

Table S6: Significantly differentially expressed ($p < 0.05$; \log_2 fold change >1) *Thalassiosira pseudonana* genes and expression values under different growth limitations in relation to control growth.

ID	Si	Fe	N	T	Co2	PFAM
6363	0	0	0	1.27	0	Ribosomal_L23eN
5259	0	0	0	1.14	0	Ribosomal_L44
2848	-2.6	-1.56	-4.74	-1.55	0	PsbU
25772	0	0	-1.33	0	0	Actin
28496	-2.89	1.44	-2.04	2.42	0	AdoHcyase
38715	-5.85	-1.17	-3.96	-3.62	0	Chloroa_b-bind
41829	1.38	0	0	0	0	GTP_EFTU;GTP_EFTU_D2;GTP_EFTU_D3
6285	0	0	0	1.34	0	HATPase_c;HSP90
42962	0	0	1.38	0	0	Chloroa_b-bind
31383	-3.61	-1.01	-3.43	1.04	0	Gp_dh_N;Gp_dh_C
575	-3.58	0	-4.11	0	0	Aminotran_3
866	0	0	-1.32	0	0	CLP_protease
12152	-2.94	0	-2.9	2.28	0	ketoacyl-synt;Ketoacyl-synt_C
26893	0	0	0	1.47	0	Ribosomal_S13
25933	0	0	-1.62	0	0	TPT
41256	-1.31	0	0	0	0	ATP-synt_ab_N;ATP-synt_ab_C
41548	0	0	0	0	1.7	Epimerase
26051	0	0	0	1.68	0	Gln-synt_N;Gln-synt_C
31705	-1.84	-1.13	0	-2.18	0	Mpv17_PMP22
264201	0	0	0	1.28	0	Ribosomal_L2;Ribosomal_L2_C
38583	-4.98	-1.28	-4.31	-2.28	0	Chloroa_b-bind
9716	0	0	0	1.69	0	DEAD;Helicase_C
268127	-5.69	-1.11	-7.68	-5.58	0	Chloroa_b-bind
268304	-3.86	-1.19	-4.27	0	0	0
33018	-6.19	-1.67	-6.41	-3.45	0	Chloroa_b-bind
802	0	0	0	1.02	0	Ribosomal_L18p
32924	-3.56	-2.49	-3.43	0	0	Ribul_P_3_epim
39143	1.16	0	0	0	0	Mito_carr
264921	-4.12	-2.46	-1.86	2.68	0	Chloroa_b-bind
428	-4.88	-2.57	-2.2	0	0	F_bP_aldolase
1326	-2.16	0	0	0	0	ATP-sulfurylase
29825	0	0	0	1.23	0	Ribosomal_S8e
32201	-4.33	0	-3.08	0	0	Mg_chelatase;VWA
39936	0	0	0	1.57	0	Metallophos
1738	0	0	-1.59	0	0	CLP_protease
21175	-4.53	-1.14	-5.62	0	0	Transketolase_N;Transket_pyr;Transketolase_C
32546	0	0	-1.6	2.13	0	Cyt-b5;FA_desaturase

262125	-3.45	-1.49	0	0	0	NIR_SIR_ferr
3622	-1.09	0	-1.19	0	0	IspD
21815	0	1.47	-1.84	1.53	0	S-AdoMet_synt_N;S-AdoMet_synt_M;S-AdoMet_synt_C
22565	-2.12	0	1.44	0	0	Sugar_tr
26046	0	0	0	1.11	0	Ribosomal_S3Ae
28189	0	0	0	3.65	0	HSP70;NAD-GH
31012	-3.51	-1.87	-2.97	0	0	Coprogen_oxidas
31516	0	0	0	1.46	0	NOP5NT;NOSIC;Nop
32555	-1.58	0	0	0	0	Ribonuc_red_sm
32752	0	0	0	1.16	0	Ribosomal_L24e
39278	-1.17	0	0	0	0	ATP-synt_C
42326	-2.22	0	-2.37	-1.87	0	UDPGP
269274	-3.27	0	0	-2	0	MFS_1
2343	-2.21	0	-3.64	1.87	0	0
3741	-1.71	-1.41	0	2.13	0	ELO
4830	0	1.64	0	0	0	Cofilin_ADF
5021	0	0	0	2.02	0	ketoacyl-synt;Ketoacyl-synt_C
5174	-3.9	0	-5.07	-4.63	0	Chloroa_b-bind
10234	-4.48	-2.55	-3.98	-1.15	0	FAD_binding_3
11411	0	0	2.09	0	0	Citrate_synt
20603	-6.96	-2.64	-7.64	-2.61	0	0
25892	-4.33	-1.44	-3.64	0	0	NAD_binding_1
26221	0	0	0	1.02	0	Ribosomal_S13_N;Ribosomal_S15
26367	0	0	0	1.21	0	Ribosomal_S8
28125	-1.81	0	0	0	0	GlutR_N;Shikimate_DH;GlutR_dimer
31446	0	0	0	1.11	0	Ribosomal_S21
33008	0	0	0	1.86	0	EPSP_synthase
36235	-2.24	0	-1.52	0	0	p450
36979	0	0	0	2.01	0	Fcfl
38667	-5.92	-1.49	-4.18	-3.48	0	Chloroa_b-bind
39901	0	0	0	0	1.39	PGK
40391	-1.82	0	1.83	0	0	Enolase_N;Enolase_C
269240	0	0	1.83	1.63	0	HSP70;NAD-GH
3815	-5.93	-3.43	-3.8	-5.97	0	Chloroa_b-bind
4914	-3.23	0	-3.32	0	0	NAD_binding_1
5219	-2.66	-2.41	-2.69	0	0	Acyl_transf_1
5240	-2.5	0	-2.92	-3.08	0	ALAD
8522	-2.23	0	0	0	-2.35	Ribonuc_red_sm
9021	-2.95	0	0	0	0	Porphobil_deam;Porphobil_deamC
10233	-1.74	0	-1.45	0	0	0
11501	-5.78	-1.87	-5.7	-2.24	0	Chloroa_b-bind

13806	-1.17	0	0	0	0	tRNA-synt_1c;tRNA-synt_1c_C
20008	0	0	0	1.36	0	Ribosomal_S26e
20965	-7.71	-2.61	-7.03	-3.37	-1.4	0
21261	-2.28	0	0	0	0	Rubredoxin
21292	1.31	0	0	0	0	CitMHS
21327	-1.62	0	-1.93	0	0	DUF1625
21972	-1.75	0	0	3.01	0	0
22350	0	0	0	1.38	0	Ribosomal_S21e
22476	0	0	0	1.43	0	Ribosomal_L13e
23283	-1.74	0	-2.07	0	0	0
24250	-1.5	0	1.76	0	0	SSF
26436	0	0	0	1.7	0	Peptidase_M3
26573	-3.65	-1.62	-3.28	0	0	DUF3479;CobN-Mg_chel
27873	0	0	1.55	0	0	IMPDH
29217	0	0	0	1.17	0	Ribosomal_L7Ae
29375	-5.89	-1.9	-6.91	-4	0	Chloroa_b-bind
29728	0	0	0	0	1.67	Epimerase
29842	-4.9	-1.85	-4.56	-1.78	0	0
29861	0	0	1.65	0	0	GATase_2;Glu_syn_central;Glu_synthase;GX GXG
31014	0	0	0	1.59	0	Adap_comp_sub
31091	-2.13	0	-1.72	0	0	NDK
31851	-1.58	0	-1.94	2.95	0	adh_short
31912	-1.36	0	0	0	0	Pro_isomerase
32955	-2.59	-1.71	-3.24	0	0	ADH_N;ADH_zinc_N
33871	0	0	0	1.69	0	Metallophos
34585	-2.72	-2.43	-3.81	0	0	Radical_SAM;BATS
34830	-4.34	-1.9	-5.16	-1.91	0	MSP
34864	0	0	-1.2	2.39	0	FKBP_N;FKBP_C
35180	-7.04	0	-1.56	-1.08	-1.87	Mpv17_PMP22
35712	-4.7	0	-5.16	1.56	0	PGK
35816	0	0	-1.51	0	0	Gp_dh_N;Gp_dh_C
35934	-4.71	-1.26	-4.14	0	0	Cytochrom_C
37083	0	0	0	1.17	0	DnaJ;DnaJ_C
39003	0	0	2.91	3.93	0	UPF0113
39666	-1.14	0	0	0	0	cobW;CobW_C
40156	-2.65	0	-2.08	0	0	ATP-synt
40312	0	0	0	1.15	0	Ribosomal_S9
41005	-2.34	0	-2.43	0	0	Transket_pyr;Transketolase_C
41113	0	0	0	1.79	0	Cyt-b5;FA_desaturase
262796	-3.1	-1.28	-4.57	0	0	PP-binding
264039	-2.02	0	-2.37	0	0	p450

268374	0	0	2.49	0	0	E1_dh
268895	7.15	0	-1.35	0	0	Silic_transp
269348	-1.97	0	-2.4	0	0	Pyrophosphatase
269942	-2.92	0	-2.57	0	0	SHMT
105	0	0	0	1.55	0	S1;EIF_2_alpha
174	0	0	1.6	0	0	CoA_trans
225	0	0	-1.44	0	0	RRF
233	-7.44	-6.88	-5.57	-7.99	0	0
283	-1.8	0	-1.19	0	0	HIT
370	-3.98	0	0	2.63	-1.51	Ribonuc_red_lgC;ATP-cone;Ribonuc_red_lgN
411	0	0	0	1.64	0	CoA_binding;Ligase_CoA
412	-4.68	-2.58	-3.32	-2.01	0	Aminotran_1_2
511	0	0	0	1.2	0	FeoB_N;MMR_HSR1;YchF-GTPase_C
547	-2.07	0	-2.82	2.11	0	Biotin_lipoyl;E3_binding;2-oxoacid_dh
574	-1.83	0	-1.9	0	0	TPP_enzyme_C;Transket_pyr;Transketolase_C
595	0	0	0	1.39	0	eIF-1a
644	-3.46	0	-2.63	1.37	0	PfkB
656	0	-1.66	2.43	0	0	GST_C
681	3.06	0	0	0	0	0
711	0	0	-1.29	0	0	SBF
795	2.64	0	4.83	-2.61	0	E1_dh
799	0	0	0	1.25	0	ABC_membrane;ABC_tran
843	-1.08	0	0	0	0	Ras
874	-6.26	-1.87	-5.24	0	0	0
896	1.62	1.94	0	0	0	0
899	0	0	2.14	-1.96	1.95	0
928	0	0	0	1.58	1.87	DAGAT
932	0	1.2	1.2	0	0	Choline_transpo
985	0	0	2.3	0	1.89	0
997	-1.34	0	0	0	0	OTCace_N
1010	0	0	1.56	0	0	0
1022	0	0	0	2.11	0	0
1049	-3.57	-2.35	-3.67	-2.79	0	GFO_IDH_MocA;GFO_IDH_MocA_C
1060	0	0	1.97	1.87	0	GFA
1093	-3.69	-2.84	-3.82	-2.77	0	DUF803
1122	0	0	0	1.17	0	Nuc_sug_transp
1160	1.99	1.65	0	0	0	FKBP_C
1203	0	0	0	2.07	0	PPI_Ypi1
1210	0	1.3	0	0	-1.94	0
1238	0	0	0	-1.65	0	Glyoxalase
1243	-1.78	0	0	0	-1.35	0
1247	1.63	1.53	-1.49	0	0	PALP

1254	-2.59	0	-2.32	-1.92	0	Chalcone
1309	1.77	0	0	0	0	0
1344	2.32	2.3	0	0	0	0
1356	0	0	0	-1.06	0	0
1374	0	0	1.24	2.32	0	RRM_1
1388	0	0	1.9	0	0	0
1393	-1.39	1.24	0	0	0	SMC_N
1397	0	0	0	1.1	-1.03	0
1456	0	0	-1.38	0	0	IDH
1463	2.63	0	0	0	0	zf-DHHC
1481	0	0	0	-1.26	0	0
1515	-1.39	0	0	0	0	NifU
1526	0	0	0	2.3	0	CRAL_TRIO
1557	0	0	0	2.26	0	0
1584	-1.89	0	-1.56	0	0	Pro_isomerase
1591	4.04	2.39	0	0	0	0
1594	-2.3	0	0	0	0	0
1637	-2.6	-2.29	-2.58	0	0	0
1665	-1.56	0	0	0	0	Fer2
1666	0	0	0	2.63	0	Tic22
1711	0	0	1.69	-1.58	0	CRAL_TRIO
1724	-1.26	0	-1.36	0	0	0
1734	0	0	0	2	0	PPR
1754	0	0	-1.7	0	0	GST_C
1761	0	0	0	2.18	0	DUF1499
1779	0	0	1.37	-1.61	0	SPX
1798	0	0	1.49	0	0	0
1843	4.31	2.56	0	0	0	Bestrophin
1869	0	0	0	1.7	0	0
1870	-1.29	0	0	3.24	0	0
1889	-1.19	0	0	0	0	EFP_N;Elong-fact-P_C
1899	0	0	0	-2.31	1.63	0
1903	1.55	0	0	0	0	0
1908	-1.63	0	0	0	0	Spindle_Spc25
1909	0	0	0	2.09	0	0
1932	5.42	2.98	3.15	-1.23	0	HA
1945	2.68	0	0	0	0	zf-C3HC4
1951	0	0	0	2.23	0	SET
1953	-4.58	-1.23	-3.92	0	0	0
1962	0	0	0	1.56	0	Peptidase_M48
1965	-1.26	0	-2.31	-1.44	0	0
1968	-1.57	0	0	0	0	0

1989	-2.27	0	-1.95	-1.81	0	FKBP_C
2028	2.43	0	1.71	0	0	RCC1
2078	-7.16	-6.32	-5.72	-7.58	0	0
2157	0	0	1.03	0	0	D123
2220	1.37	0	0	0	0	HSF_DNA-bind
2237	1.67	0	0	0	0	0
2243	1.62	1.54	0	0	0	0
2287	0	0	-1.12	-1.19	0	0
2320	0	0	1.39	-1.42	0	0
2335	-1.8	0	0	0	-1.68	CXC
2352	-1.8	0	0	0	0	ClpS
2375	0	0	0	2.04	0	Polyketide_cyc
2420	0	0	0	2.87	0	S1
2462	-2.54	-1.44	0	0	0	0
2465	-1.94	0	0	-1.91	0	0
2483	0	0	1.65	0	0	0
2524	0	-2.37	0	0	0	Cyclin_N;Cyclin_C
2535	0	0	0	1.76	0	0
2540	0	0	0	1.19	0	Acetyltransf_1
2553	-1.29	0	0	-1.34	0	ADH_N
2577	-1.17	0	-1.19	0	0	0
2601	-4.6	-1.7	-4.57	-2.1	0	Chloroa_b-bind
2642	2.17	0	0	0	0	0
2671	0	0	0	1.13	0	NUDIX
2673	-3.4	0	-2.8	-3.52	0	Rieske
2698	0	0	0	-1.52	0	0
2769	-1.28	-1.36	-1.2	0	0	Mito_carr
2772	0	0	1.56	1.54	0	Utp14
2818	0	-1.27	0	0	0	0
2845	-4.81	-1.42	-5.5	-1.95	0	Chloroa_b-bind
2846	-1.68	0	-1.76	-1.6	0	2-Hacid_dh;2-Hacid_dh_C
2877	2.05	0	0	0	3.27	0
2880	0	0	0	0	1.26	TspO_MBR
2892	0	0	0	2.77	0	UBA;EF_TS
2916	1.22	1.26	-1.72	0	0	TENA_THI-4
2921	0	0	0	1.09	0	SAP;RRM_1
2928	0	0	0	-1.92	0	0
2942	2.46	1.32	0	0	0	0
2957	0	0	0	-1.71	0	0
3073	0	0	0	1.34	0	Polyketide_cyc
3085	0	1.53	0	0	0	0
3105	0	0	0	1.43	0	SKN1

3111	0	0	0	-1.65	0	0
3114	0	0	0	6.9	0	AhpC-TSA
3132	0	0	0	1.64	0	Ank
3141	-2.57	0	-2.69	0	0	0
3143	-1.98	-1.86	-2.16	2.38	0	FA_desaturase
3148	0	0	0	-1.51	0	Inhibitor_I29;Peptidase_C1
3189	0	0	0	1.45	0	WHEP-TRS
3201	4.58	2.01	0	1.38	0	0
3215	0	0	0	1.71	0	Cyclin_N;Cyclin_C
3222	1.78	0	0	0	0	TauD
3244	0	0	0	-1.39	1.94	PLA2G12
3250	5.85	0	0	1.56	1.58	0
3275	0	-1.71	1.49	0	0	TLD
3298	0	0	0	2.35	0	MtN3_slv
3300	0	0	0	1.81	0	0
3313	3.62	2.8	0	3.09	0	peroxidase
3322	0	2	-2.47	0	0	0
3326	-2.5	-1.96	-1.69	0	0	TauD
3330	0	0	0	0	2.15	cNMP_binding;RGS
3344	0	0	0	2.82	0	Mpv17_PMP22
3353	-4.96	-3.07	-4.51	0	0	FMN_dh
3397	1.57	0	0	0	0	ETF_QO
3426	0	0	0	0	1.53	zf-DNL
3428	-2.4	0	-2.08	0	0	0
3453	-2.31	-2.19	-2.73	-2.7	-1.92	0
3463	-3.73	-2.36	-2.84	0	0	0
3481	0	0	-2.17	0	0	0
3482	-2.48	0	0	0	-1.51	0
3524	1.22	0	0	0	0	Mito_carr
3554	0	0	2.52	0	0	0
3583	0	0	1.34	0	0	0
3601	1.09	0	1.53	2.13	0	Ion_trans_2
3604	1.69	1.98	0	0	3.2	0
3614	0	0	2.65	2.11	2.1	0
3627	1.65	0	0	0	0	Thiolase_N;Thiolase_C
3706	3.25	0	0	0	0	0
3748	-1.98	0	0	6.58	0	Mito_carr
3755	0	0	0	1.48	0	0
3781	1.77	0	1.97	3.55	0	0
3839	1.28	1.27	0	0	0	0
3840	0	1.54	0	0	0	PPR
3845	0	0	0	1.54	0	0

3863	3.52	0	0	0	0	DAO
3878	-1.67	0	-1.66	0	0	Pro_isomerase
3883	-1.7	0	-2.5	1.29	0	0
3903	0	0	0	1.57	0	adh_short
3906	0	0	1.76	0	0	Mito_carr
3944	0	0	0	1.42	0	MMR_HSR1
3956	0	0	0	2.11	0	FUN14
3974	-2.85	-1.4	0	-1.7	0	URO-D
3975	3.32	2.97	0	0	0	0
3976	3.22	2.71	0	0	0	0
4000	0	0	1.28	0	0	0
4002	-1.83	0	-1.87	-1.53	0	Peptidase_M14
4007	0	0	1.97	0	0	0
4026	0	0	0	0	3.06	0
4050	3	1.76	0	0	1.54	0
4058	0	0	0	-2.7	2.38	Cyclin_N
4067	0	0	2.33	0	0	0
4086	0	0	1.95	0	0	0
4117	0	0	0	2.72	0	0
4146	0	0	0	0	1.95	0
4170	-1.62	0	0	0	-1.21	0
4214	-1.18	0	0	0	0	0
4225	0	1.52	-2.05	0	1.91	0
4261	0	0	0	-1.73	0	0
4270	-1.43	0	0	0	0	Scramblase
4315	-1.76	0	0	-2.65	0	0
4349	0	0	0	2.99	0	0
4355	0	0	3.27	0	0	0
4376	-1.73	0	0	0	0	PRK
4382	0	0	-1.69	3.33	0	DUF2854
4439	-5.15	-2.67	-5.37	0	0	0
4456	0	0	0	-1.19	0	0
4495	-1.41	0	0	0	0	0
4536	0	0	0	0	-1.9	0
4576	0	0	0	1.59	0	MatE
4608	1.51	1.49	0	0	0	0
4616	2.34	3.01	0	0	0	0
4624	0	0	0	1.24	0	DEAD;Helicase_C
4633	0	0	0	1.31	0	0
4654	0	0	3.05	0	0	0
4659	0	0	0	0	-1.75	0
4668	-1.96	0	0	0	0	0

4700	-2.93	0	-1.38	0	0	0
4718	-1.55	0	-1.71	-1.6	0	Epimerase
4726	0	0	0	-2.07	0	0
4755	0	0	2	0	0	0
4765	1.82	0	0	0	0	RRM_1
4767	0	0	-1.41	0	0	0
4781	-1.52	0	0	0	0	0
4782	0	0	0	0	-1.19	0
4804	0	0	-1.58	0	0	Aldo_ket_red
4819	-3.98	-3.64	-4.19	-3.27	0	Bestrophin
4820	-7.85	-4.81	-6.44	-5.62	0	Bestrophin
4834	0	0	0	-2.01	0	PTPS
4875	0	0	-1.83	0	0	PK;PK_C
4878	3.1	2.49	0	0	0	0
4888	-1.89	-1.57	-2.55	0	0	0
4891	0	0	0	1.59	0	DSPc
4900	0	0	0	1.38	0	DUF1997
4919	0	0	2.51	0	0	0
4985	0	1.39	0	1.57	1.33	0
5009	0	-1.17	0	0	0	0
5026	-1.16	0	0	0	0	ATP-synt
5028	1.25	0	0	0	0	RdRP
5077	-3.74	-1.45	-2.74	-1.53	0	adh_short
5078	0	0	0	3.14	0	tRNA-synt_2b;HGTP_anticodon
5108	0	0	0	1.76	0	DUF3727
5110	7.62	7.82	0	0	0	0
5130	0	0	2.11	2.62	0	Sell
5147	-1.71	0	0	0	0	0
5186	0	0	1.56	-2.21	0	PEPCK_ATP
5193	0	0	1.12	0	0	DUF2263
5201	0	0	0	-1.29	1.45	MatE
5293	0	0	0	1.7	0	Kri1;Iso_dh;MobB;Clp1
5362	0	0	0	1.35	0	0
5371	0	0	1.4	0	0	0
5377	0	0	0	2.76	0	0
5380	0	0	0	2.36	0	DUF1092
5393	0	0	0	-1.33	0	0
5394	-1.96	0	2.8	1.47	0	0
5424	-2.12	-1.24	2.74	-3.55	0	zf-C3HC4
5470	-1.6	0	0	0	0	CBS
5484	0	0	0	1.39	0	DUF914
5500	0	-3.03	0	-2.77	1.5	PPDK_N;PEP-utilizers_C

5513	0	0	0	2.06	0	0
5515	0	0	0	1.32	0	SAM_2
5532	0	0	0	3.57	0	0
5533	0	0	0	5	0	Chloroa_b-bind
5545	-1.27	0	-1.75	2.95	1.37	0
5584	0	0	0	0	1.15	2OG-FeII_Oxy
5600	0	-1.56	0	0	0	0
5607	-1.53	0	0	-1.68	0	Choline_transpo
5647	0	0	0	1.05	0	0
5675	-1.24	0	0	1.23	0	0
5763	1.25	0	0	0	0	SAP
5778	0	0	0	-1.71	1.68	0
5832	0	0	0	0	1.68	Cytochrom_B561
5835	4.22	2.47	0	0	1.63	0
5954	-3.12	1.59	-2.12	2.55	0	AdoHcyase
5989	1.91	0	0	0	0	Inositol_P
6048	0	0	2.99	-1.93	0	0
6114	0	0	0	0	1.31	Guanylate_cyc_2
6123	0	0	0	1.84	0	Ank
6139	-1.85	-1.56	-1.76	0	0	Chloroa_b-bind
6155	-2.35	-1.69	-2.66	0	0	0
6203	-2.3	0	0	-2.63	0	Bestrophin
6204	0	0	0	-2.13	0	Bestrophin
6211	5.74	4.5	0	0	0	Cyclin_N
6248	0	0	0	-1.75	0	0
6250	0	0	1.53	1.34	0	0
6253	0	0	0	1.47	0	0
6258	0	0	0	-1.43	0	NUDIX
6290	0	0	-1.9	2.89	0	NDK
6330	0	0	0	0	-1.87	0
6332	0	0	0	-3.06	0	0
6383	0	0	0	2.08	0	RNA_pol_Rpb7_N;S1
6489	0	0	0	1.69	0	0
6551	0	1.72	-3.16	0	0	0
6562	-1.25	0	0	0	0	Ribosomal_L23
6564	0	0	-1.38	0	0	TspO_MBR
6581	1.5	0	0	0	0	0
6607	0	0	0	1.73	0	SpoU_methylase
6670	0	0	0	-1.58	0	ATG_C;DUF1162
6731	0	0	-3.23	-2.64	0	0
6743	1.57	2.33	0	0	0	0
6750	0	0	0	-2.56	0	0

