Supplementary Information

Appendix 1. FLG synthesis details

Crucibles containing the expandable graphite were placed for 4 min pre-heated and in a furnace maintained at 900°C under air flow after what, they were retrieved and allowed to cool down to room temperature. A dispersion of the 52 wt.% of resulting expanded graphite was performed by two successive mechanical exfoliations in 2.2 L of propan-2-ol to reach a 3 g.L^{-1} nominal concentration. The first one consisted in a homogenization with a shear mixer (Silverson L5M) for 15 min at 8000 rpm for each batch. During the second one, a probe sonication at 50% amplitude for 90 min (Vibra cell 75042, 13mm-diameter probe, 500 W, 20 kHz) was carried out by batches of 200 mL. The collected material was diluted to reach a nominal concentration of 0.2 g.L^{-1}.

Selection of FLG by removal of too thick (> 100 nm) particles and agglomerates was performed by centrifugation at 2000 rpm for 1h (Thermofisher scientific Heraeus Megafuge 40, rotation acceleration = 9, rotation deceleration = 3). Because, after storage, particles may agglomerate at the bottom of the containers, a brief sonication of 10 min in the same conditions as described above was carried out immediately prior to centrifugation. The residue was discarded. Once the supernatant collected, a filtration on a cellulose nitrate membrane (45 mm diameter, 0.45 µm pore size) was performed followed by washing the particles with deionised water (1 volume of deionised water per volume of suspension).

Table S1*. Identification and description of DEGs involved in* N. palea *exposed to* FLG_{50mg}

DEGs identification	Description	GO Terms	Log2FC	E-value
TT00_diatome_CL78Contig1_1	extracellular matrix	P:positive regulation of catalytic activity, F:calcium ion binding, C:membrane, P:lipid catabolic process, C:integral component of membrane, P:digestion, F:enzyme activator activity, C:extracellular region	5.82	2.32395E-10
OG50_diatome_CL11Contig3_2	filamentous hemagglutinin family N-terminal domain	P:intein-mediated protein splicing, C:membrane, P:proteolysis, C:integral component of membrane, F:peptidase activity	5.06	1.40079E-49
TC01_diatome_k49_Locus_10503_Transcript_2_1	ubiquitin thioesteraseVirion core	P:DNA-templated transcription, termination	5.06	2.94065E-13
TG01_diatome_k37_Locus_4954_Transcript_4_1	SPT2 homolog	F:DNA binding, F:histone binding, P:regulation of chromatin assembly, P:histone exchange, P:regulation of transcription, DNA-templated, P:nucleosome assembly	4.96	5.95629E-92
TG01_diatome_k25_Locus_4662_Transcript_10_1	Rho termination factor	P:DNA-templated transcription, termination	4.45	7.3469E-16
TT00_diatome_k25_Locus_575_Transcript_22_1	vegetative cell wall gp1-like	P:metabolic process, F:hydrolase activity, hydrolyzing O-glycosyl compounds, F:cellulase activity, P:carbohydrate metabolic process, P:polysaccharide catabolic process, F:catalytic activity, C:membrane, C:integral component of membrane, F:carbohydrate binding, P:cellulose catabolic process, F:cellulose binding, F:polysaccharide binding, F:hydrolase activity, F:hydrolase activity, acting on glycosyl bonds	4.31	2.4908E-20
TG01_diatome_k49_Locus_14252_Transcript_2_1	vegetative cell wall gp1-like	F:calcium ion binding, C:membrane, C:integral component of membrane, C:extracellular region, P:pathogenesis	4.14	1.44095E-37
TG01_diatome_k49_Locus_8534_Transcript_3_1	winged helix DNA-binding domain-containing	F:DNA binding, C:nucleus, F:ATP binding, F:transcription factor activity, sequence-specific DNA binding, P:regulation of transcription, DNA-templated, F:sequence-specific DNA binding, F:protein kinase activity, P:protein phosphorylation	3.86	6.40682E-17
OG50_diatome_CL37Contig1_3	lpxtg-motif cell wall anchor domain	F:sigma factor activity, F:DNA binding, F:transcription factor activity, sequence-specific DNA binding, P:transcription, DNA-templated, C:cell wall, C:membrane, C:integral component of membrane, P:regulation of transcription, DNA-templated, P:DNA-templated transcription, initiation, C:extracellular region	3.81	2.60566E-19
OG50_diatome_CL14Contig2_1	adhesin [	P:intein-mediated protein splicing, P:proteolysis, C:membrane, C:integral component of membrane, F:serine-type endopeptidase activity, F:peptidase activity	3.79	1.50536E-53
OG50_diatome_k37_Locus_2316_Transcript_2_2	pyridine nucleotide-disulfide oxidoreductase	F:oxidoreductase activity, acting on a sulfur group of donors, NAD(P) as acceptor, C:cell, F:oxidoreductase activity, F:flavin adenine dinucleotide binding, F:mercury (II) reductase activity, C:membrane, C:integral	3.72	3.77326E-160

		component of membrane, P:cell redox homeostasis, P:oxidation-reduction process		
TG01_diatome_k49_Locus_7415_Transcript_3_1	non-classical arabinogalactan 31 *(peptidoglycane)*	F:DNA binding, C:integral component of membrane, F:deoxyribonuclease II activity, P:DNA metabolic process	3.70	1.34501E-37
TG01_diatome_k31_Locus_1520_Transcript_5_1	filamentous hemagglutinin family N-terminal domain	P:carbohydrate metabolic process, C:membrane, C:integral component of membrane	3.68	7.20383E-56
TT00_diatome_CL1248Contig1_1	axoneme-associated mst101(2)-like isoform X2	P:carbohydrate metabolic process, F:catalytic activity	3.63	1.56664E-29
OG50_diatome_CL15Contig2_3	beta strand repeat-containing	P:intein-mediated protein splicing, C:membrane, P:proteolysis, C:integral component of membrane, F:peptidase activity	3.62	1.96448E-168
TC01_diatome_CL17Contig1_1	possible RNA polymerase sigma factor	F:sigma factor activity, F:DNA binding, F:transcription factor activity, sequence-specific DNA binding, P:transcription, DNA-templated, C:membrane, C:integral component of membrane, P:regulation of transcription, DNA-templated, P:DNA-templated transcription, initiation	3.51	5.48801E-12
TT00_diatome_CL1923Contig1_2	5 -3 exoribonuclease 1	F:nucleic acid binding, P:nucleic acid phosphodiester bond hydrolysis, F:exonuclease activity	3.51	0.0
TT00_diatome_CL28Contig1_1	family 18 chitinase	P:carbohydrate metabolic process, P:macromolecule catabolic process, F:hydrolase activity, hydrolyzing O-glycosyl compounds, F:carbohydrate binding	3.40	4.59927E-22
TT00_diatome_k25_Locus_914_Transcript_4_2	DNA-binding heat shock factor	F:DNA binding, C:nucleus, F:ATP binding, F:transcription factor activity, sequence-specific DNA binding, P:regulation of transcription, DNA-templated, F:sequence-specific DNA binding, F:protein kinase activity, P:protein phosphorylation	3.30	6.41012E-18
TT00_diatome_k25_Locus_5168_Transcript_2_1	autotransporter-associated beta strand repeat	P:intein-mediated protein splicing, F:calcium ion binding, C:membrane, P:proteolysis, C:integral component of membrane, F:peptidase activity	3.26	4.11169E-26
TC01_diatome_k25_Locus_6918_Transcript_1_1	hypothetical protein THAOC_30976, partial	F:DNA binding, P:DNA integration, P:DNA recombination	3.24	1.44114E-107
TC01_diatome_k25_Locus_2944_Transcript_6_1	glycosyl transferase family 8	F:transferase activity, transferring glycosyl groups, C:membrane, C:integral component of membrane, P:protein glycosylation, F:transferase activity	3.23	2.35408E-37
TT00_diatome_CL33Contig1_1	choice-of-anchor A domain-containing	F:collagen binding, C:cell wall, C:membrane, C:integral component of membrane, P:cell adhesion, P:DNA-templated transcription, termination, C:extracellular region	3.19	5.49928E-114
TG01_diatome_k49_Locus_2422_Transcript_14_1	basic proline-rich -	P:intein-mediated protein splicing, C:membrane, P:proteolysis, C:integral component of membrane, F:peptidase activity, C:cellular_component	3.15	7.52329E-103
TC01_diatome_CL2100Contig1_1	patatin-like phospholipase domain-containing 2 isoform X1	P:metabolic process, P:lipid metabolic process, P:lipid catabolic process, F:hydrolase activity	3.14	1.44665E-52
OG50_diatome_k25_Locus_4840_Transcript_1_1	hypothetical protein FisN_12Lh033	F:DNA binding, C:nucleus, F:transcription factor activity, sequence-specific DNA binding, P:regulation of transcription, DNA-templated, F:sequence-specific DNA binding	3.14	9.76254E-43
OG50_diatome_k49_Locus_3837_Transcript_14_1	cell surface receptor	F:hydrolase activity, acting on carbon-nitrogen (but not peptide) bonds,	3.06	1.51773E-76

		P:signal transduction, P:nitrogen compound metabolic process, F:phosphorus-oxygen lyase activity, C:membrane, C:integral component of membrane, P:intracellular signal transduction, P:cyclic nucleotide biosynthetic process, C:intracellular, F:3',5'-cyclic-nucleotide phosphodiesterase activity		
TT00_diatome_k43_Locus_21_Transcript_66_2	hypothetical protein FRACYDRAFT_251158	P:carbohydrate metabolic process	3.05	1.12553E-29
TT00_diatome_CL97Contig1_1	filamentous hemagglutinin family N-terminal domain	P:intein-mediated protein splicing, C:membrane, P:proteolysis, C:integral component of membrane, F:peptidase activity	3.02	2.12447E-116
OG50_diatome_CL14Contig1_1	DUF3494 domain-containing	F:chitin binding, P:intein-mediated protein splicing, C:membrane, P:proteolysis, P:chitin metabolic process, C:integral component of membrane, F:peptidase activity, C:extracellular region	2.97	1.93628E-61
TC01_diatome_k25_Locus_107_Transcript_7_3	conserved repeat domain	P:cell communication, F:calcium ion binding, C:membrane, C:integral component of membrane, C:extracellular region, P:pathogenesis	2.92	8.81572E-129
OG50_diatome_k31_Locus_2735_Transcript_2_1	malate synthase A	P:glyoxylate cycle, C:cytoplasm, F:malate synthase activity, P:tricarboxylic acid cycle	2.91	0.0
TG01_diatome_CL1766Contig1_3	predicted protein	F:hydrolase activity, acting on carbon-nitrogen (but not peptide) bonds, P:signal transduction, P:nitrogen compound metabolic process, F:phosphorus-oxygen lyase activity, C:membrane, C:integral component of membrane, P:intracellular signal transduction, C:intracellular, P:cyclic nucleotide biosynthetic process, F:3',5'-cyclic-nucleotide phosphodiesterase activity	2.82	1.9617E-15
TG01_diatome_k43_Locus_2504_Transcript_14_1	basic proline-rich -	P:intein-mediated protein splicing, C:membrane, P:proteolysis, C:integral component of membrane, F:peptidase activity, C:cellular_component	2.81	1.52985E-107
TT00_diatome_k49_Locus_7584_Transcript_1_1	possible RNA polymerase sigma factor	F:sigma factor activity, F:DNA binding, F:transcription factor activity, sequence-specific DNA binding, P:transcription, DNA-templated, P:regulation of transcription, DNA-templated, P:DNA-templated transcription, initiation	2.78	6.3829E-22
TC01_diatome_k31_Locus_2434_Transcript_2_1	acyl- dehydrogenase	F:acyl-CoA dehydrogenase activity, P:fatty acid beta-oxidation using acyl-CoA dehydrogenase, F:fatty-acyl-CoA binding, F:flavin adenine dinucleotide binding, F:electron carrier activity, F:oxidoreductase activity, acting on the CH-CH group of donors, with a flavin as acceptor, P:lipid homeostasis, C:plasma membrane	2.76	0.0
TC01_diatome_k49_Locus_8575_Transcript_9_1	Serineaspartate repeat-containing	P:proteolysis, C:membrane, C:integral component of membrane, F:serine-type endopeptidase activity	2.71	1.89357E-27
OG50_diatome_k37_Locus_300_Transcript_5_3	isocitrate lyase	P:glyoxylate cycle, C:cytoplasm, F:isocitrate lyase activity, F:transferase activity, transferring acyl groups, acyl groups converted into alkyl on transfer	2.70	0.0
TG01_diatome_CL8Contig3_1	Serineaspartate repeat-containing	P:proteolysis, C:membrane, C:integral component of membrane, F:serine-type endopeptidase activity	2.69	1.56487E-29
TT00_diatome_CL216Contig1_1	accessory Sec-dependent LPXTG-anchored adhesin	F:calcium ion binding, C:cell wall, C:membrane, C:integral component of membrane, C:extracellular region, P:pathogenesis	2.69	8.27702E-47
TT00_diatome_k49_Locus_13474_Transcript_1_1	predicted protein	P:signal transduction, F:phosphorus-oxygen lyase activity, C:membrane,	2.68	4.19228E-4

		C:integral component of membrane, P:intracellular signal transduction, P:cyclic nucleotide biosynthetic process, C:intracellular, F:3',5'-cyclic-nucleotide phosphodiesterase activity		
OG50_diatome_k43_Locus_2399_Transcript_9_2	cell surface receptor	C:guanylate cyclase complex, soluble, F:hydrolase activity, acting on carbon-nitrogen (but not peptide) bonds, P:cGMP biosynthetic process, C:integral component of membrane, F:guanylate cyclase activity, C:plasma membrane, F:adenylate cyclase activity, P:intracellular signal transduction, F:3',5'-cyclic-nucleotide phosphodiesterase activity	2.61	7.15756E-43
OG50_diatome_CL74Contig1_1	Rho termination factor	P:DNA-templated transcription, termination	2.61	5.96955E-24
TC01_diatome_k25_Locus_953_Transcript_1_1	predicted protein	F:DNA binding, C:nucleus, F:transcription factor activity, sequence-specific DNA binding, P:transcription, DNA-templated, P:regulation of transcription, DNA-templated	2.60	3.5171E-165
TT00_diatome_CL66Contig2_2	non-classical arabinogalactan 31	F:chitin binding, C:membrane, P:chitin metabolic process, C:integral component of membrane, C:extracellular region	2.59	3.05487E-57
TC01_diatome_k25_Locus_1257_Transcript_1_1	Dihydroxyacetone kinase (Fragment)	P:regulation of transcription from RNA polymerase II promoter in response to oxidative stress, P:transcription, DNA-templated, P:regulation of cell size, P:regulation of transcription, DNA-templated, F:sequence-specific DNA binding, P:response to singlet oxygen, P:negative regulation of flocculation, P:negative regulation of filamentous growth, P:response to stress, F:phosphorelay response regulator activity, P:regulation of transcription from RNA polymerase II promoter, F:DNA binding, C:nucleus, F:transcription factor activity, sequence-specific DNA binding, P:phosphorelay signal transduction system, C:cytosol	2.59	9.42816E-46
TG01_diatome_k31_Locus_1935_Transcript_5_2	proteophosphoglycan ppg4	F:chitin binding, C:membrane, P:chitin metabolic process, C:integral component of membrane, C:extracellular region	2.57	2.00167E-40
TC01_diatome_k49_Locus_2160_Transcript_2_3	nucleoredoxin 2	C:commitment complex, C:prespliceosome, F:zinc ion binding, P:mRNA 5'-splice site recognition, F:pre-mRNA 5'-splice site binding, C:U1 snRNP, P:spliceosomal snRNP assembly	2.56	3.23276E-53
TG01_diatome_k37_Locus_8080_Transcript_11_2	predicted protein	F:hydrolase activity, acting on carbon-nitrogen (but not peptide) bonds, P:signal transduction, P:nitrogen compound metabolic process, F:phosphorus-oxygen lyase activity, C:membrane, C:integral component of membrane, P:intracellular signal transduction, C:intracellular, P:cyclic nucleotide biosynthetic process, F:3',5'-cyclic-nucleotide phosphodiesterase activity	2.54	1.48954E-13
TT00_diatome_k25_Locus_4897_Transcript_1_2	peptidase	P:proteolysis, C:membrane, P:cell adhesion, F:metalloendopeptidase activity, F:metallopeptidase activity	2.53	6.56896E-45
TT00_diatome_k43_Locus_7278_Transcript_7_1	retinol dehydrogenase 12-like isoform X1	P:regulation of cellular process, C:cytoplasm, C:intracellular membrane-bounded organelle, P:cellular response to stimulus, F:binding, P:single-organism process	2.51	9.5258E-30
TC01_diatome_k31_Locus_758_Transcript_6_2	NAD(P) mitochondrial-like	F:NADP binding, P:proton transport, F:NAD binding, C:integral component of membrane, P:NADPH regeneration, F:NAD(P)+ transhydrogenase (AB-specific) activity, C:mitochondrial inner membrane	2.49	0.0
TT00_diatome_k31_Locus_5856_Transcript_3_2	hypothetical protein	P:transcription, DNA-templated, F:transcription factor binding	2.45	9.46209E-71

	FisN_3Hh170			
TG01_diatome_k25_Locus_4881_Transcript_8_1	hypothetical protein FRACYDRAFT_264505	C:cytoplasm, P:glutathione metabolic process, F:glutathione transferase activity	2.38	1.65361E-35
TG01_diatome_k37_Locus_2687_Transcript_3_1	squash family serine protease inhibitor	P:proteolysis, F:peptidase activity, C:extracellular region	2.38	1.51008E-101
TG01_diatome_CL1517Contig1_2	winged helix DNA-binding domain-containing	C:nucleus, F:transcription factor activity, sequence-specific DNA binding, P:regulation of transcription, DNA-templated, F:sequence-specific DNA binding	2.38	1.69334E-82
OG50_diatome_k49_Locus_1808_Transcript_5_1	ADP-ribosylation factor GTPase-activating 1	F:GTPase activator activity, C:membrane, C:integral component of membrane, P:cellular protein modification process, P:positive regulation of GTPase activity	2.37	1.01663E-148
TT00_diatome_CL2334Contig1_1	serine threonine kinase	P:regulation of cellular process, F:transferase activity, transferring phosphorus-containing groups, P:single-organism process, P:cellular process	2.35	1.74548E-57
TT00_diatome_k37_Locus_680_Transcript_4_2	alpha beta-hydrolase	P:lipid metabolic process, C:membrane, C:integral component of membrane, F:hydrolase activity	2.35	2.59202E-156
TT00_diatome_k25_Locus_2038_Transcript_5_4	ubiquitin thiolesterase	P:intein-mediated protein splicing, C:membrane, P:proteolysis, C:integral component of membrane, F:peptidase activity	2.34	8.09434E-47
TG01_diatome_k49_Locus_8806_Transcript_3_1	predicted protein	P:signal transduction, F:phosphorus-oxygen lyase activity, C:membrane, C:integral component of membrane, P:intracellular signal transduction, P:cyclic nucleotide biosynthetic process, C:intracellular, F:3',5'-cyclic-nucleotide phosphodiesterase activity	2.32	2.6295E-5
TC01_diatome_k37_Locus_6057_Transcript_1_1	RNA recognition motif-containing	C:commitment complex, F:nucleotide binding, C:precatalytic spliceosome, F:U1 snRNA binding, F:mRNA binding, C:U2-type prespliceosome, C:U1 snRNP, P:mRNA splicing, via spliceosome	2.29	2.93012E-89
TT00_diatome_k37_Locus_1121_Transcript_1_1	thioredoxin-disulfide reductase	C:cell, F:protein disulfide oxidoreductase activity, C:cytoplasm, F:oxidoreductase activity, P:removal of superoxide radicals, F:electron carrier activity, C:membrane, C:integral component of membrane, F:thioredoxin-disulfide reductase activity, P:cell redox homeostasis, P:oxidation-reduction process	2.29	3.5067E-93
TG01_diatome_CL1773Contig1_3	pyruvate:ferredoxin oxidoreductase NADPH-cytochrome	F:thiamine pyrophosphate binding, P:response to oxidative stress, F:iron ion binding, F:oxidoreductase activity, acting on the aldehyde or oxo group of donors, C:mitochondrion, P:cellular respiration, F:4 iron, 4 sulfur cluster binding, P:electron transport chain, P:pyruvate metabolic process	2.26	0.0
OG50_diatome_k25_Locus_3888_Transcript_6_1	serine-rich adhesin for	F:chitin binding, P:chitin metabolic process, C:membrane, C:integral component of membrane, C:extracellular region	2.25	2.15579E-17
TG01_diatome_k25_Locus_842_Transcript_2_1	Monoglyceride lipase	P:regulation of cellular process, P:cellular lipid metabolic process, C:intracellular part, F:hydrolase activity	2.17	1.25028E-25
TG01_diatome_CL271Contig1_1	tyrosine- phosphatase non-receptor type 9-like isoform X2	F:phosphoprotein phosphatase activity, F:protein tyrosine phosphatase activity, P:protein dephosphorylation, F:phosphatase activity, P:dephosphorylation, P:peptidyl-tyrosine dephosphorylation, F:hydrolase activity	2.17	6.93223E-82
TT00_diatome_k49_Locus_9893_Transcript_1_1	cleavage stimulation	C:nucleus, P:RNA 3'-end processing, F:mRNA binding, P:RNA	2.16	2.38383E-38

	factor subunit 3	processing, P:mRNA processing, P:mRNA cleavage		
TC01_diatome_k25_Locus_69_Transcript_7_3	DUF4116 domain-containing	F:ATP binding, F:actin binding, C:membrane, C:integral component of membrane, F:protein kinase activity, P:protein phosphorylation	2.15	4.79418E-153
TG01_diatome_CL26Contig1_2	predicted protein	P:signal transduction, F:phosphorus-oxygen lyase activity, C:membrane, C:integral component of membrane, P:intracellular signal transduction, C:intracellular, P:cyclic nucleotide biosynthetic process, F:3',5'-cyclic-nucleotide phosphodiesterase activity	2.15	3.74344E-18
TC01_diatome_k31_Locus_388_Transcript_36_1	LEPR-XLL domain-containing	F:coenzyme binding, F:calcium ion binding, P:proteolysis, C:membrane, C:integral component of membrane, P:coenzyme A metabolic process, P:oxidation-reduction process, C:extracellular region, F:hydroxymethylglutaryl-CoA reductase (NADPH) activity, P:pathogenesis, F:metallopeptidase activity	2.13	0.0
TT00_diatome_k25_Locus_8529_Transcript_1_2	hypothetical protein FRACYDRAFT_208755	P:regulation of transcription, DNA-templated	2.10	0.0
TC01_diatome_k37_Locus_3659_Transcript_3_2	PAB1 binding	P:stress granule assembly, C:cytoplasmic stress granule, F:RNA binding, P:regulation of cytoplasmic mRNA processing body assembly, F:RNA binding	2.10	5.15154E-109
TG01_diatome_CL1725Contig1_2	pyruvate carboxylase	F:DNA binding, F:ATP binding, P:gluconeogenesis, F:pyruvate carboxylase activity, F:metal ion binding, F:biotin binding, F:biotin carboxylase activity, P:pyruvate metabolic process	2.09	0.0
TC01_diatome_k25_Locus_9115_Transcript_1_1	ATP-dependent RNA helicase DDX54 DBP10	F:nucleic acid binding, F:ATP binding, P:RNA secondary structure unwinding, F:ATP-dependent RNA helicase activity	2.09	0.0
TC01_diatome_k31_Locus_6356_Transcript_1_1	mitochondrial carrier	F:structural constituent of ribosome, C:intracellular membrane-bounded organelle, C:membrane, P:transport, P:translation	2.07	2.43819E-127
TC01_diatome_k25_Locus_821_Transcript_6_1	hypothetical protein FisN_20Lh177	F:hydrolase activity, acting on carbon-nitrogen (but not peptide) bonds, P:signal transduction, P:nitrogen compound metabolic process, F:phosphorus-oxygen lyase activity, C:membrane, C:integral component of membrane, P:intracellular signal transduction, C:intracellular, P:cyclic nucleotide biosynthetic process, F:3',5'-cyclic-nucleotide phosphodiesterase activity	2.07	3.48437E-6
TG01_diatome_k25_Locus_2747_Transcript_2_1	squash family serine protease inhibitor	P:proteolysis, F:peptidase activity	2.06	2.19085E-53
OG50_diatome_k43_Locus_3019_Transcript_2_1	fatty acid oxidation alpha mitochondrial	F:3-hydroxyacyl-CoA dehydrogenase activity, F:lyase activity, P:oxidation-reduction process, P:fatty acid metabolic process	2.05	0.0
OG50_diatome_k31_Locus_3489_Transcript_4_3	homebox domain-containing	C:nucleus, F:DNA binding, F:zinc ion binding, P:regulation of transcription, DNA-templated	2.02	0.0
TC01_diatome_k31_Locus_2689_Transcript_10_2	TKL DICTY4 kinase	F:catalytic activity, C:membrane, P:primary metabolic process, P:single-organism process, P:organic substance metabolic process, P:phosphate-containing compound metabolic process	2.02	0.0
TG01_diatome_k25_Locus_7763_Transcript_2_3	U3 small nucleolar ribonucleo	C:nucleus, C:intracellular ribonucleoprotein complex, C:Mpp10 complex, C:viral nucleocapsid, P:rRNA processing, C:small nucleolar ribonucleoprotein complex	2.01	5.46641E-130
TC01_diatome_k49_Locus_3015_Transcript_23_2	predicted protein	C:cytoplasm, P:glutathione metabolic process, F:glutathione transferase	2.00	5.7505E-38

