

Supporting Information for

# Phylogenetic and phenogenetic diversity of *Synechococcus* along a Yellow Sea Section Reveal its Environmental Dependent Distribution and Co-occurrence Microbial Pattern

Ting Wang<sup>1,2,3,4,†</sup>, Xi Chen<sup>5,†</sup>, Song Qin<sup>1,6</sup>, Jialin Li<sup>1,6,\*</sup>

<sup>1</sup> Key Lab of Coastal Biology and Biological Resource Utilization, Yantai Institute of Coastal Zone Research, Chinese Academy of Sciences, Yantai 264003, China

<sup>2</sup> College of Environmental Science and Engineering, Ocean University of China, Qingdao 266100, China

<sup>3</sup> Institute of Deep-sea Science and Engineering, Chinese Academy of Sciences, Sanya 572000, China

<sup>4</sup> University of Chinese Academy of Sciences, Beijing, China

<sup>5</sup> College of Marine Life Science, Ocean University of China, Qingdao 266005, China

<sup>6</sup> Center for Ocean Mega-Science, Chinese Academy of Sciences, Qingdao 266071, China

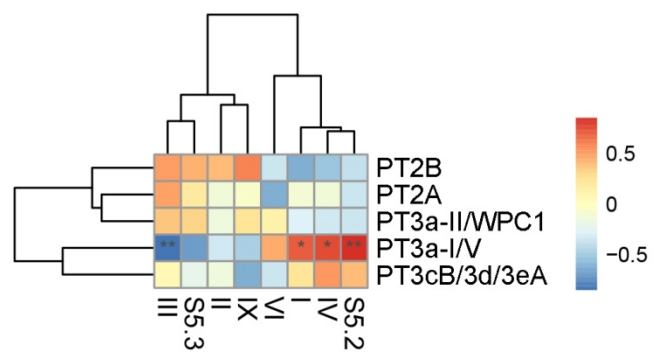
\* Correspondence: jlli@yic.ac.cn

† Co-first authors

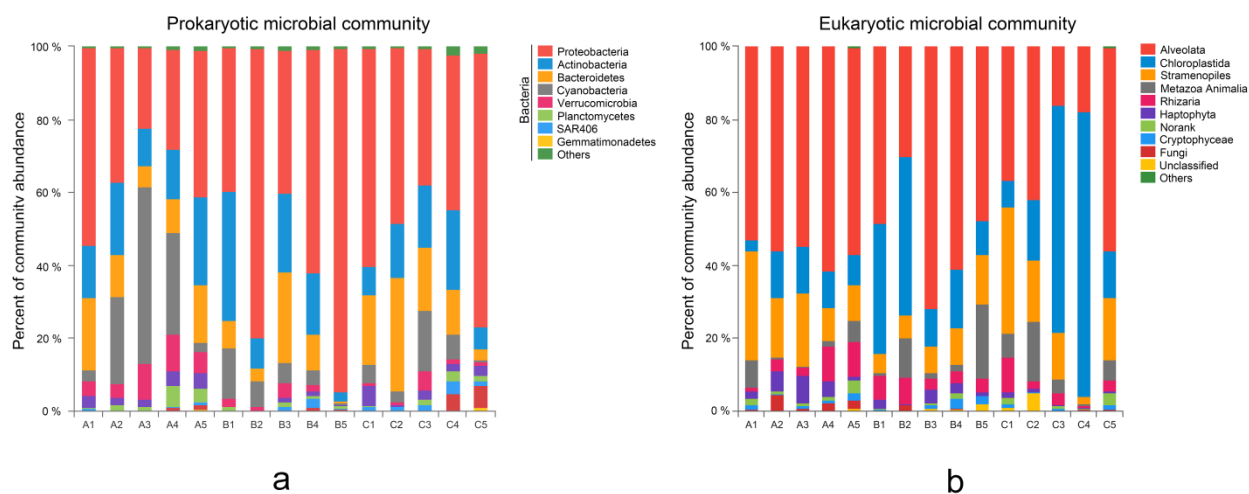
## Contents of this file

Figures S1 to S6

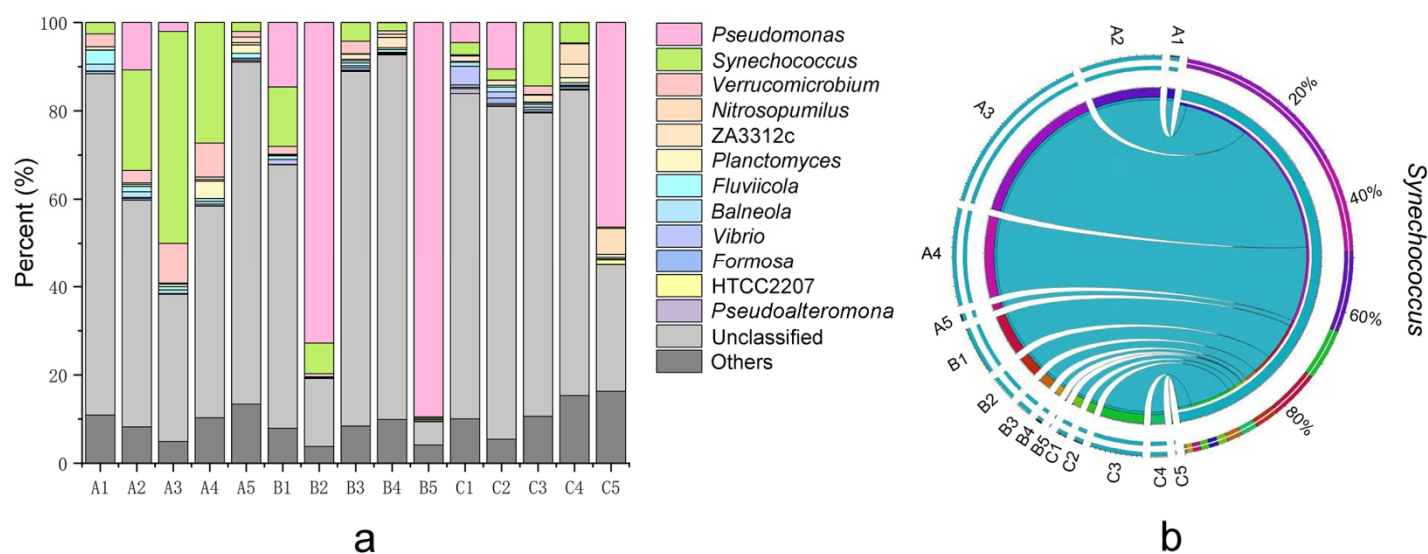
Tables S1 to S6



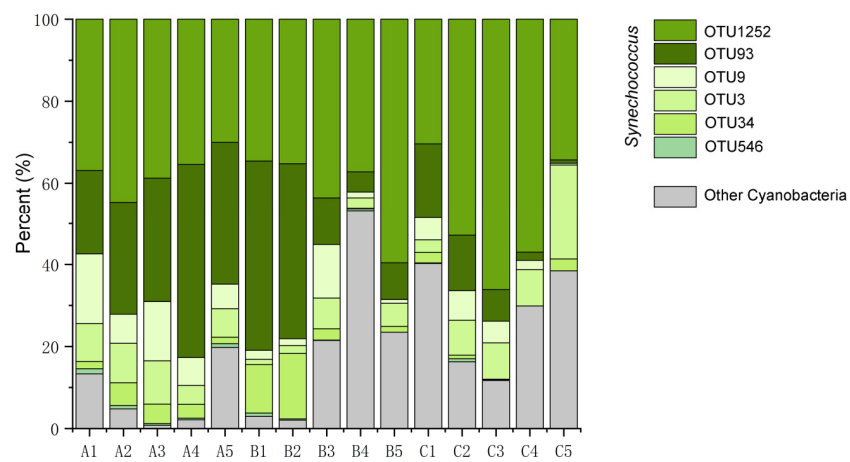
**Figure S1.** Spearman rank correlation analysis between *Synechococcus* clades as determined using *rpoC1* and pigment types as indirectly assessed using the *cpeBA* operon.



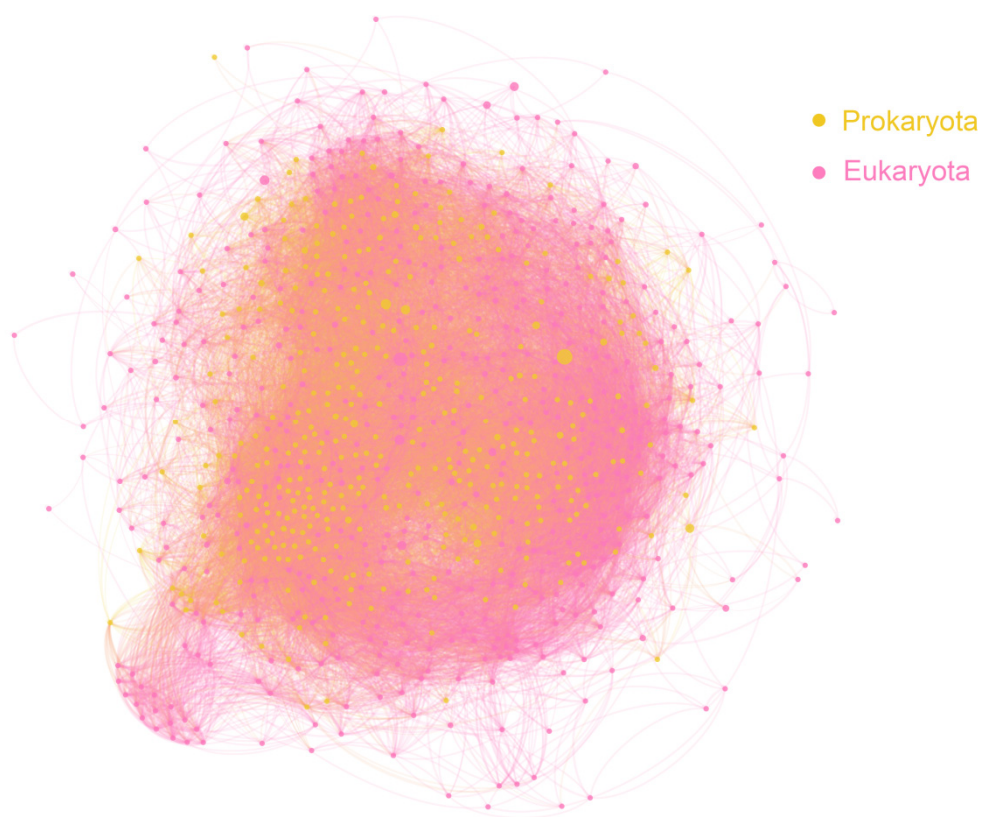
**Figure S2.** The relative abundances of predominant taxa in the prokaryotic community at the phylum level (a) and the eukaryotic community at the kingdom level (b).