6770	-4.39	-1.46	-4.97	-1.74	0	CPSase_L_chain;CPSase_L_D2;Biotin_carb_C;Biotin_lipoyl;ACC_central;Carboxyl_trans
6807	0	0	0	0	-1.25	0
6817	-1.69	0	-1.42	0	0	PAP_fibrillin;PEMT
6876	0	0	0	-1.73	0	0
6894	0	0	3.71	1.45	0	Pirin;Pirin_C
6931	0	0	0	1.45	0	Mpv17_PMP22
6948	0	0	0	1.14	0	Histone
6949	0	0	0	0	1.59	Peptidase_S41
6950	1.13	0	0	0	0	Peptidase_S41
6958	0	0	1.31	0	0	HSF_DNA-bind
6971	0	0	2.28	0	0	0
6979	0	0	0	0	1.58	DJ-1_PfpI
6988	0	0	-1.47	0	0	tRNA_anti;tRNA-synt_2
7019	0	0	1.25	0	0	mTERF
7023	-1.74	0	0	0	-1.35	0
7031	0	0	0	1.2	0	CIA30
7060	-1.77	0	-1.54	0	0	0
7070	0	0	1.93	0	0	0
7093	0	0	0	1.57	0	Lipase_3
7094	0	0	0	1.47	0	Amino_oxidase
7110	0	0	0	-1.77	-1.45	0
7123	-1.28	0	0	0	0	Exonuc_X-T
7134	0	1.66	1.62	0	0	Mem_trans
7155	-1.05	0	-1.13	0	0	0
7166	0	0	0	1.46	0	PGAM
7186	3.31	3.13	0	-2.18	1.99	0
7265	0	0	0	1.27	0	NOB1_Zn_bind
7268	0	0	0	-2.46	1.09	Cation_ATPase_N;E1-E2_ATPase;Hydrolase
7270	-2.31	-2.04	-1.7	-1.93	0	0
7341	0	0	-1.67	0	0	TPT
7349	0	0	0	0	3.25	0
7372	0	0	0	0	2.3	Trypsin
7491	0	0	3.2	0	0	HA
7509	1.03	0	0	0	0	0
7558	0	0	0	2.14	0	DUF525
7582	0	0	0	0	2.65	Guanylate_cyc
7583	0	0	0	1.51	0	DUF1995
7642	0	0	0	2.07	0	Hydrolase_4
7669	0	0	0	-1.98	0	0
7678	0	0	0	1.33	0	0
7704	0	0	0	-2.1	0	Pyr_redox_2;Pyr_redox_dim;Rhodanese

7709	-3.68	-2.02	3.15	-3.82	0	0
7719	2.25	0	0	0	0	YbaK
7742	0	0	0	2.11	0	KTI12
7752	0	0	1.37	-1.56	0	0
7776	6.44	3.91	0	0	1.6	0
7805	0	0	0	4.78	0	Aldo_ket_red
7815	0	0	0	-2.34	0	0
7838	0	0	0	1.62	0	0
7859	0	0	0	0	1.31	0
7863	1.31	0	-1.39	0	0	0
7865	2.76	1.74	0	0	0	DUF839
7873	-1.58	0	0	0	0	0
7881	-2.62	0	-3.3	0	0	0
7883	-4.65	-2.83	-2.25	1.71	0	0
7887	0	0	0	0	1.51	Snf7
7916	-6.56	-2.87	-6.92	-5.96	0	Chloroa_b-bind
7940	-2.64	0	0	2.93	0	0
7950	-2.56	-1.71	0	-2.5	0	0
7974	0	0	0	-2.87	0	0
7997	-1.4	0	0	0	0	TLD
7999	2.16	0	0	1.96	0	0
8014	0	0	-1.56	0	0	0
8028	-1.66	-1.04	0	-1	0	0
8031	-2.29	0	0	-1.36	0	0
8044	-1.39	-1.41	0	0	1.27	Pentapeptide
8062	0	0	0	1.17	0	0
8073	-1.86	0	-1.61	-2.19	0	TauD
8086	2.67	1.69	0	0	0	0
8164	0	0	0	1.78	0	0
8180	2.29	0	0	0	0	0
8181	0	0	0	0	-1.46	0
8216	0	-1.37	1.58	0	0	0
8219	-6.31	0	0	0	0	0
8248	-3.24	-1.73	-2.99	0	0	HopJ
8270	0	0	0	1.47	0	0
8281	0	0	1.6	2.66	0	0
8329	-1.94	-1.41	0	0	0	0
8355	0	0	0	-1.44	0	0
8365	1.93	2.62	0	0	0	0
8407	2.84	0	2.91	-4.6	1.94	0
8409	-1.72	0	0	0	0	0
8426	-1.26	0	0	0	0	Mito_carr

8437	0	0	0	1.45	0	E1-E2_ATPase
8439	1.17	1.07	1.57	0	0	Epimerase
8469	1.16	0	1.49	1.65	0	0
8521	0	0	4.56	1.55	0	PseudoU_synth_1
8537	0	2.28	0	0	0	Peptidase_M50
8571	0	0	0	1.6	0	0
8611	0	0	0	2	0	FG-GAP
8670	-1.33	-1.53	-1.61	2.06	0	0
8672	-1.58	-1.85	0	-3.3	0	NAD_binding_4
8673	1.33	0	0	0	0	0
8698	1.56	0	1.62	0	0	0
8704	-1.38	0	0	0	-1.65	0
8713	-5.78	-2.91	-5.09	0	0	0
8733	0	0	0	-1.35	0	BHD_1;BHD_2;BHD_3
8740	2.62	1.82	0	0	0	Bestrophin
8775	0	0	0	2.84	0	Peptidase_S9
8778	0	0	2.99	0	0	Transket_pyr;Transketolase_C
8808	0	0	0	2.43	0	SNARE_assoc
8811	0	0	0	1.26	0	RPE65
8845	1.74	0	0	0	0	0
8861	0	0	1.75	2.06	0	GST_C
8952	-1.9	0	0	-2.5	2.56	GATase_2;SIS
8974	-2.14	-2.25	0	0	0	0
8979	1.24	0	0	0	0	MS_channel
8982	0	1.67	0	0	0	0
8997	0	0	0	1.68	0	DEAD;Helicase_C
9003	0	0	0	0	1.52	0
9007	1.69	0	0	0	0	0
9057	0	0	0	1.28	0	0
9060	0	0	1.72	0	0	0
9086	0	0	0	1.62	0	0
9087	0	0	0	1.51	0	Mito_carr
9118	0	0	0	2.17	0	MoaC
9122	0	0	0	1.84	-1.95	0
9152	0	0	0	-2.38	2.8	0
9173	0	0	0	-2	0	0
9240	-2.84	-2.88	0	-2.37	0	PT
9242	-2.55	-2.7	0	-2.33	0	0
9252	0	0	-1.63	0	0	SET
9255	0	1.29	0	0	0	0
9268	-1.63	-1.82	-2.06	-2.4	0	0
9284	0	0	0	-1.25	0	Guanylate_cyc

9352	-2.07	0	-3.15	0	0	LrgB
9394	0	0	-1.5	0	0	0
9406	0	-1.09	0	-1.86	1.45	0
9432	0	1.33	0	0	0	CAP
9442	0	0	0	2.96	0	Fibrillarin
9475	0	0	1.26	0	0	0
9479	2.14	1.62	0	0	0	ATG22
9485	-1.94	-1.47	0	0	0	mTERF
9499	0	0	1.71	0	0	Hydrolase_3
9502	-1.9	0	0	0	0	0
9511	0	0	0	1.96	0	ADK
9524	2.55	1.78	0	0	0	PAP_fibrillin
9557	-6.42	0	0	0	-2.1	0
9558	-2.53	0	0	0	0	0
9619	6.95	0	0	0	0	0
9689	0	0	0	2.19	0	PAS
9705	0	0	0	1.66	0	DUF2431
9714	1.14	1.93	1.34	-1.35	0	0
9722	0	0	0	-1.08	0	0
9737	0	0	1.02	0	0	0
9742	0	0	0	3.43	0	HA
9746	0	0	1.2	0	0	RNA_pol_Rpb4
9754	0	0	1.46	0	0	0
9795	0	0	-1.84	0	0	0
9830	0	0	-1.71	0	0	Cys_Met_Meta_PP
9840	0	1.9	0	0	0	Nramp
9874	0	0	0	0	-1.57	0
9878	-1.82	0	0	0	0	0
9903	-2.24	-2.11	-1.8	-2.44	0	0
9918	-2.08	0	-2.5	0	0	Cupin_3
9958	0	0	5.88	0	0	0
9976	0	0	0	1.3	0	0
10081	0	0	0	-1.1	0	Metallophos
10093	0	0	0	1.72	0	FAD_binding_3
10106	-1.12	0	0	0	-1.46	0
10156	-1.31	0	0	0	-1.35	Tcp10_C
10181	-1.51	0	0	0	0	0
10228	0	0	0	-1.48	0	0
10254	0	0	0	3.98	0	FAD_binding_2
10256	0	0	0	-2.55	0	0
10311	0	0	0	-3.97	1.75	0
10313	-1.61	0	0	-3.41	1.6	0

10360	-1.74	0	-1.54	-1.73	0	0
10363	5.41	0	1.36	-2.07	1.89	0
10378	-1.12	-1.11	0	0	0	0
10385	3.85	3.51	0	0	1.56	CMD
10416	0	0	0	1.47	0	0
10417	-3.3	0	-2.54	0	0	0
10425	0	1.48	0	-1.47	0	DUF1409
10457	0	0	0	-1.14	0	Alpha_kinase
10472	0	0	0	1.59	0	0
10497	0	-1.22	0	0	0	Gly_transf_sug
10518	0	0	1.33	0	0	0
10552	4.71	3	0	0	0	Beta_propel
10556	1.49	0	0	0	0	0
10604	0	0	0	3.31	0	Epimerase
10626	0	0	1.15	0	0	0
10661	0	1.58	0	0	0	0
10677	0	0	0	1.64	0	FA_desaturase
10723	1.83	0	-1.92	0	0	0
10741	0	0	0	-1.52	0	0
10767	-2.28	-1.78	-1.86	0	0	0
10791	-2.14	-2.57	0	-2.84	-2.78	RCC1
10850	0	1.26	0	0	0	FA_hydroxylase
10885	0	0	0	2.35	2.16	0
10899	3.17	0	0	-3.23	0	0
10945	0	0	3.03	0	0	0
10983	1.54	0	0	0	0	0
10997	4.09	4.05	0	0	0	0
11029	0	0	0	-1.77	0	0
11101	1.62	1.69	0	0	0	TauE
11118	0	0	-2.12	1.77	0	0
11133	-1.15	0	0	0	0	0
11145	0	0	1.67	0	0	0
11320	0	0	0	2.53	2.42	DAHPSynth_2
11352	0	0	1.35	0	0	0
11357	0	0	0	0	-1.62	0
11360	1.51	1.41	0	-1	0	0
11366	2.09	2.29	0	-1.85	0	0
11375	0	0	0	-1.24	0	Ferric_reduct;FAD_binding_8;NAD_binding_6
11383	0	0	0	0	3.03	0
11392	0	1.98	-1.49	0	0	0
11430	-1.26	-1.37	0	0	0	0

11487	0	1.95	1.2	3.83	0	PhyH
11499	-1.04	0	0	0	0	0
11500	0	0	0	1.98	0	0
11508	0	0	0	1.82	0	Prefoldin_2
11523	0	-1.52	0	-1.54	0	Sulfotransfer_1
11548	-1.3	0	0	0	0	0
11557	0	0	0	0	-1.09	PhyH
11576	0	0	0	0	1.58	0
11676	0	0	0	1.06	0	LON
11757	-2.44	0	-2.53	0	0	0
11777	0	0	0	1.58	0	Methyltransf_16
11794	0	0	2.13	-2.2	0	0
11796	0	0	1.6	-2.45	0	0
11824	0	0	0	1.59	0	GidB
11836	-1.75	0	0	1.42	0	0
11858	0	-1.41	0	0	0	0
11902	-4.98	-1.28	-4.31	-2.28	0	Telo_bind
11905	0	2.07	0	0	0	0
11924	-2.23	0	-1.69	-2.25	0	PPR
11977	1.49	0	0	0	0	0
11978	0	0	0	2.21	0	Cyt-b5;DAO
12012	0	0	0	0	1.81	DSBA
12040	-1.47	0	-1.27	-1.58	2.34	0
12047	0	0	0	0	2.21	0
12061	0	0	0	1.78	0	0
12070	0	0	0	2.67	0	NDK
12072	0	0	0	0	1.9	0
12141	0	0	0	1.5	0	Abhydrolase_1
12171	0	1.65	0	0	1.52	0
12179	6.15	3.56	0	0	0	0
12594	2.11	4	0	0	0	Chitin_bind_1
12637	1.21	0	0	0	0	Myosin_head
12695	-2.2	0	-4.1	0	-1.46	Glucan_synthase
13064	0	0	2.15	0	0	GCS
13089	1.95	1.51	0	0	2.6	ABC_tran
13224	0	1.25	0	0	0	RRM_1;PABP
13254	0	0	0	1.89	0	DEAD;Helicase_C
13459	0	0	0	-1.34	0	AAA_2;ClpB_D2-small
13485	-2.79	-1.78	3.07	-4.51	0	Xan_ur_permease
13982	0	0	0	3.2	0	DEAD;Helicase_C
14147	-2.05	-2.19	-1.94	-2.23	0	PALP
14322	4.06	0	0	0	2.4	Pkinase

14370	1.52	0	0	0	0	WD40
14389	0	0	0	3.06	0	Pyridoxal_deC
14563	-1.56	0	0	0	0	Kinesin;6PF2K;PGAM
14597	0	0	1.72	0	0	DEAD;Helicase_C
14700	1.52	0	0	0	0	WD40
14942	0	0	-1.12	0	0	Kinesin
15027	0	0	0	1.47	0	CitMHS
15093	0	0	1.1	-1.4	0	Peptidase_S10
15226	0	0	0	1.07	0	GHMP_kinases_N
15259	0	0	0	1.43	0	S1
15638	1.52	0	0	-1.31	0	PHD;SET
15916	0	1.33	0	0	0	cNMP_binding;Pkinase
15961	2.17	1.26	0	0	0	5-FTHF_cyc-lig
16210	1.5	0	2.26	-2.33	0	0
16344	-2.52	-1.59	-2.77	-3.08	0	Nuc_sug_transp
16372	0	0	0	0	1.43	Aldo_ket_red
16390	0	0	1.36	0	0	Peptidase_C1;Inhibitor_I29
16746	0	2.11	0	2.41	0	Mito_carr
16772	0	0	0	1.47	0	Mito_carr
16777	0	0	0	0	1.54	0
16947	0	0	0	1.43	0	DEAD;Helicase_C
17031	2.08	2.14	0	-1.41	0	PI3_PI4_kinase
17073	-1.15	0	0	0	0	DUF1295
17140	3.04	2.52	0	0	0	Spermine_synth
17242	0	0	0	0	1.07	Band_7
17302	0	0	1.87	1.58	0	Inositol_P
17362	0	0	0	4.43	0	Kua-UEV1_localn
17439	-1.08	0	0	0	0	DUF818
17443	0	0	-1.6	1.86	0	Inositol_P
17480	0	0	0	1.58	0	Pkinase
17492	1.55	0	0	0	0	ThiF
17623	0	0	2.59	0	0	TP_methylase
17687	0	0	1.82	0	0	AAA
17704	-1.09	0	-1.5	0	0	Peptidase_C12
17854	0	0	-1.91	0	0	Heme_oxygenase
17859	0	0	0	1.47	0	DER1
17961	0	0	0	2.1	0	UPF0005
18076	2.43	0	0	2.24	0	ADK
18099	1.42	1.63	0	0	1.7	Nfu_N;NifU
18109	0	0	0	2.27	0	UPF0016
18198	0	0	1.5	1.61	0	RRM_1
18351	0	0	0	2.39	0	Maf

18536	1.42	1.48	-3.01	1.46	1.29	Chloroa_b-bind
18624	0	0	3.07	-2.01	0	Mpv17_PMP22
18662	0	0	2.17	0	0	Ank;ADK
18741	0	0	0	0	1.26	0
18820	1.04	0	0	0	0	Myb_DNA-binding
18841	0	0	0	0	1.59	RRM_1
19048	3.16	2.35	0	0	0	Pkinase
19094	0	0	0	0	1.54	Pkinase
19141	0	0	2.57	3.36	0	Flavodoxin_1
19351	0	0	0	1.22	0	LRR_1
19421	0	0	0	-1.4	0	HECT
19501	0	0	0	1.1	0	S10_plectin
19541	0	0	0	1.18	0	Ribosomal_L28e
19793	-3.03	0	0	1.23	0	Histone
19813	2.39	2.23	0	0	1.9	AdoMet_dc;Spermine_synth
19818	0	0	0	1.21	0	Ribosomal_S15
19895	1.58	0	0	0	0	BTB
19928	0	0	0	2.16	0	Ribosomal_L20
20065	-1.35	0	0	0	0	bZIP_1
20186	-1.61	-1.77	4.68	-1.74	2.02	DnaJ
20194	-3.7	0	-3.37	1.77	0	zf-CDGSH
20223	0	0	0	2.18	0	RRM_1
20266	0	0	0	2.25	0	RRM_1
20335	-3.97	-1.82	-5.32	-3.49	0	Rotamase
20567	1.47	0	0	0	0	MS_channel
20590	2.52	2.03	0	0	0	IQ
20593	0	0	-1.22	3.42	0	FA_hydroxylase
20605	2.23	1.01	0	0	0	DEAD
20609	0	0	1.9	0	0	0
20625	0	0	0	1.48	0	0
20629	0	0	0	1.73	0	YCII
20641	0	0	0	1.82	0	0
20648	0	0	0	0	1.7	0
20649	0	0	0	-2.18	0	0
20658	0	0	0	1.85	0	Nop53
20670	0	0	2.31	0	-1.84	0
20671	2.95	2.41	0	0	0	0
20678	0	0	0	1.53	0	Cupin_4
20707	0	0	0	0	1.04	0
20731	0	0	0	2.63	0	Mito_carr
20740	0	0	0	0	1.17	0
20743	1.31	0	0	0	0	0

20751	0	0	0	-1.53	1.47	MORN
20786	0	1.41	0	0	0	0
20795	0	1.69	0	0	0	CAP
20797	-1.2	0	-1.51	0	0	Methyltransf_11
20810	0	0	0	-1.11	0	FTR1
20812	-1.22	0	-2.05	0	0	0
20814	0	0	0	2.21	0	0
20816	0	0	2.11	0	0	Aminotran_4
20827	-1.94	0	2.27	0	0	TauE;GYF
20829	0	0	1.26	0	0	HPP
20832	0	0	0	-1.27	0	HPP
20833	0	0	0	3.01	0	Methyltransf_16
20837	0	0	2.17	-1.47	0	0
20845	1.27	0	0	0	0	Tic22
20847	-4.37	1.88	0	2.11	-1.94	0
20877	0	0	0	1.66	0	Ubiq_cyt_C_chap;WW
20880	1.49	0	-2.58	0	0	PhoD
20888	-1.36	0	0	0	0	0
20909	0	0	0	0	1.53	0
20930	0	0	0	1.26	0	0
20931	-2.36	0	0	0	-1.62	0
20946	0	0	0	0	2.55	0
20950	0	0	0	1.2	1.68	DAGAT
20953	0	0	0	-1.44	0	Trypsin
20959	1.2	1.95	0	-1.96	0	Myb_DNA-binding
20962	2.17	0	0	0	0	0
20966	0	0	0	0	1.71	CIA30
20972	2.56	0	0	0	0	0
20974	0	0	0	-2.22	0	0
20993	0	0	0	0	1.39	AAA_5;AAA_2;ClpB_D2-small
20998	0	0	0	0	1.59	HOOK
20999	0	-1.8	0	0	0	Cyclin_N
21000	0	-1.16	0	-2.07	1.63	Cyclin_N
21001	0	0	0	-2.21	1.44	Cyclin_N;Cyclin_C
21020	0	2.82	0	0	0	0
21043	-1.1	0	0	0	0	0
21050	0	0	0	1.85	0	NOG1
21059	-1.4	-1.62	-1.47	-1.29	0	0
21061	0	0	0	0	1.83	0
21067	0	0	2.5	0	0	FMN_red
21068	1.92	2.32	0	0	0	0
21076	-1.74	-2.21	5.2	0	1.59	0

21081	-5	-2.86	-6.27	-3.28	0	0
21085	4.31	4.57	0	0	0	0
21087	1.35	0	0	0	0	0
21094	0	0	0	0	-2.22	0
21124	0	0	0	-1.69	0	0
21139	0	0	1.29	0	0	0
21149	0	1.51	1.62	2.64	0	0
21152	0	0	0	0	1.11	zf-C3HC4
21159	0	1.16	0	0	0	Cyclin_N;Cyclin_C
21161	0	0	0	0	1.53	Patched
21170	0	0	0	-1.53	0	0
21177	0	0	1.82	0	0	Biotin_lipoyl;UBX
21193	0	0	0	1.48	0	ubiquitin
21203	0	0	0	-1.55	0	SET
21208	0	0	1.76	-1.72	2.05	0
21213	0	0	0	0	1.63	0
21216	3.01	2.96	0	0	0	0
21224	0	0	3.28	2.45	0	0
21234	1.31	0	0	0	0	0
21237	-1.65	0	0	0	0	TPR_1
21240	0	0	0	0	1.66	0
21250	0	0	-1.89	0	0	0
21255	-1.77	0	0	-1.48	1.22	DUF500
21258	0	0	0	2.43	0	DUF3523;AAA
21279	0	0	0	0	1.52	0
21290	-2.27	0	0	0	0	0
21299	0	0	2.77	0	0	AMP-binding
21300	0	0	-1.81	0	0	Epimerase
21306	-2.17	0	0	0	0	0
21312	0	0	2.93	0	0	0
21342	0	0	0	0	1.53	0
21348	-3.24	0	-3.41	0	0	0
21351	-1.07	0	0	0	0	0
21362	1.08	1.06	1.7	0	0	0
21374	0	0	1.24	1.8	0	Muc_lac_enz
21381	1.88	2.19	0	0	0	0
21386	0	0	0	0	2.47	Aldo_ket_red
21389	-2.5	0	0	-1.42	0	0
21390	-2.48	0	0	0	0	0
21392	1.11	0	0	0	1.11	0
21403	-1.61	0	0	0	0	0
21416	1.7	0	0	0	0	0

21438	0	0	0	-1.96	0	0
21446	1.42	0	1.3	0	0	0
21449	0	0	0	-1.49	0	0
21472	-5.28	-2.04	-4.24	-2.43	0	Chloroa_b-bind
21477	-2.99	-1.09	-1.56	0	0	0
21480	1.61	0	0	0	0	Choline_transpo
21489	0	0	0	1.3	0	0
21515	0	0	0	0	1.24	0
21517	-1.89	-1.74	-1.65	0	0	Methyltransf_6
21519	0	0	0	2.42	0	0
21587	0	2.88	0	0	0	0
21594	0	0	0	0	1.46	0
21598	0	0	0	0	1.19	Acetyltransf_1
21605	0	1.97	0	0	-1.92	0
21611	0	0	0	-1.37	0	Inhibitor_I29;Peptidase_C1
21612	0	0	0	1.86	0	GARS_A
21613	4.91	2.79	0	0	0	0
21640	0	0	1.73	0	0	Iso_dh
21651	0	0	0	-1.53	0	Abhydrolase_1
21656	2.16	0	0	0	0	0
21661	0	0	0	-3.04	1.57	Pro_isomerase
21663	0	0	0	-1.7	1.29	0
21664	2.43	1.15	0	0	0	0
21665	5.85	0	0	1.56	1.58	0
21666	0	-1.2	0	-1.84	0	0
21680	0	0	0	-1.26	0	0
21683	4.82	4.32	0	0	0	Kringle;peroxidase
21690	0	0	0	-1.86	0	0
21692	-1.94	0	-1.43	0	0	DUF2470
21707	3.2	2.19	0	0	0	0
21720	0	0	1.96	0	1.58	ZZ
21725	0	0	1.62	2.63	0	Brix
21727	1.16	0	0	0	0	DENN;PDZ
21748	-2.45	0	-2.16	0	0	F_bP_aldolase
21753	0	0	1.65	0	0	PGAM
21774	0	0	0	-1.59	0	0
21776	2.4	0	0	0	-1.47	0
21779	1.64	2.06	0	0	0	0
21781	0	0	1.17	2.43	0	0
21784	1.45	1.5	0	0	0	0
21785	-1.37	0	2.65	2.32	0	Pyr_redox_2
21795	3.54	3.54	0	0	0	0