		activity		
TC01_diatome_k31_Locus_4528_Transcript_1_1	RHS repeat-associated core domain-containing	F:GTP binding, F:nucleotide binding, P:self proteolysis, F:ATP binding, P:small GTPase mediated signal transduction, C:membrane, C:integral component of membrane, F:protein kinase activity, P:protein phosphorylation, C:intracellular	2.00	3.43661E-56
TG01_diatome_k49_Locus_5469_Transcript_9_2	beta-1,3-galactosyltransferase 1-like	F:transferase activity, transferring glycosyl groups, C:membrane, C:integral component of membrane, P:protein glycosylation, F:galactosyltransferase activity, C:Golgi apparatus, C:Golgi membrane, F:transferase activity	1.99	1.5502E-17
OG50_diatome_CL1815Contig1_3	hypothetical protein THAOC_14013, partial	F:DNA binding, P:DNA integration, P:DNA recombination	1.98	3.01879E-121
TC01_diatome_k31_Locus_422_Transcript_1_1	winged helix DNA-binding domain-containing	F:DNA binding, C:nucleus, F:transcription factor activity, sequence-specific DNA binding, P:regulation of transcription, DNA-templated, F:sequence-specific DNA binding	1.98	3.13389E-14
OG50_diatome_k31_Locus_1066_Transcript_11_2	TKL DICTY4 kinase	F:catalytic activity, C:membrane, P:primary metabolic process, P:single-organism process, P:organic substance metabolic process, P:phosphate-containing compound metabolic process	1.98	0.0
OG50_diatome_k43_Locus_3058_Transcript_5_2	short-chain specific acyl-mitochondrial	F:acyl-CoA dehydrogenase activity, C:nucleus, F:acryloyl-CoA reductase activity, P:fatty acid beta-oxidation using acyl-CoA dehydrogenase, F:fatty-acyl-CoA binding, F:flavin adenine dinucleotide binding, F:butyryl-CoA dehydrogenase activity, F:electron carrier activity, P:lipid homeostasis, C:mitochondrion, C:integral component of membrane, P:butyrate catabolic process	1.95	0.0
TC01_diatome_k25_Locus_4432_Transcript_8_4	ATP-dependent Clp ATP-binding subunit	F:ATP binding, C:mitochondrial matrix, P:protein catabolic process, P:proteolysis, F:unfolded protein binding, F:ATP-dependent peptidase activity, P:protein folding	1.95	0.0
OG50_diatome_k49_Locus_2008_Transcript_6_2	cyclin-dependent kinase 12 isoform X4	F:ATP binding, F:protein serine/threonine kinase activity, P:protein phosphorylation	1.94	8.86483E-36
TC01_diatome_k25_Locus_527_Transcript_5_4	carbohydrate 4-sulfotransferase 9	P:carbohydrate biosynthetic process, C:membrane, C:integral component of membrane, F:sulfotransferase activity, F:transferase activity	1.93	6.50873E-27
TG01_diatome_k43_Locus_7213_Transcript_6_1	Cardiolipin synthetase	P:intein-mediated protein splicing, P:proteolysis, C:membrane, C:integral component of membrane, F:serine-type endopeptidase activity, F:peptidase activity	1.93	4.53034E-119
TC01_diatome_k49_Locus_4065_Transcript_4_2	hypothetical protein FRACYDRAFT_268903	P:histone H3-K79 methylation, F:histone methyltransferase activity (H3-K79 specific), P:regulation of cell cycle	1.92	2.26099E-49
TG01_diatome_k37_Locus_1000_Transcript_3_1	NLRC3 isoform X2	F:GTP binding, P:small GTPase mediated signal transduction, C:intracellular	1.92	3.62338E-21
TG01_diatome_k37_Locus_2296_Transcript_14_6	RING finger 11-like	F:ubiquitin protein ligase activity, F:zinc ion binding, P:proteasome-mediated ubiquitin-dependent protein catabolic process, F:metal ion binding, P:protein polyubiquitination, C:membrane, C:integral component of membrane, P:protein ubiquitination involved in ubiquitin-dependent protein catabolic process, F:ligase activity, P:protein ubiquitination	1.91	1.77603E-18
OG50_diatome_k25_Locus_1955_Transcript_6_2	ATP-dependent RNA	F:nucleic acid binding, P:regulation of gene expression, P:RNA secondary	1.88	0.0

	helicase DDX46 PRP5	structure unwinding, F:ATP-dependent RNA helicase activity, P:mRNA splicing, via spliceosome		
TT00_diatome_k49_Locus_1293_Transcript_1_1	bZIP tanscription factor	F:transcription factor activity, sequence-specific DNA binding, P:regulation of transcription, DNA-templated, F:sequence-specific DNA binding	1.87	4.73385E-90
OG50_diatome_k31_Locus_2551_Transcript_10_1	TKL DICTY4 kinase	F:catalytic activity, C:membrane, P:primary metabolic process, P:single-organism process, P:organic substance metabolic process, P:phosphate-containing compound metabolic process	1.85	0.0
OG50_diatome_k25_Locus_319_Transcript_4_3	DNase I	F:hydrolase activity, P:phosphatidylinositol dephosphorylation	1.85	3.37095E-141
TC01_diatome_k43_Locus_2325_Transcript_30_1	predicted protein	P:signal transduction, F:phosphorus-oxygen lyase activity, C:membrane, C:integral component of membrane, P:intracellular signal transduction, P:cyclic nucleotide biosynthetic process, C:intracellular, F:3',5'-cyclic-nucleotide phosphodiesterase activity	1.85	3.88185E-100
TG01_diatome_CL1835Contig1_2	TKL DICTY4 kinase	F:catalytic activity, C:membrane, P:primary metabolic process, P:single-organism process, P:organic substance metabolic process, P:phosphate-containing compound metabolic process	1.85	0.0
TG01_diatome_k49_Locus_5449_Transcript_39_1	predicted protein	F:hydrolase activity, acting on carbon-nitrogen (but not peptide) bonds, P:signal transduction, P:nitrogen compound metabolic process, F:phosphorus-oxygen lyase activity, C:membrane, C:integral component of membrane, P:intracellular signal transduction, P:cyclic nucleotide biosynthetic process, C:intracellular, F:3',5'-cyclic-nucleotide phosphodiesterase activity	1.84	3.49552E-156
TT00_diatome_k37_Locus_670_Transcript_5_4	predicted protein	F:hydrolase activity, acting on carbon-nitrogen (but not peptide) bonds, P:signal transduction, P:nitrogen compound metabolic process, F:phosphorus-oxygen lyase activity, C:membrane, C:integral component of membrane, P:intracellular signal transduction, C:intracellular, P:cyclic nucleotide biosynthetic process, F:3',5'-cyclic-nucleotide phosphodiesterase activity	1.84	1.01447E-10
OG50_diatome_k31_Locus_5713_Transcript_1_1	dienelactone hydrolase	F:1-alkyl-2-acetylglycerophosphocholine esterase activity, P:lipid catabolic process, F:hydrolase activity	1.83	3.35145E-99
TT00_diatome_CL2242Contig1_1	DNA-directed RNA polymerase II subunit RPB7	P:positive regulation of translational initiation, F:DNA-directed 5'-3' RNA polymerase activity, F:single-stranded RNA binding, P:nuclear-transcribed mRNA catabolic process, exonucleolytic, C:P-body, F:translation initiation factor binding, P:positive regulation of nuclear-transcribed mRNA poly(A) tail shortening, P:transcription initiation from RNA polymerase II promoter, C:DNA-directed RNA polymerase II, core complex, F:single-stranded DNA binding	1.83	7.01135E-110
TT00_diatome_CL63Contig1_2	piccolo isoform X1	C:postsynaptic density, C:intracellular organelle, P:cytoskeleton organization, P:insulin secretion, F:ion binding, C:cytoplasmic part, C:neuron projection, C:membrane-bounded organelle, F:profilin binding, C:presynapse, C:cell projection part, P:regulation of exocytosis, P:protein localization to synapse, P:cAMP-mediated signaling	1.82	4.69164E-13
TT00_diatome_k25_Locus_2271_Transcript_2_2	SCY1 kinase	F:ATP binding, F:protein kinase activity, P:phosphorylation, P:protein	1.82	0.0

		phosphorylation, F:kinase activity		
TT00_diatome_k25_Locus_6611_Transcript_3_1	glycerol-3-phosphate mitochondrial	P:glycerol-3-phosphate metabolic process, C:glycerol-3-phosphate dehydrogenase complex, F:sn-glycerol-3-phosphate:ubiquinone-8 oxidoreductase activity, P:oxidation-reduction process	1.82	0.0
TG01_diatome_k43_Locus_10262_Transcript_1_1	pyruvate kinase	F:magnesium ion binding, F:pyruvate kinase activity, F:potassium ion binding, P:glycolytic process, F:kinase activity	1.81	0.0
TT00_diatome_k25_Locus_3998_Transcript_2_3	electron transfer flavo subunit alpha	F:acyl-CoA dehydrogenase activity, P:fatty acid beta-oxidation using acyl-CoA dehydrogenase, F:fatty-acyl-CoA binding, F:flavin adenine dinucleotide binding, F:electron carrier activity, F:oxidoreductase activity, acting on the CH-CH group of donors, with a flavin as acceptor, P:lipid homeostasis, C:mitochondrion	1.81	1.51011E-107
OG50_diatome_CL2188Contig1_3	probable leucine-rich repeat receptor kinase At1g35710	F:nucleotide binding, F:ATP binding, C:membrane, C:integral component of membrane, F:protein kinase activity, P:protein phosphorylation	1.80	2.48782E-68
OG50_diatome_k31_Locus_2960_Transcript_2_2	Abortive infection	F:calcium ion binding, C:membrane, P:proteolysis, C:integral component of membrane, F:peptidase activity	1.80	4.35812E-115
OG50_diatome_CL12Contig3_1	winged helix DNA-binding domain-containing	F:DNA binding, C:nucleus, F:transcription factor activity, sequence-specific DNA binding, P:regulation of transcription, DNA-templated, F:sequence-specific DNA binding	1.80	2.2077E-15
TT00_diatome_k25_Locus_4124_Transcript_2_1	DEAD DEAH box RNA	F:nucleic acid binding, C:cytoplasmic ribonucleoprotein granule, F:ATP binding, P:regulation of gene expression, P:RNA secondary structure unwinding, P:chromosome segregation, P:translational initiation, F:ATP-dependent RNA helicase activity	1.80	0.0
TC01_diatome_k37_Locus_2171_Transcript_2_1	transcription elongation factor SPT6	F:nucleic acid binding, P:regulation of transcription, DNA-templated, P:cellular nitrogen compound metabolic process, P:primary metabolic process, P:organic substance metabolic process	1.80	0.0
TG01_diatome_k49_Locus_9850_Transcript_6_1	apoptotic chromatin condensation inducer in the nucleus-like	C:cytoplasm, F:catalytic activity, C:membrane, C:integral component of membrane, C:extracellular region, P:pathogenesis	1.79	0.0
OG50_diatome_k31_Locus_3090_Transcript_12_4	bifunctional acetaldehyde-alcohol dehydrogenase	F:metal ion binding, F:lyase activity, F:acetaldehyde dehydrogenase (acetylating) activity, P:alcohol metabolic process, P:oxidation-reduction process, F:alcohol dehydrogenase (NAD) activity, P:carbon utilization	1.78	0.0
OG50_diatome_k31_Locus_2349_Transcript_7_2	predicted protein	P:lipid metabolic process, C:membrane, C:integral component of membrane, F:hydrolase activity	1.78	1.6033E-159
OG50_diatome_k37_Locus_89_Transcript_25_1	hypothetical protein FRACYDRAFT_264505	C:cytoplasm, P:glutathione metabolic process, C:membrane, P:proteolysis, C:integral component of membrane, F:glutathione transferase activity, F:metallopeptidase activity	1.77	1.37428E-63
OG50_diatome_k25_Locus_342_Transcript_1_2	Chromatin modification-related vid-21	F:transcription factor activity, sequence-specific DNA binding, P:regulation of transcription, DNA-templated, F:sequence-specific DNA binding	1.75	0.0
TC01_diatome_k25_Locus_7017_Transcript_7_1	hypothetical protein FRACYDRAFT_234916	F:DNA binding, C:nucleus, F:transcription factor activity, sequence-specific DNA binding, P:regulation of transcription, DNA-templated, F:sequence-specific DNA binding	1.75	1.17865E-107

OG50_diatome_k49_Locus_3866_Transcript_2_1	M6 metalloprotease	P:proteolysis, F:peptidase activity, F:metallopeptidase activity	1.74	2.4411E-62
TG01_diatome_k25_Locus_6415_Transcript_3_1	signal peptide peptidase-like 3	P:proteolysis, C:integral component of membrane, C:endoplasmic reticulum, C:intracellular organelle part, P:transport	1.74	1.1639E-98
TT00_diatome_CL457Contig1_2	E3 ubiquitin- ligase RNF13	F:ubiquitin protein ligase activity, P:proteasome-mediated ubiquitin-dependent protein catabolic process, F:zinc ion binding, F:metal ion binding, C:membrane, C:integral component of membrane, C:Golgi apparatus, C:fungal-type vacuole, F:ligase activity, P:protein ubiquitination	1.74	6.56351E-71
TC01_diatome_k25_Locus_4906_Transcript_9_2	predicted protein	F:G-protein coupled receptor activity, P:G-protein coupled receptor signaling pathway, C:membrane, C:integral component of membrane	1.74	1.96579E-7
TC01_diatome_k49_Locus_1281_Transcript_6_2	monoglyceride lipase isoform X1	P:acylglycerol acyl-chain remodeling, C:nucleoplasm, C:endoplasmic reticulum membrane, P:inflammatory response, F:acylglycerol lipase activity, P:acylglycerol catabolic process, C:cytosol, P:arachidonic acid metabolic process, F:protein homodimerization activity, P:fatty acid biosynthetic process, P:regulation of signal transduction, P:fatty acid metabolic process, C:plasma membrane, F:lysophospholipase activity, C:cytoplasm, C:membrane, P:lipid catabolic process, P:lipid metabolic process, C:integral component of membrane, P:regulation of endocannabinoid signaling pathway, P:regulation of inflammatory response, P:triglyceride catabolic process, C:extrinsic component of membrane, P:regulation of sensory perception of pain, F:carboxylic ester hydrolase activity, F:hydrolase activity	1.73	2.43888E-7
TT00_diatome_k25_Locus_2647_Transcript_1_1	wiskott-Aldrich syndrome	F:actin binding, C:membrane, C:integral component of membrane, P:actin filament organization, P:positive regulation of Arp2/3 complex-mediated actin nucleation, P:endocytosis, C:actin cortical patch	1.72	1.14494E-29
OG50_diatome_k25_Locus_5496_Transcript_3_1	formin 20	F:zinc ion binding, F:actin binding, P:actin filament organization, P:positive regulation of Arp2/3 complex-mediated actin nucleation, P:endocytosis, C:actin cortical patch	1.72	1.39511E-123
TC01_diatome_k31_Locus_3375_Transcript_3_1	predicted protein	P:proteolysis, C:membrane, C:integral component of membrane, F:metallopeptidase activity	1.72	7.39612E-62
OG50_diatome_CL1519Contig1_1	Cardiolipin synthetase	P:proteolysis, C:membrane, C:integral component of membrane, F:serine-type endopeptidase activity	1.72	2.53512E-79
TT00_diatome_k43_Locus_4334_Transcript_1_1	conserved secreted	F:chitinase activity, P:cell wall macromolecule catabolic process, P:chitin catabolic process, C:membrane, C:integral component of membrane	1.71	2.40867E-27
OG50_diatome_CL1945Contig1_2	1-aminocyclopropane-1-carboxylate synthase	P:1-aminocyclopropane-1-carboxylate biosynthetic process, F:pyridoxal phosphate binding, F:1-aminocyclopropane-1-carboxylate synthase activity	1.70	0.0
TG01_diatome_k25_Locus_66_Transcript_13_2	hypothetical protein B7Z37_07345	P:carbohydrate metabolic process, F:carbohydrate binding, F:hydrolase activity, hydrolyzing O-glycosyl compounds, F:polysaccharide binding	1.70	1.12734E-34
TC01_diatome_k25_Locus_3587_Transcript_3_1	g- coupled receptor	F:G-protein coupled receptor activity, F:transmembrane signaling receptor activity, P:G-protein coupled receptor signaling pathway, C:membrane, C:integral component of membrane, P:cell surface receptor signaling pathway	1.70	6.63131E-38

OG50_diatome_k43_Locus_1918_Transcript_3_1	WEE kinase	F:nucleotide binding, F:ATP binding, F:protein kinase activity, P:phosphorylation, F:protein serine/threonine kinase activity, P:protein phosphorylation, F:kinase activity	1.69	5.85202E-166
TC01_diatome_k25_Locus_736_Transcript_1_1	serine threonine phosphatase 2C	F:protein serine/threonine phosphatase activity, F:phosphoprotein phosphatase activity, F:catalytic activity, F:metal ion binding, P:protein dephosphorylation, C:membrane, C:integral component of membrane, F:cation binding, F:hydrolase activity	1.69	4.10934E-98
TG01_diatome_k49_Locus_182_Transcript_22_1	hypothetical protein FRACYDRAFT_266620	F:GTP binding, P:small GTPase mediated signal transduction, F:[protein-PII] uridylyltransferase activity, C:intracellular	1.69	0.0
OG50_diatome_k37_Locus_3105_Transcript_3_2	1,3-beta-glucanase	P:carbohydrate metabolic process, F:hydrolase activity, hydrolyzing O-glycosyl compounds	1.69	5.86601E-89
TT00_diatome_k49_Locus_4875_Transcript_5_1	phosphoribosylformylglycinamidine synthase	F:ATP binding, C:cytoplasm, P:'de novo' IMP biosynthetic process, P:glutamine metabolic process, F:phosphoribosylformylglycinamidine synthase activity	1.68	0.0
TG01_diatome_k43_Locus_734_Transcript_3_2	predicted protein	F:hydrolase activity, acting on carbon-nitrogen (but not peptide) bonds, P:signal transduction, P:nitrogen compound metabolic process, F:phosphorus-oxygen lyase activity, C:membrane, C:integral component of membrane, P:intracellular signal transduction, C:intracellular, P:cyclic nucleotide biosynthetic process, F:3',5'-cyclic-nucleotide phosphodiesterase activity	1.68	3.35889E-32
TT00_diatome_k49_Locus_77_Transcript_10_4	ULK ULK kinase	F:ATP binding, F:protein serine/threonine kinase activity, P:protein phosphorylation	1.68	0.0
OG50_diatome_CL448Contig1_1	predicted protein	F:galactosylceramide sulfotransferase activity, C:membrane, C:integral component of membrane, P:glycolipid biosynthetic process, C:Golgi apparatus, F:sulfotransferase activity	1.68	1.74335E-38
TT00_diatome_k25_Locus_1511_Transcript_3_1	serine hydroxymethyltransferase	F:pyridoxal phosphate binding, P:L-serine metabolic process, F:glycine hydroxymethyltransferase activity, P:tetrahydrofolate interconversion, F:methyltransferase activity, P:glycine metabolic process, P:methylation	1.68	0.0
TT00_diatome_k31_Locus_17_Transcript_2_1	ubiquitin C	C:cell wall, P:proteolysis, C:membrane, C:integral component of membrane, F:serine-type peptidase activity, F:serine-type endopeptidase activity, F:peptidase activity, F:hydrolase activity	1.67	6.96599E-63
OG50_diatome_CL148Contig1_1	proteophosphoglycan ppg4	F:chitin binding, C:cytoplasm, C:membrane, P:chitin metabolic process, C:integral component of membrane, P:mRNA processing, C:extracellular region	1.67	8.68717E-16
OG50_diatome_k25_Locus_3228_Transcript_3_2	family transcriptional regulator	F:G-protein coupled receptor activity, F:G-protein coupled GABA receptor activity, P:G-protein coupled receptor signaling pathway, F:iron ion binding, F:metal ion binding, F:oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen, C:membrane, C:integral component of membrane, P:oxidation-reduction process, F:monooxygenase activity, F:heme binding	1.67	0.0
TG01_diatome_k49_Locus_6767_Transcript_1_2	E3 ubiquitin- ligase RNF181 isoform X1	F:ubiquitin protein ligase activity, P:proteasome-mediated ubiquitin-dependent protein catabolic process, F:zinc ion binding, F:metal ion binding, C:membrane, C:integral component of membrane, P:protein	1.66	4.01031E-41

		ubiquitination		
OG50_diatome_k25_Locus_2614_Transcript_8_3	alkyl hydroperoxide reductase	F:antioxidant activity, F:oxidoreductase activity, P:cellular oxidant detoxification, P:oxidation-reduction process	1.65	1.61765E-41
TG01_diatome_k31_Locus_5273_Transcript_3_1	predicted protein	F:transcription factor activity, sequence-specific DNA binding, P:regulation of transcription, DNA-templated, F:sequence-specific DNA binding, P:transport, F:transporter activity, C:intracellular	1.64	1.27584E-41
TC01_diatome_k43_Locus_1130_Transcript_10_1	glycoside hydrolase	P:carbohydrate metabolic process, F:hydrolase activity, hydrolyzing O-glycosyl compounds, F:hydrolase activity	1.63	7.48043E-82
TG01_diatome_k31_Locus_264_Transcript_3_3	DNA ligase	P:DNA metabolic process, P:cellular response to DNA damage stimulus	1.63	0.0
TT00_diatome_CL1525Contig1_2	rhomboid family intramembrane serine protease	C:membrane, P:proteolysis, C:integral component of membrane, F:serine-type endopeptidase activity, F:peptidase activity, F:hydrolase activity	1.63	2.83099E-79
TC01_diatome_k49_Locus_157_Transcript_10_1	predicted protein	F:DNA binding, C:nucleus, P:histone lysine methylation, F:oxidoreductase activity, C:membrane, C:integral component of membrane, F:histone-lysine N-methyltransferase activity, P:oxidation-reduction process, F:N-acetyltransferase activity	1.62	5.99443E-96
TG01_diatome_k43_Locus_790_Transcript_11_2	alkyl hydroperoxide reductase	F:peroxidase activity, F:antioxidant activity, F:oxidoreductase activity, P:cellular oxidant detoxification, P:oxidation-reduction process, F:peroxiredoxin activity	1.61	2.4762E-42
TG01_diatome_CL2288Contig1_2	DUF1295 domain-containing	F:oxidoreductase activity, acting on the CH-CH group of donors, C:cytoplasm, P:metabolic process, P:lipid metabolic process, C:membrane, C:integral component of membrane, P:oxidation-reduction process, F:CoA-transferase activity, F:transferase activity	1.61	2.20029E-59
OG50_diatome_k43_Locus_6619_Transcript_3_1	lipopolysaccharide-induced transcription factor regulating tumor necrosis factor	P:transmembrane transport, C:membrane, C:integral component of membrane, P:transport, P:auxin-activated signaling pathway	1.60	1.27309E-100
OG50_diatome_k37_Locus_4276_Transcript_2_1	TKL DICTY4 kinase	F:catalytic activity, C:membrane, P:primary metabolic process, P:single-organism process, P:organic substance metabolic process, P:phosphate-containing compound metabolic process	1.60	0.0
TT00_diatome_k31_Locus_971_Transcript_200_1	predicted protein	F:hydrolase activity, acting on carbon-nitrogen (but not peptide) bonds, P:signal transduction, P:nitrogen compound metabolic process, F:phosphorus-oxygen lyase activity, C:membrane, C:integral component of membrane, P:intracellular signal transduction, P:cyclic nucleotide biosynthetic process, C:intracellular, F:3',5'-cyclic-nucleotide phosphodiesterase activity	1.60	4.61858E-37
TC01_diatome_k49_Locus_448_Transcript_1_1	Na-Ca exchanger integrin-beta4 domain	F:GTP binding, F:ATP binding, P:small GTPase mediated signal transduction, C:membrane, C:integral component of membrane, F:protein kinase activity, P:protein phosphorylation, C:intracellular	1.58	9.45064E-33
TG01_diatome_k31_Locus_3169_Transcript_2_2	flap endonuclease GEN	F:DNA binding, P:nucleic acid phosphodiester bond hydrolysis, P:DNA repair, F:catalytic activity, F:endonuclease activity, F:nuclease activity, C:membrane, C:integral component of membrane	1.58	0.0