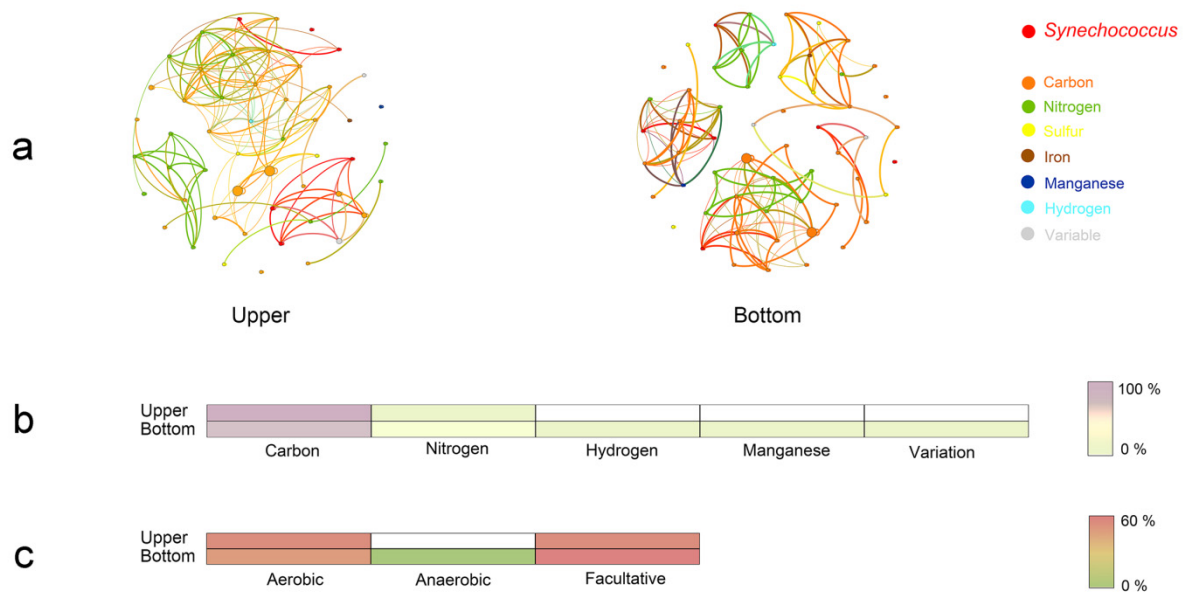
**Figure S3.** The relative abundance of taxa in the prokaryotic community at the genus level. **(a)** Community bar map showing the relative abundance of the genus; The unclassified does not represent a single taxon, but the sum of all taxa not classified to genus level; **(b)** Chord diagram reveals the relationship between samples and *Synechococcus* abundance. The length of the left semicircle represents the relative abundance of the *Synechococcus* in the corresponding samples. The right semicircle represents the distribution proportion of *Synechococcus* in different samples.



**Figure S4.** The relative abundances of OTUs belonging to phyla Cyanobacteria.



**Figure S5.** Network of microbial community encompassing all prokaryotic and eukaryotic OTUs constructed from the correlation matrix. OTUs with Spearman coefficients  $> 0.6$  and  $p < 0.05$  were connected and graphed using a force-directed layout algorithm.



**Figure S6.** Network of microbial metabolic function correlations encompassing metabolic functions constructed from the correlation matrix of upper and bottom samples. **(a)** Metabolic functions with the absolute value of Spearman coefficients  $> 0.6$  and  $p < 0.05$  were connected and graphed using a force-directed layout algorithm. Red nodes represent six OTUs belonging to *Synechococcus*. **(b)** Metabolic heat map associated with *Synechococcus* showing the relative abundance of predominant metabolic functions classified based on the main metabolic elements. **(c)** Metabolic heat map associated with *Synechococcus* showing the relative abundance of predominant metabolic functions classified based on respiratory types.

**Table S1.** Reference sequences of *rpoC1* gene.

Representative strain	Cluster	Clade	Accession number
<i>Synechococcus</i> sp. CC9617	S5.1	I	AF154562.1
<i>Synechococcus</i> sp. PROS-9-1	S5.1	I	CP047961.1:1791816-1792218
<i>Synechococcus</i> sp. SYN20	S5.1	I	CP047959.1:2224046-2224381
<i>Synechococcus</i> sp. CC9311	S5.1	I	AF013607.1
<i>Synechococcus</i> sp. M16.1	S5.1	II	CP047954.1:1570118-1570520
<i>Synechococcus</i> sp. RS9911	S5.1	II	AJ621009.1
<i>Synechococcus</i> sp. RS9907	S5.1	II	AJ621007.1
<i>Synechococcus</i> sp. WH6501	S5.1	II	AF448106.1
<i>Synechococcus</i> sp. Minos02	S5.1	III	AJ621016.1
<i>Synechococcus</i> sp. Minos12	S5.1	III	AJ621019.1
<i>Synechococcus</i> sp. RS9905	S5.1	III	AJ621006.1
<i>Synechococcus</i> sp. C129	S5.1	III	AF153339.1
<i>Synechococcus</i> sp. CC9703	S5.1	III	AF153338.1
<i>Synechococcus</i> sp. CC9902	S5.1	IV	CP000097.1:614302-614704
<i>Synechococcus</i> sp. RS9901	S5.1	IX	AJ621003.1
<i>Synechococcus</i> sp. UW01	S5.1	V	AJ621020.1
<i>Synechococcus</i> sp. WH8018	S5.1	VI	AJ621015.1
<i>Synechococcus</i> sp. WH7805	S5.1	VI	L34062.1
<i>Synechococcus</i> sp. RS9920	S5.1	VII	AJ621012.1
<i>Synechococcus</i> sp. KORDI-49	S5.1	WPC1	CP006270.1:928342-928744
<i>Synechococcus</i> sp. A15-127	S5.1	WPC1	CP047948.1:1883957-1884359
<i>Synechococcus</i> sp. WH8007	S5.2	CB5	AF448107.1
<i>Synechococcus</i> sp. Minos11	S5.3		AJ621021.1
<i>Synechococcus</i> sp. Minos01	S5.3		AJ621022.1
<b>Outgroup-<i>Escherichia coli</i> sp. U5/41</b>			NR024570.1