21807	0	0	0	-2.27	0	PDZ
21808	0	0	0	-1.36	0	0
21821	-2.49	0	-3.19	0	0	0
21830	0	0	0	0	2.41	WLM
21844	2.32	2.64	0	0	1.84	0
21847	0	0	0	1.62	0	FAD_binding_2
21850	1.96	1.81	0	0	-1.52	Cyclin_N
21855	1.91	0	1.77	1.48	0	PH;DUF1336
21886	0	0	0	1.41	0	0
21896	0	0	0	0	1.48	0
21897	-2.76	0	0	-1.92	2.55	0
21898	-1.62	0	0	0	0	0
21900	0	0	0	1.55	0	FAD_binding_2
21923	0	0	0	0	-1.39	0
21948	-1.29	0	0	0	0	DUF179
21965	0	0	0	0	2.08	Thioredoxin
21966	0	0	1.49	2.5	0	0
21968	3.62	0	0	0	0	0
21979	0	0	1.69	1.7	0	DUF2373
22002	0	0	0	-1.38	0	0
22016	-1.37	0	0	0	0	ABC_membrane;ABC_tran
22025	0	0	0	0	1.31	0
22030	4.4	3.02	0	0	0	Hydrolase
22052	0	0	3.27	0	0	0
22057	1.7	0	0	0	0	0
22064	0	0	0	-2.8	2.39	0
22074	-1.87	-2.93	0	-2.44	0	0
22114	0	0	0	3.86	0	0
22117	-5.04	-1.76	-1.84	-1.24	0	0
22127	0	0	0	-2.18	0	0
22155	0	0	0	0	1.56	K_tetra
22163	0	0	0	1.24	0	0
22166	0	0	0	-1.3	0	0
22171	-1.04	0	0	0	0	Cation_efflux
22187	0	0	0	0	3.04	HSP20
22194	-1.36	-1.59	-1.73	-2.44	0	DUF1995
22197	0	0	0	2.18	0	Aldo_ket_red
22198	-1.33	0	-1.73	2.59	0	0
22199	0	1.43	0	0	0	0
22200	0	0	1.83	2.45	0	DnaJ
22203	0	0	1.93	1.81	0	0
22208	-3.1	-2.45	-2.56	-2.31	0	Aminotran_5

22213	0	0	1.61	1.72	0	PFK
22214	-2.04	0	-2.64	0	0	0
22215	0	0	0	-1.37	0	CBM_14
22218	0	1.99	0	0	0	0
22220	-3.75	0	0	0	0	0
22223	0	0	0	0	1.85	Serinc
22227	0	0	0	0	1.83	0
22231	0	0	0	-1.67	0	0
22234	0	0	2.1	0	0	PAS
22240	0	0	0	1.71	0	eRF1_1;eRF1_2;eRF1_3
22251	0	0	2.36	0	0	0
22277	1.27	1.02	0	0	0	0
22323	0	0	0	2.3	0	SRP19
22332	3.42	2.22	0	0	1.61	Peptidase_S51
22337	1.56	0	0	1.21	0	0
22339	0	0	0	-1.43	1.28	DnaJ;U-box
22345	0	0	6.21	4.07	0	PK;PK_C
22349	0	1.31	0	0	0	0
22356	0	0	0	1.3	0	TruD
22368	0	0	0	1.36	1.96	ArsA_ATPase;ParA
22378	0	0	0	1.33	0	0
22379	0	0	0	2.64	0	0
22396	-2.21	-1.04	-1.66	0	0	0
22404	0	0	0	1.56	0	DEAD;Helicase_C
22413	-1.54	-1.16	0	-1.25	0	0
22428	0	1.44	0	0	0	0
22429	0	0	0	3.09	0	0
22430	0	0	1.23	0	0	SOUL
22454	-1.77	-2.05	1.9	0	0	HSF_DNA-bind
22455	0	0	0	-1.97	0	0
22462	0	0	1.45	1.27	0	FtsJ
22481	0	0	0	0	1.89	0
22483	0	0	1.42	0	0	0
22486	0	1.87	0	0	0	0
22490	0	0	0	0	1.5	DOMON;Cytochrom_B561
22495	1.32	2.23	0	2.05	1.47	Cyclin_N
22522	0	1.9	0	0	0	0
22526	-1.3	0	0	0	0	ABC_membrane;ABC_tran;DUF1602
22527	-1.48	0	-1.55	0	0	NAD_binding_1
22566	0	0	1.75	0	0	0
22582	0	0	0	1.28	0	S1
22610	0	0	0	1.05	0	Ribosomal_L4;NAC;CIA30

22635	0	0	0	1.94	0	Nop;CSD;NOP5NT;NOSIC;IF3_N;IF3_C;Pet191_N
22640	0	0	3.17	0	0	0
22643	0	1.07	0	0	0	0
22645	1.3	0	0	0	0	0
22656	0	0	0	0	1.27	TatD_DNase
22658	1.52	0	0	0	0	DUF1800;DUF1501
22670	0	0	2.61	0	0	0
22671	0	0	2.83	0	0	FAD_binding_3
22683	0	0	0	-1.38	0	0
22701	-4.01	0	0	0	0	0
22702	-1.85	0	1.37	0	0	0
22712	0	0	0	2.08	0	Fer2
22714	0	0	-1.35	0	0	0
22721	0	0	2.07	0	0	0
22725	0	0	0	1.25	0	SAP
22731	0	0	1.69	0	0	zf-C3HC4
22734	-3.31	0	0	0	-1.8	0
22748	-2.19	-1.44	0	0	0	0
22752	0	0	1.42	0	0	0
22772	0	1.68	0	0	0	0
22781	2.29	1.99	0	0	0	0
22783	0	0	0	0	1.62	CRCB
22794	0	0	-1.73	0	0	TRAM_LAG1_CLN8
22795	0	0	2.43	-1.55	0	0
22796	0	0	0	0	1.33	UBA;PUB
22855	0	0	0	-2.15	0	0
22860	-2.03	0	0	0	0	0
22861	0	0	1.54	1.76	0	0
22863	0	0	-1.89	1.34	0	Peptidase_M16;Peptidase_M16_C;M16C_assoc
22864	0	0	0	-1.54	0	DAO;GCV_T;GCV_T_C
22867	-1.44	0	0	0	0	0
22876	0	0	0	1	0	0
22877	0	0	0	-1.4	0	MgtC
22879	0	0	0	1.55	0	0
22880	0	0	0	-1.88	0	Fasciclin
22891	-1.74	0	0	0	0	0
22941	-3.88	-3.92	0	-4.33	0	peroxidase
22984	2.01	1.55	0	0	0	Gelsolin
22985	0	0	0	1.84	0	NLE;WD40
22993	2.87	3	0	0	0	GARS_A
23036	0	1.82	0	0	0	0

23040	0	1.68	1.73	0	0	DUF1800;DUF1501
23071	1.65	0	0	0	0	0
23143	4.36	2.21	0	2.8	0	Cyclin_N
23159	1.3	0	0	0	0	0
23160	2.86	2.37	4.13	0	0	0
23209	0	0	0	1.27	0	0
23224	0	1.52	1.57	1.98	0	0
23225	0	0	0	0	-1.67	0
23232	0	0	0	2.41	0	0
23245	0	0	1.45	1.6	0	0
23246	0	0	0	3.02	0	0
23253	-2.99	0	0	0	0	0
23264	0	1.56	1.39	0	0	0
23272	0	0	0	0	1.39	Adap_comp_sub
23292	0	0	0	2.39	0	FA_desaturase
23295	-2.07	0	0	-4.34	0	Trp_Tyr_perm
23296	0	0	1.53	0	0	0
23303	0	-1.3	0	0	0	0
23308	-1.02	0	0	-1.12	1.36	0
23329	0	0	0	1.4	0	Cpn60_TCP1
23354	0	0	0	2.26	0	CPL
23357	0	0	-1.56	1.61	0	Hydrolase
23359	0	0	0	-1.32	0	0
23363	0	-3.54	-4.44	-5.52	0	0
23369	0	1.6	0	0	2.48	0
23374	0	0	0	-2.64	2.26	0
23377	0	0	1.63	0	0	VWA
23390	-1.5	0	0	0	0	0
23391	0	0	1.45	-1.66	0	Ammonium_transp;Cyt-b5;FA_desaturase
23393	0	0	0	1.66	0	0
23396	2.23	1.39	0	-1.18	0	0
23399	-1.86	0	0	0	0	efhand
23409	0	0	0	0	1.01	0
23416	1.01	1.45	0	0	0	0
23431	0	0	0	-1.88	1.7	0
23446	0	0	0	-1.87	1.79	0
23466	0	0	1.15	0	0	0
23481	-1.18	0	0	0	0	Sulfotransfer_1
23486	0	0	0	0	3.16	0
23503	0	0	1.23	-1.1	0	Ank
23504	3.79	1.37	0	0	0	0
23505	2.86	1.79	0	0	0	0

23509	0	1.64	0	0	0	0
23510	2.87	3.49	0	0	0	0
23511	0	1.51	0	0	0	0
23519	0	0	0	-1.6	0	PAH;HDAC_interact;Pkinase
23526	1.44	0	0	0	0	Glyoxalase
23527	0	0	0	1.66	0	Prefoldin_2
23528	0	0	-1.36	0	0	Ras
23543	0	0	0	-1.43	2.04	0
23565	0	0	0	-1.04	0	0
23603	-1.03	0	0	0	0	0
23607	0	0	-1.72	0	0	TRAM_LAG1_CLN8
23620	-1.25	0	-1.73	-1.88	5.16	0
23623	-2.08	-1.79	4.82	0	0	0
23624	2.19	2.11	0	0	0	CAP
23653	0	0	0	0	1.71	Cyclin_N
23654	0	-1.27	0	0	0	0
23655	0	0	0	1.66	0	MAM33
23657	-1.98	0	0	0	0	Globin
23662	0	0	0	-1.87	3.05	Trypsin
23665	-1.99	0	0	0	0	HSF_DNA-bind
23669	0	0	0	0	1.4	0
23671	1.6	0	0	0	0	0
23684	-1.94	0	0	0	1.21	0
23685	-1.94	0	0	0	1.21	0
23700	0	0	0	-1.49	0	0
23701	0	-1.35	0	-2.28	0	0
23716	0	0	1.62	0	0	0
23719	1.79	1.99	0	0	0	0
23720	2.17	2.81	0	0	0	0
23757	-1.16	0	0	0	0	0
23771	-2.9	0	0	0	1.95	0
23794	-1.13	-1.23	0	-1.99	1.21	0
23796	1.69	0	0	0	1.66	0
23798	0	0	0	2.89	0	FA_desaturase
23801	-2.01	0	1.36	0	0	HSF_DNA-bind
23811	0	0	0	3.89	0	ABC_tran
23813	0	1.57	-1.56	0	0	Kazal_1
23814	0	1.73	-1.56	0	0	Kazal_1
23821	0	-1.54	0	-2.45	0	0
23827	0	0	0	-2.48	0	0
23850	-1.48	0	0	0	0	WD40
23857	0	1.78	0	0	1.67	Thioredoxin;PUB

23861	2.46	2.72	0	0	0	0
23862	1.14	0	0	0	0	0
23867	0	0	2.18	-3.78	0	PCMT
23872	0	0	1.79	3.6	0	GLTP
23881	-1.22	0	0	0	0	0
23888	0	0	0	-2.29	0	0
23899	0	0	0	0	1.23	0
23918	-3.89	0	-4.57	0	0	0
23927	1.75	1.9	0	-2.7	2.77	Smr
23929	0	0	0	1.94	0	0
23932	1.92	2.1	0	0	0	0
23933	0	0	0	-1.31	0	0
23934	-2.28	-2.05	0	0	2.43	0
23937	0	0	0	-1.36	0	0
23947	0	0	0	-1.23	0	0
23976	2.23	2.75	0	0	0	SBF
23986	2.09	1.84	0	-1.95	4.92	0
23993	-1.63	-1.77	0	0	1.75	0
24000	0	0	0	0	1.43	uDENN
24008	0	1.55	0	0	0	0
24011	0	0	0	-1.33	0	0
24016	0	0	0	1.31	0	Ebp2
24017	2.37	0	0	0	0	0
24023	1.73	0	0	0	0	HA
24028	2.63	1.68	0	0	0	0
24039	2.6	1.82	0	0	0	0
24046	0	0	0	0	2.45	0
24056	-1.16	0	0	0	0	Pkinase
24060	-2.29	0	0	0	0	GFO_IDH_MocA
24072	0	0	0	1.33	0	0
24074	0	0	0	0	1.35	0
24077	0	0	0	-1.47	0	0
24099	-1.13	0	-1.55	0	0	0
24112	0	0	0	0	1.32	HSF_DNA-bind
24126	0	0	0	1.59	0	Sld5
24134	0	0	0	-1.73	1.73	0
24149	0	0	0	1.96	2.33	0
24153	2.05	0	0	0	0	0
24160	-3.58	0	0	0	-1.97	0
24163	0	0	-2.17	0	0	tRNA-synt_2d;FDX-ACB
24164	4.12	2.01	0	2.18	1.98	0
24165	1.25	0	0	0	0	0

24172	0	0	0	1.75	0	0
24198	0	0	0	-3.44	3.96	0
24199	0	0	0	0	1.8	0
24205	0	0	0	0	1.21	0
24217	0	0	1.87	1.83	0	CS;SAP
24224	-1.37	0	0	0	0	0
24225	-1.72	0	0	0	0	ClpS
24248	-3.79	-2.97	-2.46	-2.59	0	GATase;CPSase_L_chain;CPSase_L_D2;CPSase_L_D3;MGS;CPSase_sm_chain
24257	0	0	0	-1.93	0	0
24261	0	0	1.68	1.87	0	0
24292	1.35	0	0	0	0	zf-CCCH
24303	1.47	1.35	0	1.16	0	DUF647
24307	2.59	2.5	0	-2.08	0	0
24309	0	0	-2.43	0	0	PsbP
24319	1.26	0	0	1.36	0	0
24325	0	0	0	-3.38	0	Cna_B
24341	0	0	0	1.4	0	DnaJ
24346	0	0	0	1.24	0	0
24361	0	0	1.01	0	0	0
24362	0	0	1.58	0	0	0
24369	0	0	0	1.88	0	RRM_1
24376	-1.38	0	0	0	2.44	C2;TerD
24379	0	0	2.84	1.56	0	0
24385	4.18	3.61	-2.22	2.09	2.22	0
24396	0	0	1.33	2.04	0	HSF_DNA-bind
24428	0	1.17	0	0	0	0
24441	2.1	2.17	0	0	1.65	0
24443	0	2.21	0	0	0	0
24445	1.24	0	0	0	0	0
24448	0	0	1.78	0	0	0
24456	0	0	0	0	1.69	0
24486	0	0	0	0	1.29	0
24500	0	0	0	-3.45	2.54	0
24507	0	0	0	1.49	0	0
24511	0	0	0	0	1.45	0
24512	-2.79	0	-3.01	0	0	0
24521	0	0	0	-2.31	2.16	GATase_2;SIS
24534	0	-2.24	1.86	-3.17	0	0
24535	-2.23	0	0	0	0	ADH_N
24557	-1.17	-1.47	0	-1.88	0	0
24559	-1.58	-1.87	0	0	0	0

24564	-2.68	-2.99	0	-2.28	0	0
24566	-2.22	-1.94	0	-1.97	-2.37	0
24569	-1.86	0	0	0	0	0
24571	-2.02	-1.97	0	-1.55	0	0
24575	0	0	0	-1.23	0	Guanylate_cyc
24597	0	0	0	1.45	0	0
24599	0	0	0	0	2.12	0
24602	1.76	0	0	0	0	0
24606	0	-1.5	0	0	1.91	0
24649	-2.78	0	0	0	-2.33	0
24655	0	0	1.41	0	0	0
24657	1.4	0	0	0	0	0
24659	0	0	0	-1.47	2	3_5_exonuc;KH_1
24669	-4.43	-2.26	-4.11	0	0	0
24677	0	-1.84	0	-2.13	1.51	Smr
24680	1.48	1.28	0	0	0	Sulfotransfer_2
24694	0	0	-1.12	-1.94	0	DUF1800;DUF1501
24699	-2.01	0	0	0	0	0
24700	-1.73	0	-2.1	0	0	PMSR
24704	0	0	1.52	-1.63	0	0
24718	0	0	0	1.63	0	ABC1
24726	3.38	2.48	0	0	0	0
24738	0	0	0	0	1.53	0
24760	4.72	3.56	0	-4.01	2.54	0
24761	5.16	3.58	0	-4.04	2.57	0
24769	-4.51	-1.02	-4.87	-1.7	0	0
24770	0	0	-1.14	0	0	DUF498
24812	0	0	0	2.26	0	GFO_IDH_MocA
24816	0	1.63	0	2.32	-2.26	AsnA
24818	4.19	4.03	0	0	0	0
24849	0	0	1.41	0	0	Exonuc_X-T
24850	0	0	0	1.21	0	0
24858	6.34	5.13	0	2.23	0	0
24862	0	0	0	-1.74	0	0
24882	-1.89	0	-1.43	-1.83	0	0
24900	1.84	1.6	0	0	0	0
24904	0	0	1.18	2.33	0	Fcf1
24910	0	0	0	0	1.99	0
24918	2.73	1.04	0	0	0	0
24923	0	0	5.21	0	0	0
24932	0	0	-1.06	0	0	Thioredoxin
24935	-2.11	0	0	-1.77	0	0

24961	0	0	0	0	1.84	Kelch_1
24962	0	0	0	0	1.4	0
24963	2.12	2.51	0	0	0	0
24977	0	0	2.05	0	0	TRAUB
24980	1.21	1.23	0	1.51	0	0
24999	-1.76	-1.33	3.53	-2.63	0	0
25012	0	-1.33	0	1.15	0	MAPEG
25041	-1.31	0	0	0	0	TPR_1
25058	-4.81	-4.09	0	-3.73	-3.21	0
25059	0	0	0	2.6	0	0
25060	-4.54	-4.91	0	-4.19	-3.17	0
25061	-4.41	-4.24	0	-4.32	-3.84	0
25064	0	0	0	1.91	0	0
25069	0	0	0	0	1.97	0
25075	0	0	0	1.74	0	0
25092	0	0	0	0	1.8	0
25100	0	0	0	2.22	0	PAP_fibrillin
25104	-1.89	0	0	1.65	-2.35	0
25107	0	0	0	-1.36	2.17	U-box
25115	1.17	0	0	0	0	0
25116	-2.01	0	-1.38	0	0	PGK
25123	0	0	1.34	0	0	0
25127	0	0	0	0	2.05	DUF1625
25130	0	0	0	2.45	0	2-Hacid_dh_C
25156	0	1.23	-1.66	0	2.08	0
25157	0	0	0	-1.38	1.79	0
25159	0	0	2.35	2.32	0	0
25161	0	0	1.48	0	0	0
25164	0	0	0	-2.56	0	0
25171	-1.49	0	0	0	1.85	DUF1517
25183	0	0	0	1.44	0	0
25190	0	0	0	-1.29	0	0
25193	-1.92	0	0	0	0	0
25202	1.75	0	0	0	0	0
25205	4.16	2.58	0	0	0	Beta_propel
25206	0	0	0	0	2.78	0
25207	0	0	0	0	2.07	0
25217	0	0	0	-1.69	0	0
25231	0	0	0	0	2.01	Acetyltransf_1
25235	0	0	0	0	-1.19	0
25243	0	1.9	1.54	1.77	0	0
25246	1.45	0	0	0	0	RRM_1

25264	0	0	0	-2	0	0
25277	0	0	0	1.92	0	0
25280	6.74	5.45	0	0	2.02	0
25290	2.11	1.72	0	0	0	0
25295	0	0	0	1.51	0	0
25299	-2.05	0	0	0	0	Oxidored_molyb;Mo-co_dimer;Cyt-b5;FAD_binding_6;NAD_binding_1;Glyco_hydro_38C
25306	0	0	0	-1.45	0	0
25335	0	0	0	0	1.62	0
25337	-2.34	-2.54	0	-3.62	-3.18	RCC1
25347	-1.15	-1.51	0	0	0	0
25353	0	0	0	0	1.83	0
25355	0	0	0	1.33	0	Plug_translocon;SecY
25357	6.02	5.39	0	0	0	0
25372	1.51	1.92	0	0	0	0
25381	1.79	1.34	0	0	0	0
25382	0	1.35	0	0	0	Glyco_transf_10
25386	0	0	0	0	2.33	0
25387	-1.5	0	0	0	0	0
25389	0	0	4.43	0	0	0
25393	-1.67	0	0	0	0	0
25396	0	0	0	0	1.2	0
25398	1.44	0	0	0	0	0
25414	4.03	2.91	0	0	2.65	0
25415	0	0	0	-1.62	1.67	0
25428	0	0	0	-1.89	0	0
25430	0	0	0	-1.84	0	0
25432	1.72	2.38	0	0	0	0
25439	-2.96	-2.43	0	-1.66	0	0
25463	0	0	0	0	1.76	0
25464	-2.45	0	0	0	-1.7	0
25528	0	0	0	1.62	-1.77	0
25544	0	0	-1.21	0	0	0
25548	1.2	0	0	0	0	0
25551	0	-1.37	0	0	0	0
25560	-2.62	-1.78	-2	0	0	PseudoU_synth_2
25572	0	0	2.45	0	0	Acetyltransf_1;CoA_binding
25582	3.17	0	0	0	1.96	RRM_1
25590	0	0	0	-1.97	2.02	0
25594	0	-1.4	0	0	0	0
25604	0	0	0	1.52	0	0
25610	-1.22	0	-1.87	0	0	Fasciclin;Methyltransf_11

25613	0	0	0	-2.72	0	FAT
25623	1.62	0	0	0	0	0
25626	0	1.44	0	0	0	0
25629	0	0	0	1.77	0	GTP_EFTU;GTP_EFTU_D2;EFG_IV;EFG_C
25635	0	0	0	0	2.33	0
25637	1.42	2	0	0	1.45	0
25639	0	0	0	0	1.75	Choline_kinase
25649	1.35	2.26	0	0	0	0
25650	0	0	1.01	0	0	0
25659	-1.57	0	1.9	-1.71	1.46	0
25692	-1.45	0	0	0	0	0
25698	0	0	0	1.74	0	IFRD
25713	3.54	3.69	0	0	0	0
25739	1.3	0	0	0	0	VWA
25742	1.68	1.02	0	0	0	0
25746	0	0	0	1.6	0	DUF2039
25750	0	0	0	0	1.59	0
25766	0	0	0	1.65	0	0
25775	1.42	0	0	0	0	zf-C3HC4
25783	1.2	2.09	0	0	0	0
25797	0	0	0	2.58	0	0
25805	2.6	3.05	0	1.47	0	0
25807	-3.59	0	0	0	0	0
25814	1.4	0	0	0	0	0
25839	0	0	-1.33	0	0	0
25840	-5.65	-3.03	-1.33	-4.98	0	CdCA1
25843	0	0	0	0	1.75	0
25848	-1.42	0	-1.28	-1.59	2.27	0
25898	-4.03	0	0	0	0	0
25904	4.55	3.82	0	0	2.76	0
25905	1.26	0	0	0	0	DUF23
25908	1.47	0	0	0	0	0
25909	0	0	1.57	0	2.06	0
25912	-1.9	0	0	0	0	0
25917	0	0	0	0	-1.98	0
25921	-5.64	0	0	0	0	0
25949	0	0	0	1.14	0	Ribosomal_L5;Ribosomal_L5_C
26022	0	0	2.48	2.05	0	Pam16
26031	0	0	0	2.12	0	SHMT
26041	6.18	6.58	0	0	0	Chitin_bind_1
26131	-4.22	-1.84	-2.16	0	0	CytB6-F_Fe-S;Rieske
26137	0	0	0	1.21	0	Ribosomal_L6