TT00_diatome_k43_Locus_1165_Transcript_15_1	conserved repeat domain	P:cell communication, F:calcium ion binding, C:membrane, C:integral component of membrane, C:extracellular region, P:pathogenesis	1.58	4.02192E-141
TT00_diatome_k31_Locus_7268_Transcript_1_1	pyrophosphate-dependent phosphofructose kinase	F:ATP binding, F:diphosphate-fructose-6-phosphate 1-phosphotransferase activity, C:membrane, P:fructose 6-phosphate metabolic process, P:glycolytic process through fructose-6-phosphate, P:carbohydrate phosphorylation, F:6-phosphofructokinase activity	1.57	0.0
TG01_diatome_CL26Contig2_3	3 ,5 -cyclic-nucleotide phosphodiesterase	P:signal transduction, F:phosphorus-oxygen lyase activity, C:membrane, C:integral component of membrane, P:intracellular signal transduction, P:cyclic nucleotide biosynthetic process, C:intracellular, F:3',5'-cyclic-nucleotide phosphodiesterase activity	1.56	2.29615E-80
TT00_diatome_k37_Locus_561_Transcript_1_2	winged helix DNA-binding domain-containing	C:nucleus, F:transcription factor activity, sequence-specific DNA binding, P:regulation of transcription, DNA-templated, F:sequence-specific DNA binding	1.56	5.05415E-53
OG50_diatome_k43_Locus_10414_Transcript_4_1	molybdenum cofactor biosynthesis 1 isoform X2	F:binding, F:GTP 3',8'-cyclase activity, F:cyclic pyranopterin monophosphate synthase activity, P:molybdopterin cofactor biosynthetic process	1.56	0.0
TT00_diatome_k25_Locus_5944_Transcript_2_1	predicted protein	P:signal transduction, F:phosphorus-oxygen lyase activity, C:membrane, C:integral component of membrane, P:intracellular signal transduction, P:cyclic nucleotide biosynthetic process, C:intracellular, F:3',5'-cyclic-nucleotide phosphodiesterase activity	1.56	0.0
TG01_diatome_k25_Locus_10006_Transcript_3_1	T9SS C-terminal target domain-containing	C:postsynaptic density, F:ionotropic glutamate receptor binding, P:GDP metabolic process, P:nervous system development, P:chemical synaptic transmission, P:GMP metabolic process, F:guanylate kinase activity, P:receptor clustering, C:ionotropic glutamate receptor complex, P:receptor localization to synapse, C:postsynaptic membrane, P:establishment or maintenance of epithelial cell apical/basal polarity, C:membrane, C:integral component of membrane, C:basolateral plasma membrane	1.55	9.06634E-34
TG01_diatome_k25_Locus_3628_Transcript_1_1	phosphoglycerate kinase isoform X1	P:RNA (guanine-N7)-methylation, F:tRNA (guanine-N7-)-methyltransferase activity, F:phosphoglycerate kinase activity, P:glycolytic process, P:phosphorylation, F:transferase activity, F:kinase activity, P:tRNA modification	1.55	2.33669E-120
TC01_diatome_k31_Locus_3040_Transcript_2_2	exosome component 10	C:nuclear part, P:ncRNA processing, F:organic cyclic compound binding, F:heterocyclic compound binding, P:nuclear polyadenylation-dependent ncRNA catabolic process, F:exonuclease activity, P:nuclear-transcribed mRNA catabolic process	1.55	0.0
TG01_diatome_k49_Locus_819_Transcript_3_1	spore coat polysaccharide synthesis	C:membrane, C:integral component of membrane, P:regulation of transcription, DNA-templated, P:intracellular protein transport, F:Ran GTPase binding, C:intracellular	1.55	6.61471E-57
OG50_diatome_k43_Locus_8796_Transcript_1_1	geranylgeranylglycerol-phosphate geranylgeranyltransferase	C:membrane, F:transferase activity, P:primary metabolic process, P:organic substance metabolic process	1.54	8.69674E-85
OG50_diatome_k25_Locus_834_Transcript_7_1	DNA-directed RNA polymerase II subunit	F:DNA binding, F:RNA polymerase II activity, P:transcription from RNA polymerase II promoter, C:DNA-directed RNA polymerase II, core	1.54	0.0

	RPB1	complex		
TT00_diatome_k25_Locus_3569_Transcript_8_1	hypothetical protein FRACYDRAFT_264505	C:cytoplasm, P:glutathione metabolic process, F:glutathione transferase activity	1.54	1.89225E-70
TT00_diatome_k37_Locus_175_Transcript_2_1	hypothetical protein FRACYDRAFT_277076	P:autophagy, C:cytoplasmic part	1.54	0.0
TG01_diatome_k37_Locus_12131_Transcript_2_1	ATP-binding subfamily G (WHITE) member 2	F:ATPase activity, F:ATPase activity, coupled to transmembrane movement of substances, P:transmembrane transport, P:cellular response to drug, F:xenobiotic-transporting ATPase activity, C:plasma membrane, F:nucleotide binding, F:ATP binding, P:drug transmembrane transport, C:membrane, C:integral component of membrane, P:xenobiotic transport, F:drug transmembrane transporter activity	1.54	2.72421E-12
TC01_diatome_k37_Locus_595_Transcript_4_1	E3 ubiquitin- ligase RNF181 isoform X1	F:ubiquitin protein ligase activity, F:zinc ion binding, P:proteasome-mediated ubiquitin-dependent protein catabolic process, F:metal ion binding, P:protein polyubiquitination, C:membrane, C:integral component of membrane, F:ligase activity, P:protein ubiquitination involved in ubiquitin-dependent protein catabolic process, P:protein ubiquitination	1.53	3.17961E-15
TT00_diatome_k25_Locus_5557_Transcript_3_3	acyl- dehydrogenase NM domain	F:acyl-CoA dehydrogenase activity, P:fatty acid beta-oxidation using acyl-CoA dehydrogenase, F:fatty-acyl-CoA binding, F:flavin adenine dinucleotide binding, F:electron carrier activity, F:oxidoreductase activity, acting on the CH-CH group of donors, with a flavin as acceptor, P:lipid homeostasis, C:mitochondrion	1.53	0.0
TG01_diatome_k37_Locus_4650_Transcript_10_1	viral A-type inclusion	F:GTP binding, F:nucleotide binding, C:nucleus, F:ATP binding, F:transcription factor activity, sequence-specific DNA binding, F:microtubule motor activity, P:signal transduction, C:membrane, C:integral component of membrane, P:regulation of transcription, DNA-templated, P:microtubule-based movement, F:microtubule binding	1.53	1.59032E-56
OG50_diatome_k31_Locus_255_Transcript_8_1	predicted protein	F:catalytic activity, P:primary metabolic process, P:organic substance metabolic process	1.53	3.64095E-36
TG01_diatome_k25_Locus_8386_Transcript_5_2	hypothetical protein FisN_4Hh568	P:spermidine biosynthetic process, F:adenosylmethionine decarboxylase activity	1.53	9.0122E-146
TC01_diatome_k43_Locus_1377_Transcript_6_5	isovaleryl- dehydrogenase	F:acyl-CoA dehydrogenase activity, P:fatty acid beta-oxidation using acyl-CoA dehydrogenase, F:fatty-acyl-CoA binding, F:flavin adenine dinucleotide binding, F:electron carrier activity, F:oxidoreductase activity, acting on the CH-CH group of donors, with a flavin as acceptor, P:lipid homeostasis, C:mitochondrion	1.52	0.0
OG50_diatome_CL169Contig1_3	NAD nucleotidase	F:nucleotide binding, F:hydrolase activity, acting on ester bonds, F:metal ion binding, P:nucleotide catabolic process, F:5'-nucleotidase activity, C:membrane, C:integral component of membrane, P:dephosphorylation, F:hydrolase activity	1.52	2.09297E-74
TC01_diatome_k25_Locus_3198_Transcript_43_1	TKL DICTY4 kinase	F:catalytic activity, C:membrane, P:primary metabolic process, P:single-organism process, P:organic substance metabolic process, P:phosphate-containing compound metabolic process	1.51	0.0
OG50_diatome_k49_Locus_5011_Transcript_5_1	predicted protein	P:signal transduction, F:phosphorus-oxygen lyase activity, C:membrane,	1.51	9.36609E-8

		C:integral component of membrane, P:intracellular signal transduction, P:cyclic nucleotide biosynthetic process, C:intracellular, F:3',5'-cyclic-nucleotide phosphodiesterase activity		
TT00_diatome_k49_Locus_649_Transcript_10_1	tyrosine kinase	F:ATP binding, C:membrane, F:protein serine/threonine kinase activity, P:protein phosphorylation	1.50	0.0
TC01_diatome_k31_Locus_1298_Transcript_20_1	cell surface receptor	F:hydrolase activity, acting on carbon-nitrogen (but not peptide) bonds, P:nitrogen compound metabolic process, P:signal transduction, F:phosphorus-oxygen lyase activity, C:membrane, C:integral component of membrane, P:intracellular signal transduction, P:cyclic nucleotide biosynthetic process, C:intracellular, F:3',5'-cyclic-nucleotide phosphodiesterase activity	1.50	2.57072E-117
TG01_diatome_CL744Contig1_2	histone deacetylase 6 10	C:heterochromatin, C:nuclear chromatin, P:chromatin silencing, F:hydrolase activity	1.49	1.08175E-90
OG50_diatome_k43_Locus_8370_Transcript_2_1	probable leucine-rich repeat receptor kinase At1g35710	F:nucleotide binding, F:ATP binding, C:membrane, C:integral component of membrane, F:protein kinase activity, P:phosphorylation, F:transferase activity, F:protein serine/threonine kinase activity, P:protein phosphorylation, F:kinase activity	1.48	1.1662E-24
TT00_diatome_k43_Locus_1049_Transcript_29_1	serine esterase	C:membrane, C:integral component of membrane, P:cellular lipid metabolic process, F:carboxylic ester hydrolase activity, F:hydrolase activity	1.48	3.26152E-77
TT00_diatome_k25_Locus_3384_Transcript_2_1	Glyco gp2	C:cell, F:protein disulfide oxidoreductase activity, F:electron carrier activity, P:cell redox homeostasis, P:oxidation-reduction process	1.48	1.33947E-24
OG50_diatome_k49_Locus_335_Transcript_7_3	tRNA pseudouridine(38-40) synthase	P:pseudouridine synthesis, F:RNA binding, P:tRNA pseudouridine synthesis, P:tRNA processing, P:RNA modification, F:pseudouridine synthase activity, F:isomerase activity	1.47	3.55239E-49
TG01_diatome_k37_Locus_3215_Transcript_1_1	caffeoylshikimate esterase-like	C:membrane, P:lipid metabolic process, F:lipase activity	1.47	1.43432E-126
TC01_diatome_k25_Locus_2479_Transcript_6_2	glutamate dehydrogenase	P:glutamate catabolic process to 2-oxoglutarate, P:oxidation-reduction process, F:glutamate dehydrogenase (NAD+) activity	1.46	0.0
TC01_diatome_k37_Locus_4080_Transcript_1_3	N2,N2-dimethylguanosine tRNA methyltransferase	P:tRNA processing, F:transferase activity, P:methylation	1.46	0.0
TG01_diatome_k43_Locus_2401_Transcript_8_1	DNA helicase	F:DNA binding, C:nucleus, F:transcription factor activity, sequence-specific DNA binding, F:protein heterodimerization activity, P:transcription, DNA-templated, P:regulation of DNA-templated transcription, elongation, P:regulation of transcription, DNA-templated, F:helicase activity	1.45	0.0
TT00_diatome_k31_Locus_8866_Transcript_2_1	beta-1,4-mannosyl-glyco beta-1,4-N-acetylglucosaminyltransferase	F:beta-1,4-mannosylglycoprotein 4-beta-N-acetylglucosaminyltransferase activity, F:transferase activity, transferring glycosyl groups, C:membrane, C:integral component of membrane, P:protein N-linked glycosylation, F:transferase activity	1.45	7.14601E-135
TG01_diatome_k31_Locus_5830_Transcript_1_1	hypothetical protein FRACYDRAFT_264505	C:membrane, P:proteolysis, C:integral component of membrane, F:metallopeptidase activity	1.44	4.87009E-26
TG01_diatome_k31_Locus_4062_Transcript_3_1	zinc C3HC4 type (RING	F:ubiquitin protein ligase activity, F:zinc ion binding, F:metal ion binding,	1.44	2.15279E-48

	finger) domain-containing	C:Hrd1p ubiquitin ligase complex, C:membrane, C:integral component of membrane, P:ER-associated ubiquitin-dependent protein catabolic process, C:nucleolus, P:protein ubiquitination		
TC01_diatome_CL336Contig1_1	glyceraldehyde-3-phosphate dehydrogenase	F:NADP binding, F:NAD binding, P:glycolytic process, P:oxidation-reduction process, P:glucose metabolic process, F:glyceraldehyde-3-phosphate dehydrogenase (NAD+) (phosphorylating) activity, F:isomerase activity	1.43	0.0
TC01_diatome_CL1816Contig1_4	probable leucine-rich repeat receptor kinase At1g35710	F:GTP binding, F:ATP binding, P:small GTPase mediated signal transduction, C:membrane, C:integral component of membrane, F:protein kinase activity, P:protein phosphorylation, C:intracellular	1.42	9.05749E-74
TC01_diatome_CL111Contig1_2	predicted protein	F:hydrolase activity, acting on carbon-nitrogen (but not peptide) bonds, P:nitrogen compound metabolic process, P:signal transduction, F:phosphorus-oxygen lyase activity, C:membrane, C:integral component of membrane, P:intracellular signal transduction, P:cyclic nucleotide biosynthetic process, C:intracellular, F:3',5'-cyclic-nucleotide phosphodiesterase activity	1.42	3.98342E-75
TT00_diatome_k25_Locus_1886_Transcript_3_2	phosphate dikinase	F:ATP binding, F:metal ion binding, C:intracellular membrane-bounded organelle, F:pyruvate, phosphate dikinase activity, C:cytoplasmic part, P:phosphorylation, F:kinase activity, P:pyruvate metabolic process	1.42	0.0
TG01_diatome_k37_Locus_4818_Transcript_1_1	glutamate synthase large subunit	P:glutamate biosynthetic process, C:cytoplasm, F:glutamate synthase (ferredoxin) activity, P:ammonia assimilation cycle, P:oxidation-reduction process	1.42	0.0
TT00_diatome_k25_Locus_1271_Transcript_1_1	g-patch domain containing	F:nucleic acid binding, P:box C/D snoRNA 3'-end processing, P:positive regulation of catalytic activity, F:enzyme activator activity, P:negative regulation of telomere maintenance via telomerase, C:nucleolus, P:negative regulation of telomerase activity, F:telomerase inhibitor activity, C:nucleoplasm	1.41	1.96131E-5
TC01_diatome_k25_Locus_378_Transcript_33_2	fibro-slime domain-containing	F:chitinase activity, P:cell wall macromolecule catabolic process, P:chitin catabolic process, C:membrane, C:integral component of membrane	1.41	5.24289E-14
TC01_diatome_CL4Contig1_4	3 ,5 -cyclic-nucleotide phosphodiesterase	F:hydrolase activity, acting on carbon-nitrogen (but not peptide) bonds, P:signal transduction, P:nitrogen compound metabolic process, F:phosphorus-oxygen lyase activity, C:membrane, C:integral component of membrane, P:intracellular signal transduction, P:cyclic nucleotide biosynthetic process, C:intracellular, F:3',5'-cyclic-nucleotide phosphodiesterase activity	1.40	7.44609E-16
TG01_diatome_k49_Locus_8751_Transcript_1_1	fucoxanthin chlorophyll a c	F:pigment binding, C:integral component of membrane, P:protein-chromophore linkage, F:chlorophyll binding, P:response to light stimulus, P:photosynthesis, light harvesting in photosystem I, C:chloroplast thylakoid membrane	1.40	7.61265E-96
TG01_diatome_k49_Locus_4789_Transcript_7_1	ubiquitin thiolesterase	P:macromolecule metabolic process, P:nitrogen compound metabolic process, C:membrane	1.38	2.38499E-33
TC01_diatome_k25_Locus_6522_Transcript_1_1	phosphoribosylamine-glycine ligase	F:phosphoribosylglycinamide formyltransferase activity, F:ATP binding, C:cytoplasm, F:phosphoribosylamine-glycine ligase activity, F:metal ion	1.38	0.0

		binding, P:'de novo' IMP biosynthetic process, P:purine nucleobase biosynthetic process, F:phosphoribosylformylglycinamidine cyclo-ligase activity		
TC01_diatome_k31_Locus_4016_Transcript_6_2	alpha,alpha-trehalose-phosphate synthase (UDP-forming)	F:catalytic activity, P:trehalose biosynthetic process	1.38	0.0
TT00_diatome_k25_Locus_7275_Transcript_2_1	5 -3 exoribonuclease 2	P:RNA metabolic process, F:hydrolase activity	1.37	0.0
OG50_diatome_k43_Locus_68_Transcript_28_2	cell surface receptor	F:hydrolase activity, acting on carbon-nitrogen (but not peptide) bonds, P:signal transduction, P:nitrogen compound metabolic process, F:phosphorus-oxygen lyase activity, C:membrane, C:integral component of membrane, P:intracellular signal transduction, P:cyclic nucleotide biosynthetic process, C:intracellular, F:3',5'-cyclic-nucleotide phosphodiesterase activity	1.37	0.0
TG01_diatome_k49_Locus_5935_Transcript_21_1	acyl :acetate 3-ketoacid transferase	F:3-oxoacid CoA-transferase activity, C:mitochondrion, P:ketone body catabolic process	1.36	0.0
TT00_diatome_k37_Locus_9052_Transcript_1_1	hypothetical protein FRACYDRAFT_236886	P:signal transduction	1.36	0.0
TG01_diatome_CL361Contig1_4	RING finger 11-like	F:ubiquitin protein ligase activity, F:zinc ion binding, P:proteasome-mediated ubiquitin-dependent protein catabolic process, F:metal ion binding, P:protein polyubiquitination, C:membrane, C:integral component of membrane, P:protein ubiquitination involved in ubiquitin-dependent protein catabolic process	1.36	1.97758E-18
TG01_diatome_k25_Locus_6242_Transcript_3_1	TKL DICTY4 kinase	P:signal transduction, F:transferase activity, transferring phosphorus-containing groups, P:primary metabolic process, P:organic substance metabolic process, P:phosphate-containing compound metabolic process	1.36	0.0
TC01_diatome_k49_Locus_1463_Transcript_53_1	P type ATPase	C:integral component of plasma membrane, F:ATP binding, F:metal ion binding, C:intracellular membrane-bounded organelle, P:calcium ion transmembrane transport, F:calcium-transporting ATPase activity, P:cellular calcium ion homeostasis	1.36	5.81177E-96
TT00_diatome_k25_Locus_413_Transcript_1_1	serine-rich repeat glyco adhesin	P:proteolysis, F:peptidase activity, C:nucleolus	1.36	3.92329E-9
OG50_diatome_CL1749Contig1_2	CAMK CAMK1 kinase	F:nucleotide binding, C:nucleus, F:calmodulin binding, C:cytoplasm, P:protein autophosphorylation, F:calmodulin-dependent protein kinase activity, P:peptidyl-serine phosphorylation, P:intracellular signal transduction, F:calcium-dependent protein serine/threonine kinase activity	1.35	1.48309E-138
OG50_diatome_k49_Locus_6837_Transcript_7_1	predicted protein	F:hydrolase activity, acting on carbon-nitrogen (but not peptide) bonds, P:signal transduction, P:nitrogen compound metabolic process, F:phosphorus-oxygen lyase activity, C:membrane, C:integral component of membrane, P:intracellular signal transduction, P:cyclic nucleotide biosynthetic process, C:intracellular, F:3',5'-cyclic-nucleotide phosphodiesterase activity	1.35	2.29134E-88
TG01_diatome_k37_Locus_8115_Transcript_3_1	phosphatidate cytidylyltransferase	F:phosphatidate cytidylyltransferase activity, C:membrane, P:CDP-diacylglycerol biosynthetic process, P:phosphatidylglycerol biosynthetic	1.34	2.52497E-180

		process		
OG50_diatome_k49_Locus_1987_Transcript_9_2	probable leucine-rich repeat receptor kinase At1g35710	F:nucleotide binding, F:ATP binding, F:calcium ion binding, C:membrane, C:integral component of membrane, F:protein kinase activity, P:phosphorylation, P:protein phosphorylation, F:kinase activity	1.34	8.577E-105
OG50_diatome_k25_Locus_5187_Transcript_1_1	Eukaryotic translation initiation factor 3 subunit D	F:translation initiation factor activity, P:translational initiation, C:eukaryotic translation initiation factor 3 complex	1.33	0.0
TG01_diatome_k49_Locus_2304_Transcript_1_1	AFG3 family	P:protein import into mitochondrial intermembrane space, F:ATP binding, F:zinc ion binding, P:cristae formation, P:protein complex assembly, P:mitochondrial fusion, C:integral component of membrane, F:ATP-dependent peptidase activity, P:mitochondrial protein processing, F:metalloendopeptidase activity, C:mitochondrial inner membrane	1.33	0.0
TC01_diatome_k43_Locus_3778_Transcript_2_2	DENN domain-containing 1B-like isoform X3	C:mitochondrion, F:double-stranded DNA binding, P:regulation of transcription, DNA-templated, F:Rab guanyl-nucleotide exchange factor activity, P:positive regulation of GTPase activity	1.33	0.0
TC01_diatome_k25_Locus_9287_Transcript_6_1	threonine ammonia-lyase	F:L-serine ammonia-lyase activity, F:pyridoxal phosphate binding, C:cytoplasm, C:membrane, P:threonine catabolic process, F:L-threonine ammonia-lyase activity, P:L-serine catabolic process	1.32	0.0
TT00_diatome_k25_Locus_2830_Transcript_1_2	serine protease	P:proteolysis, F:serine-type endopeptidase activity	1.31	4.37307E-164
TC01_diatome_k25_Locus_821_Transcript_6_2	cell surface receptor	P:nitrogen compound metabolic process, P:signal transduction, C:membrane, F:hydrolase activity	1.31	0.0
TC01_diatome_k37_Locus_3153_Transcript_1_1	tetratricopeptide TPR_2	F:microtubule motor activity, P:signal transduction, C:kinesin complex	1.30	1.29794E-79
TG01_diatome_k43_Locus_708_Transcript_2_2	isocitrate dehydrogenase	F:isocitrate dehydrogenase (NADP+) activity, P:tricarboxylic acid cycle	1.30	0.0
TC01_diatome_k43_Locus_5333_Transcript_1_1	splicing factor 3B subunit 1	C:U12-type spliceosomal complex, C:catalytic step 2 spliceosome, F:mRNA binding, C:U2-type prespliceosome, C:U2 snRNP, P:spliceosomal complex assembly	1.29	0.0
TT00_diatome_k43_Locus_348_Transcript_1_2	CAMK CAMKL AMPK kinase	C:nucleus, F:ATP binding, C:cytoplasm, F:protein serine/threonine kinase activity, P:protein phosphorylation, P:intracellular signal transduction	1.29	0.0
TC01_diatome_k37_Locus_787_Transcript_1_1	hypothetical protein FRACYDRAFT_267251	F:RNA binding, C:U2-type prespliceosome, C:U1 snRNP, P:mRNA splicing, via spliceosome	1.29	7.22948E-44
TT00_diatome_k25_Locus_813_Transcript_4_1	diacylglycerol kinase	F:ATP binding, F:diacylglycerol kinase activity, P:phosphorylation, P:protein kinase C-activating G-protein coupled receptor signaling pathway	1.29	0.0
OG50_diatome_CL94Contig1_2	phosphatase 2C	F:protein serine/threonine phosphatase activity, P:protein dephosphorylation	1.28	0.0
TG01_diatome_k25_Locus_5139_Transcript_3_1	Cold shock domain-containing E1	F:nucleic acid binding, F:DNA binding, P:regulation of transcription, DNA-templated	1.27	0.0
OG50_diatome_k25_Locus_1030_Transcript_3_1	hemolysin-type calcium-binding region	C:extracellular space, F:calcium ion binding, C:membrane, P:proteolysis, C:integral component of membrane, F:serine-type endopeptidase activity	1.27	2.54194E-53
TG01_diatome_k25_Locus_3005_Transcript_1_1	ribosomal S2	P:rRNA export from nucleus, P:endonucleolytic cleavage to generate mature 3'-end of SSU-rRNA from (SSU-rRNA, 5.8S rRNA, LSU-rRNA), F:structural constituent of ribosome, C:cytosolic small ribosomal subunit,	1.26	5.25969E-155