**Table S2.** Reference sequences of *cpeBA* operon.

Representative strain	Cluster	Clade	Pigment type	Accession number
<i>Synechococcus</i> sp. BMK-MC-1	S5.1	V	2A	KF528784.1
<i>Synechococcus</i> sp. G10.1	S5.2		2B	DQ248025.1
<i>Synechococcus</i> sp. A15-44	S5.1	II	2B	KF528782.1
<i>Synechococcus</i> sp. PROS-7-1	S5.1	VI	2B	KF528783.1
<i>Synechococcus</i> sp. G11	S5.2		2B	DQ248026.1
<i>Synechococcus</i> sp. M12.1	S5.1	II	2B	JN566232.1
<i>Synechococcus</i> sp. M16.1	S5.1	II	3a	KF528774.1
<i>Synechococcus</i> sp. M16B.1	S5.1	II	3a	JN566234.1
<i>Synechococcus</i> sp. ROS8604	S5.1	I	3a	KF528765.1
<i>Synechococcus</i> sp. SYN20	S5.1	I	3a	MG018776.1
<i>Synechococcus</i> sp. WH7803	S5.1	V	3a	X72961.1
<i>Synechococcus</i> sp. RS9907	S5.1	II	3a	KF528775.1
<i>Synechococcus</i> sp. NOUM97013	S5.1	VII	3a	KF528781.1
<i>Synechococcus</i> sp. M16.3	S5.1	II	3a	JN566233.1
<i>Synechococcus</i> sp. KORDI-49	S5.1	WPC1	3a	CP006270.1
<i>Synechococcus</i> sp. RCC307	S5.3		3b/ 3e	CT978603.1
<i>Synechococcus</i> sp. BIOS-E4-1	S5.1	CRD1	3cB	KF528767.1
<i>Synechococcus</i> sp. MITS9920	S5.1	CRD1	3d	MG018774.1
<i>Synechococcus</i> sp. CC9902	S5.1	IV	3d	CP000097.1
<i>Synechococcus</i> sp. BIOS-U3-1	S5.1	CRD1	3dA	KF528768.1
Outgroup- <i>Escherichia coli</i> sp. U5/41				NR024570.1

**Table S3.** Spearman correlation coefficients between environmental variables.

	Longit ude	Water depth	Sampling depth	Tempera ture	Salin ity	Oxyg en	NO <sub>2</sub> <sup>-</sup>	NO <sub>3</sub> <sup>-</sup>	NH <sub>4</sub> <sup>+</sup>	DT N	PO <sub>4</sub> <sup>3-</sup>	DT P	DSi
<b>Longitude</b>	1	0.99**	0.23	-0.47	0.59*	0.89**	-0.3 2	0.1 1	0.14	-0.1 9	0.16	0.25	-0.1 9
<b>Water depth</b>	0.99**	1	0.23	-0.47	0.59*	0.89**	-0.3 2	0.1 1	0.14	-0.1 9	0.16	0.25	-0.1 9
<b>Sampling depth</b>	0.23	0.23	1	-0.91**	0.82**	0.10	0.5 1	0.4 0	-0.7 3**	0.5 0	0.72 **	0.85 **	0.77 **
<b>Temperatu re</b>	-0.47	-0.47	-0.91**	1	-0.87**	-0.28	-0.4 8	-0.5 2*	0.67 **	-0.4 0	-0.8 1**	-0.8 9**	-0.6 8**
<b>Salinity</b>	0.59*	0.59*	0.82**	-0.87**	1	0.43	0.1 5	0.2 0	-0.5 6*	0.4 0	0.66 **	0.84 **	0.42
<b>Oxygen</b>	0.89**	0.89**	0.10	-0.28	0.43	1	-0.5 2*	-0.2 0	0.15	-0.3 7	-0.0 7	0.04	-0.3 1
<b>NO<sub>2</sub><sup>-</sup></b>	-0.32	-0.32	0.51	-0.48	0.15	-0.52*	1 7**	0.6 0	-0.5 0	0.3 5	0.57 *	0.42	0.73 **
<b>NO<sub>3</sub><sup>-</sup></b>	0.11	0.11	0.40	-0.52*	0.20	-0.20	0.6 7**	1	-0.1 1	0.2 1	0.63 *	0.40	0.63 *
<b>NH<sub>4</sub><sup>+</sup></b>	0.14	0.14	-0.73**	0.67**	-0.56*	0.15	-0.5 0	-0.1 1	1	-0.4 0	-0.6 2*	-0.7 4**	-0.7 4**
<b>DTN</b>	-0.19	-0.19	0.50	-0.40	0.40	-0.37	0.3 5	0.2 1	-0.4 0	1	0.66 **	0.72 **	0.50
<b>PO<sub>4</sub><sup>3-</sup></b>	0.16	0.16	0.72**	-0.81**	0.66**	-0.07	0.5 7*	0.6 3*	-0.6 2*	0.6 6**	1	0.92 **	0.76 **
<b>DTP</b>	0.25	0.25	0.85**	-0.89**	0.84**	0.04	0.4 2	0.4 0	-0.7 4**	0.7 2**	0.92 **	1	0.72 **
<b>DSi</b>	-0.19	-0.19	0.77**	-0.68**	0.42	-0.31	0.7 3**	0.6 3*	-0.7 4**	0.5 0	0.76 **	0.72 **	1