26190	0	0	0	1.63	0	UCH;SHMT
26365	2.18	0	0	-3.32	0	ECH;3HCDH_N
26366	0	0	3.3	2.84	0	Mito_carr
26418	0	0	0	1.34	0	Peptidase_S24
26470	0	0	0	0	1.47	Epimerase
26473	1.91	1.68	0	0	0	Metallophos
26492	0	0	0	1.37	0	GARS_N;GARS_A;GARS_C;Formyl_trans_N; AIRS;AIRS_C
26530	0	0	-1.95	0	0	Cation_efflux
26548	-3.82	-2.26	-3.88	-3.02	0	GFO_IDH_MocA;GFO_IDH_MocA_C
26678	0	0	0	1.79	0	Transketolase_N;Transket_pyr;Transketolase_C
26686	0	0	0	1.61	0	WD40
26759	-1.58	0	0	0	-1.22	adh_short
26991	-1.83	0	0	0	0	Glutaredoxin
27083	0	0	0	1.62	0	PCI;eIF3_N
27273	-2.43	0	-2.3	1.69	0	MTHFR
27292	0	0	0	1.27	0	RS4NT;Ribosomal_S4e
27414	-3.05	0	0	-2.03	0	MFS_1
27550	0	1.18	2.02	2.29	0	THF_DHG_CYH;THF_DHG_CYH_C;cNMP_binding
27776	0	0	0	0	1.1	Amidohydro_1
27836	0	0	0	-2.17	0	Chitin_synth_2
27850	0	0	2.99	0	0	PGAM
28028	0	0	-1.54	0	0	PCI
28300	0	0	1.86	0	0	RrnaAD
28326	0	-1.6	-1.64	0	0	LYTB
28350	0	0	0	2.4	-1.26	PGAM
28521	-1.72	0	-2.66	0	0	GCV_H
28544	0	1.65	1.48	4.03	0	DapB_N;DapB_C
28570	0	0	0	2.77	0	Ribosomal_L7Ae
28682	0	0	0	1.57	0	Cpn60_TCP1
28755	0	0	2	2.57	0	Ribosomal_S8e
28825	3.93	4.53	0	0	0	Cyt-b5;Chitin_synth_2
28842	1.22	0	0	0	0	Thioredoxin
28865	0	0	0	1.36	0	ABC1;APH
28920	0	0	0	-3.2	2.42	Pkinase
28998	0	0	0	1.71	1.68	Aldo_ket_red
29008	0	0	0	1.26	0	AA_kinase;NAD_binding_3;Homoserine_dh
29049	0	0	0	2.65	0	IF-2;IF2_N;GTP_EFTU
29183	0	0	0	1.45	0	HMGL-like;LeuA_dimer
29244	-1.23	0	0	0	0	Pro_isomerase
29314	-1.99	0	-2.04	0	0	Peptidase_M17

29506	0	0	0	0	1.14	Cpn10
29771	3.16	2.68	1.86	0	0	PI3_PI4_kinase;DUF3385;FAT;Rapamycin_bind;FATC
29782	0	0	0	0	1.46	eIF-6
30385	-4.26	-1.45	-5.35	-3.14	0	Chloroa_b-bind
30851	0	0	-2.68	0	0	AAA;AAA_2;ClpB_D2-small;DUF3170
30862	0	0	0	2.92	0	zf-CCHC
30871	0	0	2.36	2.91	0	Ham1p_like
30887	0	0	1.6	0	0	Cyt-b5
30939	-1.66	0	0	2.94	0	eIF-1a
30976	-2.39	0	-2.06	0	0	FKBP_C
30977	0	0	0	2.15	0	Pep_deformylase
30979	0	0	0	1.41	0	HIT
31001	1.46	0	0	0	0	Glycos_trans_3N;Glycos_transf_3;PYNP_C
31006	-1.45	0	0	0	0	Ribosomal_S30AE
31011	0	0	0	-1.61	0	Mito_carr
31035	0	0	0	2.05	0	Trypsin
31037	0	0	0	3.15	0	DEAD;Helicase_C
31047	0	0	0	2.13	0	Brix
31085	2.74	3.15	0	0	0	Aa_trans
31108	0	0	0	-1.69	0	Glyco_transf_20;Trehalose_PPase
31125	0	0	0	1.88	0	adh_short
31128	-4.22	-4.03	-4.35	0	0	Chloroa_b-bind
31166	0	2.11	0	0	0	AdoMet_dc
31169	-2.09	0	0	-1.6	0	AhpC-TSA
31216	0	0	-1.27	0	0	Aminotran_1_2
31226	1.24	0	0	0	0	Sugar_tr
31232	0	0	1.96	0	0	PFK
31259	0	0	0	1.75	0	HA
31266	0	0	1.73	0	0	NUDIX
31362	-1.26	0	0	0	0	ATP-grasp_2;Ligase_CoA
31394	0	0	-2.24	1.6	0	Aminotran_1_2
31402	0	0	-1.74	1.52	0	DUF3007
31406	1.21	0	1.34	0	0	Arf
31412	0	0	0	1.47	0	THF_DHG_CYH_C
31415	0	0	0	1.35	0	Cons_hypoth95
31447	0	0	0	1.63	0	Mito_carr
31451	0	0	0	1.55	0	Ribosomal_L18e
31465	0	0	0	2.52	0	Brix
31535	-1.74	0	0	0	0	FKBP_C;Pro_isomerase
31564	0	0	-1.24	0	0	LSM
31569	-2.09	0	0	0	0	Tubulin;Tubulin_C

31635	0	0	0	3.59	0	TPT
31636	-1.91	-2.2	-1.57	0	0	Aldose_epim
31673	0	0	-1.46	0	0	Radical_SAM
31732	0	0	0	-1.78	0	Ank
31749	-6.62	-3.19	-7.08	-5.07	0	Chloroa_b-bind
31771	0	0	0	1.08	0	ABC1
31783	2.48	2.75	0	0	0	PrmA
31818	0	0	3.08	0	0	Mito_carr
31819	0	0	0	1.71	0	DUF2419
31923	0	0	0	1.37	0	0
31930	-1.39	0	-1.63	1.51	0	AAA;Peptidase_M41
31938	0	0	0	2.01	0	PUF
31951	-1.69	0	0	0	0	Cation_efflux
31979	0	0	0	1.05	0	HhH-GPD
31983	-2.41	-1.92	-2.72	-2.38	0	Chloroa_b-bind
32003	1.49	0	0	0	1.54	Lipase_GDSL
32029	0	0	0	-1.63	0	Methyltransf_11;Sterol_MT_C
32053	0	0	-1.51	0	0	WHEP-TRS;tRNA-synt_2b;HGTP_anticodon;ProRS-C_1
32066	-1.11	0	0	1.87	0	Mito_carr
32067	0	0	1.67	-1.88	0	Transket_pyr;Transketolase_C
32137	0	0	0	2.22	0	Hydrolase
32140	0	0	0	2.73	0	DHDPS
32145	-2.75	0	-1.6	1.85	0	Lipid_DES;FA_desaturase
32153	-1.1	0	-1.57	2.31	0	0
32158	0	0	1.83	1.27	0	NOC3p;CBF
32176	0	0	0	0	1.06	MAP1_LC3
32216	0	0	0	1.35	0	Ribosomal_S5;Ribosomal_S5_C
32223	-1.27	0	-1.5	0	0	Ras
32252	0	0	0	1.46	0	Rib_5-P_isom_A
32261	-2.15	0	-1.9	0	0	DUF2237
32325	0	0	0	1.38	0	ABC_membrane;ABC_tran;DUF1602
32332	-3.45	-2.57	-2.85	1.85	0	Rib_5-P_isom_A
32374	0	0	0	1.44	0	0
32430	1.59	0	0	0	0	DUF1336
32431	-1.53	-1.4	-1.06	0	0	Fe_bilin_red
32459	-1.72	0	1.61	0	0	PspA_IM30
32485	0	0	0	-1.62	0	Pro_dh
32493	0	0	2.42	-1.52	0	Aldo_ket_red
32557	-2.73	0	0	0	0	zf-C3HC4
32577	0	0	0	0	1.43	Semialdehyde_dh;Semialdehyde_dhC
32596	0	1.56	0	0	0	Trypsin

32610	0	0	0	0	1.42	EamA
32678	1.76	1.83	0	0	0	Archease
32723	-4.08	-1.84	-4.11	-4.05	0	Chloroa_b-bind
32736	0	0	0	0	2.02	DEAD;Helicase_C
32738	4.38	4.08	0	-1.83	0	Pkinase
32795	0	0	0	1.23	0	Arf
32807	0	0	0	2.07	0	DEAD;Helicase_C
32827	0	0	0	1.25	0	Metallophos
32860	-1.18	0	-1.69	3.26	0	0
32874	-2.36	0	-2.02	-1.7	0	Sod_Fe_N;Sod_Fe_C
32964	-6.19	-2.6	-5.39	-1.95	-1.2	PsbM
32971	0	0	0	-1.86	0	Trypsin
33000	-3.48	-1.99	-3.07	0	0	FTHFS
33021	0	0	0	4.2	0	FBPase
33024	0	0	0	-2.37	0	Isochorismatase
33035	0	0	-1.43	0	0	YGGT
33044	0	0	0	1.5	0	WHEP-TRS;tRNA_anti;tRNA-synt_2
33067	-1.51	0	0	0	0	CBFD_NFYB_HMF
33131	-6.1	-2.94	-6.52	-5.2	0	Chloroa_b-bind
33169	0	0	0	2.52	0	Mpv17_PMP22
33219	0	0	0	3.11	0	Sdh5
33220	0	0	0	2.86	2.56	PMSR
33241	0	0	0	1.12	0	Ribosomal_L22
33270	-2.45	0	0	1.25	0	Histone
33316	0	0	-1.37	0	1.44	Epimerase
33330	0	0	0	1.65	0	Glycos_transf_2
33340	-1.63	0	0	0	0	bZIP_1;PAS
33343	-1.53	0	0	0	0	NAD_binding_2;6PGD
33407	-1.34	0	0	0	0	bZIP_2;PAS
33476	0	0	0	2.45	0	Diphthamide_syn
33558	0	0	0	1.42	0	SecA_DEAD;SecA_SW
33578	-1.13	0	0	0	0	Ras
33580	0	0	1.49	0	0	ABC_membrane;ABC_tran
33589	0	0	0	2.4	0	Brix
33606	-5.58	-2.25	-5.52	-5.05	0	Chloroa_b-bind
33653	0	2.35	0	2.51	0	GrpE
33663	-1.47	0	-1.06	0	0	PGI
33680	0	2.29	0	0	0	HMG-CoA_red
33701	-3.21	-1.73	-3.18	0	0	0
33718	0	0	1.73	3.25	0	Methyltransf_4
33772	2.26	2.43	0	0	0	Pkinase
33855	0	0	-2.38	0	0	FKBP_C

33883	-1.69	0	0	0	-2.03	Cyclin_N;Cyclin_C
33891	-2.42	-1.43	-1.72	0	0	Sigma70_r2;Sigma70_r3;Sigma70_r4
33911	0	0	0	3.2	0	Steroid_dh
33937	0	0	0	1.98	0	FAD_binding_6;NAD_binding_1
33941	0	0	0	2.56	0	Mito_carr
33973	0	0	0	-1.17	0	DUF3336;Patatin
33979	-1.72	0	0	0	-1.53	Pkinase;POLO_box
33985	0	0	0	1.28	0	PseudoU_synth_1
33995	0	0	0	1.71	0	DUF1077
34006	0	0	0	1.84	0	Nol1_Nop2_Fmu
34030	-2.64	0	-2.46	0	0	malic;Malic_M
34044	0	0	0	1.96	0	Peptidase_M24
34094	0	0	-2.44	-2.92	2.32	0
34104	0	0	0	2.37	0	FKBP_C
34125	-7.14	-6.86	-8.58	-6.92	0	0
34170	0	0	0	1.52	0	Peptidase_M18
34191	1.12	1.04	0	0	0	CobN-Mg_chel
34210	-3.81	0	0	0	0	Histone
34211	-2	0	0	-1.9	1.85	Cytochrom_C
34276	-6.26	-2.41	-6.38	-4.6	0	Chloroa_b-bind
34280	0	0	0	-1.31	2.24	0
34283	0	0	0	1.95	0	adh_short
34340	0	0	0	1.42	0	0
34357	0	0	0	1.85	0	Fcf2
34379	0	0	-1.23	0	-1.13	NIF
34447	0	0	0	1.1	0	Cyt-b5
34543	-2.6	0	-2.79	0	0	PEPcase
34551	0	0	-2.46	0	0	60KD_IMP
34554	0	0	0	3.49	0	Psb28
34559	0	0	0	1.16	0	Pkinase
34592	1.48	0	2.18	2.28	0	FAD_binding_6;NAD_binding_1
34681	0	0	-1.59	2.16	0	FabA
34738	0	0	0	0	1.81	0
34746	0	0	1.5	0	0	Abhydrolase_2
34771	0	0	0	1.74	0	Formyl_trans_N;Formyl_trans_C
34809	2.7	0	0	0	0	Thiolase_N;Thiolase_C
34878	1.93	0	0	0	0	Abhydrolase_1
34881	0	0	0	1.66	0	Pescadillo_N;BRCT
35041	0	0	2.4	1.86	0	0
35094	0	0	2.94	0	0	2-Hacid_dh_C;Aldolase_II
35189	1.8	0	0	0	0	DNA_pol_B_exo
35206	0	0	1.82	0	0	LRR_1

35310	-1.74	1.43	0	0	-1.6	Kinesin
35407	-1.74	0	0	1.39	0	Histone
35409	0	0	-2.51	0	0	peroxidase
35464	-1.31	0	0	0	0	SAP;HhH-GPD
35499	0	0	0	-1.45	0	SMC_N;SMC_hinge
35523	0	0	-1.18	-1.6	0	ICL
35532	0	0	-1.11	-1.46	0	Epimerase
35639	0	0	0	3.22	0	Abhydrolase_1
35685	0	0	1.82	0	1.68	CS
35710	1.56	0	0	0	0	Acyl-CoA_dh_N;Acyl-CoA_dh_M;Acyl-CoA_dh_I
35740	0	0	0	1.93	0	adh_short
35871	-2.96	-1.93	-2.48	0	0	2-Hacid_dh_C
35878	-1.96	0	-1.47	0	0	PGM_PMM_I;PGM_PMM_II;PGM_PMM_III
35911	0	0	0	2.34	0	Methyltrans_SAM
35963	1.63	1.36	1.73	0	0	Ureidogly_hydro;Polysacc_deac_1;Isochorismatase
35968	-3.03	0	-1.3	1.64	-1.58	0
36015	0	0	3.33	0	0	Mpv17_PMP22
36053	0	0	0	1.45	0	Ank;Pkinase;Pkinase_Tyr
36078	0	0	-1.75	0	0	Redoxin
36081	-5.96	-2.32	-4.98	-5.35	0	Chloroa_b-bind
36186	0	0	0	1.99	0	DUF143
36208	-2.71	-1.62	-1.53	-1.44	0	GCV_T;GCV_T_C
36263	0	1.32	0	0	0	Ammonium_transp
36291	0	0	2.12	0	0	Biotin_lipoyl;E3_binding;2-oxoacid_dh
36297	0	0	0	-2	0	Asp
36322	0	0	0	2.41	0	tRNA_U5-meth_tr
36339	0	0	1.22	0	0	tRNA-synt_1;Anticodon_1
36406	0	0	2.28	1.73	0	Ribosomal_L30
36420	0	2.23	0	0	0	HATPase_c;DNA_gyraseB;DNA_topoisoIV
36431	0	0	-1.25	0	0	Pro_isomerase
36434	0	0	0	1.87	0	DUF1253
36456	0	0	0	1.94	0	eIF-5_eIF-2B
36462	-4.11	0	-4.06	0	0	TIM
36477	1.06	0	0	0	0	ABC_tran;ABC2_membrane;DUF1602
36522	0	1.62	0	0	0	HATPase_c;DNA_gyraseB;DNA_topoisoIV
36527	0	0	0	1.91	0	Methyltransf_11
36539	0	0	1.65	0	0	Trm112p
36557	0	0	0	3.61	0	PAP_fibrillin
36572	0	0	0	-1	0	GFO_IDH_MocA
36576	0	0	0	2.65	0	GTP_EFTU;GTP_EFTU_D2;EFG_C
36679	0	1.1	0	2.94	0	ICMT

36689	0	0	1.87	0	1.13	PFL;Gly_radical
36702	0	0	1.42	0	1.06	PFL;Gly_radical
36709	0	0	-1.25	2.99	0	Epimerase
36716	0	0	2.37	0	0	Pyr_redox_2;Pyr_redox_dim
36788	-1.8	0	0	0	0	NAD_binding_5
36837	0	0	0	-1.71	0	ABC_membrane;ABC_tran;DUF1602
36917	0	0	0	1.36	0	TGT
36929	0	0	0	1.86	0	KH_1
36958	1.83	0	0	0	0	Pkinase_Tyr
36995	0	0	0	0	1.26	0
37071	0	1.64	1.81	3.1	0	OMPdecase;Pribosyltran
37098	0	0	1.7	1.77	0	Pterin_4a
37127	-2.07	1.16	0	0	-1.42	Glyco_hydro_31
37280	-1.26	0	0	2.35	0	ABC1
37288	0	0	-2.25	0	0	Amino_oxidase
37294	-2.54	0	-2.41	-2.02	0	ABC1
37306	1.23	0	0	0	0	Sigma70_r2;Sigma70_r4
37322	2.08	2.81	0	0	0	Pkinase
37338	0	0	-1.82	0	0	Thioredoxin
37357	-1.67	0	0	0	0	Histone
37359	0	0	0	1.59	0	CLP_protease
37376	0	1.34	0	0	0	Myosin_head;IQ
37431	-1.58	0	0	1.21	0	Histone
37444	0	0	0	3.42	0	Methyltransf_11
37450	0	0	-1.71	0	0	Peptidase_M16;Peptidase_M16_C
37493	0	0	0	-1.51	0	Formyl_trans_N
37509	-1.72	0	0	0	0	vATP-synt_AC39
37534	-1.67	0	-1.68	-1.89	0	DUF59;ParA;DUF971
37562	0	0	0	1.26	0	Pkinase;Pkinase_Tyr
37584	0	0	0	-3.05	0	Cupin_3
37592	0	1.42	0	0	0	Pkinase
37599	0	0	0	2.99	0	Peptidase_M41
37615	-1.08	0	0	-1.24	0	Epimerase
37707	2.44	1.63	0	0	0	MORN
37739	0	0	0	0	1.47	adh_short
37803	3.25	2.25	0	0	0	DUF208
37928	0	0	1.67	0	0	MOZ_SAS
37961	0	0	0	2.3	0	zf-Tim10_DDP
37965	0	0	1.35	1.43	0	S1
37976	-1.34	0	-2.19	0	0	Pro_isomerase
37988	0	1.56	0	0	0	Arf
38006	0	0	1.61	1.63	0	FKBP_C

38030	0	0	-1.5	0	0	ABM
38051	0	0	1.64	0	0	6PF2K;PGAM
38054	-1.43	0	0	0	0	MtN3_slv
38085	-3.02	0	-3.5	0	0	EamA;TPT
38121	0	0	0	-1.96	0	AAA_2;ClpB_D2-small;DUF3170
38122	-5.89	-3	-5.71	-5.99	0	Chloroa_b-bind
38139	0	0	0	3.02	0	Chloroa_b-bind
38191	0	1.57	0	1.64	0	Cpn60_TCP1
38221	0	0	0	2.01	0	0
38360	0	0	1.31	0	0	Peptidase_C1
38494	-3.95	0	-3.64	-2.65	0	Chloroa_b-bind
38512	-1.97	0	-2.2	0	0	Hydrolase_4
38513	0	0	0	2.47	0	ABC1
38574	0	0	0	0	1.9	DnaJ
38575	-1.37	0	0	0	0	adh_short
38597	0	0	1.42	0	1.06	PFL;Gly_radical
38608	-1.95	0	-1.72	1.97	0	Semialdehyde_dh;NmrA
38646	1.39	0	1.93	1.82	0	Thioredoxin
38724	-3.08	0	-1.76	0	0	peroxidase
38760	0	0	1.87	0	1.13	PFL;Gly_radical
38767	0	0	0	0	1.78	Peptidase_C1
38776	0	0	0	1.2	0	BOP1NT;WD40
38780	0	0	0	-1.35	0	DSPc
38800	0	0	-1.05	0	0	peroxidase
38807	-4.06	-2.32	-3.63	0	0	Aldolase
38845	1.15	0	0	0	0	ABC_membrane;ABC_tran
38879	-4.6	-2.6	-1.84	2.65	0	Chloroa_b-bind
38924	0	0	-1.88	0	0	tRNA-synt_1c;tRNA_bind
38964	0	0	0	1.98	0	Chorismate_synt
38973	0	0	0	0	2.24	DEP;TBC
38987	0	-1.6	0	2.58	0	ABC_tran;DUF1602
39032	0	0	0	0	1.29	Fe-S_biosyn
39098	0	1.25	0	0	0	HSP70
39149	0	0	0	0	1.17	HATPase_c;HSP90
39173	-1.15	0	0	0	0	ATP-synt_D
39286	0	0	1.57	1.69	0	ABC_tran;DUF1602
39550	0	0	0	1.23	0	Ribosomal_S7e
39622	0	0	0	1.72	0	NAC;UBA
39677	-1.82	1.66	0	0	0	Myb_DNA-binding
39710	0	0	0	2.12	0	MMR_HSR1;YchF-GTPase_C
39799	-4.64	-2.1	-4.38	-2.54	0	GDC-P
39813	-5.1	-1.47	-3.87	-3.26	0	Chloroa_b-bind

39824	1.5	0	0	0	2.36	Clp_N;AAA;AAA_2;ClpB_D2-small;DUF3170
39845	0	0	0	1.53	0	DNA_topoisoIV;DNA_gyraseA_C
39864	0	0	0	0	1.51	DEAD;Helicase_C
39924	0	0	0	1.98	0	HATPase_c;DNA_gyraseB;Toprim;DNA_gyraseB_C
39941	0	0	0	2.34	0	Aminotran_4
39953	0	0	1.88	0	0	DEAD;Helicase_C
40044	0	0	0	1.77	0	Peptidase_M24
40193	0	0	-3.93	0	0	AAA
40233	0	0	0	1.59	0	CSD
40323	-4.55	-2.94	-1.24	0	0	CPSase_sm_chain;GATase;CPSase_L_chain;CPSase_L_D2;CPSase_L_D3;MGS
40329	0	0	0	1.29	0	Ribosomal_L18ae
40341	0	0	0	2.97	0	WD40
40385	0	0	-1.07	0	0	ABC_membrane;ABC_tran;DUF1602
40393	0	0	6.17	4.24	0	PK;PK_C
40509	0	0	2.01	2.53	0	Ribosomal_L24e
40586	-2.06	0	0	0	1.61	Epimerase
40597	0	0	0	1.39	0	RPE65
40630	-2.06	0	0	0	0	Band_7
40747	-5.83	-1.96	-5.21	-4.24	0	Chloroa_b-bind
40771	0	0	0	1.58	0	Enolase_N;Enolase_C
40788	-2.09	0	-2.04	0	0	RmlD_sub_bind
40801	0	0	0	2.55	0	polyprenyl_synt
40958	3.22	3.49	3.3	4.92	0	TIM
40966	0	0	0	2.38	0	Sigma70_r2;Sigma70_r3
40985	0	0	0	2.71	0	GN3L_Grn1;MMR_HSR1
41014	0	0	0	5.33	0	FA_desaturase
41169	0	0	0	0	1.68	Peptidase_M16;Peptidase_M16_C
41178	0	0	0	1.69	0	HisG;HisG_C
41392	3.15	0	-1.45	0	0	Silic_transp
41425	0	0	2.12	-1.53	1.82	Ldh_1_N;Ldh_1_C
41433	-1.81	0	3.04	0	0	Pyr_redox_dim;Pyr_redox_2
41632	-1.54	0	0	0	0	Asp
41655	0	0	0	2.79	0	Chloroa_b-bind
41697	-1.29	0	0	0	0	Thioredoxin
41733	0	-1.37	0	0	-1.28	ThiC
41979	0	0	1.83	0	0	Pyr_redox_2;Pyr_redox_dim
42123	0	0	0	-2.49	2.32	GATase_2;SIS
42133	0	0	0	-1.55	0	Guanylate_cyc
42194	0	0	0	2.42	0	cNMP_binding
42258	4.7	3.41	0	0	0	WD40