		P:endonucleolytic cleavage in ITS1 to separate SSU-rRNA from 5.8S rRNA and LSU-rRNA from tricistronic rRNA transcript (SSU-rRNA, 5.8S rRNA, LSU-rRNA), P:ribosomal small subunit assembly, C:90S preribosome, P:translation		
OG50_diatome_k43_Locus_341_Transcript_1_1	arginine N-methyltransferase	P:protein methylation	1.26	0.0
TG01_diatome_k43_Locus_2542_Transcript_4_2	LOV domain-containing	F:phosphorelay sensor kinase activity, F:transcription factor activity, sequence-specific DNA binding, P:phosphorelay signal transduction system, P:regulation of transcription, DNA-templated, F:sequence-specific DNA binding, P:signal transduction by protein phosphorylation, C:intracellular	1.26	4.35762E-75
TG01_diatome_k49_Locus_110_Transcript_6_1	TBC1 domain family member 20-like	P:regulation of Rho protein signal transduction, C:nucleus, F:O-methyltransferase activity, P:vesicle-mediated transport, C:membrane, C:integral component of membrane, C:cytosol, C:endoplasmic reticulum, P:cell separation after cytokinesis, F:methyltransferase activity, P:methylation	1.25	1.56816E-12
OG50_diatome_CL447Contig1_2	regulator of nonsense transcripts 1 (RENT1)	F:nucleotide binding, P:nucleic acid phosphodiester bond hydrolysis, F:ATP binding, F:endonuclease activity, F:helicase activity	1.25	0.0
TC01_diatome_k25_Locus_2555_Transcript_2_1	CCR4-NOT transcription complex subunit 6	P:nucleic acid phosphodiester bond hydrolysis, F:exonuclease activity, F:endonuclease activity	1.25	0.0
TG01_diatome_CL378Contig1_2	FAM203 family	F:DNA binding, C:nucleus, P:transcription, DNA-templated	1.25	1.77682E-119
OG50_diatome_k31_Locus_2249_Transcript_1_1	60S ribosomal L11	F:structural constituent of ribosome, C:cytosolic large ribosomal subunit, P:ribosomal large subunit assembly, P:translation	1.25	1.87328E-106
TC01_diatome_k37_Locus_8365_Transcript_2_1	branched-chain amino acid aminotransferase	F:L-leucine transaminase activity, F:L-valine transaminase activity, P:branched-chain amino acid biosynthetic process, F:L-isoleucine transaminase activity	1.25	0.0
TT00_diatome_k43_Locus_3020_Transcript_8_1	DUF4116 domain-containing	F:ATP binding, F:actin binding, C:membrane, C:integral component of membrane, F:protein kinase activity, P:protein phosphorylation	1.25	3.53916E-57
TG01_diatome_k25_Locus_6716_Transcript_2_2	arf guanine-nucleotide exchange factor gnom-like	F:ARF guanyl-nucleotide exchange factor activity, P:regulation of ARF protein signal transduction, P:positive regulation of GTPase activity	1.24	0.0
TT00_diatome_k25_Locus_2511_Transcript_1_1	Zinc finger CCCH domain-containing O74823	C:nucleus, C:nuclear body, C:NURS complex, C:nuclear chromatin, F:metal ion binding, P:nuclear-transcribed mRNA catabolic process, meiosis-specific transcripts	1.24	5.02262E-32
TG01_diatome_k31_Locus_962_Transcript_5_1	adenylyl cyclase	F:phosphorus-oxygen lyase activity, C:membrane, C:integral component of membrane, P:intracellular signal transduction, P:cyclic nucleotide biosynthetic process, C:intracellular	1.24	0.0
TC01_diatome_k25_Locus_1512_Transcript_2_3	probable ATP-dependent DNA helicase HFM1	F:nucleotide binding, F:nucleic acid binding, F:ATP binding, P:meiotic cell cycle, P:resolution of meiotic recombination intermediates, F:helicase activity, F:hydrolase activity	1.23	0.0
OG50_diatome_k31_Locus_6107_Transcript_2_2	3-oxoacid -transferase	F:3-oxoacid CoA-transferase activity, C:mitochondrion, P:ketone body catabolic process	1.23	0.0
TT00_diatome_k43_Locus_1018_Transcript_1_1	ATP-dependent RNA helicase DB10	F:nucleic acid binding, F:ATP binding, C:mitochondrion, P:RNA secondary structure unwinding, F:ATP-dependent RNA helicase activity	1.22	0.0

TC01_diatome_CL34Contig1_1	hypothetical protein FRACYDRAFT_264505	C:cytoplasm, P:glutathione metabolic process, C:membrane, P:proteolysis, C:integral component of membrane, F:glutathione transferase activity, F:metallopeptidase activity	1.22	3.78836E-65
TG01_diatome_k37_Locus_3920_Transcript_1_1	histidine kinase	F:aspartic-type endopeptidase activity, F:starch binding, P:proteolysis, P:phosphorylation, F:carbohydrate binding, F:kinase activity	1.21	8.94325E-128
TG01_diatome_k31_Locus_6963_Transcript_12_1	G- -coupled receptor family 3 5	F:G-protein coupled receptor activity, F:G-protein coupled GABA receptor activity, P:G-protein coupled receptor signaling pathway, P:signal transduction, P:nucleotide catabolic process, C:membrane, P:lipid metabolic process, C:integral component of membrane, F:signal transducer activity, F:hydrolase activity	1.21	9.9211E-159
TG01_diatome_k43_Locus_7087_Transcript_2_1	aspartyl protease	F:aspartic-type endopeptidase activity, C:membrane, P:proteolysis, C:integral component of membrane, F:peptidase activity	1.21	9.79756E-18
OG50_diatome_k37_Locus_398_Transcript_22_1	cell surface receptor	F:hydrolase activity, acting on carbon-nitrogen (but not peptide) bonds, P:nitrogen compound metabolic process, P:signal transduction, F:phosphorus-oxygen lyase activity, C:membrane, C:integral component of membrane, P:intracellular signal transduction, P:cyclic nucleotide biosynthetic process, C:intracellular, F:3',5'-cyclic-nucleotide phosphodiesterase activity	1.21	4.30266E-99
TG01_diatome_k31_Locus_57_Transcript_9_4	G1 S-specific cyclin-D1	P:regulation of cellular process, P:single-organism cellular process, P:response to stimulus	1.21	3.9137E-26
TT00_diatome_k25_Locus_7047_Transcript_1_1	casein kinase II subunit beta-4	P:regulation of cellular process, C:intracellular part	1.21	3.43069E-52
OG50_diatome_k43_Locus_2931_Transcript_5_1	hypothetical protein FRACYDRAFT_264505	C:cytoplasm, P:glutathione metabolic process, C:membrane, P:proteolysis, C:integral component of membrane, F:glutathione transferase activity, F:metallopeptidase activity	1.21	1.30833E-67
TC01_diatome_k25_Locus_8774_Transcript_1_1	ornithine carbamoyltransferase	C:cytoplasm, C:intracellular membrane-bounded organelle, P:urea cycle, P:arginine biosynthetic process via ornithine, F:amino acid binding, F:ornithine carbamoyltransferase activity	1.21	4.85901E-174
TT00_diatome_k37_Locus_2515_Transcript_3_1	phosphoenolpyruvate carboxykinase (ATP)	F:phosphoenolpyruvate carboxykinase (ATP) activity, F:ATP binding, P:gluconeogenesis, C:cytosol, P:phosphorylation, F:kinase activity	1.20	0.0
TC01_diatome_k37_Locus_1320_Transcript_5_1	kinase	F:nucleotide binding, F:protein kinase activity, P:protein phosphorylation, C:intracellular part	1.20	0.0
TT00_diatome_k25_Locus_6991_Transcript_6_1	ribose-phosphate pyrophosphokinase 4-like	F:magnesium ion binding, F:transferase activity, transferring glycosyl groups, P:nucleotide biosynthetic process, F:ribose phosphate diphosphokinase activity, P:nucleoside metabolic process	1.20	0.0
TT00_diatome_CL174Contig1_2	Nucleolar and coiled-body phospho 1	F:chitin binding, P:chitin metabolic process, C:extracellular region	1.20	1.62015E-21
TC01_diatome_k49_Locus_3191_Transcript_3_1	ATP-binding cassette superfamily	F:ATP binding, P:phosphate ion transport, C:membrane, C:integral component of membrane, F:phosphate ion binding, P:cellular response to phosphate starvation, P:transport, F:ATPase-coupled phosphate ion transmembrane transporter activity, P:phosphate ion transmembrane transport, C:ATP-binding cassette (ABC) transporter complex, C:plasma membrane	1.20	3.79323E-57

TT00_diatome_k25_Locus_1333_Transcript_10_3	cell wall anchor	F:chitin binding, P:chitin metabolic process, C:extracellular region	1.19	2.89389E-27
OG50_diatome_k49_Locus_232_Transcript_11_1	acyl- dehydrogenase	F:acyl-CoA dehydrogenase activity, P:fatty acid beta-oxidation using acyl-CoA dehydrogenase, F:fatty-acyl-CoA binding, F:flavin adenine dinucleotide binding, F:electron carrier activity, F:oxidoreductase activity, acting on the CH-CH group of donors, with a flavin as acceptor, P:lipid homeostasis	1.18	0.0
TT00_diatome_k25_Locus_1273_Transcript_6_1	mannosyl-oligosaccharide 1,2-alpha-mannosidase MNS1	F:organic cyclic compound binding, F:heterocyclic compound binding, P:glycoprotein ERAD pathway, F:calcium ion binding, P:N-glycan processing, C:membrane, F:mannosyl-oligosaccharide 1,2-alpha-mannosidase activity, C:endoplasmic reticulum, P:ER-associated ubiquitin-dependent protein catabolic process	1.17	0.0
TG01_diatome_CL28Contig2_2	cell surface receptor	F:hydrolase activity, acting on carbon-nitrogen (but not peptide) bonds, P:nitrogen compound metabolic process, P:signal transduction, F:phosphorus-oxygen lyase activity, C:membrane, C:integral component of membrane, P:intracellular signal transduction, P:cyclic nucleotide biosynthetic process, C:intracellular, F:3',5'-cyclic-nucleotide phosphodiesterase activity	1.17	0.0
TG01_diatome_k31_Locus_4301_Transcript_3_2	ATP-dependent RNA helicase DDX50 isoform X2	F:nucleotide binding, C:nucleus, F:RNA binding, F:ion binding, P:RNA secondary structure unwinding, F:ATP-dependent RNA helicase activity	1.17	0.0
TT00_diatome_k25_Locus_879_Transcript_8_4	mitochondrial carnitine acylcarnitine carrier	F:structural constituent of ribosome, C:membrane, P:transport, P:translation	1.16	1.62851E-92
TG01_diatome_CL245Contig1_1	tuberin isoform X2	P:negative regulation of signal transduction, P:regulation of intracellular signal transduction	1.16	2.26691E-55
TT00_diatome_CL370Contig1_2	long chain acyl-synthetase	P:long-chain fatty acid metabolic process, F:long-chain fatty acid-CoA ligase activity	1.16	9.84871E-95
OG50_diatome_k31_Locus_5704_Transcript_6_1	LRR receptor-like serine threonine- kinase GSO1	F:nucleotide binding, F:ATP binding, C:mitochondrion, C:membrane, C:integral component of membrane, F:protein kinase activity, P:phosphorylation, F:transferase activity, F:protein serine/threonine kinase activity, P:protein phosphorylation, F:kinase activity	1.15	2.17562E-77
TT00_diatome_k25_Locus_4475_Transcript_1_1	kinesin KIN-12D	F:protein homodimerization activity, F:structural molecule activity, F:protein kinase activity, C:intermediate filament, P:flocculation, F:transcription factor binding, F:protein serine/threonine kinase activity, P:protein phosphorylation, P:microtubule-based movement, F:dynein complex binding, C:intracellular, F:microtubule binding, F:nucleotide binding, F:ATP binding, F:microtubule motor activity, F:metal ion binding, P:phosphorylation, F:transferase activity, F:kinase activity, P:intracellular signal transduction	1.15	3.38399E-6
TC01_diatome_k31_Locus_4385_Transcript_3_1	AAA domain	C:nucleus, F:ATP binding, P:regulation of double-strand break repair via homologous recombination, P:cytoplasmic microtubule organization, F:microtubule-severing ATPase activity	1.15	1.15472E-170
TC01_diatome_k37_Locus_1341_Transcript_1_1	predicted protein	C:cytosol, F:pseudouridine synthase activity, P:enzyme-directed rRNA pseudouridine synthesis	1.15	4.84041E-103

TC01_diatome_k49_Locus_3394_Transcript_2_1	predicted protein	F:ATPase activity, C:MutLalpha complex, P:mismatch repair, F:single-stranded DNA binding	1.15	6.20441E-20
TC01_diatome_k37_Locus_7338_Transcript_9_1	transmembrane chitin glycosaminyl transferas	F:transferase activity, transferring glycosyl groups, F:transferase activity, transferring hexosyl groups, P:chitin biosynthetic process, C:membrane, C:integral component of membrane, F:chitin synthase activity, F:transferase activity	1.14	6.46706E-69
OG50_diatome_k49_Locus_4154_Transcript_2_1	mitochondrial carnitine acylcarnitine carrier	F:structural constituent of ribosome, C:membrane, P:transport, P:translation	1.13	9.96666E-127
OG50_diatome_k25_Locus_4471_Transcript_2_2	Pectin lyase fold virulence factor	P:carbohydrate metabolic process, P:metabolic process, C:membrane, C:integral component of membrane, F:lyase activity, F:polygalacturonase activity, P:cell wall organization, C:extracellular region, F:hydrolase activity, F:hydrolase activity, acting on glycosyl bonds	1.13	1.57435E-76
TT00_diatome_k43_Locus_2212_Transcript_2_2	L domain	F:nucleotide binding, F:ATP binding, C:membrane, C:integral component of membrane, F:protein kinase activity, P:protein phosphorylation	1.13	2.12673E-43
TC01_diatome_k25_Locus_803_Transcript_1_1	RHOMBOID 13	P:proteolysis, C:membrane, C:integral component of membrane, F:serine-type endopeptidase activity	1.12	3.43297E-56
OG50_diatome_k37_Locus_655_Transcript_87_1	predicted protein	F:hydrolase activity, acting on carbon-nitrogen (but not peptide) bonds, P:nitrogen compound metabolic process, P:signal transduction, F:phosphorus-oxygen lyase activity, C:membrane, C:integral component of membrane, P:intracellular signal transduction, P:cyclic nucleotide biosynthetic process, C:intracellular, F:3',5'-cyclic-nucleotide phosphodiesterase activity	1.12	7.45597E-90
TT00_diatome_k43_Locus_2852_Transcript_4_1	cell surface receptor	F:hydrolase activity, acting on carbon-nitrogen (but not peptide) bonds, P:nitrogen compound metabolic process, P:signal transduction, F:phosphorus-oxygen lyase activity, C:membrane, C:integral component of membrane, P:intracellular signal transduction, P:cyclic nucleotide biosynthetic process, C:intracellular, F:3',5'-cyclic-nucleotide phosphodiesterase activity	1.12	0.0
TT00_diatome_k49_Locus_4983_Transcript_4_1	E3 ubiquitin- ligase NEDD4	C:nucleus, F:ubiquitin-protein transferase activity, C:cytoplasm, F:ligase activity, P:protein ubiquitination involved in ubiquitin-dependent protein catabolic process	1.12	0.0
TT00_diatome_k49_Locus_2113_Transcript_11_1	polymorphic Outer membrane G I family	F:chitinase activity, P:cell wall macromolecule catabolic process, P:chitin catabolic process, C:membrane, C:integral component of membrane	1.11	3.33725E-23
TG01_diatome_k37_Locus_2842_Transcript_2_2	Serineaspartate repeat-containing	P:intein-mediated protein splicing, P:polysaccharide catabolic process, F:metal ion binding, F:calcium ion binding, C:membrane, P:proteolysis, C:integral component of membrane, F:serine-type endopeptidase activity, F:peptidase activity, F:carbohydrate binding, C:mucus layer	1.11	3.63154E-69
TT00_diatome_k37_Locus_114_Transcript_2_6	MYB DNA binding transcription factor	C:nucleus, F:DNA binding, P:transcription, DNA-templated, P:regulation of transcription, DNA-templated	1.11	1.40781E-33
TC01_diatome_k49_Locus_7650_Transcript_3_1	alpha 1,2-mannosyltransferase	P:glycosylation, P:glycoprotein biosynthetic process	1.10	6.66178E-111
OG50_diatome_k37_Locus_422_Transcript_8_2	monogalactosyldiacylglycerol synthase	F:transferase activity, transferring hexosyl groups, P:glycolipid biosynthetic process	1.10	0.0

TT00_diatome_k37_Locus_757_Transcript_12_2	hypothetical protein FisN_14Hh150	F:chalcone isomerase activity, C:membrane, C:integral component of membrane, F:intramolecular lyase activity, P:flavonoid biosynthetic process	1.10	1.98324E-149
OG50_diatome_k25_Locus_1229_Transcript_4_1	thiol:disulfide interchange	F:protein disulfide oxidoreductase activity, C:cytoplasm, F:oxidoreductase activity, acting on a sulfur group of donors, disulfide as acceptor, P:cellular response to oxidative stress, P:cell redox homeostasis, P:oxidation-reduction process, P:protein folding, P:sulfate assimilation	1.10	2.65717E-71
TG01_diatome_CL74Contig1_4	peptide-methionine (S)-S-oxide reductase	P:cellular protein metabolic process, F:oxidoreductase activity, acting on a sulfur group of donors, disulfide as acceptor	1.10	9.19323E-57
OG50_diatome_k31_Locus_200_Transcript_2_1	G- -coupled receptor family 3 5	P:G-protein coupled receptor signaling pathway, P:signal transduction, P:small GTPase mediated signal transduction, F:signal transducer activity, P:transport, C:plasma membrane, F:transporter activity, C:intracellular, F:GTP binding, F:G-protein coupled receptor activity, F:G-protein coupled GABA receptor activity, C:membrane, P:lipid metabolic process, C:integral component of membrane, F:hydrolase activity	1.09	0.0
TG01_diatome_k37_Locus_6457_Transcript_2_1	filamentous hemagglutinin family N-terminal domain	C:membrane, P:proteolysis, C:integral component of membrane, C:extracellular region, P:defense response, F:metalloendopeptidase activity, P:pathogenesis, F:metallopeptidase activity	1.09	1.92134E-41
TT00_diatome_k25_Locus_3710_Transcript_6_1	transcription initiation factor IIB	F:zinc ion binding, P:regulation of transcription, DNA-templated, P:DNA-templated transcription, initiation, F:TBP-class protein binding	1.09	0.0
TC01_diatome_k25_Locus_2285_Transcript_1_1	2-isopropylmalate synthase	F:transferase activity, transferring acyl groups, acyl groups converted into alkyl on transfer, P:branched-chain amino acid biosynthetic process	1.09	0.0
OG50_diatome_k31_Locus_3735_Transcript_2_1	peptidase P60	F:DNA binding, C:nucleus, P:histone lysine methylation, F:oxidoreductase activity, F:metal ion binding, F:histone-lysine N-methyltransferase activity, P:oxidation-reduction process, F:N-acetyltransferase activity	1.09	0.0
TC01_diatome_k31_Locus_1250_Transcript_9_3	CAMK kinase	F:nucleotide binding, F:ion binding, F:protein serine/threonine kinase activity, P:protein phosphorylation, C:intracellular part	1.09	5.2527E-177
TC01_diatome_k25_Locus_3830_Transcript_1_1	histidine kinase	P:regulation of cellular process, P:metabolic process, F:transferase activity, transferring phosphorus-containing groups, P:cellular process, P:response to stimulus	1.08	1.29482E-118
TC01_diatome_CL236Contig1_1	Phospho involved in cytoplasm to vacuole targeting and autophagy	F:alternative oxidase activity, P:autophagy, C:ATG1/ULK1 kinase complex, C:membrane, C:integral component of membrane, P:oxidation-reduction process	1.08	1.9391E-105
OG50_diatome_k25_Locus_4309_Transcript_8_2	PEK kinase	F:ATP binding, F:protein kinase activity, P:protein phosphorylation	1.08	6.15071E-140
TG01_diatome_k49_Locus_10754_Transcript_1_1	pre-mRNA-splicing factor RBM22	F:nucleotide binding, F:U6 snRNA binding, F:pre-mRNA binding, F:metal ion binding, P:multicellular organism development, C:U2-type catalytic step 1 spliceosome, C:U2-type catalytic step 2 spliceosome, C:Prp19 complex, P:spliceosomal snRNP assembly	1.08	0.0
TG01_diatome_k25_Locus_559_Transcript_8_1	3-deoxy-7-phosphoheptulonate synthase	P:aromatic amino acid family biosynthetic process, F:protein binding, C:chloroplast thylakoid, C:integral component of membrane, F:3-deoxy-7-phosphoheptulonate synthase activity, P:chorismate biosynthetic process	1.08	0.0
TC01_diatome_k37_Locus_6957_Transcript_1_1	exodeoxyribonuclease V	P:nucleic acid phosphodiester bond hydrolysis, F:exonuclease activity	1.08	1.03364E-131

	subunit beta			
OG50_diatome_k37_Locus_853_Transcript_3_2	beta-glucan synthase	P:nucleic acid phosphodiester bond hydrolysis, P:carbohydrate metabolic process, F:endonuclease activity, C:membrane, C:integral component of membrane, F:hydrolase activity, hydrolyzing O-glycosyl compounds	1.07	1.70063E-72
TG01_diatome_k25_Locus_5708_Transcript_3_1	Phosphocholine transferase	P:signal transduction, C:membrane, F:transferase activity, F:NAD+ ADP-ribosyltransferase activity	1.07	1.67303E-48
TT00_diatome_k25_Locus_1110_Transcript_1_1	DNA mismatch repair C-terminal domain-containing	F:DNA binding, F:ATP binding, P:mismatch repair, F:mismatched DNA binding	1.06	1.05504E-28
TG01_diatome_k49_Locus_123_Transcript_8_1	GABAR1 G -coupled GABA receptor	F:G-protein coupled receptor activity, F:zinc ion binding, F:G-protein coupled GABA receptor activity, P:G-protein coupled receptor signaling pathway, P:nucleotide catabolic process, C:membrane, C:integral component of membrane, F:N-acylphosphatidylethanolamine-specific phospholipase D activity, F:hydrolase activity	1.06	0.0
OG50_diatome_k37_Locus_1216_Transcript_6_1	hypothetical protein FRACYDRAFT_241601	F:ATPase activity, C:MutLalpha complex, P:mismatch repair, F:single-stranded DNA binding	1.06	2.43945E-54
TT00_diatome_k25_Locus_2344_Transcript_4_1	cysteine ase	P:proteolysis, P:cellular protein metabolic process, F:thiol-dependent ubiquitinyl hydrolase activity	1.06	1.67281E-173
TC01_diatome_k25_Locus_2729_Transcript_15_1	acetyl-coenzyme A synthetase	F:ATP binding, F:acetate-CoA ligase activity, F:AMP binding, C:intracellular part, P:acetyl-CoA biosynthetic process from acetate	1.05	0.0
OG50_diatome_k49_Locus_5629_Transcript_2_1	hypothetical protein FisN_2Lh474	F:DNA binding, C:nucleus, F:transcription factor activity, sequence-specific DNA binding, P:regulation of transcription, DNA-templated, F:sequence-specific DNA binding	1.05	3.72943E-58
OG50_diatome_k25_Locus_1783_Transcript_2_2	ATP-dependent RNA helicase DOB1	F:ATP binding, F:RNA binding, F:RNA helicase activity, P:RNA catabolic process	1.05	0.0
TG01_diatome_k37_Locus_5066_Transcript_10_2	Sterol desaturase sphingolipid fatty acid hydroxylase superfamily	F:iron ion binding, F:oxidoreductase activity, C:membrane, C:integral component of membrane, P:oxidation-reduction process, P:fatty acid biosynthetic process	1.04	3.64256E-6
TG01_diatome_k25_Locus_4056_Transcript_2_2	serine threonine-phosphatase pp1	P:mitotic spindle assembly checkpoint, C:cell division site, P:mitotic DNA damage checkpoint, C:condensed nuclear chromosome kinetochore, P:cell budding, C:CENP-A containing chromatin, P:rRNA processing, C:nucleolus, C:mating projection base, C:protein phosphatase type 1 complex, P:response to heat, P:termination of RNA polymerase II transcription, poly(A)-coupled, C:mRNA cleavage and polyadenylation specificity factor complex, C:growing cell tip, C:DPS complex, P:termination of RNA polymerase II transcription, exosome-dependent, C:non-growing cell tip, P:protein localization to kinetochore, P:dephosphorylation of RNA polymerase II C-terminal domain, C:cytosol, P:replication fork processing, P:histone dephosphorylation, P:negative regulation of chromosome condensation, P:transfer RNA gene-mediated silencing, P:regulation of cell shape during vegetative growth phase, P:cellular ion homeostasis, P:meiotic nuclear division, F:protein serine/threonine phosphatase activity, P:regulation of carbohydrate	1.04	0.0