\*\*\*" represents  $p < 0.01$ ; "\*\*" represents  $p < 0.05$

**Table S4.** Sequencing information and alpha diversity indices of *rpoC1* and *cpeBA* gene.

Samples	<i>rpoC1</i> gene				<i>cpeBA</i> operpn			
	Number of sequences	Coverage	NP-Shannon	Chao1	Number of sequences	Coverage	NP-Shannon	Chao1
A1	21898	0.99	1.75	85	34	0.82	2.28	19
A2	21998	0.99	1.60	66	1	0	0	1
A3	13737	0.99	1.46	60	36	0.99	1.82	7
A4	9747	0.99	1.81	78	/	/	/	/
A5	11031	0.99	2.09	84	119	0.97	1.78	14
B1	12988	0.99	1.79	61	38	0.92	1.75	10
B2	13527	0.99	2.09	63	31	0.81	2.18	25
B3	14730	0.99	2.40	95	25	0.84	2.18	11
B4	20763	0.99	1.64	89	44	0.86	2.41	21
B5	3458	0.99	1.87	64	/	/	/	/
C1	21211	0.99	1.52	88	30	0.97	1.57	6
C2	19162	0.99	2.30	87	51	0.98	1.76	7
C3	15257	0.99	2.07	69	31	0.84	2	19
C4	16570	0.99	1.90	80	31	0.97	1.59	6
C5	/	/	/	/	26	0.73	2.57	17

“/” represents representative clone library of this sample was unsuccessful.

**Table S5.** Sequencing information and alpha diversity indices of 16S and 18S gene.

Samples	16S gene				18S gene			
	Number of sequences	Coverage	NP-Shannon	Chao1	Number of sequences	Coverage	NP-Shannon	Chao1
A1	59596	0.99	4.19	731	66257	0.99	3.55	600
A2	50565	0.99	4.08	597	70836	0.99	3.78	442
A3	68369	0.99	3.45	673	48965	0.99	3.81	600
A4	71235	0.99	4.28	1102	47679	0.99	4.16	795
A5	60001	0.99	4.51	1083	51777	0.99	4.65	449
B1	49932	0.99	3.48	470	72661	0.99	3.22	264
B2	50960	0.99	2.02	381	36802	0.99	3.06	108
B3	47704	0.99	4.19	914	65422	0.99	3.82	535
B4	40938	0.99	3.72	804	61141	0.99	4.33	651
B5	55793	0.99	1.38	471	79711	0.99	3.68	110
C1	49515	0.99	4.30	725	51156	0.99	4.05	657
C2	60950	0.99	4.01	653	42940	0.99	3.62	445
C3	70528	0.99	4.22	907	40305	0.99	2.71	567
C4	52073	0.99	4.18	869	54969	0.99	1.92	391
C5	52162	0.99	3.47	735	60206	0.99	4.39	373