42320	-1.66	0	0	0	1.72	Snf7
42515	0	0	0	1.85	0	Helicase_C;DEAD
42545	0	0	0	0	1.62	PA
42577	-2.28	-1.06	0	-2.04	0	PGK
42594	0	0	2.28	2.74	0	Ribosomal_L10
42612	0	0	0	1.41	0	SOR_SNZ
42660	0	0	0	2.21	0	0
42704	0	0	0	1.15	0	Aconitase;Aconitase_C
42804	0	0	0	0	1.5	Trypsin
43120	0	0	0	1.67	0	Thioredoxin;COPIIcoated_ERV
43128	0	0	-1.27	0	0	Saccharop_dh
260748	0	0	0	2.59	0	TRM
260761	-1.8	0	0	0	0	HA
260906	1.55	0	0	0	0	Phos_pyr_kin
260925	1.71	0	0	0	0	dCMP_cyt_deam_1
260926	-1.92	0	0	0	0	LRR_1
260934	0	0	3.08	-1.35	0	Aminotran_4
260941	0	0	0	1.26	0	CDP-OH_P_transf
260942	-2.67	-1.69	-2.47	-2.13	0	Ribonuc_L-PSP
260953	-6.13	-4.4	-5.91	-3.01	0	OCD_Mu_crystall
260962	-1.13	0	0	0	0	Rhodanese
260974	0	0	-2.02	0	0	0
260975	0	0	1.38	0	0	Na_H_Exchanger
260991	0	0	0	1.7	0	DnaJ;DnaJ_C
261036	-3.83	0	0	0	-2.26	LRR_1
261087	0	0	0	-3.48	0	Aminotran_3
261109	0	0	0	3.44	0	HSP70
261112	0	0	0	1.45	0	NUDIX
261124	1.47	0	0	0	0	AlaDh_PNT_C;Saccharop_dh_N
261161	0	2.5	0	1.4	0	Spermine_synth
261226	0	0	0	2.19	0	Pentapeptide
261232	-1.94	0	-1.57	0	0	URO-D
261242	0	0	0	2.62	0	PsbP
261275	-1.52	0	0	2.42	0	ThylakoidFormat
261284	0	0	0	1.54	0	Aldo_ket_red
261287	-1.19	0	0	0	0	SUI1
261476	0	0	0	0	1.48	Biotin_lipoyl
261525	0	0	0	2.54	0	p450
261541	-1.35	0	0	0	0	RRM_1
261636	0	0	0	1.81	0	Glutaredoxin
261641	-3.32	-2.13	0	-3.44	2.35	Ferric_reduct;FAD_binding_8;NAD_binding_6

261684	0	0	-1.81	0	0	tRNA-synt_1;Anticodon_1
261690	0	0	-1.37	0	0	ABC_tran;ABC2_membrane
261702	2.2	2.43	0	0	2.77	HSP20
261705	0	-1.38	0	0	0	Trypsin
261711	0	0	0	-1.38	1.5	Sulfotransfer_1
261726	0	0	0	-2.24	0	Metallophos;Acetyltransf_1
261727	1.2	0	0	0	0	Kringle
261748	-2.48	-1.84	-3.15	-2.06	0	cobW;CobW_C
261777	0	0	0	1.71	0	MIF4G
261820	3.27	2.36	0	0	0	Pkinase
261823	0	0	0	1.65	0	FBPase
261827	-2.1	0	0	0	0	Thioredoxin
261878	0	0	0	1.71	0	Peptidase_M50
261882	-1.77	0	0	0	1.62	Glutaredoxin
261885	0	0	1.64	0	0	RRM_1
261895	0	0	0	0	1.33	Glyco_hydro_18
261925	-1.45	0	0	0	0	PP2C
261935	0	0	0	1.39	0	Thioredoxin
261965	3.3	2.97	0	0	0	HSF_DNA-bind
261966	1.5	0	0	0	0	Pyr_redox_2
262006	0	0	0	0	-1.49	Carb_anhydrase
262009	-3.07	0	0	0	-1.98	Carb_anhydrase
262032	-2.07	0	0	-1.84	0	0
262041	0	0	1.74	1.92	0	MIF4G;MA3
262099	2.4	2.05	0	0	0	Ala_racemase_N;Ala_racemase_C
262129	2.06	2.15	0	0	0	zf-C3HC4
262146	0	0	0	-1.71	0	Cyt-b5;Chitin_synth_2
262148	0	0	0	-1.72	0	Cyt-b5
262149	0	0	0	-1.75	0	Cyt-b5
262151	0	0	0	-1.73	0	Cyt-b5;Chitin_synth_2
262153	0	0	0	-3.16	0	PT;Glyco_hydro_18
262217	-1.44	0	0	0	0	LRR_1
262229	0	0	0	1.65	0	adh_short
262236	0	0	1.42	0	0	AA_permease
262242	1.98	0	0	-1.83	0	AMP-binding
262249	-2.16	0	0	0	0	LRR_1
262250	0	0	0	0	1.22	TPR_4;IU_nuc_hydro
262254	0	0	-1.17	1.66	0	ABC_tran
262258	0	0	0	1.11	0	CitMHS
262279	-3.07	0	-2.77	1.67	0	UbiA
262307	0	0	0	-1.43	0	BCCT
262313	-5.67	-1.8	-4.27	-6.09	0	Chloroa_b-bind

262322	0	0	0	0	-1.23	Homeobox
262332	-6.81	-2.83	-6.38	-5.06	0	Chloroa_b-bind
262335	0	0	0	1.48	0	Methyltransf_11
262414	0	0	0	2.02	0	CSD
262433	0	0	1.98	-3.26	0	PUF
262455	0	0	0	0	1.86	HlyIII
262457	0	0	0	2.67	0	60KD_IMP
262506	0	0	-1.17	0	0	0
262517	1.81	0	0	-1.11	0	Glyco_hydro_18
262535	0	0	2.48	0	0	TPR_4;TPR_1
262564	-1.73	0	0	0	0	V-ATPase_H_N;V-ATPase_H_C
262567	0	0	0	0	1.75	Aldo_ket_red
262572	0	0	-1.86	0	0	Octopine_DH
262610	0	0	0	1.19	0	NUDIX
262619	0	0	0	-1.35	0	Spc97_Spc98
262620	0	0	0	4.17	0	Ank
262630	0	0	0	1.92	0	DnaJ
262659	1.94	1.99	0	0	1.31	Trypsin
262677	1.8	2.27	0	0	0	PrmA
262679	-1.88	0	0	-1.55	0	Cation_ATPase_N;E1-E2_ATPase;Hydrolase;Cation_ATPase_C
262743	-1.94	0	0	0	1.61	Choline_transpo
262753	-3.49	0	-3.7	3.35	0	peroxidase
262775	0	0	1.36	2.04	0	RBFA
262849	-3.61	-2	-4.3	-2.39	0	Chromate_transp
262946	0	0	0	2.3	0	DNA_photolyase;FAD_binding_7
262963	1.61	0	0	0	0	Phos_pyr_kin;TMP-TENI
262977	0	0	0	2.02	0	Fer2
263081	2.55	1.35	0	0	0	LRR_1
263116	0	0	0	1.48	0	Rubredoxin
263121	2.92	3.65	0	0	0	Peptidase_M8
263132	-1.74	0	-1.86	0	0	Phytochelatin
263142	1.59	1.4	0	0	0	FtsJ
263182	0	0	0	1.43	0	DUF1350
263212	1.08	1.42	-1.22	0	0	CAP
263213	1.37	1.47	0	0	0	CAP
263240	1.51	0	0	0	0	SNF2_N
263246	2.08	0	0	0	0	PI-PLC-X;PI-PLC-Y;C2
263268	0	0	0	-1.31	0	Peptidase_M8
263271	-1.8	0	0	-1.36	0	LRR_1
263287	0	0	0	0	4.27	DUF347
263298	0	0	0	-1.4	0	Cyt-b5;Chitin_synth_2

263301	0	0	0	-1.4	0	Cyt-b5;Chitin_synth_2
263313	2.05	1.73	0	0	0	Peptidase_M8
263343	1.3	0	0	0	0	HpcH_HpaI;MaoC_dehydratas
263346	0	0	0	0	1.74	LRR_1
263355	-1.46	0	0	0	0	0
263365	0	0	0	2.42	0	WW;SpoIIE
263371	0	0	0	1.54	0	DcpS_C
263431	0	0	-1.39	0	0	Peptidase_M16;Peptidase_M16_C
263451	1.51	0	0	0	0	Trypsin
263452	-1.48	0	0	0	1.78	Trypsin
263456	2.49	2.09	0	1.43	0	DUF938
263461	0	0	0	0	1.41	Methyltransf_11
263528	-2.02	0	0	-1.9	0	zf-TRAF
263641	0	0	0	1.45	0	GTP_EFTU;IF-2
263658	-1.87	0	-2.34	0	0	GUN4
263660	0	0	0	1.57	0	Acyltransferase
263661	0	0	0	3.06	0	Mito_carr
263707	0	0	0	1.61	0	Mito_carr
263781	0	0	-1.99	0	0	Sulfate_transp;STAS
263801	0	1.89	0	2.74	1.47	PseudoU_synth_2
263816	0	1.28	0	0	0	Chromo;SNF2_N;Helicase_C
263830	0	1.58	4.01	0	3.21	PFL;Gly_radical
263883	0	0	0	0	1.48	0
263887	0	0	0	0	2.83	Pkinase
263902	0	0	0	1.71	0	UbiA
263906	0	0	0	-2.75	1.81	GSHPx
263924	-1.86	-1.45	-2.05	-2.23	0	MFS_1
263935	-1.81	-1.89	-2.26	0	1.09	PAS
263938	0	0	0	-1.42	2.12	0
263953	0	0	0	-2.08	0	Guanylate_cyc
263992	-1.84	0	-1.44	-2.67	0	Thioredoxin
264004	0	1.38	0	0	0	E1-E2_ATPase
264005	0	0	2.63	0	0	Glyco_hydro_16
264008	2.25	3.53	0	0	2.12	TylF
264043	0	0	0	0	-1.1	Myb_DNA-binding
264095	0	0	0	0	1.49	TBP
264109	0	0	0	-1.51	0	adh_short
264149	-1.37	0	0	0	0	Ribosomal_L28
264157	0	0	0	-2.49	1.19	CBS
264181	-7.87	-7.66	-7.09	-9.28	0	CaMKII_AD
264269	0	0	0	0	1.49	0
264275	0	0	-1.44	0	0	CRAL_TRIO

264289	0	0	2.36	0	0	HSP20
264293	1.5	1.74	0	1.59	0	0
264295	0	1.08	0	0	0	PP2C
264335	0	0	0	2.55	0	PIP5K
264337	0	0	0	-1.8	0	0
264353	2.34	0	0	0	0	Mito_carr
264361	-1.99	0	0	0	0	Peptidase_M1;DUF3458
264384	-2.04	-2.66	-2.42	-2.48	3	0
264395	1.79	0	0	0	0	PI3_PI4_kinase
264421	-1.45	0	0	-1.35	0	ABC2_membrane
264439	0	0	0	-1.15	0	DAO
264494	0	0	0	-2.13	1.76	SIR2
264496	0	0	-1.79	0	0	Aldo_ket_red
264651	0	0	0	-2.58	1.64	Thioredoxin
264663	0	0	0	1.87	0	Thioredoxin
264664	0	0	1.66	0	0	Thioredoxin
264670	0	0	1.57	0	0	Redoxin
264671	1.01	0	0	-1.63	2.52	Pkinase
264688	0	0	0	1.97	1.29	GSHPx
264730	2.72	3.05	0	0	2.16	AdoMet_dc;Spermine_synth
264732	1.8	2.27	0	0	0	PrmA
264753	0	1.58	4.01	0	3.21	PFL;Gly_radical
264781	0	0	0	1.82	0	0
264786	0	0	0	1.27	0	RNA_pol_Rpc34
264804	0	0	0	-1.44	2.09	0
264807	-2.4	0	0	0	0	ATP-synt_C
264815	0	0	0	0	1.7	Peptidase_M3
264846	0	0	0	-1.44	1.84	Inhibitor_I29;Peptidase_C1
264854	-1.72	0	0	0	0	Pkinase
264865	-1.42	0	-2.03	0	0	CSD
264891	0	0	2.34	0	0	Glyco_hydro_30;Ricin_B_lectin
264901	-1.29	0	0	0	0	Amino_oxidase
264903	0	0	0	0	1.35	Glyco_hydro_18
267958	1.61	1.75	0	0	0	An_peroxidase
267971	0	0	1.75	0	0	MORN
268003	0	0	2.2	0	0	0
268009	0	0	0	-1.11	0	FTR1
268024	0	0	0	-2.32	0	0
268027	0	0	0	1.55	0	Met_10
268043	0	0	0	0	1.74	DUF231
268054	0	0	0	0	1.82	DUF1632;Sugar_transport
268059	0	0	0	1	0	0

268062	0	0	0	1.62	0	DnaJ;DnaJ_CXXCXGXG
268064	0	0	0	0	1.93	HSF_DNA-bind
268070	0	0	0	1.1	0	0
268117	0	1.63	0	0	-1.66	Histone
268160	-2.01	0	0	0	0	Band_7
268172	0	0	0	1.65	1.29	0
268185	0	-1.64	0	0	1.06	0
268187	0	0	-1.52	0	0	YGGT
268204	3.87	0	0	0	4.06	0
268220	0	0	0	-1.36	1.49	Peptidase_M6
268234	0	0	0	-1.78	0	0
268238	0	0	0	1.88	0	GIDA
268242	-2.18	-1.34	0	0	0	0
268270	0	0	0	1.96	0	Patched
268271	0	0	0	2.53	0	SRP54;SRP_SPB;SRP54_N
268296	0	0	0	1.59	0	Ribosomal_L12
268300	0	0	0	0	1.84	DUF493
268316	2.34	3	0	0	1.45	Annexin
268329	3.33	3.18	0	-1.42	0	Synaptobrevin
268335	0	0	0	-2.46	0	Bac_GDH;ELFV_dehydrog
268343	-2.17	-1.59	-2.21	1.48	0	0
268350	0	0	0	1.79	0	SpoU_methylase
268354	0	0	0	-1.39	1.35	Cyclin_N
268410	1.88	0	0	0	0	Pkinase
268447	-2.09	-1.63	0	0	0	Thioredoxin
268449	0	0	0	2.69	0	GST_C
268474	-2.52	0	0	0	0	NmrA
268480	-3.19	-1.66	-1.84	-1.7	0	polyprenyl_synt
268481	0	0	0	0	1.5	HSF_DNA-bind
268500	0	0	1.29	0	0	HATPase_c;HSP90;NAD_binding_1;FAD_binding_6
268546	-3.15	-2.59	0	-2.79	0	PEPcase
268548	1.48	1.49	0	0	0	Esterase;ADH_N
268594	0	0	3.63	0	0	Aminotran_1_2
268596	0	0	0	1.26	0	CBF
268619	0	0	0	1.21	0	Arf
268621	-2.57	0	-2.12	0	0	PGM_PMM_I;PGM_PMM_II;PGM_PMM_III;PGM_PMM_IV
268644	0	0	0	1.07	0	RNase_PH;RNase_PH_C;PNPase;KH_1;S1
268653	0	0	0	0	1.59	0
268657	0	0	-1.19	2.72	0	Pyr_redox_2;Pyr_redox_dim
268669	0	0	0	1.49	0	Rieske;PaO
268678	0	0	0	1.22	0	DnaJ;Myb_DNA-binding

268695	0	0	1.47	0	1.48	GTP_cyclohydro2;GTP_CH_N
268713	0	0	-2.64	0	0	0
268714	0	0	0	1.38	0	GTP_EFTU;GTP_EFTU_D2;EFG_C
268773	0	0	-1.18	0	0	0
268788	0	0	1.78	0	0	0
268839	2.58	2.04	0	0	0	RRM_1
268858	2.23	2.61	0	0	0	0
268881	0	0	0	0	1.46	Mod_r
268889	0	0	0	0	1.48	SNF2_N
268958	0	0	0	0	-2.3	0
268963	-2.12	0	1.63	-1.55	0	PUF
268965	0	0	1.96	0	0	Aconitase_B_N;Aconitase_2_N
268966	0	0	0	-1.83	0	Glyco_hydro_18
268970	1.42	0	1.62	2.39	0	2-Hacid_dh_C
269049	0	0	0	1.88	0	eIF-1a
269057	2.98	1.86	0	0	0	PGK
269086	0	0	0	1.09	0	Ribosomal_S24e
269095	-1.77	-1.8	4.45	0	0	Methyltransf_11
269115	0	1.34	0	0	0	0
269127	0	0	2	0	0	Acyl-CoA_dh_N;Acyl-CoA_dh_M;Acyl-CoA_dh_1
269135	0	0	0	0	1.56	Tic22
269141	0	0	2.4	0	0	0
269160	0	0	1.71	0	0	Pyr_redox_2
269238	0	0	2.57	0	0	HSF_DNA-bind
269258	1.86	1.69	0	0	1.72	0
269273	0	0	0	-1.56	1.9	0
269325	-2.1	0	0	0	0	HSF_DNA-bind
269328	0	0	0	-2	0	Carboxyl_trans
269355	0	0	0	0	2.65	Kazal_1
269386	0	1.49	0	0	0	Trypsin
269393	-1.82	0	0	0	0	Epimerase
269434	0	0	1.44	1.29	0	Methyltrans_SAM
269459	-1.52	0	0	0	0	0
269475	0	0	0	0	1.6	SIR2
269513	0	0	0	-1.92	1.41	Acyl-CoA_dh_N;Acyl-CoA_dh_1;Acyl-CoA_dh_M
269541	0	0	0	0	2.79	Peptidase_M20
269557	-3.08	0	1.56	-1.57	0	NAD_binding_4
269559	0	0	0	1.56	0	rRNA_processing
269575	0	0	0	0	1.27	0
269633	0	4.34	0	0	0	0
269653	-2.45	-1.49	0	-1.93	2.27	0

269655	0	2.53	0	0	0	Tubulin;FtsZ_C
269696	-4.53	-3.62	-5.46	-2.25	3.03	0
269699	-4.53	-3.62	-5.49	-2.22	3.03	0
269714	0	1.2	0	0	0	APS_kinase;ATP-sulfurylase;Pyrophosphatase
269764	0	0	0	2.19	0	PseudoU_synth_2
269776	0	0	1.84	2.23	0	0
269779	0	0	0	1.42	0	Ribosomal_S6e
269792	0	0	0	0	2.04	Annexin;WD40
269826	0	0	0	-1.95	0	Cyclin_N
269844	-1.41	0	1.61	-1.66	0	Glyco_transf_28;UDPGT
269866	0	-1.13	1.67	0	0	GST_N;GST_C
269876	0	-1.54	0	-2.08	2	0
269889	0	0	-1.26	-1.18	0	Pkinase
269900	0	0	1.89	0	0	GATase_2;Glu_syn_central;Glu_synthase;GX GXG
269908	-3.97	-2.29	-3.72	-2.69	0	CPSase_L_chain;CPSase_L_D2;Biotin_carb_ C;HMGL-like;PYC_OADA;Biotin_lipoyl
269952	2.14	1.77	0	0	0	MtN3_slv
269968	0	0	-2.07	-1.47	0	Rhodanese
269975	0	0	1.51	1.65	0	0
269997	1.68	0	0	0	0	0
270013	0	0	0	1.52	0	3_5_exonuc;SAP;DNA_pol_A
270038	-1.25	0	0	0	0	Peptidase_C14
270092	-3.73	-2.63	-3.66	-2.45	-1.58	Chloroa_b-bind
270113	0	0	0	0	2.15	cNMP_binding
270127	0	0	0	0	1.64	Glyco_hydro_18;CBM_14
270136	0	0	1.77	0	0	Aminotran_3
270137	-1.85	0	0	-5.1	0	efhand

Table S7: List of *Thalassiosira pseudonana* proteins returning hits from NPAC, bacillariophyta-like sequences.

ID	# Hits	Si	Fe	N	T	Co2	PFAM
6363	7821	0	0	0	1.27	0	Ribosomal_L23eN
5259	1228	0	0	0	1.14	0	Ribosomal_L44
2848	111	-2.6	-1.56	-4.74	-1.55	0	PsbU
25772	73	0	0	-1.33	0	0	Actin
28496	40	-2.89	1.44	-2.04	2.42	0	AdoHcyase
38715	29	-5.85	-1.17	-3.96	-3.62	0	Chloroa_b-bind
41829	28	1.38	0	0	0	0	GTP_EFTU;GTP_EFTU_D2;GTP_EFTU_D3
6285	20	0	0	0	1.34	0	HATPase_c;HSP90
42962	20	0	0	1.38	0	0	Chloroa_b-bind
31383	19	-3.61	-1.01	-3.43	1.04	0	Gp_dh_N;Gp_dh_C
575	17	-3.58	0	-4.11	0	0	Aminotran_3
866	16	0	0	-1.32	0	0	CLP_protease
12152	15	-2.94	0	-2.9	2.28	0	ketoacyl-synt;Ketoacyl-synt_C
26893	14	0	0	0	1.47	0	Ribosomal_S13
25933	13	0	0	-1.62	0	0	TPT
41256	12	-1.31	0	0	0	0	ATP-synt_ab_N;ATP-synt_ab_C
41548	12	0	0	0	0	1.7	Epimerase
26051	11	0	0	0	1.68	0	Gln-synt_N;Gln-synt_C
31705	10	-1.84	-1.13	0	-2.18	0	Mpv17_PMP22
264201	10	0	0	0	1.28	0	Ribosomal_L2;Ribosomal_L2_C
38583	9	-4.98	-1.28	-4.31	-2.28	0	Chloroa_b-bind
9716	8	0	0	0	1.69	0	DEAD;Helicase_C
268127	8	-5.69	-1.11	-7.68	-5.58	0	Chloroa_b-bind
268304	8	-3.86	-1.19	-4.27	0	0	
33018	7	-6.19	-1.67	-6.41	-3.45	0	Chloroa_b-bind
802	6	0	0	0	1.02	0	Ribosomal_L18p
32924	6	-3.56	-2.49	-3.43	0	0	Ribul_P_3_epim
39143	6	1.16	0	0	0	0	Mito_carr
264921	6	-4.12	-2.46	-1.86	2.68	0	Chloroa_b-bind
428	5	-4.88	-2.57	-2.2	0	0	F_bP_aldolase
1326	5	-2.16	0	0	0	0	ATP-sulfurylase
29825	5	0	0	0	1.23	0	Ribosomal_S8e
32201	5	-4.33	0	-3.08	0	0	Mg_chelatase;VWA
39936	5	0	0	0	1.57	0	Metallophos
1738	4	0	0	-1.59	0	0	CLP_protease
21175	4	-4.53	-1.14	-5.62	0	0	Transketolase_N;Transket_pyr;Transketolase_C
32546	4	0	0	-1.6	2.13	0	Cyt-b5;FA_desaturase