		metabolic process, C:endocytic vesicle, P:DNA replication checkpoint, C:nuclear chromatin, P:glycogen metabolic process, C:cellular bud neck, F:metal ion binding, C:cell cortex, C:spindle pole body, P:positive regulation of protein dephosphorylation, C:PTW/PP1 phosphatase complex, P:attachment of mitotic spindle microtubules to kinetochore		
TC01_diatome_k49_Locus_1297_Transcript_12_3	G- -coupled receptor family 3 5	F:G-protein coupled receptor activity, F:G-protein coupled GABA receptor activity, P:G-protein coupled receptor signaling pathway, P:signal transduction, C:membrane, P:lipid metabolic process, C:integral component of membrane, F:signal transducer activity, P:transport, F:transporter activity, F:hydrolase activity	1.03	0.0
TC01_diatome_k49_Locus_5337_Transcript_4_3	cell surface receptor	F:catalytic activity, P:signal transduction, C:membrane	1.02	4.00636E-127
TT00_diatome_k31_Locus_3806_Transcript_2_1	proteophosphoglycan 5	C:integral component of nuclear inner membrane, P:proteolysis, C:membrane, C:integral component of membrane, F:serine-type endopeptidase activity	1.02	1.53274E-27
TG01_diatome_CL642Contig1_1	guanylyl cyclase	P:signal transduction, F:phosphorus-oxygen lyase activity, P:intracellular signal transduction, P:cyclic nucleotide biosynthetic process, C:intracellular, F:3',5'-cyclic-nucleotide phosphodiesterase activity	1.02	0.0
TG01_diatome_k37_Locus_794_Transcript_3_1	mitochondrial carrier	F:structural constituent of ribosome, C:membrane, P:transport, P:translation	1.01	3.50947E-120
TG01_diatome_k25_Locus_8476_Transcript_1_1	E3 ubiquitin- ligase	P:positive regulation of protein binding, C:neuronal cell body, P:learning or memory, C:endoplasmic reticulum membrane, C:growth cone, C:dendrite, P:positive regulation of transcription, DNA-templated, F:chaperone binding, P:positive regulation of protein ubiquitination, F:ubiquitin protein ligase activity involved in ERAD pathway, F:zinc ion binding, P:pattern specification process, C:protein complex, F:ubiquitin-specific protease binding, F:receptor activity, P:protein ubiquitination involved in ubiquitin-dependent protein catabolic process, P:ubiquitin-dependent SMAD protein catabolic process, C:nucleus, P:proteasome-mediated ubiquitin-dependent protein catabolic process, F:protein binding, P:movement of cell or subcellular component, F:metal ion binding, C:integral component of endoplasmic reticulum membrane, P:global genome nucleotide-excision repair, P:protein oligomerization, C:Derlin-1 retrotranslocation complex, P:protein ubiquitination, F:ubiquitin protein ligase activity, C:Hrd1p ubiquitin ligase ERAD-M complex, P:multicellular organism development, F:ubiquitin-ubiquitin ligase activity, P:positive regulation of transcription from RNA polymerase II promoter, C:nucleolus, C:nucleoplasm, P:endoplasmic reticulum unfolded protein response, F:ligase activity, P:ERAD pathway, P:protein autoubiquitination, P:protein K48-linked ubiquitination, P:signal transduction, F:SUMO polymer binding, P:protein polyubiquitination, F:BAT3 complex binding, C:endoplasmic reticulum, P:aging, P:ubiquitin-dependent protein catabolic process, F:ubiquitin-protein transferase activity, C:perinuclear region of cytoplasm, F:SMAD binding,	0.99	1.88468E-7

		C:cytoplasm, C:membrane, C:integral component of membrane, P:ER-associated ubiquitin-dependent protein catabolic process, F:protein binding, bridging, P:positive regulation of transforming growth factor beta receptor signaling pathway		
TG01_diatome_k25_Locus_7174_Transcript_6_1	clumping factor A-like isoform X1	F:chitin binding, P:chitin metabolic process, P:mismatch repair, C:extracellular region, C:proteinaceous extracellular matrix, P:cellular response to cell-matrix adhesion, F:ATP binding, C:cytoplasm, P:positive regulation of enamel mineralization, C:membrane, C:integral component of membrane, F:mismatched DNA binding, P:biomineral tissue development	0.99	4.77604E-8
TC01_diatome_k25_Locus_1715_Transcript_9_2	nucleoside diphosphate kinase B	F:ATP binding, P:UTP biosynthetic process, P:CTP biosynthetic process, P:GTP biosynthetic process, P:nucleoside diphosphate phosphorylation, F:nucleoside diphosphate kinase activity, C:intracellular	0.99	3.63884E-148
TG01_diatome_CL1003Contig1_1	transcription elongation factor SPT5	C:intracellular organelle, P:translation	0.99	0.0
TT00_diatome_k25_Locus_6468_Transcript_1_1	pre-mRNA-splicing factor ATP-dependent RNA helicase	F:nucleic acid binding, C:nucleus, F:ATP binding, C:cytoplasm, P:RNA processing, F:ATP-dependent RNA helicase activity	0.99	0.0
TC01_diatome_k25_Locus_5938_Transcript_3_1	serine threonine- kinase ctr1	F:ATP binding, F:protein kinase activity, P:protein phosphorylation	0.99	0.0
TT00_diatome_k43_Locus_5847_Transcript_1_1	RIP metalloprotease	F:metal ion binding, P:proteolysis, C:membrane, C:integral component of membrane, F:peptidase activity, F:metalloendopeptidase activity, C:plasma membrane, F:metallopeptidase activity, F:hydrolase activity	0.99	1.44258E-28
TC01_diatome_k37_Locus_7630_Transcript_1_1	hect domain and rld	P:carbohydrate metabolic process, F:hydrolase activity, hydrolyzing O-glycosyl compounds, F:ligase activity	0.99	0.0
TT00_diatome_k37_Locus_2709_Transcript_14_1	G- -coupled receptor family 3 5	F:G-protein coupled receptor activity, F:G-protein coupled GABA receptor activity, P:G-protein coupled receptor signaling pathway, P:signal transduction, P:nucleotide catabolic process, C:membrane, P:lipid metabolic process, C:integral component of membrane, F:signal transducer activity, F:hydrolase activity	0.98	1.36933E-151
TG01_diatome_k31_Locus_2220_Transcript_9_3	pas pac sensor hybrid histidine kinase	F:DNA binding, F:transcription factor activity, sequence-specific DNA binding, C:RNA polymerase II transcription factor complex, F:RNA polymerase II regulatory region sequence-specific DNA binding, P:regulation of transcription, DNA-templated, F:protein dimerization activity, P:phosphorylation, F:kinase activity, P:regulation of transcription from RNA polymerase II promoter	0.98	1.29741E-98
TC01_diatome_k25_Locus_3046_Transcript_1_2	lipoate ligase	P:primary metabolic process, P:cellular metabolic process, P:organic substance metabolic process	0.98	1.71728E-27
TT00_diatome_k37_Locus_2610_Transcript_3_1	predicted protein	P:phosphorelay signal transduction system, C:intracellular	0.98	5.99087E-48
OG50_diatome_k37_Locus_3728_Transcript_3_1	ATG2 Autophagy-related homolog	P:autophagy	0.97	0.0
TG01_diatome_k31_Locus_256_Transcript_3_2	serine threonine-phosphatase 4 regulatory	F:ATP binding, F:protein kinase activity, P:protein phosphorylation	0.96	0.0

	subunit 3A			
OG50_diatome_k31_Locus_6522_Transcript_3_2	Mitochondrial carnitine carrier	P:transmembrane transport, C:mitochondrion, C:membrane, C:fungal-type vacuole membrane, C:integral component of membrane, F:carnitine:acyl carnitine antiporter activity, P:transport, P:fatty acid metabolic process, P:macroautophagy, C:mitochondrial inner membrane	0.96	5.99901E-6
TG01_diatome_k37_Locus_2248_Transcript_1_2	gag-pol poly	F:nucleic acid binding, P:DNA integration	0.96	0.0
OG50_diatome_k25_Locus_5399_Transcript_2_1	AGC kinase	F:phosphoprotein phosphatase activity, P:cellular protein modification process, F:cation binding, P:phosphate-containing compound metabolic process	0.95	0.0
TC01_diatome_k37_Locus_4145_Transcript_10_3	DNA polymerase zeta catalytic subunit isoform X2	C:nucleus, F:organic cyclic compound binding, F:heterocyclic compound binding, P:error-prone translesion synthesis, C:zeta DNA polymerase complex, F:transferase activity	0.95	0.0
TT00_diatome_k25_Locus_1218_Transcript_3_1	ARM repeat-containing	C:nucleus, F:ubiquitin-protein transferase activity, C:cytoplasm, F:ligase activity, P:protein ubiquitination	0.94	9.25796E-155
TC01_diatome_k25_Locus_3170_Transcript_1_1	tetratricopeptide repeat 28-like isoform X1	F:DNA binding, C:nucleus, F:microtubule motor activity, F:transcription factor activity, sequence-specific DNA binding, P:signal transduction, P:regulation of transcription, DNA-templated, C:kinesin complex, F:sequence-specific DNA binding	0.94	3.98564E-120
TG01_diatome_k31_Locus_3772_Transcript_5_3	plant adhesion molecule 1	P:regulation of vesicle fusion, P:activation of GTPase activity, F:GTPase activator activity, C:endomembrane system, P:intracellular protein transport, F:Rab GTPase binding, C:intracellular	0.92	4.22194E-112
TT00_diatome_k49_Locus_2276_Transcript_1_1	E1A CREB-binding	C:nucleus, F:histone acetyltransferase activity, F:zinc ion binding, F:transcription cofactor activity, P:regulation of transcription, DNA-templated, P:histone acetylation	0.91	0.0
TT00_diatome_k31_Locus_5065_Transcript_1_2	aarF domain-containing kinase	F:ATP binding, F:protein kinase activity, P:protein phosphorylation	0.91	0.0
TT00_diatome_k31_Locus_4643_Transcript_4_1	cyclic nucleotide-binding domain	F:carboxypeptidase activity, C:membrane, P:proteolysis, C:integral component of membrane	0.90	8.47665E-141
TG01_diatome_CL99Contig1_1	secreted peptidase	F:ATP binding, F:dipeptidase activity, P:proteolysis, C:membrane, C:integral component of membrane	0.90	0.0
OG50_diatome_k31_Locus_2181_Transcript_3_1	cell surface receptor	F:hydrolase activity, acting on carbon-nitrogen (but not peptide) bonds, P:signal transduction, P:nitrogen compound metabolic process, F:phosphorus-oxygen lyase activity, C:membrane, C:integral component of membrane, P:intracellular signal transduction, P:cyclic nucleotide biosynthetic process, C:intracellular, F:3',5'-cyclic-nucleotide phosphodiesterase activity	0.89	5.69444E-170
TG01_diatome_k49_Locus_3512_Transcript_4_2	DUF946 domain-containing	F:hydrolase activity, hydrolyzing N-glycosyl compounds, C:membrane, P:proteolysis, C:integral component of membrane, F:serine-type peptidase activity, F:serine-type endopeptidase activity, F:peptidase activity, F:hydrolase activity	0.89	4.46098E-101
TT00_diatome_k31_Locus_2095_Transcript_15_1	hypothetical protein FisN_6Hh373	F:zinc ion binding, F:metallocarboxypeptidase activity, P:phosphorelay signal transduction system, P:proteolysis, C:intracellular	0.87	0.0

OG50_diatome_k31_Locus_1260_Transcript_2_1	kinase domain	C:nucleus, F:ATP binding, F:calmodulin binding, C:cytoplasm, F:calcium ion binding, P:protein autophosphorylation, F:calmodulin-dependent protein kinase activity, P:peptidyl-serine phosphorylation, P:intracellular signal transduction, F:calcium-dependent protein serine/threonine kinase activity	0.87	0.0
TT00_diatome_k25_Locus_4550_Transcript_2_1	winged helix DNA-binding domain-containing	F:DNA binding, C:nucleus, F:transcription factor activity, sequence-specific DNA binding, P:regulation of transcription, DNA-templated, F:sequence-specific DNA binding	0.86	1.64804E-20
OG50_diatome_k31_Locus_903_Transcript_9_2	LOV domain-containing	F:phosphorelay sensor kinase activity, P:phosphorelay signal transduction system, P:signal transduction by protein phosphorylation, C:intracellular	0.86	6.68813E-110
TT00_diatome_k31_Locus_5640_Transcript_1_1	oligopeptidase B	C:cytoplasm, P:proteolysis, F:serine-type peptidase activity, F:serine-type endopeptidase activity, F:peptidase activity, F:serine-type exopeptidase activity	0.86	3.81924E-58
TG01_diatome_k25_Locus_4222_Transcript_2_3	hect e3 ubiquitin	F:ubiquitin-protein transferase activity, C:nucleus, C:cytoplasm, F:metal ion binding, P:protein ubiquitination involved in ubiquitin-dependent protein catabolic process, F:ligase activity, P:protein ubiquitination	0.85	0.0
TG01_diatome_k49_Locus_11880_Transcript_1_1	phosphoserine phosphatase	F:magnesium ion binding, F:phosphoserine phosphatase activity, C:cytoplasm, P:L-serine biosynthetic process	0.85	8.05403E-95
TG01_diatome_k31_Locus_256_Transcript_3_1	dentin sialophospho	F:phosphoprotein phosphatase activity, P:protein dephosphorylation, F:hydrolase activity	0.81	2.19502E-23
TC01_diatome_k49_Locus_303_Transcript_24_1	notch receptor	F:chitinase activity, P:cell wall macromolecule catabolic process, P:chitin catabolic process, C:membrane, C:integral component of membrane	0.78	4.6757E-22
TC01_diatome_k25_Locus_2264_Transcript_2_1	serine threonine	F:phosphoprotein phosphatase activity, P:protein dephosphorylation	0.77	0.0
TT00_diatome_k37_Locus_2323_Transcript_7_1	DNA repair RAD50	F:ATPase activity, F:DNA binding, P:DNA repair, P:DNA recombination, C:nuclear chromosome, P:telomere maintenance, P:single-organism cellular process, C:chromosomal part	0.75	1.57733E-38
OG50_diatome_k25_Locus_3200_Transcript_5_1	phosphatase 2A regulatory B	P:signal transduction, C:protein phosphatase type 2A complex	0.74	0.0
TG01_diatome_k43_Locus_4033_Transcript_1_1	jumonji domain-containing 2	F:ubiquitin protein ligase binding, P:negative regulation of transcription, DNA-templated, C:cytoplasm, F:methylated histone binding, P:negative regulation of autophagy, C:nucleolus, F:histone demethylase activity (H3-K36 specific), P:histone demethylation	0.74	0.0
TT00_diatome_k31_Locus_3488_Transcript_6_1	ATP-dependent RNA helicase DDX46 PRP5	F:nucleic acid binding, F:ATP binding, P:regulation of gene expression, P:RNA secondary structure unwinding, F:ATP-dependent RNA helicase activity, P:mRNA splicing, via spliceosome	0.72	0.0
OG50_diatome_k25_Locus_7969_Transcript_2_1	endoplasmic reticulum lectin 1 isoform X2	C:endoplasmic reticulum lumen, P:negative regulation of retrograde protein transport, ER to cytosol, C:membrane, C:integral component of membrane, F:glycoprotein binding, P:retrograde protein transport, ER to cytosol, F:unfolded protein binding, P:ER-associated ubiquitin-dependent protein catabolic process	0.69	1.15097E-85
OG50_diatome_k25_Locus_4642_Transcript_2_1	SR related	P:positive regulation of vulval development, C:nucleus, P:chromatin remodeling, P:nematode larval development, P:locomotion, P:embryo development ending in birth or egg hatching, C:cytosol, C:Ino80 complex,	0.67	6.3367E-5

		P:mRNA processing, P:reproduction		
TC01_diatome_k37_Locus_22_Transcript_6_3	cathepsin X	C:extracellular space, F:cysteine-type endopeptidase activity, P:proteolysis involved in cellular protein catabolic process, C:lysosome	0.65	1.06079E-38
TT00_diatome_k25_Locus_2904_Transcript_2_1	methyltransferase family	F:fucosyltransferase activity, P:fucosylation, C:membrane, P:protein glycosylation, F:methyltransferase activity, F:transferase activity, P:methylation	0.62	1.44205E-31
TC01_diatome_k25_Locus_4558_Transcript_2_1	mitochondrial-processing peptidase subunit alpha	C:membrane, P:primary metabolic process, P:organic substance metabolic process	0.61	0.0
TT00_diatome_k25_Locus_4503_Transcript_6_2	cathepsin X	C:extracellular space, F:cysteine-type endopeptidase activity, P:proteolysis involved in cellular protein catabolic process, C:lysosome	0.60	5.31313E-139
TG01_diatome_k37_Locus_1272_Transcript_2_4	cathepsin X	C:extracellular space, F:cysteine-type endopeptidase activity, P:proteolysis involved in cellular protein catabolic process, C:lysosome	0.55	3.24219E-147
TC01_diatome_k25_Locus_1714_Transcript_1_2	ubiquitin carboxyl-terminal hydrolase	P:proteolysis, P:cellular protein metabolic process, F:hydrolase activity	-0.62	0.0
OG50_diatome_k37_Locus_2461_Transcript_30_1	wd-40 repeat	F:phosphorelay sensor kinase activity, F:ion channel activity, P:ion transport, P:transmembrane transport, P:phosphorelay signal transduction system, P:ion transmembrane transport, C:membrane, C:integral component of membrane, P:regulation of transcription, DNA-templated, P:signal transduction by protein phosphorylation, P:transport, C:intracellular	-0.66	2.13069E-93
TT00_diatome_CL2026Contig1_3	hypothetical protein FRACYDRAFT_259230	P:signal transduction, C:membrane, C:integral component of membrane, F:phosphoric diester hydrolase activity, F:3',5'-cyclic-nucleotide phosphodiesterase activity	-0.69	3.10352E-33
OG50_diatome_k25_Locus_3188_Transcript_9_3	platelet-activating factor acetylhydrolase cytoplasmic	F:1-alkyl-2-acetylglycerophosphocholine esterase activity, P:lipid catabolic process, F:hydrolase activity	-0.72	2.14918E-68
OG50_diatome_k43_Locus_5243_Transcript_7_4	26S protease regulatory subunit 8 homolog A	F:ATP binding, C:proteasome regulatory particle, base subcomplex, C:cytosolic proteasome complex, C:nuclear proteasome complex, F:peptidase activity, F:TBP-class protein binding, P:ER-associated ubiquitin-dependent protein catabolic process, P:positive regulation of proteasomal protein catabolic process, F:proteasome-activating ATPase activity, C:plasma membrane, P:positive regulation of RNA polymerase II transcriptional preinitiation complex assembly	-0.73	0.0
OG50_diatome_k25_Locus_3407_Transcript_3_1	ubiquitin carboxyl-terminal	F:metal ion binding, P:proteolysis, P:cellular protein metabolic process, F:thiol-dependent ubiquitinyl hydrolase activity	-0.74	0.0
OG50_diatome_k25_Locus_1341_Transcript_29_1	Crinkler (CRN) family	P:protein phosphorylation	-0.76	7.76207E-87
TT00_diatome_k49_Locus_534_Transcript_3_1	histone deacetylase 1 2	C:nucleus, P:transcription, DNA-templated, F:NAD-dependent histone deacetylase activity (H3-K14 specific), P:regulation of transcription, DNA-templated, P:histone H3 deacetylation	-0.77	0.0
OG50_diatome_k31_Locus_4893_Transcript_8_1	u6 snrna-associated sm lsm1	C:nucleus, F:RNA cap binding, P:deadenylation-dependent decapping of nuclear-transcribed mRNA, C:P-body	-0.78	1.30325E-37
TT00_diatome_k25_Locus_4461_Transcript_5_1	26S proteasome non-ATPase regulatory subunit	P:regulation of catalytic activity, P:regulation of protein catabolic process, C:proteasome regulatory particle, lid subcomplex, F:enzyme regulator	-0.78	0.0

	3	activity, P:ubiquitin-dependent protein catabolic process		
TC01_diatome_k49_Locus_2643_Transcript_6_2	alpha beta-hydrolase	P:lipid metabolic process, C:membrane, C:integral component of membrane, F:hydrolase activity	-0.80	7.84169E-161
TC01_diatome_k37_Locus_430_Transcript_1_1	116 kDa U5 small nuclear ribonucleo component	F:nucleotide binding, F:GTPase activity, C:intracellular, P:translation	-0.81	0.0
TG01_diatome_k43_Locus_9549_Transcript_1_1	Golgi apparatus membrane TVP15	P:DNA repair, P:DNA damage checkpoint, F:calcium ion binding, C:membrane, C:integral component of membrane, C:checkpoint clamp complex	-0.81	9.48092E-83
TT00_diatome_CL920Contig1_1	DNA-directed RNA polymerase II subunit J	F:DNA binding, F:RNA polymerase II activity, P:transcription from RNA polymerase II promoter, F:protein dimerization activity, C:DNA-directed RNA polymerase II, core complex	-0.82	5.11352E-67
TC01_diatome_k31_Locus_5268_Transcript_1_1	thioredoxin domain-containing 5	F:protein disulfide isomerase activity, C:endoplasmic reticulum, P:cell redox homeostasis, P:protein folding, P:response to endoplasmic reticulum stress	-0.82	2.7669E-93
OG50_diatome_k49_Locus_1970_Transcript_4_2	di-trans,poly-cis-decaprenylcistransferase	C:membrane, P:protein glycosylation, F:transferase activity, transferring alkyl or aryl (other than methyl) groups	-0.84	3.41521E-114
TG01_diatome_CL38Contig1_1	CAMK kinase	F:ATP binding, F:calmodulin-dependent protein kinase activity, P:protein phosphorylation, F:myosin light chain kinase activity	-0.85	0.0
TG01_diatome_k43_Locus_11303_Transcript_2_1	26s protease regulatory subunit 7	F:ATP binding, C:proteasome regulatory particle, base subcomplex, C:cytosolic proteasome complex, C:nuclear proteasome complex, F:peptidase activity, F:TBP-class protein binding, P:ER-associated ubiquitin-dependent protein catabolic process, P:positive regulation of proteasomal protein catabolic process, F:proteasome-activating ATPase activity, P:positive regulation of RNA polymerase II transcriptional preinitiation complex assembly	-0.86	0.0
TC01_diatome_k43_Locus_951_Transcript_7_3	hypothetical protein FRACYDRAFT_276048	F:ATP binding, F:protein kinase activity, P:protein phosphorylation, F:hydrolase activity	-0.87	1.77292E-27
TT00_diatome_k25_Locus_5998_Transcript_8_1	small nuclear ribonucleo F	C:U7 snRNP, C:U1 snRNP, C:small nucleolar ribonucleoprotein complex, C:U4 snRNP, P:spliceosomal snRNP assembly, C:U12-type spliceosomal complex, C:pICln-Sm protein complex, F:RNA binding, C:catalytic step 2 spliceosome, C:methylosome, C:SMN-Sm protein complex, C:cytosol, C:viral nucleocapsid, P:positive regulation of macromitophagy in response to mitochondrial depolarization	-0.87	1.20966E-38
TT00_diatome_k49_Locus_6109_Transcript_8_2	tryptophan synthase	F:tryptophan synthase activity, F:pyridoxal phosphate binding, P:tryptophan biosynthetic process, C:cytoplasm	-0.87	0.0
TC01_diatome_k31_Locus_436_Transcript_1_6	DNA-directed RNA polymerases and III subunit RPABC4	F:DNA binding, F:DNA-directed 5'-3' RNA polymerase activity, P:transcription, DNA-templated	-0.88	3.73742E-14
OG50_diatome_CL2298Contig1_1	26S protease regulatory subunit 6B	F:ATP binding, C:proteasome regulatory particle, base subcomplex, C:cytosolic proteasome complex, C:nuclear proteasome complex, F:peptidase activity, F:TBP-class protein binding, P:ER-associated ubiquitin-dependent protein catabolic process, P:positive regulation of proteasomal protein catabolic process, F:proteasome-activating ATPase	-0.90	0.0