**Table S6.** Correlative eukaryotic taxa of *Synechococcus* as potential *in-situ* grazers in the ecosystem.

Taxa	Abundance (%)
Eukaryota   Alveolata   Ciliophora   Intramacronucleata   Spirotrichea   Choreotrichia   <i>Eutintinnus</i> ;   <i>Eutintinnus_sp._ENB99</i>   OTU375	0.01591
Eukaryota   Alveolata   Ciliophora   Intramacronucleata   Spirotrichea   Choreotrichia   norank_Choreotrichia   <i>Leegaardiella_sp._LS803</i>   OTU601	0.02812
Eukaryota   Alveolata   Ciliophora   Intramacronucleata   Spirotrichea   Choreotrichia   norank_Choreotrichia   OTU374	0.04184
Eukaryota   Alveolata   Ciliophora   Intramacronucleata   Spirotrichea   Choreotrichia   <i>Pelagostrobilidium</i>   unclassified_ <i>Pelagostrobilidium</i>   OTU1354	0.0161
Eukaryota   Alveolata   Ciliophora   Intramacronucleata   Spirotrichea   Choreotrichia   <i>Pelagostrobilidium</i>   uncultured_ <i>Pelagostrobilidium</i>   OTU13	0.13142
Eukaryota   Alveolata   Ciliophora   Intramacronucleata   Spirotrichea   Choreotrichia   <i>Pelagostrobilidium</i>   uncultured_ <i>Pelagostrobilidium</i>   OTU593	0.06527
Eukaryota   Alveolata   Ciliophora   Intramacronucleata   Spirotrichea   Choreotrichia   <i>Steenstrupiella</i>   <i>Amphorellopsis_sp.</i>   OTU507	0.03821
Eukaryota   Alveolata   Ciliophora   Intramacronucleata   Spirotrichea   norank_Spirotrichea   OTU93	0.06307
Eukaryota   Alveolata   Ciliophora   Intramacronucleata   Spirotrichea   Oligotrichia   norank_Oligotrichia   OTU87	0.024
Eukaryota   Alveolata   Ciliophora   Intramacronucleata   Spirotrichea   Oligotrichia   <i>Spirotontonia</i>   uncultured_ <i>Spirotontonia</i>   OTU61	0.3174
Eukaryota   Alveolata   Dinoflagellata   Dinophyceae   Gymnodiniphycidae   Gymnodinium_clade   <i>Erythrospidinium</i>   uncultured_ <i>Erythrospidinium</i>   OTU7	0.51183
Eukaryota   Alveolata   Dinoflagellata   Dinophyceae   Gymnodiniphycidae   Gymnodinium_clade   <i>Gymnodinium</i>   <i>Gymnodinium_impudicum</i>   OTU590	0.04797
Eukaryota   Alveolata   Dinoflagellata   Dinophyceae   Gymnodiniphycidae   Gymnodinium_clade   <i>Polykrikos</i>   <i>Polykrikos_kofoidii</i> ; OTU911	0.01148
Eukaryota   Alveolata   Dinoflagellata   Dinophyceae   Gymnodiniphycidae   Gymnodinium_clade   <i>Proterothropsis</i>   uncultured_ <i>Proterothropsis</i>   OTU486	0.44891
Eukaryota   Alveolata   Dinoflagellata   Dinophyceae   Gymnodiniphycidae   Gymnodinium_clade   unclassified_ <i>Gymnodinium_clade</i>   OTU616	0.21283
Eukaryota   Alveolata   Dinoflagellata   Dinophyceae   Gymnodiniphycidae   Kareniaceae   <i>Karlodinium</i>   unclassified_ <i>Karlodinium</i>   OTU266	0.0333
Eukaryota   Alveolata   Dinoflagellata   Dinophyceae   Gymnodiniphycidae   norank_Gymnodiniphycidae   <i>Akashiwo_sanguinea</i>   OTU496	0.01883
Eukaryota   Alveolata   Dinoflagellata   Dinophyceae   norank_Dinophyceae   OTU488	0.01468
Eukaryota   Alveolata   Dinoflagellata   Dinophyceae   Peridiniphycidae   Gonyaulacales   <i>Alexandrium</i>   <i>Alexandrium_hiranoi</i>   OTU1440	0.03857
Eukaryota   Alveolata   Dinoflagellata   Dinophyceae   Peridiniphycidae   Gonyaulacales   <i>Azadinium</i>   unclassified_ <i>Azadinium</i>   OTU953	0.32408

Eukaryota Alveolata Dinoflagellata Dinophyceae Peridiniphycidae Gonyaulacales  <i>Fragilidium</i> ; <i>Fragilidium</i> _sp._CCMP1920 OTU604	0.03985
Eukaryota Alveolata Dinoflagellata Dinophyceae Peridiniphycidae Gonyaulacales  <i>Fragilidium</i>   <i>Fragilidium</i> _sp._G02 OTU441	0.04048
Eukaryota Alveolata Dinoflagellata Dinophyceae Peridiniphycidae Gonyaulacales  <i>Grammatodinium</i>   <i>Grammatodinium_tongyeonginum</i>  OTU631	0.04437
Eukaryota Alveolata Dinoflagellata Dinophyceae Peridiniphycidae Gonyaulacales  <i>Protoceratium</i>  unclassified_ <i>Protoceratium</i>  OTU554	0.02084
Eukaryota Alveolata Dinoflagellata Dinophyceae unclassified_Dinophyceae OTU1016	0.13246
Eukaryota Alveolata Dinoflagellata Dinophyceae unclassified_Dinophyceae OTU1389	0.01622
Eukaryota Alveolata Dinoflagellata Dinophyceae unclassified_Dinophyceae OTU510	0.0112
Eukaryota Alveolata Protalveolata Syndiniales norank_Syndiniales  <i>Amoebophrya</i>   <i>Amoebophrya</i> _sp._ex_ <i>Prorocentrum_micans</i>  OTU313	0.0269
Eukaryota Alveolata Protalveolata Syndiniales norank_Syndiniales  <i>Amoebophrya</i>  uncultured_ <i>Amoebophrya</i>  OTU954	0.16686
Eukaryota Alveolata Protalveolata Syndiniales norank_Syndiniales norank_Syndiniales  <i>Amoebophrya</i>  uncultured_ <i>Amoebophrya</i>  OTU594	0.01339
Eukaryota Alveolata Protalveolata Syndiniales norank_Syndiniales norank_Syndiniales  <i>Amoebophrya</i>  uncultured_ <i>Amoebophrya</i>  OTU321	0.02674
Eukaryota Alveolata Protalveolata Syndiniales norank_Syndiniales norank_Syndiniales  <i>Amoebophrya</i>  uncultured_ <i>Amoebophrya</i>  OTU569	0.01162
Eukaryota Alveolata Protalveolata Syndiniales norank_Syndiniales norank_Syndiniales  <i>Duboscquella</i>  unclassified_ <i>Duboscquella</i>  OTU468	0.7203
Eukaryota Alveolata Protalveolata Syndiniales norank_Syndiniales norank_Syndiniales  <i>Duboscquella</i>  unclassified_ <i>Duboscquella</i>  OTU539	0.1066
Eukaryota Alveolata Protalveolata Syndiniales norank_Syndiniales norank_Syndiniales  <i>Hematodinium</i>  unclassified_ <i>Hematodinium</i>  OTU1340	0.01582
Eukaryota Alveolata Protalveolata Syndiniales norank_Syndiniales norank_Syndiniales OTU337	0.02441
Eukaryota Alveolata Protalveolata Syndiniales norank_Syndiniales Syndiniales_Group_I OTU856	0.01974
Eukaryota Alveolata Protalveolata Syndiniales norank_Syndiniales Syndiniales_Group_I OTU121	0.13179
Eukaryota Alveolata Protalveolata Syndiniales norank_Syndiniales Syndiniales_Group_I OTU512	0.14938
Eukaryota Alveolata Protalveolata Syndiniales norank_Syndiniales Syndiniales_Group_I OTU115	0.15289
Eukaryota Alveolata Protalveolata Syndiniales norank_Syndiniales Syndiniales_Group_II OTU1266	0.01684
Eukaryota Alveolata Protalveolata Syndiniales norank_Syndiniales Syndiniales_Group_II OTU308	0.13674
Eukaryota Alveolata Protalveolata Syndiniales norank_Syndiniales Syndiniales_Group_II OTU914	0.0268
Eukaryota Alveolata Protalveolata Syndiniales norank_Syndiniales Syndiniales_Group_II OTU311	0.23895