262125	4	-3.45	-1.49	0	0	0	NIR_SIR_ferr
3622	3	-1.09	0	-1.19	0	0	IspD
21815	3	0	1.47	-1.84	1.53	0	S-AdoMet_synt_N;S-AdoMet_synt_M;S-AdoMet_synt_C
22565	3	-2.12	0	1.44	0	0	Sugar_tr
26046	3	0	0	0	1.11	0	Ribosomal_S3Ae
28189	3	0	0	0	3.65	0	HSP70;NAD-GH
31012	3	-3.51	-1.87	-2.97	0	0	Coprogen_oxidase
31516	3	0	0	0	1.46	0	NOP5NT;NOSIC;Nop
32555	3	-1.58	0	0	0	0	Ribonuc_red_sm
32752	3	0	0	0	1.16	0	Ribosomal_L24e
39278	3	-1.17	0	0	0	0	ATP-synt_C
42326	3	-2.22	0	-2.37	-1.87	0	UDPGP
269274	3	-3.27	0	0	-2	0	MFS_1
2343	2	-2.21	0	-3.64	1.87	0	
3741	2	-1.71	-1.41	0	2.13	0	ELO
4830	2	0	1.64	0	0	0	Cofilin_ADF
5021	2	0	0	0	2.02	0	ketoacyl-synt;Ketoacyl-synt_C
5174	2	-3.9	0	-5.07	-4.63	0	Chloroa_b-bind
10234	2	-4.48	-2.55	-3.98	-1.15	0	FAD_binding_3
11411	2	0	0	2.09	0	0	Citrate_synt
20603	2	-6.96	-2.64	-7.64	-2.61	0	
25892	2	-4.33	-1.44	-3.64	0	0	NAD_binding_1
26221	2	0	0	0	1.02	0	Ribosomal_S13_N;Ribosomal_S15
26367	2	0	0	0	1.21	0	Ribosomal_S8
28125	2	-1.81	0	0	0	0	GlutR_N;Shikimate_DH;GlutR_dimer
31446	2	0	0	0	1.11	0	Ribosomal_S21
33008	2	0	0	0	1.86	0	EPSP_synthase
36235	2	-2.24	0	-1.52	0	0	p450
36979	2	0	0	0	2.01	0	Fcfl
38667	2	-5.92	-1.49	-4.18	-3.48	0	Chloroa_b-bind
39901	2	0	0	0	0	1.39	PGK
40391	2	-1.82	0	1.83	0	0	Enolase_N;Enolase_C
269240	2	0	0	1.83	1.63	0	HSP70;NAD-GH
3815	1	-5.93	-3.43	-3.8	-5.97	0	Chloroa_b-bind
4914	1	-3.23	0	-3.32	0	0	NAD_binding_1
5219	1	-2.66	-2.41	-2.69	0	0	Acyl_transf_1
5240	1	-2.5	0	-2.92	-3.08	0	ALAD
8522	1	-2.23	0	0	0	-2.35	Ribonuc_red_sm
9021	1	-2.95	0	0	0	0	Porphobil_deam;Porphobil_deamC
10233	1	-1.74	0	-1.45	0	0	
11501	1	-5.78	-1.87	-5.7	-2.24	0	Chloroa_b-bind

13806	1	-1.17	0	0	0	0	tRNA-synt_1c;tRNA-synt_1c_C
20008	1	0	0	0	1.36	0	Ribosomal_S26e
20965	1	-7.71	-2.61	-7.03	-3.37	-1.4	
21261	1	-2.28	0	0	0	0	Rubredoxin
21292	1	1.31	0	0	0	0	CitMHS
21327	1	-1.62	0	-1.93	0	0	DUF1625
21972	1	-1.75	0	0	3.01	0	
22350	1	0	0	0	1.38	0	Ribosomal_S21e
22476	1	0	0	0	1.43	0	Ribosomal_L13e
23283	1	-1.74	0	-2.07	0	0	
24250	1	-1.5	0	1.76	0	0	SSF
26436	1	0	0	0	1.7	0	Peptidase_M3
26573	1	-3.65	-1.62	-3.28	0	0	DUF3479;CobN-Mg_chel
27873	1	0	0	1.55	0	0	IMPDH
29217	1	0	0	0	1.17	0	Ribosomal_L7Ae
29375	1	-5.89	-1.9	-6.91	-4	0	Chloroa_b-bind
29728	1	0	0	0	0	1.67	Epimerase
29842	1	-4.9	-1.85	-4.56	-1.78	0	
29861	1	0	0	1.65	0	0	GATase_2;Glu_syn_central;Glu_syn thase;GXGXG
31014	1	0	0	0	1.59	0	Adap_comp_sub
31091	1	-2.13	0	-1.72	0	0	NDK
31851	1	-1.58	0	-1.94	2.95	0	adh_short
31912	1	-1.36	0	0	0	0	Pro_isomerase
32955	1	-2.59	-1.71	-3.24	0	0	ADH_N;ADH_zinc_N
33871	1	0	0	0	1.69	0	Metallophos
34585	1	-2.72	-2.43	-3.81	0	0	Radical_SAM;BATS
34830	1	-4.34	-1.9	-5.16	-1.91	0	MSP
34864	1	0	0	-1.2	2.39	0	FKBP_N;FKBP_C
35180	1	-7.04	0	-1.56	-1.08	-1.87	Mpv17_PMP22
35712	1	-4.7	0	-5.16	1.56	0	PGK
35816	1	0	0	-1.51	0	0	Gp_dh_N;Gp_dh_C
35934	1	-4.71	-1.26	-4.14	0	0	Cytochrom_C
37083	1	0	0	0	1.17	0	DnaJ;DnaJ_C
39003	1	0	0	2.91	3.93	0	UPF0113
39666	1	-1.14	0	0	0	0	cobW;CobW_C
40156	1	-2.65	0	-2.08	0	0	ATP-synt
40312	1	0	0	0	1.15	0	Ribosomal_S9
41005	1	-2.34	0	-2.43	0	0	Transket_pyr;Transketolase_C
41113	1	0	0	0	1.79	0	Cyt-b5;FA_desaturase
262796	1	-3.1	-1.28	-4.57	0	0	PP-binding
264039	1	-2.02	0	-2.37	0	0	p450

268374	1	0	0	2.49	0	0	E1_dh
268895	1	7.15	0	-1.35	0	0	Silic_transp
269348	1	-1.97	0	-2.4	0	0	Pyrophosphatase
269942	1	-2.92	0	-2.57	0	0	SHMT

Table S8. Genes investigated during this study and sequences of the primers used to amplify target genes by qPCR.

Gene Target/protein ID	Primer sequence (5' - 3')	Amplicon size (bp)
Large ribosomal protein L27e/269038	Fwd: GTCCGTCATATCTTCCCAACAC Rev: TACTCGACGTTCCGCATCAAC	93
Large ribosomal protein L22/270383	Fwd: TGCACATGGTCGAATTGGTA Rev: GTTTGGCGGCCATCTTTCTG	131
Large ribosomal protein L14/271911	Fwd: TTGCCCTAACGGATTAACTGTG Rev: AGACGTGTCTTCTTGGATTGC	142
Small ribosomal protein RPS11/268264	Fwd: TACTGCCTTACACATCAAAGTTC Rev: AGAGGGGATTGGTGTGACATC	142
Small ribosomal protein S1/274976	Fwd: GATTCCTCGATGGATTAGGTGA Rev: GAATCAAGAGAATCAGAAACATCCG	89
TATA-box binding protein TBP/143154	Fwd: GCATTTGCCTCCTATGAACCAGA Rev: CTTTGCACCTGTTATCACAAACCTTC	114
RNA polymerase RNAP II/183218	Fwd: TCGGAGCTGCTTCCTTTTCTC Rev: TTGTGGACTGGATGGGTTGTAAC	128
Major allergen MA control	Fwd: TCGGTTGACAGATACCTTAAAGGAA Rev: TCAAAGGTGACGTTTCGAGTTCAT	100

Table S9: NCBI accessions and Pfam domains detected for Fucoxanthin chlorophyll binding proteins (FCPs), Nitrate reductases and Silicon transporters for *Cylindrotheca fusiformis* (C.F.), *Phaedactylum tricornutum* (P.T.) and *Thalassiosira pseudonana* (T.P). * Downloaded from NCBI RefSeq, all other gene sequences downloaded from NCBI Genbank. Based on HMM searches of Pfam-A using default gathering thresholds.

	C.F.	P.T.	T.P.	Pfam domain(s)
FCPs	AAN08838	EEC51450	ACI64366	chloroa_b-bind
Nitrate Reductase	AAY59538	AAV66996	XP_002294410*	Oxidored_molyb, Mo-co_dimer, Cyt-b5, FAD_binding_6, FAD_binding_1
Silicon Transporter	AAD13807	ABB81809	ABB81827	Silic_transp

Supplementary Figures

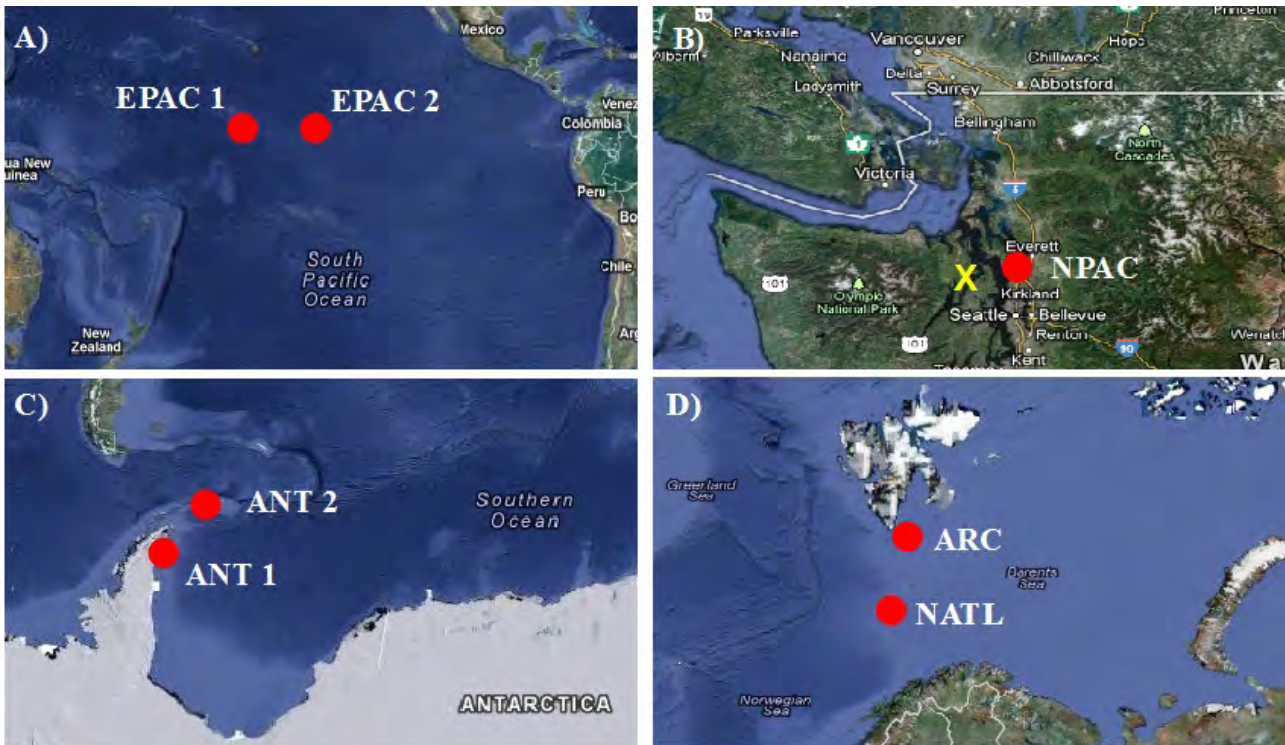
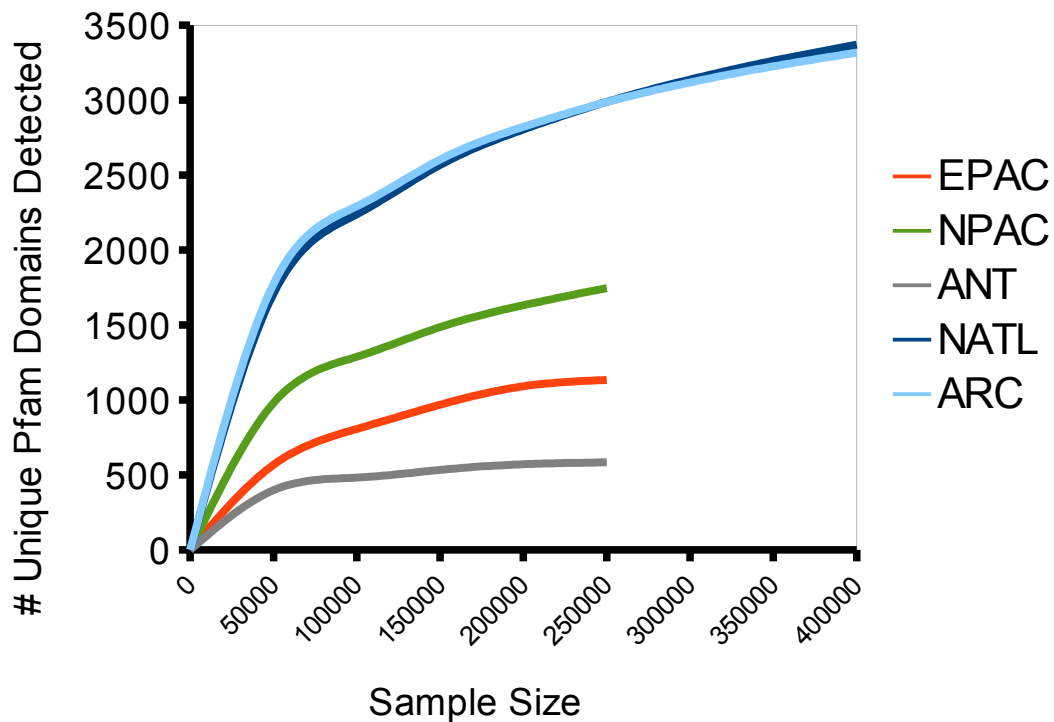


Figure S1: Sampling sites for: A) EPAC 1, 2 (Equatorial Pacific), B) NPAC (North Pacific), Hansville buoy (ORCA) (yellow X) at 47°54.44”N and 122°37.62W was used to obtain oceanographic profiles of T, S, density, O₂, and in situ fluorescence close to the sampling site. C) ANT 1, 2 (Antarctic), D) ARC (Arctic) and NATL (North Atlantic). Maps obtained from Google Maps.



	ANT	ARC	EPAC	NATL	NPAC
# Unique Pfam domains detected	583.00	3316.00	1133.00	3369.00	1746.00
Chao-1 Estimate	720.20	3873.14	1652.39	4064.53	2239.90
% of estimate detected	80.95	85.62	68.57	82.89	77.95

Figure S2: Top: Pfam protein domain rarefaction curves for Equatorial Pacific (EPAC), North Pacific (NPAC), Antarctic (ANT), North Atlantic (NATL) and Arctic (ARC) metatranscriptomes. (Chao-1 estimator of species richness using 50,000 sequence increments. <http://www.biology.ualberta.ca/jbrzusto/rarefact.php>). Bottom: table showing total number of unique Pfam domains detected in each sample, the Chao-1 estimate of unique domains and the percentage of Chao-1 estimate detected in each sample

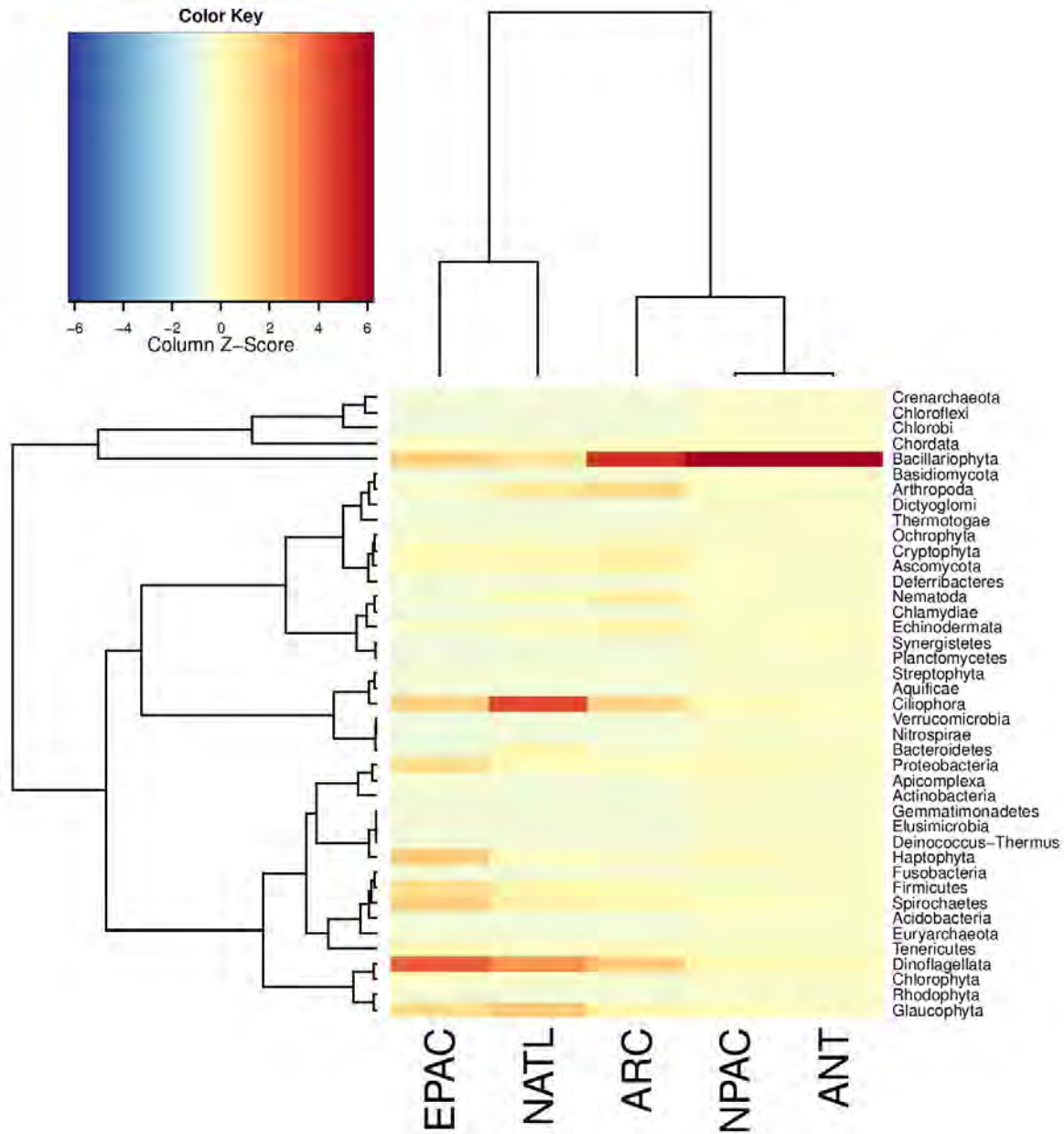


Figure S3: Heatmap for all PhymmBL-classified sequences at the Phylum level (confidence score of ≥ 0.9) Complete linkage clustering was performed based on a correlation matrix (1-Pearson correlation coefficient) of relative abundances. Heatmaps scaled and centred by column.

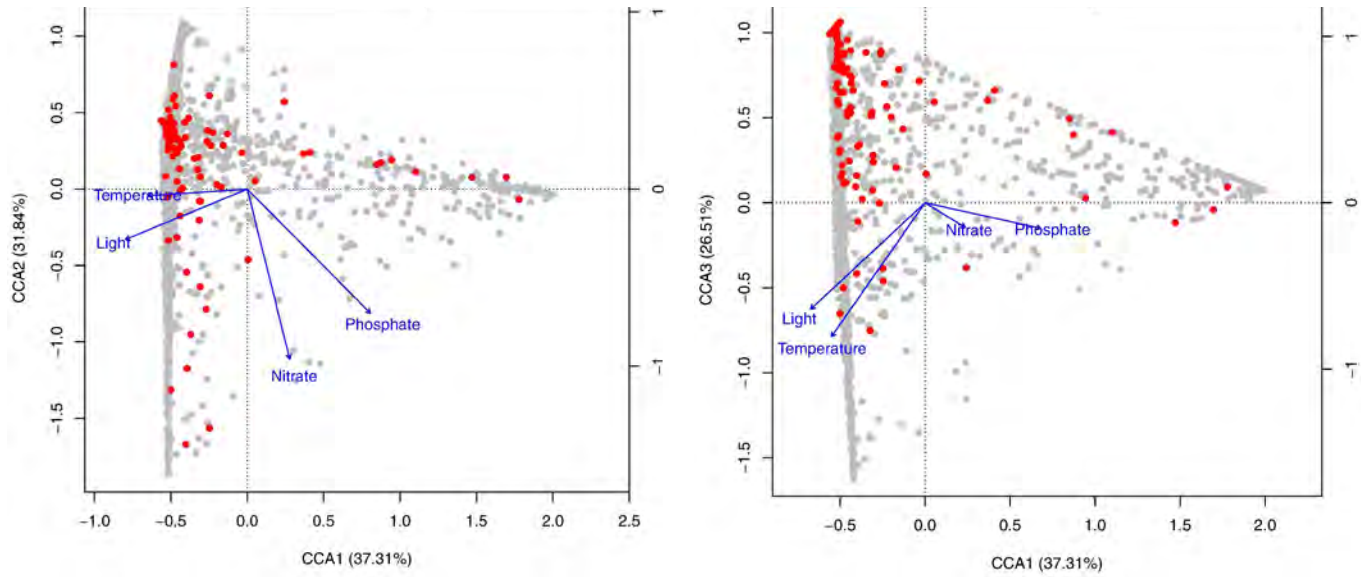


Figure S4: Canonical correspondence analysis (CCA) between protein family (Pfam) abundance and environmental conditions (Temperature, Light, Nitrate and Phosphate) deduced from ocean samples in this study, red dots represent ribosomal transcripts. Figures represent dimensions 1 and 2 (Left) and 1 and 3 (Right).

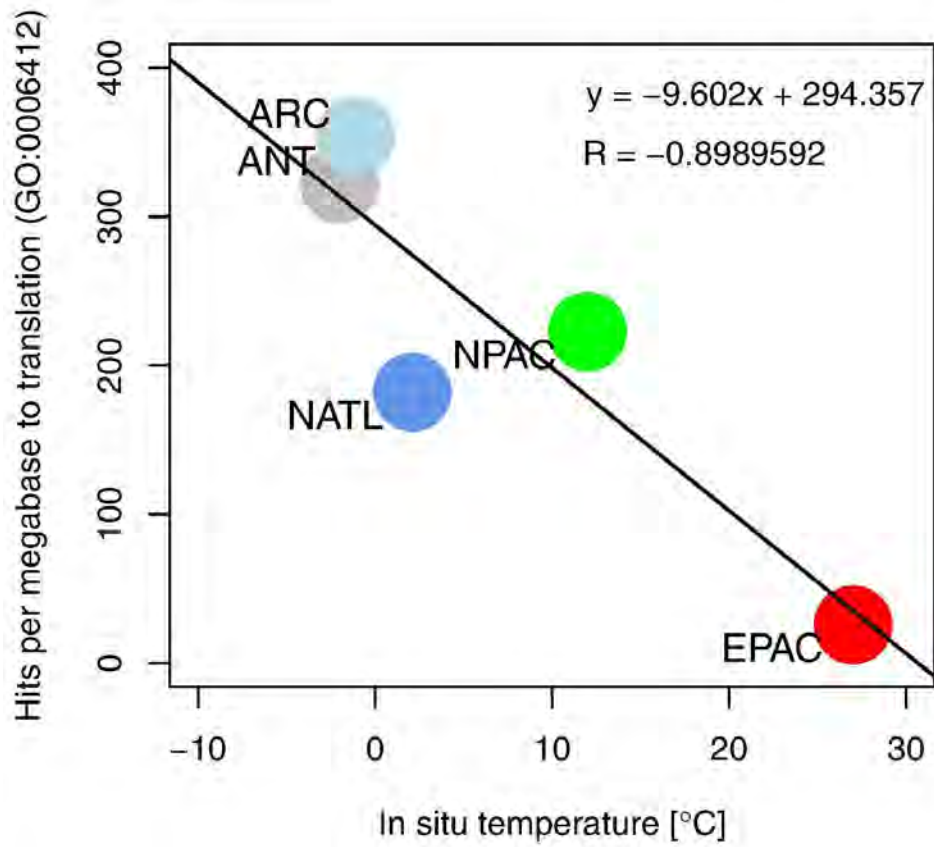


Figure S5: Correlation analysis between the normalised abundance of sequences associated with the GO term for translation and in-situ temperature of metatranscriptomes.