		activity, P:positive regulation of RNA polymerase II transcriptional preinitiation complex assembly		
OG50_diatome_CL1816Contig1_1	ubiquitin carboxyl-terminal hydrolase isozyme L5-like	P:proteolysis, P:cellular protein metabolic process, C:intracellular, F:thiol-dependent ubiquitinyl hydrolase activity	-0.90	1.7538E-127
TG01_diatome_k25_Locus_7520_Transcript_1_1	Iron-sulfur cluster assembly enzyme mitochondrial	P:cellular iron ion homeostasis, F:iron-sulfur transferase activity, P:[2Fe-2S] cluster assembly, C:mitochondrial matrix, F:ferrous iron binding, F:4 iron, 4 sulfur cluster binding, P:protein maturation by iron-sulfur cluster transfer, F:2 iron, 2 sulfur cluster binding	-0.91	3.17178E-55
TG01_diatome_k31_Locus_5199_Transcript_2_1	ubiquitin-conjugating enzyme subfamily	C:nucleus, F:ubiquitin protein ligase activity, F:ubiquitin protein ligase binding, C:cytoplasm, P:protein polyubiquitination, P:cellular response to DNA damage stimulus	-0.92	1.3105E-118
TC01_diatome_k49_Locus_5100_Transcript_4_1	methionine aminopeptidase	P:protein initiator methionine removal, F:metal ion binding, P:proteolysis, F:metalloaminopeptidase activity	-0.93	0.0
TT00_diatome_k49_Locus_4824_Transcript_7_1	ubiquinone biosynthesis COQ4	P:ubiquinone biosynthetic process, C:mitochondrial inner membrane	-0.93	2.68966E-103
TC01_diatome_k25_Locus_1274_Transcript_1_1	type 2 adenylate	F:adenylate kinase activity, F:ATP binding, P:nucleotide phosphorylation	-0.93	1.77529E-150
TG01_diatome_CL2345Contig1_1	tRNA (cytidine(32) guanosine(34)-2 -O)-methyltransferase	C:cytoplasm, F:tRNA methyltransferase activity, P:cytoplasmic translation, P:tRNA methylation	-0.94	1.10992E-145
TC01_diatome_CL1802Contig1_1	casein kinase II subunit beta	C:protein kinase CK2 complex, P:regulation of protein kinase activity, F:protein kinase regulator activity	-0.95	1.16435E-145
TC01_diatome_k43_Locus_8540_Transcript_2_1	dpy-30 like	C:Set1C/COMPASS complex, F:histone methyltransferase activity (H3-K4 specific), C:chromosome, telomeric region, C:integral component of membrane, P:chromatin silencing at telomere, P:histone H3-K4 methylation	-0.95	3.36718E-22
TC01_diatome_k31_Locus_2043_Transcript_1_1	B-cell receptor-associated 31	C:multi-eIF complex, P:mitotic G1 DNA damage checkpoint, C:endoplasmic reticulum, C:ribosome, C:eukaryotic 48S preinitiation complex, P:intracellular protein transport, P:translational initiation, F:nucleic acid binding, F:translation initiation factor activity, C:nucleus, P:formation of translation preinitiation complex, F:RNA binding, C:cytoplasm, P:regulation of cytoplasmic translational initiation in response to stress, C:membrane, C:integral component of membrane, C:cytosol	-0.96	8.31803E-39
OG50_diatome_k49_Locus_4366_Transcript_2_1	DNA-directed RNA polymerase II subunit J	F:DNA binding, F:RNA polymerase II activity, P:transcription from RNA polymerase II promoter, F:protein dimerization activity, C:DNA-directed RNA polymerase II, core complex	-0.97	1.22141E-60
TC01_diatome_CL258Contig1_2	WD40 repeat	P:nucleophagy, P:protein localization to pre-autophagosomal structure, C:pre-autophagosomal structure membrane, P:protein lipidation, C:cytosol, F:phosphatidylinositol-3,5-bisphosphate binding, F:phosphatidylinositol-3-phosphate binding, C:extrinsic component of membrane, P:mitophagy	-0.97	0.0
TT00_diatome_k25_Locus_5912_Transcript_1_1	26S protease regulatory	F:ATP binding, C:proteasome regulatory particle, base subcomplex,	-0.97	0.0

	subunit 4	C:cytosolic proteasome complex, C:nuclear proteasome complex, F:peptidase activity, F:TBP-class protein binding, P:ER-associated ubiquitin-dependent protein catabolic process, P:positive regulation of proteasomal protein catabolic process, F:proteasome-activating ATPase activity, P:positive regulation of RNA polymerase II transcriptional preinitiation complex assembly		
OG50_diatome_k31_Locus_6421_Transcript_2_2	guanylate kinase	P:GDP metabolic process, P:GMP metabolic process, F:guanylate kinase activity	-0.97	4.95123E-114
TG01_diatome_k43_Locus_10356_Transcript_6_1	ubiquitin carboxyl-terminal hydrolase isozyme l3	P:proteolysis, P:cellular protein metabolic process, C:intracellular, F:thiol-dependent ubiquitinyl hydrolase activity	-0.98	7.58932E-85
TC01_diatome_k25_Locus_2524_Transcript_2_1	26S proteasome non-ATPase regulatory	C:nucleus, P:proteasome-mediated ubiquitin-dependent protein catabolic process, C:cytosol, C:proteasome regulatory particle, lid subcomplex, P:proteasome assembly	-1.01	1.34254E-95
TG01_diatome_k43_Locus_8751_Transcript_1_1	40S ribosomal S17	F:structural constituent of ribosome, C:cytosolic small ribosomal subunit, P:ribosomal small subunit assembly, P:translation	-1.01	2.12704E-72
TT00_diatome_CL913Contig1_1	acyl carrier	P:fatty acid biosynthetic process	-1.01	4.10943E-51
TC01_diatome_k37_Locus_443_Transcript_17_3	RNA-dependent RNA polymerase	F:DNA binding, F:zinc ion binding, F:metal ion binding, F:RNA-directed 5'-3' RNA polymerase activity, P:transcription, RNA-templated, C:membrane, C:integral component of membrane, C:endoplasmic reticulum	-1.01	8.76032E-65
TG01_diatome_k25_Locus_6660_Transcript_2_1	Proteasome subunit beta type-6	C:nucleus, C:cytoplasm, C:proteasome core complex, F:threonine-type endopeptidase activity, P:proteolysis involved in cellular protein catabolic process	-1.02	4.50996E-107
OG50_diatome_k25_Locus_1868_Transcript_3_1	26S proteasome non-ATPase regulatory subunit 7	P:proteasome-mediated ubiquitin-dependent protein catabolic process, C:proteasome complex	-1.04	7.71261E-128
TT00_diatome_k25_Locus_3624_Transcript_3_2	Rhodopsin-like GPCR transmembrane domain	P:G-protein coupled receptor signaling pathway, C:membrane, C:integral component of membrane, P:response to pheromone	-1.05	0.0
TG01_diatome_k31_Locus_5931_Transcript_4_1	SWI SNF-related matrix-associated actin-dependent regulator of chromatin subfamily A member 5	F:ATPase activity, F:DNA binding, F:ATP binding, F:nucleosome binding, P:ATP-dependent chromatin remodeling, C:NURF complex	-1.05	0.0
OG50_diatome_k31_Locus_2111_Transcript_4_2	Transcription factor IIS	F:DNA binding, C:nucleus, P:transcription, DNA-templated	-1.06	0.0
OG50_diatome_CL2290Contig1_1	pyrroline-5-carboxylate reductase	F:pyrroline-5-carboxylate reductase activity, P:oxidation-reduction process, P:L-proline biosynthetic process	-1.06	7.35451E-143
OG50_diatome_k49_Locus_6450_Transcript_1_1	Nhp6ap	P:chromatin remodeling, P:RNA polymerase II transcriptional preinitiation complex assembly, P:maintenance of transcriptional fidelity during DNA-templated transcription elongation from RNA polymerase III promoter, F:nucleosome binding, C:MutSalpha complex, F:DNA binding, bending, F:sequence-specific DNA binding, P:mismatch repair, P:DNA replication-independent nucleosome organization, P:RNA polymerase III transcriptional preinitiation complex assembly	-1.06	8.15042E-8

TC01_diatome_k43_Locus_2184_Transcript_7_1	adenylate kinase	F:adenylate kinase activity, F:ATP binding, P:nucleotide phosphorylation, C:chloroplast	-1.06	3.86993E-107
OG50_diatome_k31_Locus_6109_Transcript_2_2	signal peptidase complex subunit 1	C:integral component of endoplasmic reticulum membrane, P:signal peptide processing, P:protein targeting to ER, F:peptidase activity, C:signal peptidase complex	-1.06	5.60148E-56
TT00_diatome_k25_Locus_1235_Transcript_6_1	Rab18 family GTPase	F:GTP binding, C:intracellular ribonucleoprotein complex, P:small GTPase mediated signal transduction, C:viral nucleocapsid	-1.07	4.05993E-130
OG50_diatome_k25_Locus_8756_Transcript_1_1	40s ribosomal S27	F:structural constituent of ribosome, C:cytosolic small ribosomal subunit, F:metal ion binding, P:ribosomal small subunit assembly, P:translation	-1.08	4.70457E-45
TC01_diatome_k25_Locus_6153_Transcript_2_1	lysosomal alpha-mannosidase	F:hydrolase activity, hydrolyzing O-glycosyl compounds, F:binding, P:primary metabolic process, P:organic substance metabolic process	-1.09	0.0
OG50_diatome_k25_Locus_1825_Transcript_3_1	phosphatidic acid phosphatase	F:phosphatidate phosphatase activity, P:phospholipid dephosphorylation, C:integral component of plasma membrane, P:signal transduction, C:membrane, C:integral component of membrane, P:phospholipid metabolic process	-1.09	1.64828E-55
TT00_diatome_k31_Locus_8787_Transcript_1_1	predicted protein	P:vacuolar protein processing, C:membrane, C:integral component of membrane, C:vacuole	-1.11	3.17563E-23
OG50_diatome_k37_Locus_351_Transcript_5_2	26S protease regulatory subunit 6A	F:ATP binding, C:proteasome regulatory particle, base subcomplex, C:cytosolic proteasome complex, C:nuclear proteasome complex, F:peptidase activity, F:TBP-class protein binding, P:ER-associated ubiquitin-dependent protein catabolic process, P:positive regulation of proteasomal protein catabolic process, F:proteasome-activating ATPase activity, P:positive regulation of RNA polymerase II transcriptional preinitiation complex assembly	-1.13	0.0
TC01_diatome_k25_Locus_7900_Transcript_2_1	CAMK kinase	C:nucleus, F:ATP binding, F:calmodulin binding, C:cytoplasm, P:protein autophosphorylation, F:calmodulin-dependent protein kinase activity, P:peptidyl-serine phosphorylation, P:intracellular signal transduction, F:calcium-dependent protein serine/threonine kinase activity	-1.13	0.0
TC01_diatome_k49_Locus_1907_Transcript_3_2	carbohydrate kinase	F:transferase activity, P:primary metabolic process, P:cellular metabolic process, P:organic substance metabolic process	-1.13	1.06331E-149
TC01_diatome_k43_Locus_1631_Transcript_3_1	ribosomal L1	F:RNA binding, P:cellular macromolecule metabolic process, P:gene expression, C:large ribosomal subunit, P:cellular nitrogen compound metabolic process, P:primary metabolic process	-1.13	2.35103E-116
TT00_diatome_k25_Locus_5838_Transcript_2_1	26s proteasome non-atpase regulatory subunit 12	P:proteasome-mediated ubiquitin-dependent protein catabolic process, C:cytoplasm, C:proteasome regulatory particle, lid subcomplex, C:nuclear proteasome complex	-1.15	0.0
TT00_diatome_k25_Locus_8193_Transcript_1_2	leucyl aminopeptidase	C:cytoplasm, P:proteolysis, F:metalloexopeptidase activity, F:aminopeptidase activity, F:manganese ion binding	-1.15	0.0
TT00_diatome_k49_Locus_14_Transcript_3_1	ATP synthase subunit mitochondrial	C:proton-transporting ATP synthase complex, catalytic core F(1), F:ATP binding, P:ATP hydrolysis coupled proton transport, P:ATP synthesis coupled proton transport, F:proton-transporting ATP synthase activity, rotational mechanism	-1.15	0.0
TG01_diatome_k25_Locus_6425_Transcript_2_1	20S proteasome subunit	C:nucleus, C:cytoplasm, C:membrane, C:proteasome core complex, alpha-	-1.17	8.9472E-154

	alpha 7	subunit complex, F:threonine-type endopeptidase activity, P:ubiquitin-dependent protein catabolic process		
TT00_diatome_k31_Locus_6977_Transcript_5_1	splicing factor 3B subunit 5	C:U12-type spliceosomal complex, C:precatalytic spliceosome, C:U2 snRNP, P:mRNA splicing, via spliceosome	-1.18	2.26535E-43
TC01_diatome_k25_Locus_7607_Transcript_3_2	nicotinate-nucleotide diphosphorylase (carboxylating)	F:nicotinate-nucleotide diphosphorylase (carboxylating) activity, C:cytoplasm, P:NAD biosynthetic process, P:quinolinate catabolic process	-1.18	4.53346E-163
TG01_diatome_k49_Locus_7180_Transcript_1_1	DUF84 domain-containing	F:nucleotide binding, F:metal ion binding, F:nucleoside-triphosphatase activity, P:nucleotide metabolic process, F:hydrolase activity	-1.18	6.1024E-83
TG01_diatome_CL2511Contig1_2	ATP synthase gamma subunit	C:proton-transporting ATP synthase complex, catalytic core F(1), F:proton-transporting ATPase activity, rotational mechanism, P:ATP synthesis coupled proton transport, F:proton-transporting ATP synthase activity, rotational mechanism	-1.18	6.74695E-157
OG50_diatome_CL1862Contig1_1	peptidyl-prolyl cis-trans isomerase FKBP12	C:endoplasmic reticulum membrane, F:peptidyl-prolyl cis-trans isomerase activity, F:FK506 binding, P:chaperone-mediated protein folding, C:cytosol, P:protein peptidyl-prolyl isomerization	-1.20	9.70423E-61
TG01_diatome_k37_Locus_3439_Transcript_2_2	iron-sulfur cluster scaffold	F:organic cyclic compound binding, F:heterocyclic compound binding, F:iron ion binding, F:iron-sulfur cluster binding, F:ligase activity, P:translation, P:iron-sulfur cluster assembly	-1.20	1.8556E-93
TC01_diatome_k43_Locus_9747_Transcript_2_1	S-phase kinase-associated 1	P:phosphorylation, F:kinase activity, F:ligase activity, P:ubiquitin-dependent protein catabolic process	-1.20	2.31869E-93
OG50_diatome_k25_Locus_8858_Transcript_1_1	zeta-carotene desaturase	P:carotenoid biosynthetic process, F:oxidoreductase activity, acting on the CH-CH group of donors, quinone or related compound as acceptor, F:carotene 7,8-desaturase activity, P:oxidation-reduction process	-1.20	0.0
TT00_diatome_k37_Locus_9365_Transcript_1_1	ubiquitin-conjugating enzyme subfamily	C:nucleus, F:ubiquitin protein ligase activity, F:ubiquitin protein ligase binding, C:cytoplasm, P:protein polyubiquitination, P:cellular response to DNA damage stimulus	-1.21	2.6411E-130
TG01_diatome_k25_Locus_4412_Transcript_3_1	proteasome subunit beta type-3-like	C:extracellular exosome, C:proteasome core complex, C:mitochondrion, C:actin cytoskeleton, C:Golgi apparatus, F:threonine-type endopeptidase activity, P:proteolysis involved in cellular protein catabolic process, C:nucleoplasm	-1.21	1.49281E-122
TG01_diatome_k43_Locus_10356_Transcript_6_2	pyrroline-5-carboxylate reductase	F:pyrroline-5-carboxylate reductase activity, F:oxidoreductase activity, P:proline biosynthetic process, P:oxidation-reduction process	-1.21	3.84248E-80
OG50_diatome_k25_Locus_6595_Transcript_7_2	lipid phosphate phosphatase epsilon chloroplastic-like	F:phosphatidate phosphatase activity, C:chloroplast, C:membrane, C:integral component of membrane, P:diacylglycerol biosynthetic process, P:dephosphorylation	-1.22	2.65862E-14
TG01_diatome_CL438Contig1_1	LYR motif-containing 4	C:nucleus, C:mitochondrion, P:nucleotide-excision repair	-1.22	3.59492E-32
TG01_diatome_CL533Contig1_2	plastid glutamyl tRNA	F:ATP binding, C:mitochondrion, F:glutamate-tRNA ligase activity, P:tRNA aminoacylation for mitochondrial protein translation, F:tRNA binding, P:glutamyl-tRNA aminoacylation	-1.22	0.0
OG50_diatome_k31_Locus_218_Transcript_9_1	DUF537-domain-containing	C:peroxisome, P:regulation of gene expression	-1.24	3.13019E-70
TT00_diatome_k25_Locus_6695_Transcript_1_1	DNA topoisomerase I	F:DNA binding, P:chromatin remodeling, P:DNA replication,	-1.26	0.0

		P:chromosome segregation, F:DNA topoisomerase type I activity, C:replication fork protection complex, F:DNA topoisomerase type II (ATP-hydrolyzing) activity, P:DNA topological change, C:nucleolus		
TG01_diatome_k49_Locus_3675_Transcript_4_1	geranylgeranyl reductase	F:FAD binding, P:chlorophyll biosynthetic process, F:oxidoreductase activity, acting on the CH-CH group of donors, NAD or NADP as acceptor, F:geranylgeranyl reductase activity, C:integral component of membrane, P:photosynthesis, P:oxidation-reduction process	-1.27	0.0
TG01_diatome_k25_Locus_593_Transcript_4_1	isopentenyl-diphosphate delta-isomerase	P:lipid biosynthetic process, F:transferase activity, F:isomerase activity	-1.27	3.8513E-114
TT00_diatome_k25_Locus_4960_Transcript_3_2	60S ribosomal L27a	F:structural constituent of ribosome, C:cytosolic large ribosomal subunit, P:translation	-1.27	2.13892E-89
OG50_diatome_CL1481Contig1_1	UV radiation resistance-associated	P:positive regulation of autophagy, C:endosome, P:SNARE complex assembly, C:cytosol, P:regulation of vesicle-mediated transport, F:SNARE binding, C:lytic vacuole	-1.29	5.09508E-91
OG50_diatome_k31_Locus_2713_Transcript_2_1	beta-glucan synthase	P:primary metabolic process, P:organic substance metabolic process, F:hydrolase activity	-1.29	0.0
TT00_diatome_CL396Contig1_2	hypothetical protein FisN_2Lh248	F:DNA binding, C:nucleus, P:regulation of transcription, DNA-templated, F:sequence-specific DNA binding	-1.29	3.60111E-6
TC01_diatome_k25_Locus_4300_Transcript_11_1	DNA repair RAD50	F:ATPase activity, F:DNA binding, P:DNA repair, P:DNA recombination, C:nuclear chromosome, P:telomere maintenance, P:single-organism cellular process, C:chromosomal part	-1.29	1.54339E-38
TT00_diatome_k25_Locus_2231_Transcript_2_1	copine-3-like isoform X7	F:calcium-dependent protein binding, F:protein serine/threonine kinase activity, P:protein phosphorylation, C:plasma membrane, F:calcium-dependent phospholipid binding, F:RNA binding, C:nucleus, C:extracellular exosome, C:focal adhesion, P:cellular response to calcium ion, C:cytoplasm, P:cellular response to growth factor stimulus, C:cytosol, C:cell junction, F:receptor tyrosine kinase binding, P:ERBB2 signaling pathway, P:positive regulation of cell migration	-1.31	1.55011E-73
TT00_diatome_k37_Locus_7032_Transcript_1_1	ribosomal L17	F:structural constituent of ribosome, C:large ribosomal subunit, P:translation	-1.31	7.39976E-69
TG01_diatome_k25_Locus_5693_Transcript_10_2	LOV domain-containing	F:transcription factor activity, sequence-specific DNA binding, P:signal transduction, P:regulation of transcription, DNA-templated, F:sequence-specific DNA binding	-1.31	7.35915E-140
TG01_diatome_k25_Locus_1131_Transcript_2_2	phenylalanine-tRNA alpha subunit	F:ATP binding, F:phenylalanine-tRNA ligase activity, P:phenylalanyl-tRNA aminoacylation, F:tRNA binding, C:phenylalanine-tRNA ligase complex	-1.32	0.0
TT00_diatome_k25_Locus_8432_Transcript_3_2	Kelch motif family	P:regulation of Rho protein signal transduction, F:Rho guanyl-nucleotide exchange factor activity, P:positive regulation of GTPase activity	-1.33	1.2815E-19
OG50_diatome_k49_Locus_8898_Transcript_5_3	pyrroline-5-carboxylate reductase	P:cellular amino acid biosynthetic process	-1.35	2.47125E-63
TC01_diatome_k25_Locus_746_Transcript_7_3	DNA topoisomerase 2-binding 1 isoform X2	P:biological regulation, P:DNA-dependent DNA replication, C:intracellular non-membrane-bounded organelle	-1.36	3.90054E-104
TT00_diatome_k31_Locus_1895_Transcript_4_2	ubiquitin-activating	C:nucleus, F:ubiquitin-protein transferase activity, F:ATP binding,	-1.36	0.0

	enzyme E1	C:cytosol, F:ubiquitin activating enzyme activity, P:modification-dependent protein catabolic process, P:protein ubiquitination		
TT00_diatome_k37_Locus_1443_Transcript_6_4	ABC1 family-domain-containing	F:ATP binding, F:protein kinase activity, P:protein phosphorylation	-1.38	0.0
TC01_diatome_k37_Locus_6362_Transcript_1_1	60S ribosomal	F:structural constituent of ribosome, C:cytosolic large ribosomal subunit, P:ribosomal large subunit assembly, P:assembly of large subunit precursor of preribosome, P:translation	-1.39	5.31602E-80
OG50_diatome_CL12Contig2_6	c-myc binding	F:transcription coactivator activity, P:regulation of transcription, DNA-templated	-1.39	2.94906E-35
TG01_diatome_k49_Locus_12813_Transcript_1_1	DNA-dependent metalloprotease WSS1	C:nuclear envelope, F:zinc ion binding, F:metal ion binding, P:protein sumoylation, P:proteolysis, P:response to UV-C, P:cellular response to DNA damage stimulus, F:metalloendopeptidase activity, P:translesion synthesis, P:response to UV-B	-1.39	8.45354E-46
TT00_diatome_k37_Locus_8175_Transcript_6_3	LOV domain-containing	P:signal transduction	-1.40	8.6541E-153
TC01_diatome_CL620Contig1_1	proteasome subunit alpha type-6	P:Fc-epsilon receptor signaling pathway, C:P-body, P:regulation of mRNA stability, P:positive regulation of NF-kappaB transcription factor activity, P:regulation of cellular amino acid metabolic process, C:nucleoplasm, P:stimulatory C-type lectin receptor signaling pathway, C:polysome, P:MAPK cascade, P:antigen processing and presentation of exogenous peptide antigen via MHC class I, TAP-dependent, C:extracellular exosome, F:RNA binding, F:purine ribonucleoside triphosphate binding, C:cytosol, P:Wnt signaling pathway, planar cell polarity pathway, P:T cell receptor signaling pathway, P:protein polyubiquitination, P:positive regulation of canonical Wnt signaling pathway, P:NIK/NF-kappaB signaling, F:threonine-type endopeptidase activity, F:NF-kappaB binding, P:negative regulation of canonical Wnt signaling pathway, P:tumor necrosis factor-mediated signaling pathway, P:skeletal muscle tissue development, C:proteasome core complex, alpha-subunit complex, P:anaphase-promoting complex-dependent catabolic process, C:nuclear matrix, P:regulation of inflammatory response, P:positive regulation of ubiquitin-protein ligase activity involved in regulation of mitotic cell cycle transition, C:sarcomere, P:negative regulation of ubiquitin-protein ligase activity involved in mitotic cell cycle	-1.40	2.01E-155
TT00_diatome_k31_Locus_2272_Transcript_2_3	ribulose-1,5-bisphosphate carboxylase oxygenase small subunit N-methyltransferase I	C:integral component of membrane, P:peptidyl-lysine monomethylation, F:protein-lysine N-methyltransferase activity	-1.40	0.0
TG01_diatome_k25_Locus_3443_Transcript_1_1	plastid glutamate 1-semialdehyde 2,1-	F:pyridoxal phosphate binding, F:identical protein binding, P:porphyrin-containing compound biosynthetic process, F:transaminase activity, C:integral component of membrane, F:glutamate-1-semialdehyde 2,1-aminomutase activity	-1.40	0.0
TT00_diatome_k25_Locus_4223_Transcript_1_1	proteasome subunit beta	C:proteasome core complex, F:threonine-type endopeptidase activity, P:proteolysis involved in cellular protein catabolic process	-1.41	1.49818E-135