Eukaryota Alveolata Protalveolata Syndiniales norank_Syndiniales Syndiniales_Group_II OTU905	0.10414
Eukaryota Alveolata Protalveolata Syndiniales norank_Syndiniales Syndiniales_Group_II OTU306	0.27925
Eukaryota Chloroplastida norank_Chloroplastida Chlorophyceae norank_Chlorophyceae OTU987	0.01915
Eukaryota Chloroplastida norank_Chloroplastida Clade_VII Subclade_B  <i>prasinophyte_sp._RCC2339_clade_VIIB2</i>  OTU998	4.94312
Eukaryota Chloroplastida norank_Chloroplastida Mamiellophyceae Mamiellales norank_Mamiellales  <i>Micromonas</i>   <i>Micromonas_pusilla</i>  OTU936	0.17986
Eukaryota Chloroplastida norank_Chloroplastida Mamiellophyceae norank_Mamiellophyceae  <i>Dolichomastix</i>   <i>Dolichomastix_tenuilepis</i>  OTU3	0.01197
Eukaryota Chloroplastida norank_Chloroplastida Mamiellophyceae norank_Mamiellophyceae  <i>Dolichomastix</i>   <i>Dolichomastix_tenuilepis</i>  OTU500	0.04835
Eukaryota Chloroplastida norank_Chloroplastida Prasinophytae norank_Prasinophytae  <i>Pycnococcus_sp._MBIC10637</i>  OTU1455	0.84871
Eukaryota Chloroplastida norank_Chloroplastida Prasinophytae Pseudoscourfieldiales norank_Pseudoscourfieldiales  <i>Pycnococcus</i>   <i>Pycnococcus_prova solii</i>  OTU724	0.79777
Eukaryota Chloroplastida norank_Chloroplastida Prasinophytae Pyramimonadales norank_Pyramimonadales  <i>Prasinopapilla</i>   <i>Prasinopapilla_vacuolata</i>  OTU276	0.03859
Eukaryota Chloroplastida norank_Chloroplastida Prasinophytae unclassified_Prasinophytae OTU1521	0.01075
Eukaryota Chloroplastida norank_Chloroplastida Trebouxiophyceae norank_Trebouxiophyceae OTU380	1.35874
Eukaryota Cryptophyceae norank_Cryptophyceae OTU546	0.01525
Eukaryota Fungi Chytridiomycota norank_Chytridiomycota OTU440	0.13878
Eukaryota Haptophyta Prymnesiophyceae Coccolithales norank_Coccolithales  <i>Tergestiella</i>   <i>Tergestiella_adriatica</i>  OTU708	0.01196
Eukaryota Haptophyta Prymnesiophyceae Coccolithales norank_Coccolithales  OTU47	1.27162
Eukaryota Haptophyta unclassified_Haptophyta OTU1031	0.11061
Eukaryota Metazoa_Animalia Annelida Polychaeta Phyllodocida norank_Phyllodocida  <i>Sigambra_sp._BC-2003</i>  OTU50	0.01991
Eukaryota Metazoa_Animalia Arthropoda Maxillopoda Calanoida norank_Calanoida  <i>Calanus_helgolandicus</i>  OTU1411	0.54853
Eukaryota Metazoa_Animalia Arthropoda Maxillopoda Cyclopoida norank_Cyclopoida OTU827	0.30057
Eukaryota Metazoa_Animalia Ctenophora norank_Ctenophora  <i>Euplokamis_sp._SM-2011a</i>  OTU775	0.25165
Eukaryota Metazoa_Animalia Vertebrata norank_Vertebrata  <i>Tursiops_truncatus_bottlenose_dolphin</i>  OTU988	0.58293
Eukaryota norank norank_Eukaryota OTU548	0.01988