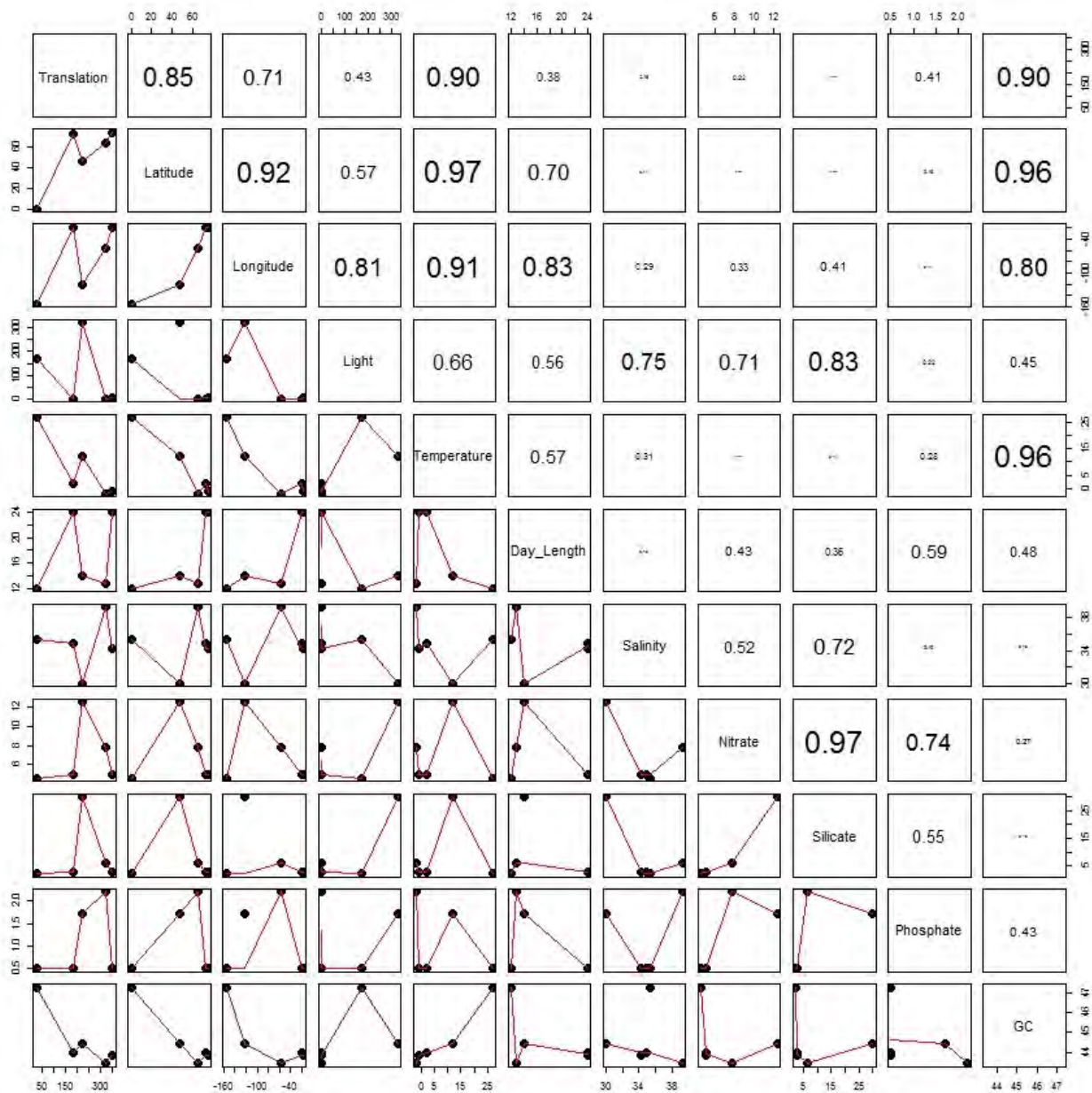


Figure S6: Multiple correlation plot between normalised abundance of metatranscriptome sequences associated with GO:0006412 – translation and environmental factors. Lower triangle displays scatter plot of factors from the central diagonal. Upper triangle displays scaled correlation coefficient between factors from central diagonal.

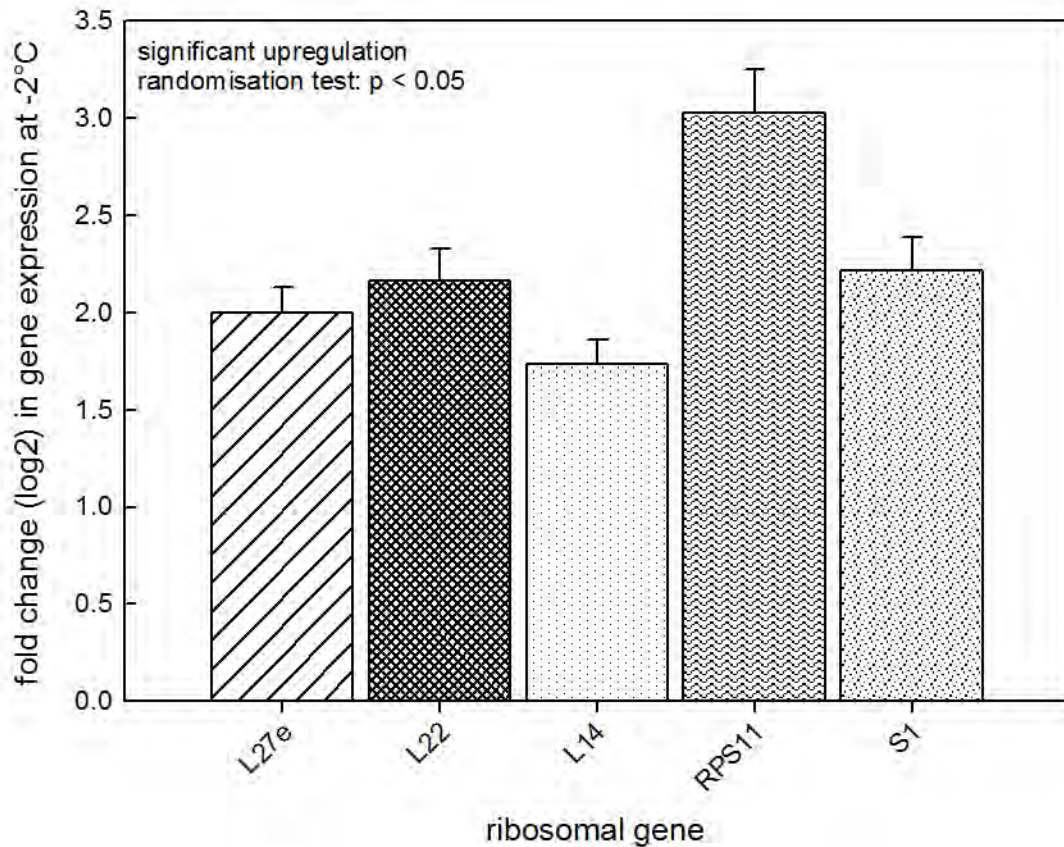
Expression of ribosomal protein genes at -2°C relative to 10°C 

Figure S7: qPCR analysis of 5 ribosomal genes determined in the polar diatom *F. cylindrus* at the freezing point of seawater (-2°C). Changes in expression are shown as log₂ of fold changes relative to *F. cylindrus* grown at $10\text{--}11^{\circ}\text{C}$. Data was normalised to the geometric mean of 3 reference genes (*TBP*, *RNAP II*, *MA*) and represents mean values and standard error from biological replicates ($n=3$) and technical replicates ($n=2$). Significances ($p < 0.05$) were tested using pair wise fixed reallocation randomisation test (*Relative Expression Software Tool*).

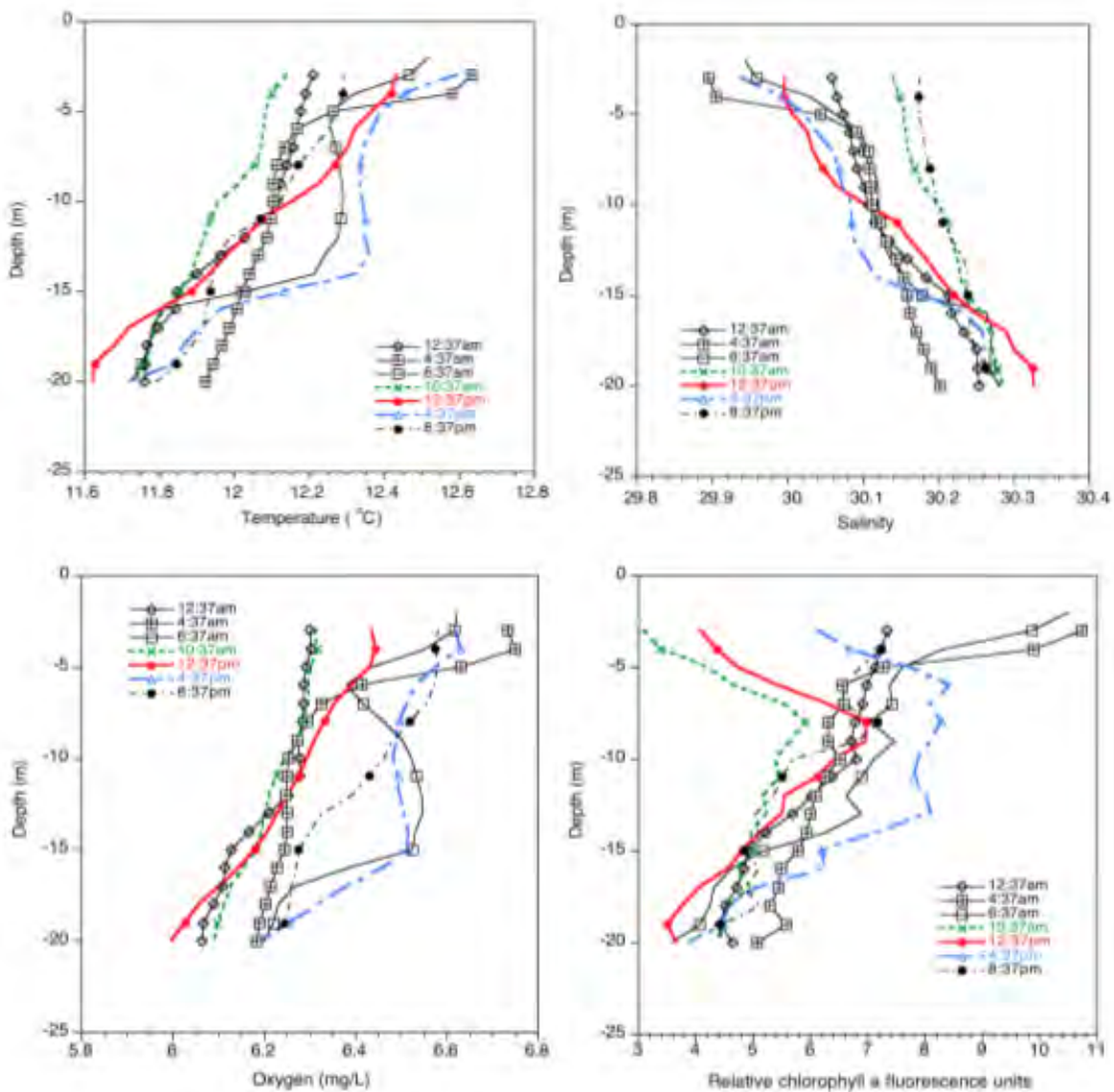


Figure S8: Hansville buoy (ORCA) (47°54.44'N, 122°37.62'W) oceanographic profiles of T , S , O_2 , and in situ fluorescence. Red line indicates time point (12:37pm) of sampling. C) and D) indicates subsurface bloom development with maximum chl a concentration between 5 and 15 m depth.

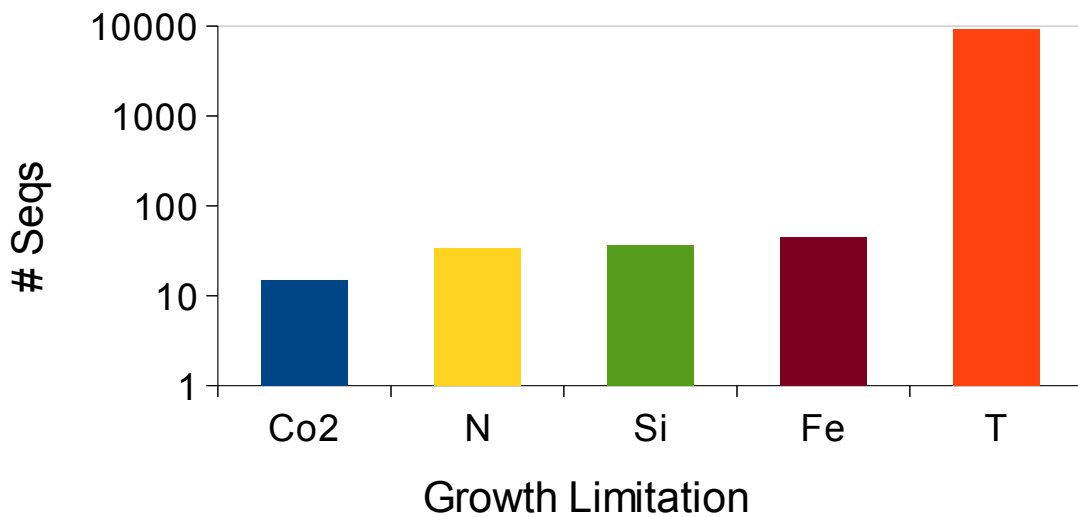
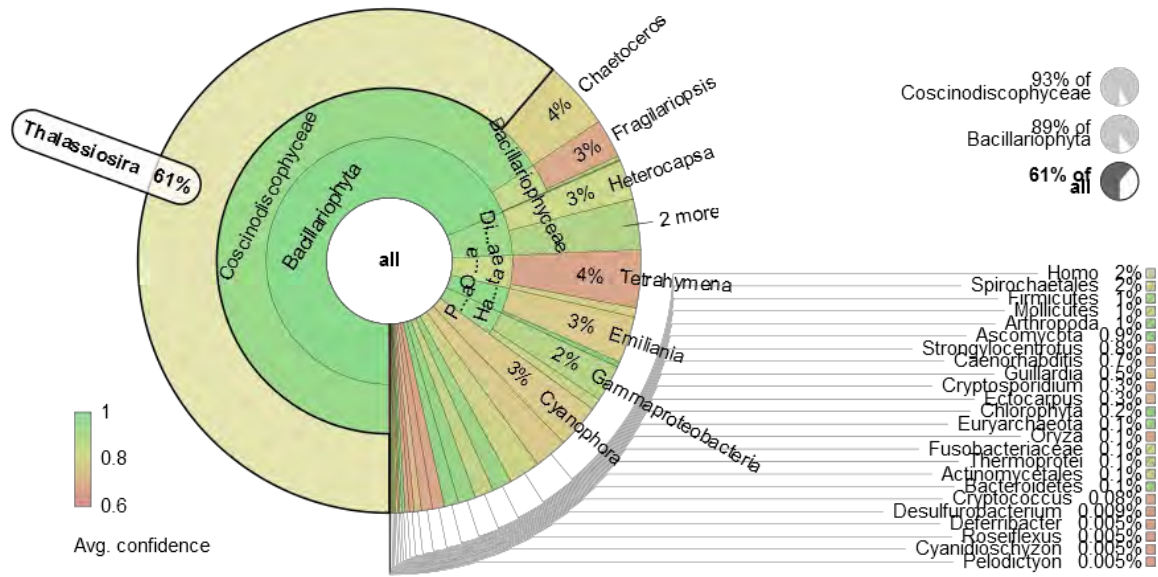


Figure S9: Top: KRONA chart of NPAC (North Pacific) taxonomic affiliations at the genus level, coloured by average confidence score. Bottom: Frequency of NPAC *Thalassiosira*-like sequences matching to *Thalassiosira pseudonana* genes (blastx with *e*-value cutoff < 1e-5, requiring ≥ 75% identity and ≥ 50% coverage of the query sequence) upregulated under different growth limitations (Note log scale on y-axis).

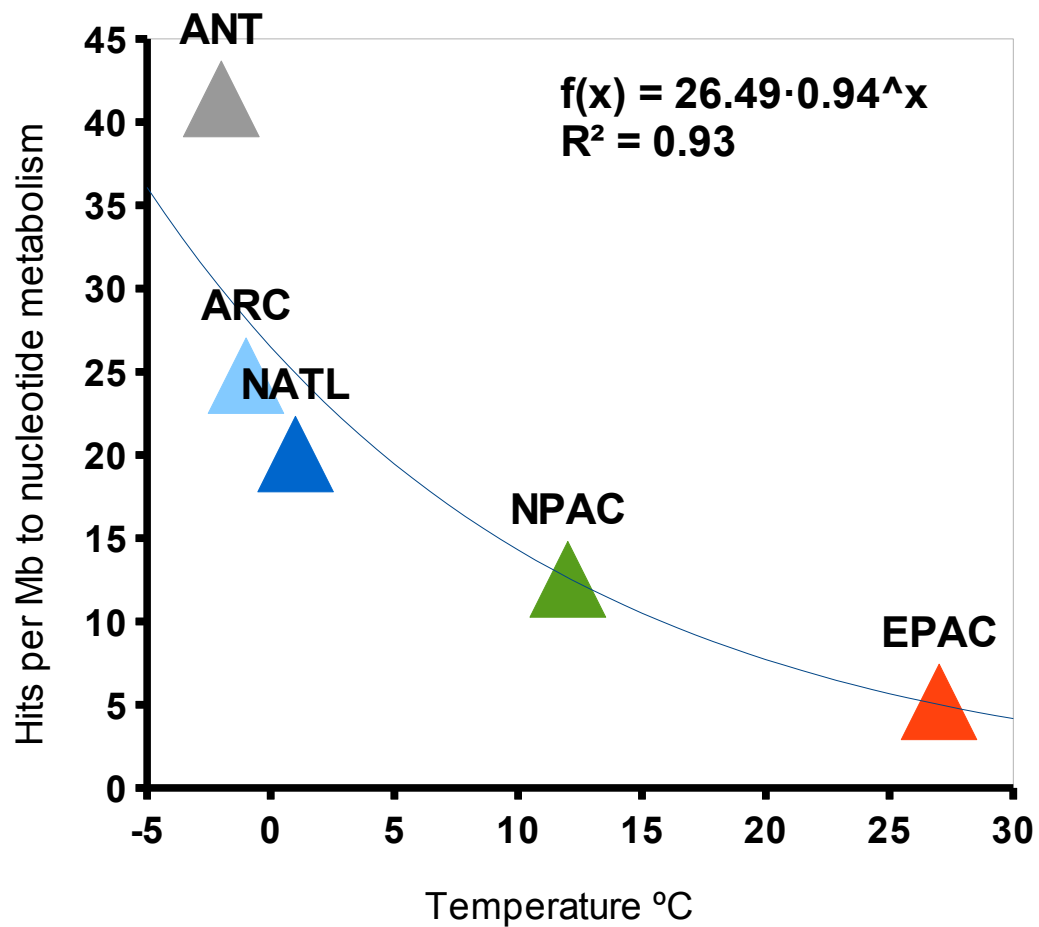


Figure S10: Plot of normalised abundance of sequences matching to nucleotide metabolism (KEGG pathways K000230: Purine metabolism and K000240: Pyrimidine metabolism) against temperature with exponential regression line.

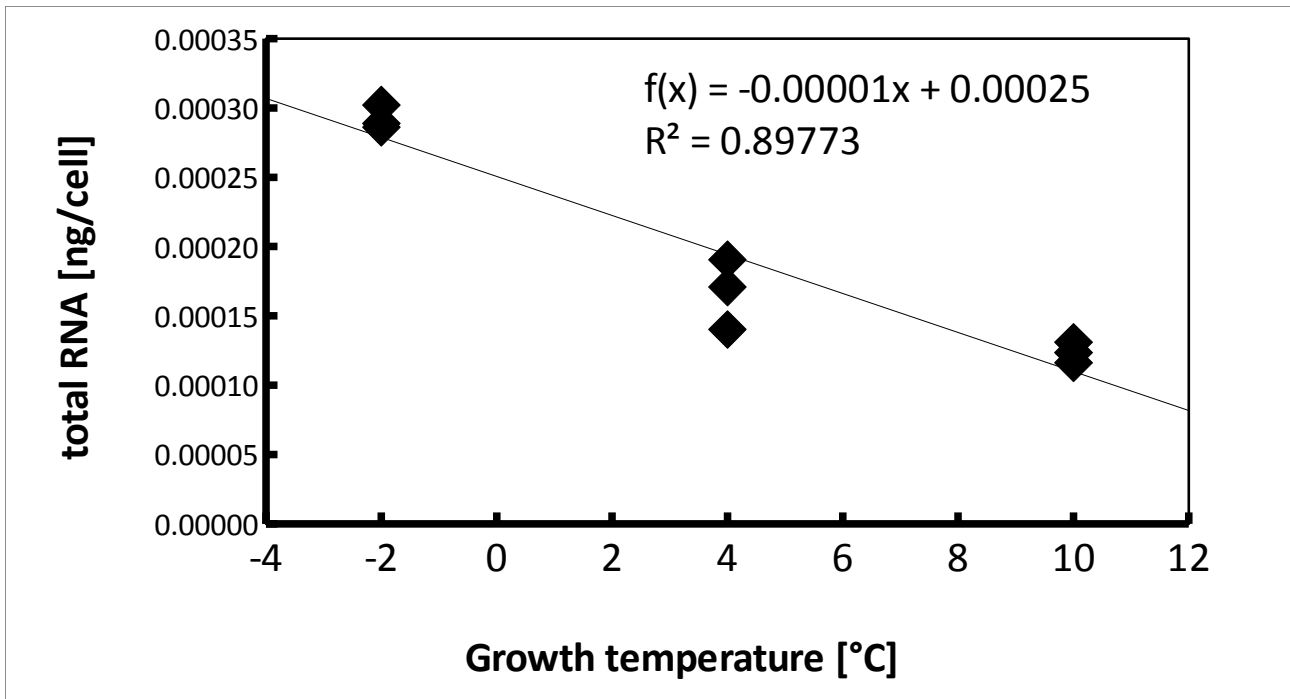


Figure S11: Correlation analysis between total RNA per cell and growth temperature. Shown are total RNA concentrations per *Fragilariopsis cylindrus* cell as calculated from biological replicates grown under -2°C, +4°C and +10°C.



Figure S12: Enriched GO terms from a pairwise comparison between EPAC (Equatorial Pacific) and ANT (Antarctic). Top: Terms enriched in EPAC compared to ANT, Bottom: Terms enriched in ANT compared to EPAC. Enriched GO terms were identified through pairwise Fisher's exact tests on relative GO term abundances (Bonferroni corrected P -value < 0.001). Term clouds created with <http://www.worditout.com> scaling terms by the absolute difference in the relative abundance of the enriched term and using direct colour blending from blue (low frequency) to red (high frequency).

6 Phytoplankton growth strategies and resource allocation in a global marine ecosystem model

6.1 Model description

The agent and trait-based global marine ecosystem model is described fully in previous publications: the agent-based modelling approach is described in Clark *et al* (2011)²³; the sub-cellular resource allocation model, integration with the agent-based model, and the coupling to the MIT-gcm is described in Clark *et al* (2013)²⁴; and the representation of rRNA, cellular stoichiometry, and extensions to a global model including predation and cell-size parameterisation for high latitudes are described in Daines *et al* (2013)²⁵. Here we summarize the key features of the model. Phytoplankton diversity is represented by a trait-based generic cell model which includes a coarse-grained representation of physiology and allocation to subcellular compartments. Phytoplankton growth strategies (PGS) and hence cellular resource allocation and composition are then an emergent result of environmental selection including multiple drivers (light, nutrients and temperature).

The cell model is described fully in references Clark *et al* (2013)²⁴ and Daines *et al* (2013)²⁵. The phytoplankton cell model represents allocation to three components: L represents cellular resource allocation (fraction of cell nitrogen) to the photosynthetic light harvesting apparatus (including chlorophyll and accessory pigments), E represents the biosynthetic apparatus (including aggregated enzyme systems and ribosomes involved in small and large molecule biosynthesis), and a size-dependent allocation to cell structure $S(r)$ including cell surface associated components involved in nutrient acquisition and assimilation, and all 'other' components not directly involved in either photosynthesis or biosynthesis. Two traits, for cell radius r which determines $S(r)$, and (2) relative allocation to L vs E , combined with the constraint that $L + E + S(r) = 1$, then determine a two-dimensional trait space. Growth rate is then given by the most limiting of light-harvesting mass-specific rate, $f_p = k_p I_z L$ (where I_z is incident light intensity and k_p is an empirically determined rate constant), temperature-dependent biosynthesis rate, $k_s Q_{10}^{(T-T_o)/10} E$ (where temperature dependence is represented by the factor Q_{10} , and k_p is an empirically determined rate constant), and mass-specific nutrient uptake (assumed diffusion limited and hence related to cell radius r by $f_N \propto 1/r^2$). C:N stoichiometry and fractional contribution of carbon and nitrogen to dry mass are assumed constant and fixed for each compartment, hence relative cellular pool allocation as biomass, carbon and nitrogen are equal. Internal fluxes are represented in carbon units. Phosphorus content is pool-specific.