TT00_diatome_k25_Locus_6553_Transcript_4_1	triose phosphate phosphate translocator	F:nucleotide-sugar transmembrane transporter activity, C:integral component of membrane, P:protein glycosylation, P:GDP-mannose transmembrane transport	-1.41	0.0
TT00_diatome_k25_Locus_3209_Transcript_1_2	arginine N-methyltransferase	F:protein-arginine omega-N asymmetric methyltransferase activity, P:mRNA export from nucleus, P:positive regulation of transcription elongation from RNA polymerase II promoter, C:nucleus, F:identical protein binding, P:histone arginine methylation, P:peptidyl-arginine methylation, to asymmetrical-dimethyl arginine, F:protein-arginine omega-N monomethyltransferase activity, C:cytosol, F:histone-arginine N-methyltransferase activity, P:negative regulation of DNA-templated transcription, termination	-1.42	0.0
TG01_diatome_k43_Locus_57_Transcript_3_2	proteasome subunit alpha type-2	C:nucleus, C:cytoplasm, C:proteasome core complex, alpha-subunit complex, F:threonine-type endopeptidase activity, P:ubiquitin-dependent protein catabolic process	-1.42	2.71347E-154
OG50_diatome_k43_Locus_10867_Transcript_2_1	26S proteasome regulatory subunit N7	P:proteasome-mediated ubiquitin-dependent protein catabolic process	-1.42	0.0
OG50_diatome_k25_Locus_5770_Transcript_1_2	plastid protoporphyrinogen	P:porphyrin-containing compound biosynthetic process, F:oxygen-dependent protoporphyrinogen oxidase activity, P:oxidation-reduction process	-1.43	0.0
TT00_diatome_k37_Locus_2574_Transcript_3_2	chloroplastic-like isoform X1	C:chloroplast, P:peptide metabolic process, P:proteolysis, C:chloroplast thylakoid, C:chloroplast envelope, F:metalloendopeptidase activity	-1.43	1.09417E-86
TC01_diatome_k37_Locus_1447_Transcript_1_3	probable leucine-rich repeat receptor kinase At1g35710	F:nucleotide binding, F:ATP binding, F:calcium ion binding, C:membrane, C:integral component of membrane, F:protein kinase activity, P:phosphorylation, P:protein phosphorylation, F:kinase activity	-1.44	4.7749E-100
TC01_diatome_CL1975Contig1_1	NADH dehydrogenase [ubiquinone] complex assembly factor 7	F:protein-arginine omega-N symmetric methyltransferase activity, C:extracellular space, C:mitochondrion, P:peptidyl-arginine methylation, to symmetrical-dimethyl arginine, P:ATP metabolic process, P:mitochondrial respiratory chain complex I assembly, F:enzyme binding	-1.44	1.85193E-167
TT00_diatome_k31_Locus_6998_Transcript_1_1	FKBP-type peptidyl-prolyl cis-trans isomerase	F:peptidyl-prolyl cis-trans isomerase activity, C:cytoplasm, F:FK506 binding, P:chaperone-mediated protein folding, P:protein peptidyl-prolyl isomerization	-1.45	5.38641E-87
OG50_diatome_k25_Locus_3721_Transcript_1_2	SUMO-activating enzyme subunit 1	C:nucleus, F:SUMO activating enzyme activity, P:protein sumoylation, P:cellular protein modification process, C:cytosol, F:small protein activating enzyme activity, P:regulation of mitotic cell cycle	-1.45	3.81409E-115
TG01_diatome_k31_Locus_8630_Transcript_3_1	proteasome subunit alpha	C:nucleus, C:cytoplasm, C:proteasome core complex, alpha-subunit complex, F:threonine-type endopeptidase activity, P:ubiquitin-dependent protein catabolic process	-1.45	6.53342E-153
TC01_diatome_k25_Locus_8135_Transcript_1_1	isoform b	P:signal transduction, C:membrane, F:transferase activity, transferring phosphorus-containing groups, P:phosphorylation	-1.45	0.0
TT00_diatome_k43_Locus_430_Transcript_4_2	RNA polymerase sigma factor	F:DNA binding, F:sigma factor activity, F:transcription factor activity, sequence-specific DNA binding, P:regulation of transcription, DNA-templated, P:DNA-templated transcription, initiation	-1.46	0.0
OG50_diatome_k25_Locus_438_Transcript_2_2	Heme-dependent	F:peroxidase activity, P:response to oxidative stress, P:cellular oxidant	-1.47	1.53868E-97

	peroxidase	detoxification, P:oxidation-reduction process, F:heme binding		
TC01_diatome_k49_Locus_5002_Transcript_4_1	SET domain-containing	P:protein targeting to Golgi, P:peptidyl-lysine monomethylation, F:protein-lysine N-methyltransferase activity, C:intracellular	-1.47	4.81313E-107
TC01_diatome_k25_Locus_5009_Transcript_1_1	60S acidic ribosomal P2	F:structural constituent of ribosome, P:cytoplasmic translation, C:cytosolic large ribosomal subunit, F:large ribosomal subunit rRNA binding, P:translational elongation, C:preribosome, large subunit precursor	-1.47	3.02772E-18
TG01_diatome_k49_Locus_12627_Transcript_3_1	glutamic acid-rich	F:ATP binding, C:cell, F:protein disulfide oxidoreductase activity, F:electron carrier activity, P:cell redox homeostasis, P:oxidation-reduction process, P:circadian rhythm	-1.47	4.07235E-5
OG50_diatome_CL1232Contig1_1	SUMO-conjugating enzyme ubc9	F:ATP binding, P:mitotic spindle elongation, F:ubiquitin protein ligase activity, F:ubiquitin protein ligase binding, P:protein sumoylation, C:cytosol, F:ligase activity, C:condensed nuclear chromosome, C:nuclear heterochromatin, F:SUMO transferase activity	-1.47	7.94679E-66
TT00_diatome_k37_Locus_2204_Transcript_2_2	beta-catenin 1	C:nucleus, P:RNA splicing, F:protein binding, P:positive regulation of apoptotic process, P:apoptotic process, C:membrane, C:spliceosomal complex, P:mRNA processing, C:Prp19 complex, P:somatic diversification of immunoglobulins, F:enzyme binding, C:nucleoplasm	-1.48	2.81054E-156
TC01_diatome_CL1395Contig1_1	Grx4 family monothiol glutaredoxin	C:cell, F:protein disulfide oxidoreductase activity, F:electron carrier activity, P:cell redox homeostasis, P:oxidation-reduction process, F:arsenate reductase (glutaredoxin) activity	-1.48	2.53142E-64
OG50_diatome_CL746Contig1_1	5 -methylthioadenosine nucleosidase	F:hydrolase activity, hydrolyzing N-glycosyl compounds, P:nucleoside metabolic process	-1.48	3.76244E-99
TC01_diatome_k25_Locus_4253_Transcript_1_1	class II fructose-bisphosphate aldolase	P:gluconeogenesis, F:zinc ion binding, C:cell wall, P:glycolytic process, C:cytosol, F:fructose-bisphosphate aldolase activity, C:plasma membrane	-1.48	0.0
TC01_diatome_k31_Locus_135_Transcript_6_1	serine threonine kinase	F:nucleotide binding, F:ATP binding, F:protein kinase activity, P:phosphorylation, F:protein serine/threonine kinase activity, P:protein phosphorylation, F:kinase activity	-1.49	1.11849E-8
TC01_diatome_k31_Locus_2814_Transcript_6_2	magnesium-dependent phosphatase-1	F:nucleic acid binding, F:DNA binding, C:membrane, F:phosphatase activity, C:integral component of membrane, P:regulation of transcription, DNA-templated, P:dephosphorylation	-1.49	2.5367E-79
TC01_diatome_k25_Locus_5100_Transcript_3_2	Histone-lysine N-methyltransferase ASHR1	F:peptidyl-prolyl cis-trans isomerase activity, C:membrane, C:integral component of membrane, P:protein peptidyl-prolyl isomerization, P:protein folding, F:isomerase activity	-1.52	1.68135E-86
TT00_diatome_k31_Locus_3660_Transcript_3_1	ubiquinol-cytochrome-c reductase	F:ubiquinol-cytochrome-c reductase activity, P:mitochondrial respiratory chain complex III assembly, C:mitochondrial respiratory chain complex III, P:mitochondrial electron transport, ubiquinol to cytochrome c, P:aerobic respiration	-1.52	2.53725E-50
TC01_diatome_k43_Locus_78_Transcript_3_3	GDP-L-fucose synthetase	F:coenzyme binding, F:oxidoreductase activity, C:integral component of membrane, P:nucleotide-sugar biosynthetic process, P:oxidation-reduction process	-1.52	0.0
TC01_diatome_k37_Locus_1705_Transcript_2_2	50S ribosomal L1	F:RNA binding, F:structural constituent of ribosome, P:maturation of LSU-rRNA, C:mitochondrion, C:cytosolic large ribosomal subunit, P:translation	-1.53	7.39004E-19

TT00_diatome_k25_Locus_5491_Transcript_2_1	proline-rich receptor kinase PERK6	F:nucleotide binding, F:nucleic acid binding, F:pyroglutamyl-peptidase activity, P:proteolysis, C:cytosol	-1.54	1.2174E-102
TT00_diatome_k31_Locus_2512_Transcript_11_1	hypothetical protein THAOC_31386	C:membrane, C:integral component of membrane, P:peptidyl-lysine monomethylation, F:protein-lysine N-methyltransferase activity	-1.54	9.19089E-32
TT00_diatome_k43_Locus_9315_Transcript_2_1	diphthamide biosynthesis 3	C:nucleus, F:zinc ion binding, P:peptidyl-diphthamide biosynthetic process from peptidyl-histidine, C:cytoplasm, F:iron ion binding, F:electron carrier activity, P:tRNA wobble uridine modification	-1.55	6.90648E-26
TT00_diatome_CL2076Contig1_2	tRNA-intron endonuclease	F:nucleic acid binding, P:RNA phosphodiester bond hydrolysis, endonucleolytic, P:tRNA splicing, via endonucleolytic cleavage and ligation, F:tRNA-intron endonuclease activity	-1.55	1.64322E-114
TG01_diatome_k25_Locus_9792_Transcript_1_1	ATP-dependent Clp protease subunit	P:proteolysis, F:serine-type endopeptidase activity	-1.56	4.72525E-152
TC01_diatome_k25_Locus_7402_Transcript_3_2	DEAD-box ATP-dependent RNA helicase 39	C:cell, F:protein disulfide oxidoreductase activity, F:electron carrier activity, C:membrane, C:integral component of membrane, P:cell redox homeostasis, P:oxidation-reduction process	-1.56	2.66267E-160
TC01_diatome_k37_Locus_374_Transcript_1_1	oligoendopeptidase f	P:peptide metabolic process, F:metalloendopeptidase activity	-1.56	0.0
TT00_diatome_k43_Locus_1683_Transcript_3_2	nicotinate-nucleotide diphosphorylase (carboxylating)	F:nicotinate-nucleotide diphosphorylase (carboxylating) activity, C:cytoplasm, P:NAD biosynthetic process, P:quinolinate catabolic process	-1.57	5.81655E-112
TC01_diatome_k43_Locus_3090_Transcript_4_1	shikimate kinase	F:magnesium ion binding, F:shikimate kinase activity, P:aromatic amino acid family biosynthetic process, P:shikimate metabolic process	-1.58	2.67647E-132
TC01_diatome_CL1620Contig1_1	50S ribosomal L3	F:structural constituent of ribosome, C:ribosome, P:translation	-1.58	6.46526E-168
OG50_diatome_k31_Locus_1701_Transcript_5_2	PUB zinc finger Thioredoxin	C:cell, F:metal ion binding, P:cell redox homeostasis	-1.59	0.0
TG01_diatome_k25_Locus_99_Transcript_1_1	prolyl oligopeptidase	P:proteolysis, F:serine-type endopeptidase activity, F:serine-type exopeptidase activity	-1.59	0.0
TT00_diatome_k31_Locus_8332_Transcript_1_1	reverse transcriptase	P:macromolecule metabolic process, P:primary metabolic process	-1.60	1.98715E-76
OG50_diatome_k31_Locus_7483_Transcript_4_1	20S proteasome subunit alpha 4	C:nucleus, C:cytoplasm, C:proteasome core complex, alpha-subunit complex, F:threonine-type endopeptidase activity, P:ubiquitin-dependent protein catabolic process	-1.60	2.88977E-115
OG50_diatome_k43_Locus_6401_Transcript_1_2	glycine cleavage system H	P:glycine decarboxylation via glycine cleavage system, C:glycine cleavage complex	-1.61	5.53493E-62
OG50_diatome_k25_Locus_44_Transcript_320_8	nitric oxide synthase-interacting	C:nucleus, C:cytoplasm, P:multicellular organism development, P:regulation of nitric-oxide synthase activity, F:ligase activity	-1.62	1.94141E-87
OG50_diatome_CL126Contig1_2	trimethylguanosine synthase	F:RNA methyltransferase activity, P:RNA methylation, P:cellular component biogenesis, C:cytoplasm, C:nuclear lumen, P:cellular component organization, P:RNA capping, F:binding, P:single-organism process	-1.62	9.38058E-87
TC01_diatome_k49_Locus_5134_Transcript_8_1	polyribonucleotide nucleotidyltransferase	P:RNA metabolic process, F:metal ion binding, F:transferase activity	-1.62	5.21768E-43
OG50_diatome_k31_Locus_3094_Transcript_1_1	gun4 domain	F:tetrapyrrole binding, C:chloroplast, P:chloroplast-nucleus signaling pathway, F:enzyme binding	-1.63	9.69332E-110

TG01_diatome_k25_Locus_6185_Transcript_1_1	insulin receptor-related receptor	F:ATP binding, F:protein kinase activity, P:protein phosphorylation	-1.63	1.82162E-19
TG01_diatome_k31_Locus_6533_Transcript_2_1	phenylalanine--tRNA ligase subunit alpha	F:ATP binding, C:cytoplasm, F:phenylalanine-tRNA ligase activity, P:phenylalanyl-tRNA aminoacylation, F:tRNA binding	-1.63	0.0
OG50_diatome_k43_Locus_871_Transcript_4_2	vacuolar -sorting-associated 25	P:protein targeting to vacuole involved in ubiquitin-dependent protein catabolic process via the multivesicular body sorting pathway, F:protein homodimerization activity, C:ESCRT II complex, F:structural molecule activity	-1.63	1.06031E-85
TT00_diatome_k25_Locus_3457_Transcript_4_1	ferrochelatase	F:ferrochelatase activity, C:membrane, P:heme biosynthetic process	-1.63	0.0
TT00_diatome_k25_Locus_4885_Transcript_5_1	atp-dependent metalloprotease	F:ATP binding, C:mitochondrion, P:proteolysis, F:ATP-dependent peptidase activity, F:metallopeptidase activity	-1.65	0.0
TC01_diatome_k31_Locus_1887_Transcript_3_1	hypothetical protein FisN_14Hu039	F:copper ion binding, C:cytoplasm, P:N-acetylglucosamine metabolic process, P:copper ion homeostasis	-1.66	7.03101E-37
OG50_diatome_k37_Locus_7519_Transcript_4_1	proteasome subunit alpha type 7	C:nucleus, C:cytoplasm, C:proteasome core complex, alpha-subunit complex, F:threonine-type endopeptidase activity, P:ubiquitin-dependent protein catabolic process	-1.67	3.05304E-156
TC01_diatome_k25_Locus_1214_Transcript_8_2	fucoxanthin chlorophyll a c	F:pigment binding, C:integral component of membrane, P:protein-chromophore linkage, F:chlorophyll binding, P:response to light stimulus, P:photosynthesis, light harvesting in photosystem I, C:chloroplast thylakoid membrane	-1.67	1.61833E-93
TT00_diatome_k31_Locus_1544_Transcript_5_2	phosphoglycerate mutase	P:gluconeogenesis, P:glycolytic process, C:cytosol, F:transferase activity, F:2,3-bisphosphoglycerate-dependent phosphoglycerate mutase activity, P:regulation of pentose-phosphate shunt	-1.67	1.18314E-155
TG01_diatome_k31_Locus_6125_Transcript_2_1	LAG1 longevity assurance homolog 2-like	F:transferase activity, transferring acyl groups, C:membrane, C:integral component of membrane, C:endoplasmic reticulum, P:vacuolar acidification, F:transferase activity	-1.68	1.04901E-90
TC01_diatome_k25_Locus_5586_Transcript_3_1	chloroplast light harvesting isoform	C:chloroplast, C:membrane, C:integral component of membrane, P:photosynthesis, light harvesting, P:protein-chromophore linkage, P:photosynthesis, F:chlorophyll binding, C:thylakoid, C:chloroplast thylakoid membrane	-1.71	3.13601E-69
OG50_diatome_k37_Locus_504_Transcript_3_2	ATP phosphoribosyltransferase	F:magnesium ion binding, C:cytoplasm, F:ATP phosphoribosyltransferase activity, P:histidine biosynthetic process	-1.71	2.48339E-153
TT00_diatome_k37_Locus_5014_Transcript_1_2	chlorophyll synthetase	P:chlorophyll biosynthetic process, C:chloroplast, F:chlorophyll synthetase activity, C:integral component of membrane	-1.71	0.0
TT00_diatome_k43_Locus_5594_Transcript_1_1	DNA damage-inducible 1	F:nucleotide binding, F:aspartic-type endopeptidase activity, F:ubiquitin binding, P:proteolysis	-1.72	1.01471E-107
TC01_diatome_k25_Locus_4834_Transcript_1_2	WD-40 repeat-containing	F:catalytic activity, C:membrane, P:nucleoside metabolic process, F:ADP binding	-1.73	3.39394E-49
TC01_diatome_k49_Locus_8591_Transcript_2_1	hypothetical protein FRACYDRAFT_205142	P:nucleic acid phosphodiester bond hydrolysis, F:DNA binding, P:transmembrane transport, F:nuclease activity, C:membrane, C:integral component of membrane, P:DNA metabolic process	-1.76	4.81114E-61
TG01_diatome_k37_Locus_245_Transcript_1_1	ATP-dependent Clp protease proteolytic	P:proteolysis, F:serine-type endopeptidase activity	-1.77	8.53682E-148

	subunit			
TC01_diatome_k31_Locus_1401_Transcript_1_1	ALA dehydratase	F:porphobilinogen synthase activity, F:zinc ion binding, P:heme biosynthetic process, C:cytosol	-1.79	0.0
TG01_diatome_k31_Locus_5059_Transcript_3_2	solute carrier family 35 member b1	P:fatty acid biosynthetic process	-1.79	0.0
TG01_diatome_CL2367Contig1_1	elongation factor P	F:translation elongation factor activity, C:cytoplasm, P:translational elongation	-1.79	4.52284E-107
TT00_diatome_k31_Locus_2727_Transcript_2_2	branched-chain amino acid aminotransferase (ilvE)	F:L-leucine transaminase activity, F:L-valine transaminase activity, P:branched-chain amino acid biosynthetic process, F:L-isoleucine transaminase activity	-1.79	8.26708E-160
OG50_diatome_k37_Locus_10265_Transcript_3_1	ATP-dependent Clp protease subunit	P:proteolysis, F:serine-type endopeptidase activity	-1.80	1.09452E-134
TC01_diatome_CL1804Contig1_3	Uroporphyrinogen decarboxylase	F:uroporphyrinogen decarboxylase activity, C:cytosol, P:protoporphyrinogen IX biosynthetic process	-1.81	0.0
OG50_diatome_k25_Locus_3339_Transcript_4_2	2-C-methyl-D-erythritol 4-phosphate cytidylyltransferase	F:2-C-methyl-D-erythritol 4-phosphate cytidylyltransferase activity, P:isoprenoid biosynthetic process	-1.81	2.87619E-141
TG01_diatome_k31_Locus_6806_Transcript_5_1	Atypical ABC1 ABC1-C kinase	P:cellular protein modification process, P:phosphorylation, F:kinase activity	-1.83	1.38044E-172
OG50_diatome_k25_Locus_6590_Transcript_2_1	F-type H+-transporting ATPase subunit gamma	C:proton-transporting ATP synthase complex, catalytic core F(1), F:proton-transporting ATPase activity, rotational mechanism, P:ATP synthesis coupled proton transport, C:chloroplast thylakoid membrane, F:proton-transporting ATP synthase activity, rotational mechanism	-1.86	0.0
TC01_diatome_k31_Locus_767_Transcript_142_7	rrna methyltransferase	C:nucleus, C:membrane, C:integral component of membrane, F:methyltransferase activity, P:rRNA processing, F:transferase activity, P:methylation	-1.87	1.27841E-16
OG50_diatome_CL2055Contig1_4	atp-dependent clp protease proteolytic subunit	P:proteolysis, F:serine-type endopeptidase activity	-1.87	4.7975E-145
TG01_diatome_k31_Locus_5565_Transcript_1_1	UDP-sulfoquinovose synthase	C:chloroplast, F:zinc ion binding, F:UDPsulfoquinovose synthase activity, F:coenzyme binding, P:glycolipid biosynthetic process, F:sulfotransferase activity	-1.88	0.0
OG50_diatome_k25_Locus_138_Transcript_4_3	glucose-6-phosphate 1-cytoplasmic isoform	F:NADP binding, P:pentose-phosphate shunt, P:oxidation-reduction process, P:glucose metabolic process, F:glucose-6-phosphate dehydrogenase activity	-1.88	0.0
TC01_diatome_k43_Locus_7614_Transcript_1_2	60S acidic ribosomal P1	F:structural constituent of ribosome, F:protein kinase activator activity, P:cytoplasmic translation, P:activation of protein kinase activity, C:cytosolic large ribosomal subunit, F:large ribosomal subunit rRNA binding, C:preribosome, large subunit precursor	-1.89	7.42559E-26
OG50_diatome_CL459Contig1_1	beta-hydroxyacyl-acyl carrier dehydratase (FABZ)	F:hydro-lyase activity, C:cytoplasm, C:membrane, P:fatty acid biosynthetic process	-1.91	2.12734E-79
TT00_diatome_k25_Locus_8813_Transcript_2_2	DNA-directed RNA polymerase II subunit	F:nucleotide binding, P:positive regulation of translational initiation, F:DNA-directed 5'-3' RNA polymerase activity, F:single-stranded RNA	-1.92	2.49116E-86