Eukaryota norank norank_Eukaryota OTU641	0.02974
Eukaryota norank Picozoa Picomonadida norank_Picomonadida OTU1369	0.01966
Eukaryota norank Picozoa Picomonadida Picomonadidae norank_Picomonadidae  <i>Picomonas</i>  OTU296	0.0175
Eukaryota Rhizaria Cercozoa Chlorarachniophyta norank_Chlorarachniophyta  <i>Lotharella</i>   <i>Chlorarachniophyceae</i> _sp._RCC531 OTU461	0.01228
Eukaryota Rhizaria Cercozoa Chlorarachniophyta norank_Chlorarachniophyta norank_Chlorarachniophyta  <i>Minorisa</i>  OTU1015	0.05346
Eukaryota Rhizaria Cercozoa Imbricatea Silicofilosea Euglyphida  <i>Paulinella</i>  OTU466	0.03602
Eukaryota Rhizaria Cercozoa Novel_Clade_2 norank_Novel_Clade_2 OTU632	0.03383
Eukaryota Rhizaria Cercozoa Thecofilosea Ebriacea norank_Ebriacea  <i>Ebria</i>  OTU505	0.06734
Eukaryota Rhizaria Cercozoa Thecofilosea Ebriacea norank_Ebriacea  <i>Ebria</i>  OTU16	0.04895
Eukaryota Rhizaria Cercozoa Thecofilosea norank_Thecofilosea OTU1028	0.98223
Eukaryota Rhizaria Cercozoa Thecofilosea unclassified_Thecofilosea OTU443	0.03384
Eukaryota Rhizaria Cercozoa unclassified_Cercozoa OTU610	0.05437
Eukaryota Rhizaria Retaria Polycystinea Nassellaria norank_Nassellaria  <i>Pseudocubus</i>   <i>Lithomelissa_setosa</i>  OTU943	0.15101
Eukaryota Stramenopiles Bicosoecida norank_Bicosoecida  <i>Bicosoeca</i>   <i>Bicosoeca_vacillans</i>  OTU1137	0.01834
Eukaryota Stramenopiles Labyrinthulomycetes norank_Labyrinthulomycetes OTU1356	0.02142
Eukaryota Stramenopiles MAST-1 MAST-1A norank_MAST-1A OTU1320	0.08885
Eukaryota Stramenopiles MAST-11 norank_MAST-11 OTU1160	0.01682
Eukaryota Stramenopiles MAST-2 norank_MAST-2 OTU1036	0.02449
Eukaryota Stramenopiles MAST-3 MAST-3B norank_MAST-3B OTU560	0.02812
Eukaryota Stramenopiles MAST-3 MAST-3C norank_MAST-3C OTU1527	0.02896
Eukaryota Stramenopiles MAST-3 MAST-3F norank_MAST-3F OTU1120	0.0127
Eukaryota Stramenopiles MAST-3 MAST-3J norank_MAST-3J norank_MAST-3J OTU34	0.03399
Eukaryota Stramenopiles Ochrophyta Chrysophyceae Ochromonadales norank_Ochromonadales  <i>Paraphysomonas</i>  uncultured_ <i>Paraphysomonas</i>  OTU33	0.0284
Eukaryota Stramenopiles Ochrophyta Chrysophyceae unclassified_Chrysophyceae OTU568	0.01472



Eukaryota   Stramenopiles   Ochrophyta   Diatomea   Bacillariophytina   Mediophyceae   <i>Brockmanniella</i>   <i>Brockmanniella_brockmannii</i>   OTU1361	0.01665
Eukaryota   Stramenopiles   Ochrophyta   Diatomea   Bacillariophytina   Mediophyceae   <i>Chaetoceros</i>   <i>Chaetoceros_muellerii</i>   OTU60	0.07502
Eukaryota   Stramenopiles   Ochrophyta   Diatomea   Bacillariophytina   Mediophyceae   <i>Chaetoceros</i>   <i>Peridinium_quinquecorne_endosymbiont</i>   OTU1488	0.3701
Eukaryota   Stramenopiles   Ochrophyta   Diatomea   Bacillariophytina   Mediophyceae   <i>Thalassiosira</i>   <i>Thalassiosira_profunda</i>   OTU250	0.02194
Eukaryota   Stramenopiles   Ochrophyta   Dictyochophyceae   Dictyochales   norank_Dictyochales   <i>Dictyocha</i>   <i>uncultured_Dictyocha</i>   OTU44	3.57247
Eukaryota   Stramenopiles   Ochrophyta   Dictyochophyceae   Florenciellales   norank_Florenciellales   <i>Pseudochattonella</i>   <i>Pseudochattonella_verruculosa</i>   OTU1463	0.14578
Eukaryota   Stramenopiles   Ochrophyta   Eustigmatophyceae   Eustigmatales   norank_Eustigmatales   OTU520	0.57533
Eukaryota   Stramenopiles   Peronosporomycetes   norank_Peronosporomycetes   OTU417	0.25777
Eukaryota   Stramenopiles   Peronosporomycetes   norank_Peronosporomycetes   OTU990	0.34125
Eukaryota   Stramenopiles   unclassified_Stramenopiles   OTU491	0.01412
Eukaryota   unclassified_Eukaryota   OTU996	0.01138