The ecosystem model uses an agent-based approach to represent a diverse phytoplankton population, sampling a trait-space (where the two traits represent cell size, and subcellular resource allocation). A population of ~ 800 individual Lagrangian agents (each representative of many real-life individuals,^{26,27}) is maintained in each grid cell of a physical Eulerian ocean model, along with the concentration of a single limiting nutrient, light, and temperature. Agents consume resources, grow, reproduce, and may be consumed by predation and cycled through particulate and dissolved detrital pools to inorganic nutrient. Biotic interactions are represented by a parameterisation of size-dependent predation.

6.2 Emergent phytoplankton growth strategies and resource allocation

The model captures major patterns between permanently-stratified, resource-limited oligotrophic gyres, high-latitude bloom-forming regions, and equatorial upwelling regions. Nutrient supply is the major driver for ecosystem structure in the oligotrophic gyres, resulting in selection for small cell size limited by an imposed trade-off such that small cells pay an increased cost in allocation to S (representing cell-surface associated structure and nutrient-uptake machinery), and slow, nutrient-limited growth rate (Figure S-13). High-latitude, bloom forming regions favour larger, fast-growing cells. In these regions, temperature and light then determine the relative allocation to biosynthesis and light-harvesting machinery.

6.3 Relating resource allocation to metagenomics

The resource-allocation patterns for S, L and E in the global model (Figure S-13) may be identified with broad classes of protein families in the global metatranscriptomic dataset (Figure S12).

7 rRNA allocation

We summarise here results from Daines *et al* (2013)²⁵. We assume that per-ribosome peptide synthesis rate $(\phi_a \sigma_a)_T = (\phi_a \sigma_a)_{T_0} Q_{10}^{(T-T_0)/10}$ is conserved across eukaryotic taxa, with a temperature dependence defined by a Q_{10} scaling. The minimum rRNA requirements (relative to cellular protein) for protein synthesis and growth are then a function of growth rate and temperature. In the coarse-grained cell model, the biosynthesis pool E represents both small and large molecule biosynthesis. This is partitioned optimally into rRNA and small molecule biosynthesis, based on a parameterization of ribosomal transcription rate and the parameterisation of overall mass-specific biomass generation rate by the E pool, with κ_S derived from laboratory measurements^{28,29}. Combined with phytoplankton growth strategies derived

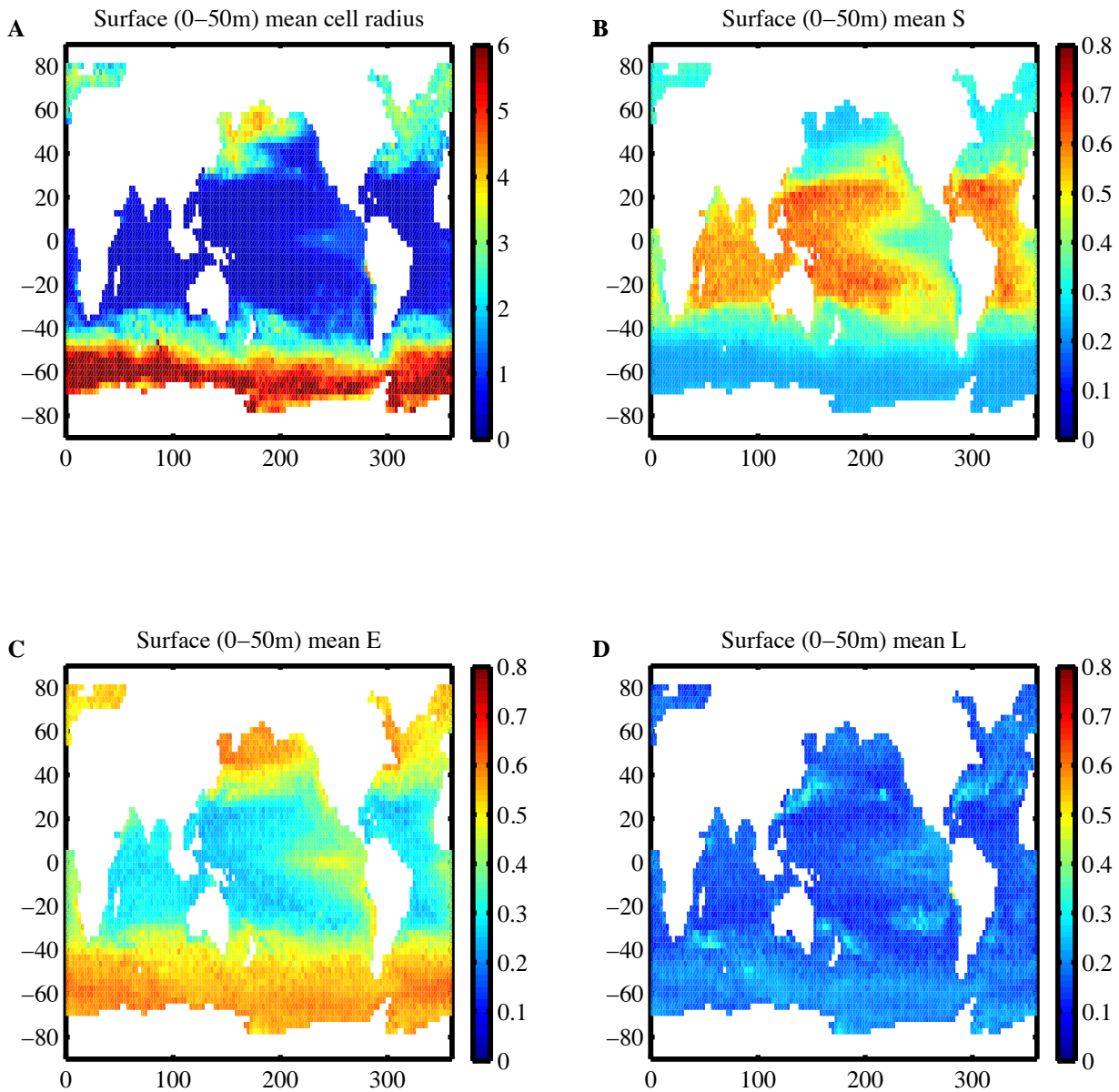


Figure S-13: Model emergent biogeography, phytoplankton growth strategies, and cellular nitrogen allocation. A (top left): cell size. B (top right): allocation to “structure” including cell-surface associated machinery. C (bottom left): Allocation to biosynthesis machinery. D (bottom right): allocation to light harvesting machinery. All properties are biomass-weighted annual means for the model surface layer (0-50m).

Table S-10: Stoichiometry of macromolecules and cellular components³⁰. Eukaryotic ribosome is assumed to have composition rRNA:protein ratio 1.2:1

Macromolecule / component	%C	%N	%P	C:N:P
protein	53	17	0	3.6:1:0
RNA	32.7	14.5	8.7	9.7:3.7:1
phospholipid	65	1.6	4.2	40.0:0.84:1
eukaryotic ribosome	41.9	15.6	4.7	23.0:7.3:1
membrane (70% protein, 30% phospholipid)	56.6	12.38	1.26	116.0:21.8:1
bacterial membrane ³⁰	55	13.7	0.86	162:35:1
'Redfield' autotroph with gC/gdw = 0.5	50	8.81	1.22	106:16:1

Table S-11: Biological constants determining minimum rRNA requirements for growth

Parameter	Description		Units
m_a^{tot}	Average mass of an amino acid in peptide changes	110	Da
m_r^{tot}	Average mass of a ribonucleotide	340	Da
σ_a	Peptide elongation rate		aa rib ⁻¹ s ⁻¹
ϕ_a	Fraction of ribosomes actively translating	0.8	-
l_r	Length in ribonucleotides of rRNA in one eukaryotic ribosome	6860	

from the global model, this then determines patterns in allocation to rRNA. We may further use absolute laboratory calibrations for per-ribosome protein synthesis rate to determine the rRNA contribution to N:P stoichiometry.

7.1 rRNA requirements for protein synthesis and growth

The minimum rRNA required to provide protein synthesis for growth (mass ratio of rRNA to protein) as a function of growth rate μ depends (only) on the empirically determined per-ribosome protein synthesis rate, and other biological parameters which are more directly related to “structural” properties of biomolecules (Table S-11, data from Loladze and Elser (2011)³¹).

The minimum cellular-level ratio of rRNA dry mass to protein dry mass required for protein synthesis for growth $r_{cellrRNA:prot}^{mass} = m_{cellrRNA}^{tot}/m_{cellprot}^{tot}$ is given by:

$$r_{cellrRNA:prot}^{mass} = 5.9 \left(\frac{\mu}{1 \text{ h}^{-1}} \right) \left(\frac{\phi_a \sigma_a}{1 \text{ aa rib}^{-1} \text{ s}^{-1}} \right)^{-1} \alpha_{comp} \quad (\text{S-1})$$

where dependency on structural parameters (Table S-11) is captured by:

$$\alpha_{comp} = \left(\frac{m_r^{tot}}{340 \text{ Da}} \right) \left(\frac{l_r}{6860} \right) \left(\frac{m_a^{tot}}{110 \text{ Da}} \right)^{-1} \quad (\text{S-2})$$

Using the stoichiometries from Table S-10, the (mass) ratio of phosphorus to nitrogen in the combination of cellular rRNA and protein is then

$$\frac{\%P_{\text{cell}}}{\%N_{\text{cell}}} = \frac{8.7r_{\text{cellrRNA:prot}}^{\text{mass}}}{17 + 14.5r_{\text{cellrRNA:prot}}^{\text{mass}}} \quad (\text{S-3})$$

where the major trend is from the ratio of phosphate-rich rRNA to nitrogen-rich protein, and the dependency on $r_{\text{cellrRNA:prot}}^{\text{mass}}$ in the denominator is a small correction due to the nitrogen content of rRNA. The fraction of cell nitrogen in ribosomes (including both the rRNA and ribosome-associated protein in ratio 1.2:1 for a eukaryotic ribosome³⁰) is

$$\frac{\%N_{\text{rib}}}{\%N_{\text{cell}}} = \frac{28.6r_{\text{cellrRNA:prot}}^{\text{mass}}}{17 + 14.5r_{\text{cellrRNA:prot}}^{\text{mass}}} \quad (\text{S-4})$$

and the ratio of rRNA mass to cell carbon mass (given an overall bulk cell C:N stoichiometry) is

$$\frac{m_{\text{rRNA}}^{\text{tot}}}{m_{\text{cell}}^{\text{C}}} = \frac{100r_{\text{cellrRNA:prot}}^{\text{mass}}}{17 + 14.5r_{\text{cellrRNA:prot}}^{\text{mass}}} \left(\frac{\%N_{\text{cell}}}{\%C_{\text{cell}}} \right) \quad (\text{S-5})$$

7.2 Relating rRNA allocation to coarse-grained phytoplankton model

The optimal allocation of cellular nitrogen to the E pool is given by $E_{\text{opt}} = \%N_{\text{E}}/\%N_{\text{cell}} = \mu/\kappa_s$. Both the allocation to E and the allocation to rRNA therefore scale linearly with growth rate, hence assuming the same temperature dependence for these rates, the optimal partitioning into rRNA and small-molecule biosynthesis within the E pool follows from the two empirical rate constants:

$$\begin{aligned} \frac{\%N_{\text{rib}}}{\%N_{\text{E}}} &= \frac{\kappa_s}{\mu} \frac{28.6r_{\text{cellrRNA:prot}}^{\text{mass}}}{17 + 14.5r_{\text{cellrRNA:prot}}^{\text{mass}}} \\ &= 1.67 \frac{\left(\frac{\kappa_s}{0.168 \text{ h}^{-1}} \right)_{25\text{C}} \left(\frac{\phi_a \sigma_a}{1 \text{ aa rib}^{-1} \text{ s}^{-1}} \right)_{25\text{C}}^{-1}}{\left(1 + 0.85E_{\text{opt}} \left(\frac{\kappa_s}{0.168 \text{ h}^{-1}} \right)_{25\text{C}} \left(\frac{\phi_a \sigma_a}{1 \text{ aa rib}^{-1} \text{ s}^{-1}} \right)_{25\text{C}}^{-1} \right)} \alpha_{\text{comp}} \end{aligned}$$

The ratio $\%N_{\text{rib}}/\%N_{\text{E}}$ is therefore close to a constant value determined by the two rate constants, with a small correction factor (arising from the non-protein contribution to cellular nitrogen in the rRNA). The growth-strategy-dependent allocation to E then determines the allocation to rRNA.

Table S-12: Representative calculations for minimum rRNA requirements for growth. Per-ribosome protein synthesis rate $(\sigma_a \phi_a)_{25C}$ scaled for temperature of 25C derived assuming temperature-dependence given by a factor $Q_{10} = 2$.

Description	μ	$\sigma_a \phi_a$ aa rib ⁻¹ s ⁻¹	$r_{cellrRNA:prot}^{mass}$	$\frac{\%N_{rib}}{\%N_{cell}}$	$\frac{\%P_{cell}}{\%N_{cell}}$	N:P	$(\sigma_a \phi_a)_{25C}$ aa rib ⁻¹ s ⁻¹
yeast, 30C ($l_r = 5470$)	0.43 h ⁻¹	8	0.25	0.35		16.2	5.7
<i>T. weissflogii</i> 20C ²⁹	1.29 d ⁻¹	1.9	0.167	0.246	0.075	29.6	2.7

7.3 Absolute laboratory calibration of rRNA synthesis rate and rRNA contribution to N:P

The absolute value of the rRNA content and hence the N:P stoichiometry of the E compartment determines the minimum rRNA contribution to overall stoichiometry, $\%P_E/\%N_E = 0.304(\%N_{rib}/\%N_E)$, $(N:P)_E = 2.21/(\%P_E/\%N_E)$. This depends on a calibration of the per-ribosome protein synthesis rate. Two representative values are shown in Table S-12, and a full sensitivity study is provided in Daines *et al* (2013)²⁵. The calculation for yeast at 30C demonstrates consistency with the data compilation and calculation from Loladze and Elser (2011)³¹. The autotroph value for the diatom *T. weissflogii* is derived by comparison with the measured RNA content of the diatom at observed maximum rate of light-limited growth at 20C²⁹, given the measured ratio of RNA mass to cell carbon mass $m_{rRNA}^{tot}/m_{cell}^C = 0.151 \text{ gRNA(gC)}^{-1}$ and measured stoichiometry with $\%N_{cell}/\%C_{cell} = 0.176 \text{ gN(gC)}^{-1}$ (Daines *et al*, 2013)²⁵.

The lowest value $(\phi_a \sigma_a)_{25C} = 2.7 \text{ aa rib}^{-1} \text{ s}^{-1}$ consistent with the *T. weissflogii* dataset²⁹ (Table S-12, scaled to a temperature of 25C by assuming $Q_{10} = 2$) then gives $\%N_{rib}/\%N_E = 0.62$ in the limit of small allocation to E, and for the highest value $E_{opt} = 0.8$ (in the high-light limit where allocation to L is small and S is 0.2), gives $\%N_{rib}/\%N_E = 0.49$, $(N:P)_E = 14.8$ and $\%N_{rib}/\%N_{cell} = 0.40$, $(N:P)_{cell} < 18.5$ (this demonstrates that the correction term $0.85E_{opt}...$ is relatively small and the optimal small and large molecule biosynthesis contributions to E have only a small sensitivity to other parameters). Taking the per-ribosome transcription rate from yeast $(\phi_a \sigma_a)_{25C} = 5.7 \text{ aa rib}^{-1} \text{ s}^{-1}$ (Table S-12, scaled to a temperature of 25C by assuming $Q_{10} = 2$) approximately halves this value for rRNA and P content at optimal growth. The highest values for maximum optimal cellular allocation to rRNA and hence maximum rRNA contribution to cellular P content are approximately half those of Klausmeier *et al* (2004)³² as we have enforced an additional constraint on per-ribosome transcription rate from consistency with laboratory data. Another overall consistency argument is that we might expect the maximum rRNA to protein ratio

in an autotroph (with additional protein requirements for growth including for light harvesting and carbon fixation, relative to a heterotroph growing on simple substrates) will always be less than the maximum in yeast.

The calculations shown here for N:P (main paper Figure 4) use $(\phi_a \sigma_a)_{25C} = 2.7 \text{ aa rib}^{-1} \text{ s}^{-1}$, and include additional P contribution from phospholipid assumed a constant 10% of total cell mass³³. A full parameter sensitivity study, discussion of optimal allocation to rRNA (the Growth Rate Hypothesis) and of potential multiple contributions to phytoplankton N:P is contained in Daines *etal* (2013)²⁵. Evidence for optimal allocation to rRNA in laboratory experiments is discussed in Loladze and Elser (2011)³¹. However, some data on microalgae do not completely agree³⁴ - the discrepancy is likely a combination of experimental uncertainties, and additional rRNA requirements in dynamic environments. The essential point for the interpretation here is that rRNA allocation for protein synthesis must represent a minimum requirement for growth (based in the model approach here on laboratory calibration) and this part of P allocation must be affected by temperature.

8 Temperature and light-dependence of optimal allocation in nutrient-unlimited environments

A simplified steady-state optimality analysis provides additional insight into the temperature dependence of cellular allocation strategies for exponential growth (unlimited nutrient) appropriate to large phytoplankton such as diatoms in high-latitude bloom forming environments or in upwelling regions. Here we solve numerically for the optimal resource allocation to L and E that gives maximum growth rate as a function of light and temperature, with cell radius fixed at a large value (the method is as described in²⁴), Figure S-14.

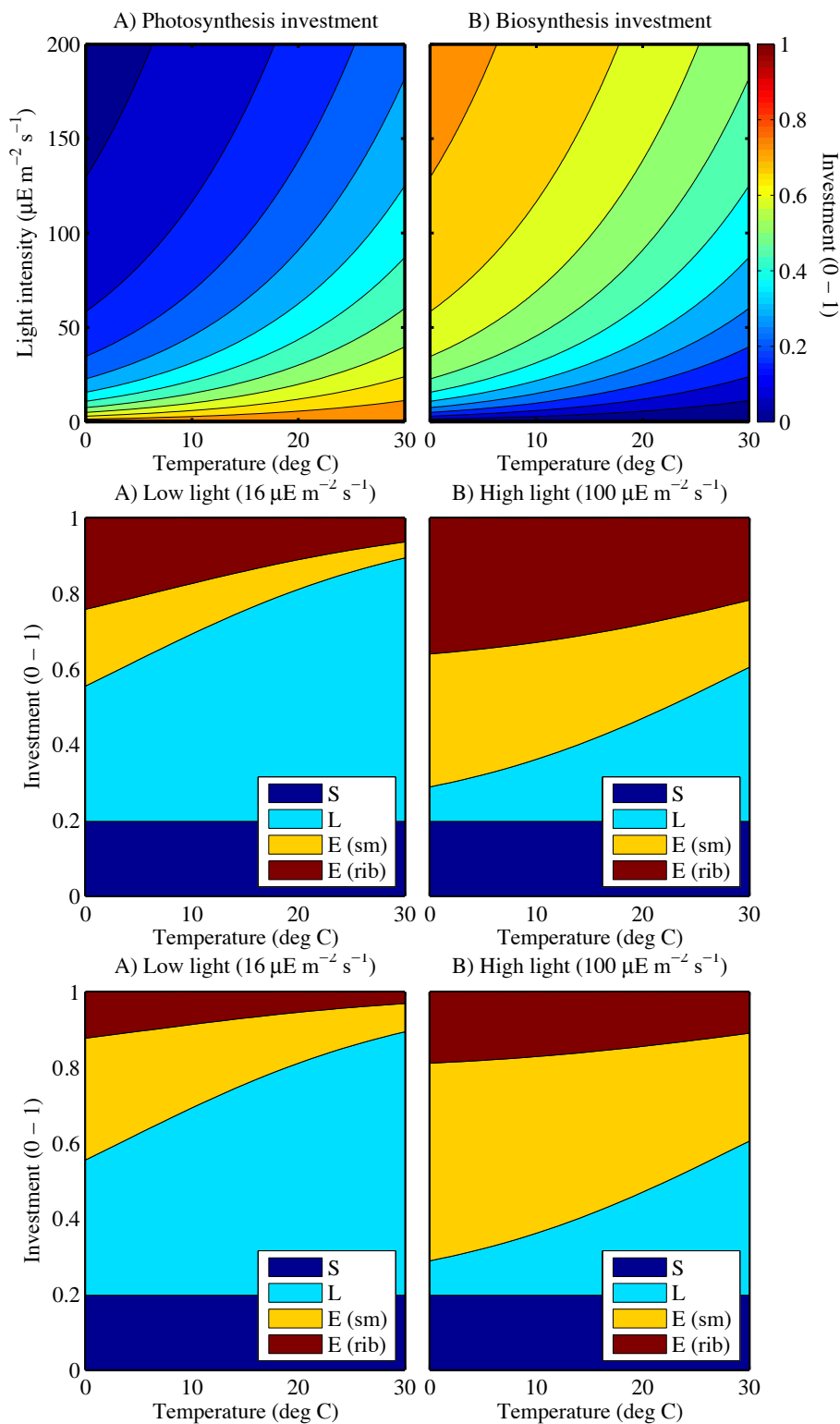


Figure S-14: Optimal allocation (fraction of cellular nitrogen) for nutrient-unlimited growth as a function of light and temperature, and demonstration of sensitivity to ribosome synthesis rate. Top row: Optimal allocation to light harvesting and biosynthesis as a function of light and temperature. Middle row: optimal allocation as a function of temperature for two light levels, showing allocation within biosynthesis component E to small and large molecule biosynthesis (ribosomes) for the lowest value $(\phi_a \sigma_a)_{25C} = 2.7 \text{ aa rib}^{-1} \text{ s}^{-1}$ consistent with the *T. weissflogii* dataset described in (Table S-12). Bottom row: as middle row, for $(\phi_a \sigma_a)_{25C} = 5.7 \text{ aa rib}^{-1} \text{ s}^{-1}$ determined for yeast³¹ (Table S-12).

Supplementary References

23. Clark, J. R., Daines, S. J., Lenton, T. M., Watson, A. J. & Williams, H. T. P. Individual-based modelling of adaptation in marine microbial populations using genetically defined physiological parameters. *Ecological Modelling* **222**, 3823–3837 (2011).
24. Clark, J. R., Lenton, T. M., Williams, H. T. P. & Daines, S. J. Environmental selection and resource allocation determine spatial patterns in picophytoplankton cell size. *Limnology and Oceanography* **58**, 1008–1022 (2013).
25. Daines, S. J., Clark, J. R. & Lenton, T. M. Multiple environmental controls on phytoplankton growth strategies suggest a key contribution of P storage to the N:P ratio. *Ecology letters* in revision (2013).
26. Rose, K. Individual-based modeling of populations with high mortality: A new method based on following a fixed number of model individuals. *Ecological Modelling* **68**, 273–292 (1993).
27. Scheffer, M., Baveco, J., DeAngelis, D. L., Rose, K. & van Nes, E. Super-individuals a simple solution for modelling large populations on an individual basis. *Ecological Modelling* **80**, 161–170 (1995).
28. Shuter, B. A model of physiological adaptation in unicellular algae. *Journal of theoretical biology* **78**, 519–52 (1979).
29. Laws, E. A., Redalje, D., Karl, D. M. & Chalup, M. S. A theoretical and experimental examination of the predictions of two recent models of phytoplankton growth. *Journal of Theoretical Biology* **105**, 469–491 (1983).
30. Sterner, R. & Elser, J. J. *Ecological stoichiometry: The biology of elements from molecules to the biosphere* (Princeton University Press, Princeton, 2002).
31. Loladze, I. & Elser, J. J. The origins of the Redfield nitrogen-to-phosphorus ratio are in a homeostatic protein-to-rRNA ratio. *Ecology letters* **14**, 244–50 (2011).
32. Klausmeier, C. A., Litchman, E., Daufresne, T. & Levin, S. A. Optimal nitrogen-to-phosphorus stoichiometry of phytoplankton. *Nature* **429**, 171–4 (2004).
33. Geider, R. J. & LaRoche, J. Redfield revisited: variability of C:N:P in marine microalgae and its biochemical basis. *European Journal of Phycology* **37**, 1–17 (2002).

34. Flynn, K. J. *et al.* Is the Growth Rate Hypothesis Applicable To Microalgae? *Journal of Phycology* **46**, 1–12 (2010).