	RPB4	binding, P:recruitment of 3'-end processing factors to RNA polymerase II holoenzyme complex, C:P-body, P:mRNA export from nucleus in response to heat stress, F:translation initiation factor binding, P:transcription initiation from RNA polymerase II promoter, C:DNA-directed RNA polymerase II, core complex, F:single-stranded DNA binding, P:nuclear-transcribed mRNA catabolic process, deadenylation-dependent decay		
TC01_diatome_k31_Locus_652_Transcript_4_1	predicted protein	C:mitochondrion, F:double-stranded DNA binding, P:regulation of transcription, DNA-templated	-1.93	1.02696E-4
TT00_diatome_k43_Locus_7876_Transcript_1_1	6,7-dimethyl-8-ribityllumazine synthase	C:chloroplast, F:6,7-dimethyl-8-ribityllumazine synthase activity, P:riboflavin biosynthetic process, C:membrane, F:transferase activity, C:riboflavin synthase complex	-1.93	5.81032E-85
TC01_diatome_k49_Locus_8632_Transcript_4_2	Grx4 family monothiol glutaredoxin	C:cell, F:protein disulfide oxidoreductase activity, F:electron carrier activity, P:cell redox homeostasis, P:oxidation-reduction process, F:arsenate reductase (glutaredoxin) activity	-1.93	1.10949E-69
OG50_diatome_k49_Locus_10108_Transcript_1_1	4-diphosphocytidyl-2-C-methyl-D-erythritol kinase	F:4-(cytidine 5'-diphospho)-2-C-methyl-D-erythritol kinase activity, P:phosphorylation, P:terpenoid biosynthetic process	-1.94	4.85289E-168
TT00_diatome_k49_Locus_4564_Transcript_1_1	mitotic spindle assembly checkpoint	P:mitotic spindle assembly checkpoint	-1.94	4.25531E-128
OG50_diatome_k25_Locus_7976_Transcript_1_2	15,16-dihydrobiliverdin:ferredoxin oxidoreductase	F:oxidoreductase activity, acting on the CH-CH group of donors, iron-sulfur protein as acceptor, P:oxidation-reduction process, P:phytochromobilin biosynthetic process, F:cobalt ion binding	-1.95	8.24455E-151
TT00_diatome_k25_Locus_6412_Transcript_3_1	4-hydroxy-3-methylbut-2-enyl diphosphate reductase	C:chloroplast, P:dimethylallyl diphosphate biosynthetic process, F:metal ion binding, P:isopentenyl diphosphate biosynthetic process, methylerythritol 4-phosphate pathway, P:oxidation-reduction process, F:iron-sulfur cluster binding, F:4-hydroxy-3-methylbut-2-en-1-yl diphosphate reductase activity	-1.95	0.0
TT00_diatome_k43_Locus_11629_Transcript_1_1	RING finger 11-like	F:ubiquitin protein ligase activity, F:zinc ion binding, P:proteasome-mediated ubiquitin-dependent protein catabolic process, F:metal ion binding, P:protein polyubiquitination, C:membrane, C:integral component of membrane, P:protein ubiquitination involved in ubiquitin-dependent protein catabolic process	-1.95	2.03097E-17
TT00_diatome_CL2461Contig1_1	uroporphyrinogen decarboxylase	F:uroporphyrinogen decarboxylase activity, P:heme biosynthetic process, C:cytosol	-1.96	0.0
TG01_diatome_k37_Locus_8064_Transcript_4_1	peptidyl-prolyl cis-trans isomerase	F:peptidyl-prolyl cis-trans isomerase activity, P:positive chemotaxis, P:positive regulation of macrophage chemotaxis, F:chemoattractant activity, P:protein peptidyl-prolyl isomerization, F:chemokine activity, P:protein folding, P:cell chemotaxis	-1.97	1.39801E-101
OG50_diatome_CL1859Contig1_2	transmembrane	C:cell, C:extracellular space, F:protein disulfide isomerase activity, C:integral component of Golgi membrane, C:membrane, C:integral component of membrane, P:cell redox homeostasis, P:oxidation-reduction process, F:flavin-linked sulfhydryl oxidase activity, P:protein folding	-1.97	5.35389E-146
TC01_diatome_CL629Contig1_1	protoporphyrin IX	P:chlorophyll biosynthetic process, C:membrane, C:chloroplast part,	-2.00	5.83844E-146

	methyltransferase	F:magnesium protoporphyrin IX methyltransferase activity, P:methylation		
TT00_diatome_CL1566Contig1_2	NAD-dependent glycerol-3-phosphate dehydrogenase	P:glycerol-3-phosphate metabolic process, F:oxidoreductase activity, acting on the CH-OH group of donors, NAD or NADP as acceptor, F:organic cyclic compound binding, F:heterocyclic compound binding, C:membrane, P:primary metabolic process	-2.01	8.3601E-145
TC01_diatome_k37_Locus_3697_Transcript_1_1	ribose 5-phosphate isomerase A	P:pentose-phosphate shunt, non-oxidative branch, C:integral component of membrane, F:ribose-5-phosphate isomerase activity	-2.02	1.47214E-148
TG01_diatome_k37_Locus_4277_Transcript_3_2	RNA polymerase sigma factor	P:regulation of gene expression, P:DNA-templated transcription, initiation	-2.02	7.83548E-146
TC01_diatome_k25_Locus_6446_Transcript_3_1	branched-chain-amino-acid aminotransferase chloroplastic-like isoform X2	F:branched-chain-amino-acid transaminase activity, P:cellular amino acid biosynthetic process, P:branched-chain amino acid metabolic process	-2.03	0.0
OG50_diatome_k37_Locus_2979_Transcript_4_1	peptidyl-prolyl cis-trans isomerase-like	F:peptidyl-prolyl cis-trans isomerase activity, P:response to hypoxia, P:protein peptidyl-prolyl isomerization, P:protein folding, C:plastid	-2.04	9.37844E-65
OG50_diatome_k25_Locus_6972_Transcript_2_1	glutaredoxin 3	C:cell, F:protein disulfide oxidoreductase activity, F:electron carrier activity, P:cell redox homeostasis, P:oxidation-reduction process	-2.04	2.72799E-30
TT00_diatome_k49_Locus_1581_Transcript_8_2	nicotinate-nucleotide pyrophosphorylase [carboxylating]	C:extracellular exosome, F:nicotinate-nucleotide diphosphorylase (carboxylating) activity, F:protein homodimerization activity, C:cytoplasm, C:membrane, P:NAD biosynthetic process, P:quinolinate catabolic process, P:protein oligomerization	-2.04	2.90052E-68
OG50_diatome_k37_Locus_1079_Transcript_3_2	trimethylguanosine synthase	F:nucleic acid binding, P:RNA methylation, P:7-methylguanosine RNA capping, F:methyltransferase activity, P:methylation	-2.06	2.68973E-92
OG50_diatome_k25_Locus_5883_Transcript_1_1	tetratricopeptide repeat family	F:L-ascorbic acid binding, P:DNA repair, P:nucleic acid phosphodiester bond hydrolysis, F:iron ion binding, F:oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen, F:oxidoreductase activity, F:nuclease activity, C:membrane, C:integral component of membrane, P:oxidation-reduction process	-2.12	3.35772E-149
TT00_diatome_k25_Locus_4808_Transcript_1_1	predicted protein	F:nucleic acid binding, C:membrane, C:integral component of membrane, P:DNA integration	-2.20	3.63203E-87
OG50_diatome_k43_Locus_5106_Transcript_1_3	G1 S-specific cyclin-E3 isoform X2	C:nucleus, P:G1/S transition of mitotic cell cycle, P:regulation of cell cycle	-2.22	4.06593E-10
TC01_diatome_k25_Locus_2376_Transcript_1_2	DUF952 domain-containing	P:carbohydrate metabolic process, F:hydrolase activity, hydrolyzing O-glycosyl compounds	-2.22	1.17713E-29
OG50_diatome_k49_Locus_9715_Transcript_1_1	cell surface receptor	F:hydrolase activity, acting on carbon-nitrogen (but not peptide) bonds, F:phosphorus-oxygen lyase activity, P:detection of hypoxia, C:integral component of membrane, P:protein autophosphorylation, F:protein histidine kinase activity, C:intracellular, P:cyclic nucleotide biosynthetic process, P:intracellular signal transduction, F:3',5'-cyclic-nucleotide phosphodiesterase activity, P:peptidyl-histidine phosphorylation	-2.23	7.52967E-11
TT00_diatome_k37_Locus_4156_Transcript_1_1	uroporphyrinogen decarboxylase	F:uroporphyrinogen decarboxylase activity, C:cytosol, P:protoporphyrinogen IX biosynthetic process	-2.24	0.0
OG50_diatome_k49_Locus_10612_Transcript_1_1	fucoxanthin chlorophyll a	C:integral component of membrane, P:photosynthesis, light harvesting,	-2.28	7.67505E-39

	c binding	P:protein-chromophore linkage, F:chlorophyll binding, C:chloroplast thylakoid membrane		
TG01_diatome_k49_Locus_6287_Transcript_3_2	triosephosphate isomerase	P:gluconeogenesis, P:pentose-phosphate shunt, P:glycolytic process, P:glyceraldehyde-3-phosphate biosynthetic process, F:triose-phosphate isomerase activity, C:cytosol, P:glycerol catabolic process	-2.30	3.50352E-146
TG01_diatome_k25_Locus_5191_Transcript_1_1	hypothetical protein FRACYDRAFT_243716	F:hydrolase activity, acting on carbon-nitrogen (but not peptide) bonds, P:signal transduction, P:nitrogen compound metabolic process, F:phosphorus-oxygen lyase activity, C:membrane, C:integral component of membrane, P:intracellular signal transduction, C:intracellular, P:cyclic nucleotide biosynthetic process, F:3',5'-cyclic-nucleotide phosphodiesterase activity	-2.32	1.72987E-21
TC01_diatome_CL1448Contig1_1	SET domain-containing	P:protein targeting to Golgi, P:peptidyl-lysine monomethylation, F:protein-lysine N-methyltransferase activity, C:intracellular	-2.55	1.05216E-120
TC01_diatome_k37_Locus_7369_Transcript_1_1	Cof-type HAD-IIB family hydrolase	P:small molecule biosynthetic process, C:cytoplasm, F:phosphatase activity, P:dephosphorylation, F:hydrolase activity	-2.56	9.84635E-87
TG01_diatome_k49_Locus_5581_Transcript_1_1	glutaredoxin	C:cell, F:protein disulfide oxidoreductase activity, F:electron carrier activity, P:cell redox homeostasis, P:oxidation-reduction process	-2.62	3.33467E-31
OG50_diatome_k43_Locus_7159_Transcript_3_1	glutathione S-transferase	C:cytoplasm, P:glutathione metabolic process, F:glutathione transferase activity, F:transferase activity	-2.71	5.81408E-84
TG01_diatome_k49_Locus_13094_Transcript_1_1	peptidase S8	P:proteolysis, F:serine-type peptidase activity, F:serine-type endopeptidase activity, F:peptidase activity, F:hydrolase activity	-2.78	3.38969E-38
TT00_diatome_k49_Locus_3285_Transcript_1_1	uroporphyrinogen-iii synthase	P:small molecule metabolic process, F:catalytic activity, C:cytoplasmic part, P:single-organism cellular process, P:cellular metabolic process	-2.86	3.97566E-98
TC01_diatome_k25_Locus_7690_Transcript_3_2	#NOM?	F:nucleic acid binding, P:DNA integration	-2.87	1.18368E-85
OG50_diatome_k43_Locus_923_Transcript_10_2	DNA helicase	P:nucleic acid phosphodiester bond hydrolysis, F:protein domain specific binding, P:tRNA processing, P:DNA-dependent DNA replication maintenance of fidelity, F:helicase activity, P:DNA-templated transcription, termination, P:rRNA processing, P:termination of RNA polymerase II transcription, P:mRNA polyadenylation, C:replication fork, C:nucleus, P:snRNA processing, C:cytoplasm, P:regulation of transcription from RNA polymerase II promoter in response to DNA damage, F:endonuclease activity, C:membrane, C:integral component of membrane, P:mRNA 3'-end processing, C:Nrd1 complex, P:snoRNA 3'-end processing	-2.96	8.70572E-13
TG01_diatome_k49_Locus_3860_Transcript_5_3	Light harvesting complex	C:integral component of membrane, P:photosynthesis, light harvesting, P:protein-chromophore linkage, F:chlorophyll binding, C:chloroplast thylakoid membrane	-3.01	2.02388E-101
OG50_diatome_k49_Locus_999_Transcript_1_1	peptidyl-prolyl cis-trans isomerase	F:peptidyl-prolyl cis-trans isomerase activity, P:protein peptidyl-prolyl isomerization, P:protein folding	-3.13	7.16764E-78
TG01_diatome_k25_Locus_2756_Transcript_6_1	FKBP-type peptidyl-prolyl cis-trans isomerase	F:peptidyl-prolyl cis-trans isomerase activity, C:cytoplasm, F:FK506 binding, P:chaperone-mediated protein folding, P:protein peptidyl-prolyl isomerization	-3.60	6.21015E-70
OG50_diatome_k25_Locus_114_Transcript_2_1	predicted protein	P:RNA phosphodiester bond hydrolysis, exonucleolytic, F:3'-5'-	-4.44	5.14558E-25

		exoribonuclease activity, P:rRNA catabolic process		
TT00_diatome_CL2065Contig1_2	Calcium calmodulin dependent kinase association-domain	F:calmodulin binding, F:calmodulin-dependent protein kinase activity, P:protein phosphorylation	-4.67	6.84004E-58

Exposure condition	Transcript ID	Description	Log2FC		E-value	Biological process															
FLG0.1	TT00_diatome_k49_Locus_3452_Transcript_7_1	probable platelet activating factor acetylhydrolase	1.15	0.30	7.73E-33	■								■		■					
FLG0.1	TG01_diatome_k49_Locus_9856_Transcript_3_1	proline rich	1.20	0.30	4.55E-05		■			■			■	■		■					
FLG50	TT00_diatome_CL78Contig1_1	extracellular matrix	5.82	1.30	2.32E-10	■								■							
FLG50	OG50_diatome_CL11Contig3_2	filamentous hemagglutinin family N-terminal domain	5.06	0.79	1.40E-49									■							
FLG50	TC01_diatome_k49_Locus_10503_Transcript_2_1	ubiquitin thioesteraseVirion core	5.06	1.35	2.94E-13					■				■							
FLG50	TG01_diatome_k37_Locus_4954_Transcript_4_1	SPT2 homolog	4.96	0.72	5.96E-92			■		■				■			■				
FLG50	TG01_diatome_k25_Locus_4662_Transcript_10_1	Rho termination factor	4.45	1.38	7.35E-16					■				■							
FLG50	TT00_diatome_k25_Locus_575_Transcript_22_1	vegetative cell wall gp1-like	4.31	0.85	2.49E-20	■				■				■							
FLG50	TG01_diatome_k49_Locus_14252_Transcript_2_1	vegetative cell wall gp1-like	4.14	1.04	1.44E-37										■						
FLG50	TG01_diatome_k49_Locus_8534_Transcript_3_1	winged helix DNA-binding domain-containing	3.86	0.33	6.41E-17					■				■			■				
FLG50	OG50_diatome_CL37Contig1_3	lpxtg-motif cell wall anchor domain	3.81	1.06	2.61E-19					■				■			■				
FLG50	OG50_diatome_CL14Contig2_1	adhesin [	3.79	0.70	1.51E-53									■							
FLG50	OG50_diatome_k43_Locus_7159_Transcript_3_1	glutathione S-transferase	-2.71	0.84	5.81E-84					■				■							
FLG50	TG01_diatome_k49_Locus_13094_Transcript_1_1	peptidase S8	-2.78	0.61	3.39E-38									■							
FLG50	TT00_diatome_k49_Locus_3285_Transcript_1_1	uroporphyrinogen-iii synthase	-2.86	0.62	3.98E-98																■
FLG50	TC01_diatome_k25_Locus_7690_Transcript_3_2	#NOM?	-2.87	0.80	1.18E-85									■							
FLG50	OG50_diatome_k43_Locus_923_Transcript_10_2	DNA helicase	-2.96	0.99	8.71E-13					■	■			■			■			■	
FLG50	TG01_diatome_k49_Locus_3860_Transcript_5_3	Light harvesting complex	-3.01	0.65	2.02E-101									■							
FLG50	OG50_diatome_k49_Locus_999_Transcript_1_1	peptidyl-prolyl cis-trans isomerase	-3.13	1.03	7.17E-78									■							
FLG50	TG01_diatome_k25_Locus_2756_Transcript_6_1	FKBP-type peptidyl-prolyl cis-trans isomerase	-3.60	0.77	6.21E-70									■							
FLG50	OG50_diatome_k25_Locus_114_Transcript_2_1	predicted protein	-4.44	1.57	5.15E-25	■				■				■							
FLG50	TT00_diatome_CL2065Contig1_2	Calcium calmodulin dependent kinase association-domain	-4.67	0.99	6.84E-58									■							
Shading FLG50	OG50_diatome_CL1759Contig1_2	Long-chain-fatty-acid--	-1.50	0.39	4.41E-158					■				■		■					■
Shading FLG50	OG50_diatome_k37_Locus_300_Transcript_5_3	isocitrate lyase	-1.69	0.40	0.00E+00					■				■		■					■
Shading FLG50	TC01_diatome_k31_Locus_2434_Transcript_2_1	acyl- dehydrogenase	-1.76	0.45	0.00E+00	■				■				■		■		■			■
Shading FLG50	OG50_diatome_k43_Locus_3019_Transcript_2_1	fatty acid oxidation alpha mitochondrial	-1.88	0.43	0.00E+00					■				■		■					■
Shading FLG50	TT00_diatome_k37_Locus_2515_Transcript_3_1	phosphoenolpyruvate carboxykinase (ATP)	-2.07	0.44	0.00E+00									■		■					■
Shading FLG50	TG01_diatome_k31_Locus_5498_Transcript_4_1	ubiquitin-superoxide dismutase fusion	-2.18	0.56	2.41E-121				■	■	■								■	■	
Shading FLG50	TC01_diatome_CL336Contig1_1	glyceraldehyde-3-phosphate dehydrogenase	-2.23	0.56	0.00E+00					■				■		■					■
Shading FLG50	TT00_diatome_k37_Locus_4335_Transcript_2_1	3-ketoacyl- mitochondrial	-2.33	0.52	0.00E+00			■				■						■			

- ■ Catabolic process
- ■ Biosynthetic process
- ■ Cellular component organization
- ■ Cellular detoxification
- ■ Cellular metabolic process
- ■ Cellular response to stimulus
- ■ Establishment of localization
- ■ Nitrogen compound metabolic process
- ■ Organic substance metabolic process
- ■ Pathogenesis
- ■ Primary metabolic process
- ■ Regulation of biological process
- ■ Regulation of biological quality
- ■ Response to chemical
- ■ Response to stress
- ■ Small molecule metabolic process

Table S3. *DEGs participating in the biosynthetic chlorophyll pathway expressed in* N. palea *exposed to* FLG_{50mg}.

DEGs Identification	Description	GO Terms	Log2FC	E-value
OG50_diatome_k25_Locus_8858_Transcript_1_1	zeta-carotene desaturase	P:carotenoid biosynthetic process, F:oxidoreductase activity, acting on the CH-CH group of donors, quinone or related compound as acceptor, F:carotene 7,8-desaturase activity, P:oxidation-reduction process	-1.20	0.0
TG01_diatome_CL533Contig1_2	plastid glutamyl tRNA	F:ATP binding, C:mitochondrion, F:glutamate-tRNA ligase activity, P:tRNA aminoacylation for mitochondrial protein translation, F:tRNA binding, P:glutamyl-tRNA aminoacylation	-1.22	0.0
TG01_diatome_k49_Locus_3675_Transcript_4_1	geranylgeranyl reductase	F:FAD binding, P:chlorophyll biosynthetic process, F:oxidoreductase activity, acting on the CH-CH group of donors, NAD or NADP as acceptor, F:geranylgeranyl reductase activity, C:integral component of membrane, P:photosynthesis, P:oxidation-reduction process	-1.27	0.0
OG50_diatome_k25_Locus_5770_Transcript_1_2	plastid protoporphyrinogen	P:porphyrin-containing compound biosynthetic process, F:oxygen-dependent protoporphyrinogen oxidase activity, P:oxidation-reduction process	-1.43	0.0
TT00_diatome_k25_Locus_3457_Transcript_4_1	ferrochelatase	F:ferrochelatase activity, C:membrane, P:heme biosynthetic process	-1.63	0.0
TC01_diatome_k25_Locus_1214_Transcript_8_2	fucoxanthin chlorophyll a c	F:pigment binding, C:integral component of membrane, P:protein-chromophore linkage, F:chlorophyll binding, P:response to light stimulus, P:photosynthesis, light harvesting in photosystem I, C:chloroplast thylakoid membrane	-1.67	1.61E-93
TC01_diatome_k25_Locus_5586_Transcript_3_1	chloroplast light harvesting isoform	C:chloroplast, C:membrane, C:integral component of membrane, P:photosynthesis, light harvesting, P:protein-chromophore linkage, P:photosynthesis, F:chlorophyll binding, C:thylakoid, C:chloroplast thylakoid membrane	-1.71	3.14E-69
TT00_diatome_k37_Locus_5014_Transcript_1_2	chlorophyll synthetase	P:chlorophyll biosynthetic process, C:chloroplast, F:chlorophyll synthetase activity, C:integral component of membrane	-1.71	0.0
TC01_diatome_k31_Locus_1401_Transcript_1_1	ALA dehydratase	F:porphobilinogen synthase activity, F:zinc ion binding, P:heme biosynthetic process, C:cytosol	-1.79	0.0
TC01_diatome_CL1804Contig1_3	Uroporphyrinogen decarboxylase	F:uroporphyrinogen decarboxylase activity, C:cytosol, P:protoporphyrinogen IX biosynthetic process	-1.81	0.0
TT00_diatome_CL2461Contig1_1	uroporphyrinogen decarboxylase	F:uroporphyrinogen decarboxylase activity, P:heme biosynthetic process, C:cytosol	-1.96	0.0
TC01_diatome_CL629Contig1_1	protoporphyrin IX methyltransferase	P:chlorophyll biosynthetic process, C:membrane, C:chloroplast part, F:magnesium protoporphyrin IX methyltransferase activity, P:methylation	-2.00	5.84E-146
TT00_diatome_k37_Locus_4156_Transcript_1_1	uroporphyrinogen decarboxylase	F:uroporphyrinogen decarboxylase activity, C:cytosol, P:protoporphyrinogen IX biosynthetic process	-2.24	0.0
OG50_diatome_k49_Locus_10612_Transcript_1_1	fucoxanthin chlorophyll a c binding	C:integral component of membrane, P:photosynthesis, light harvesting, P:protein-chromophore linkage, F:chlorophyll binding, C:chloroplast thylakoid membrane	-2.28	7.67E-39
TT00_diatome_k49_Locus_3285_Transcript_1_1	uroporphyrinogen-iii synthase	P:small molecule metabolic process, F:catalytic activity, C:cytoplasmic part, P:single-organism cellular process, P:cellular metabolic process	-2.86	3.97E-98
TG01_diatome_k49_Locus_3860_Transcript_5_3	Light harvesting complex	C:integral component of membrane, P:photosynthesis, light harvesting, P:protein-chromophore linkage, F:chlorophyll binding, C:chloroplast thylakoid membrane	-3.01	2.02E-101

Table S4. *DEGs participating to energetic pathways expressed in* N. palea *exposed to shading* FLG_{50mg}

DEGs identification	Description	GO Terms	Log2FC	E-value
OG50_diatome_CL1759Contig1_2	Long-chain-fatty-acid--	P:long-chain fatty acid metabolic process, F:catalytic activity, P:metabolic process, C:membrane, C:integral component of membrane, F:ligase activity, F:long-chain fatty acid-CoA ligase activity	-1.50	4.40E-158
OG50_diatome_k37_Locus_300_Transcript_5_3	isocitrate lyase	P:glyoxylate cycle, C:cytoplasm, F:isocitrate lyase activity, F:transferase activity, transferring acyl groups, acyl groups converted into alkyl on transfer	-1.69	0.0
TC01_diatome_k31_Locus_2434_Transcript_2_1	acyl- dehydrogenase	F:acyl-CoA dehydrogenase activity, P:fatty acid beta-oxidation using acyl-CoA dehydrogenase, F:fatty-acyl-CoA binding, F:flavin adenine dinucleotide binding, F:electron carrier activity, F:oxidoreductase activity, acting on the CH-CH group of donors, with a flavin as acceptor, P:lipid homeostasis, C:plasma membrane	-1.76	0.0
OG50_diatome_k43_Locus_3019_Transcript_2_1	fatty acid oxidation alpha mitochondrial	F:3-hydroxyacyl-CoA dehydrogenase activity, F:lyase activity, P:oxidation-reduction process, P:fatty acid metabolic process	-1.88	0.0
TT00_diatome_k37_Locus_2515_Transcript_3_1	phosphoenolpyruvate carboxykinase (ATP)	F:phosphoenolpyruvate carboxykinase (ATP) activity, F:ATP binding, P:gluconeogenesis, C:cytosol, P:phosphorylation, F:kinase activity	-2.07	0.0
TC01_diatome_CL336Contig1_1	glyceraldehyde-3-phosphate dehydrogenase	F:NADP binding, F:NAD binding, P:glycolytic process, P:oxidation-reduction process, P:glucose metabolic process, F:glyceraldehyde-3-phosphate dehydrogenase (NAD+) (phosphorylating) activity, F:isomerase activity	-2.23	0.0
TT00_diatome_k37_Locus_4335_Transcript_2_1	3-ketoacyl- mitochondrial	F:acetyl-CoA C-acyltransferase activity, C:mitochondrion, P:metabolic process, P:regulation of mitochondrial membrane permeability	-2.33	0.0

Appendix 2. Discussion of the relation between a transcription factor nuclear-encoded with the regulation of chlorophyll pigment biosynthesis pathway.

A part of the plastid genome encodes for proteins involved in photosynthesis[84]. Among all plants, chlorophyll biosynthesis pathway starts in the cytoplasm with the chloroplast glutamate tRNA, which after several enzymatic reactions forms the 5-aminolevulinic acid synthesis[85]. This plastid encoded factor was found down-regulated in diatoms exposed to high FLG concentration (TG01_diatome_CL533Contig1_2; Log2FC = -1.22). In our dataset, almost all protein complexes and enzymes involved in the chlorophyll biosynthetic pathway were down-regulated in diatoms exposed to high FLG concentration. Genes encoding for these proteins might be grouped and submitted to the same regulation process such as Rho termination factor previously discussed, found up-regulated in this condition. Genomic analysis undertaken by Yu and co-workers (2014)[86] suggested that environmental stress, such as light, can induce the formation of functional modules by nuclear-encoded transcription factors which can mediate the regulation of plastid gene expression. This could be the case here, where Rho termination factor might be nuclear-encoded and act on chloroplast gene expression. Thus, we can hypothesize that the up-regulation of the transcript homologous with a Rho termination factor could be linked with the down-regulation of all DEGs encoding for enzymes involved in chlorophyll biosynthetic pathway.