Supplementary material

Cloning of environmental sample.

Environmental clones from Salada de Monasterio (35º47’S. 57º52’W) and El Triunfo (35º47’S. 57º520’W) Argentinian Pampean shallow lakes were incorporated in the reference tree (for lake description see (1)). The samples were taken on August 2014 in the center of the lake. Fifty ml of lake water pre-filtered through a 50 µm net to remove large particles and were then filtered through a 0.22 µm pore-size polycarbonate filters (Millipore). Genomic DNA from filters was extracted using a CTAB protocol (2) as described in Llames et al (3).The 16S rRNA gene plus the 16S-23S Internal Transcribed Spacer (ITS) PCR products (2200 pb) were cloned and sequenced.

Genomic DNA was amplified with primers 27F (AGAGTTTGATCMTGGCTCAG; Lane, 1991) and PITSEND(R) (CTCTGTGTGCCAAGGTATC; Becker et al*.,* 2000). The amplification was performed using the PCR protocol described in Llames et al (3). The StrataClone PCR Cloning Kit (Agilent Technologies) was used for cloning, following the manufacturer’s instructions. Clones were screened by a direct PCR. Forty-eight positive clones of each lake were sequenced (Macrogen, South Korea) using the primer listed in Table S2 of Huber et al*.* (4)*.* The sequences were edited using Pregap4 and assembled using gap4 from the Staden package (Staden, 1996). Identical sequences (detected by cluster analysis using USEARCH; (5)) and Chimeras (UCHIME, (6)) were removed. The 16S rRNA gene was extracted from the sequences (GENEIOUS v 9.1.5, (7)) and used in the phylogenetic reconstruction.

Table S1: Full and partial genomic libraries (FLS and SLS, respectively) were constructed using 1334 sequences from 5 representative phylogenetic clades of *Synechococcus*, *Prochlorococcus* and *Cyanobium.*

Libraries	**Clades ***	**# Sequences**	**Full length sequences libraries (FLS)**	**Short length sequences libraries (SLS)**
Picocyanobacteria		1334	FLS-Pcy	SLS-Pcy$_{(V2\text{-}V4)}$ SLS-Pcy$_{(V5\text{-}V4)}$
Cyanobium	*A-Cyanobium gracile* [a]	71	FLS-Cyab	SLS-Cyab$_{(V2\text{-}V4)}$ SLS-Cyab$_{(V5\text{-}V7)}$
_Syn_1	Marine *Synechococcus* subcluster 5.1. Clades: I - II- III-IV-V-VI-VII-VIII-IX-XVI-CRD1 b	594	FLS-Syn1	SLS-Syn1$_{(V2\text{-}V4)}$ SLS-Syn1$_{(V5\text{-}V7)}$
Syn 2	Marine *Synechococcus* subcluster 5.3 [b] + Freshwater clades: I -B-E-H-U-Cz-M [c]	231	FLS-Syn2	SLS-Syn2$_{(V2\text{-}V4)}$ SLS-Syn2$_{(V5\text{-}V7)}$
Syn 3	Marine Synechococcus subcluster 5.2 [b] + undefined clades of freshwater strains closed related with *Synechococcus* PCC 7942	36	FLS-Syn3	SLS-Syn3$_{(V2\text{-}V4)}$ SLS-Syn3$_{(V5\text{-}V7)}$
Prochlorococcus	HLI-HLII-LLI-LLII-LLIII-LLIV [d]	402	FLS-Proch	SLS-Proch$_{(V2\text{-}V4)}$ SLS- Proch $_{V5\text{-}V7}$

*Phylogenetic classification as in [a] Crosbie et al.(8); Callieri et al.(9); [b] Ahlgren and Rocap (10); [c] Crosbie et al. (8); Jasser et al. (11); [d] Biller et al.(12).

Table S2: *In silico* evaluation of specificity and coverage rate of primer pairs designed in this work compared with those designed by Nübel et al. (13) allowing one mismatch.

Taxonomy [a]	coverage (%)[b]		Match [c]		Eligible [d]		specificity (%)[e]		outgroup_matched [f]		outgroup_matchable [g]	
	This work	Nübel e (13)	This work	Nübel e (13)	This work	Nübel e (13)	This work	Nübel e (13)	This work	Nübel e (13)	This work	Nübel e (13)
Bacteria	0.6	0.7	3429	4071	572584	575243	100	100	88051	96341	0	0
Bacteria;Acidobacteria	0	0.0	1	1	14486	14532	99.5	99.4	646149	657052	3428	4069
Bacteria;Actinobacteria	0	0.0	1	0	59305	59486	99.4	0	601330	612098	3428	4070
Bacteria;Cyanobacteria	25.5	30.2	3422	4064	13434	13466	100	100	647201	658118	7	6
Bacteria;Cyanobacteria;Oxyphotobacteria;Synechococcales;Cyanobiaceae	95.5	95.6	1700	1707	1781	1785	99.7	99.6	658854	669799	1729	2363
Bacteria;Cyanobacteria;Oxyphotobacteria;Synechococcales;Cyanobiaceae;Cyanobium PCC-6307	96.1	96.8	622	629	647	650	99.6	99.5	659988	670934	2807	3441
Bacteria;Cyanobacteria;Oxyphotobacteria;Synechococcales;Cyanobiaceae;Prochlorococcus MIT9313	94.9	92.5	427	417	450	451	99.5	99.5	660185	671133	3002	3653
Bacteria;Cyanobacteria;Oxyphotobacteria;Synechococcales;Cyanobiaceae;Synechococcus CC9902	95	96.5	604	614	636	636	99.6	99.5	659999	670948	2825	3456
Bacteria;Cyanobacteria;Oxyphotobacteria;Synechococcales;Cyanobiaceae;Synechococcus MBIC10613	100	100.0	5	5	5	5	99.5	99.4	660630	671579	3424	4065
Bacteria;Cyanobacteria;Oxyphotobacteria;Synechococcales;Cyanobiaceae;[Synechococcus] spongiarum group	97.6	97.6	41	41	42	42	99.5	99.4	660593	671542	3388	4029
Bacteria;Cyanobacteria;Oxyphotobacteria;Synechococcales	93.6	95.5	1700	1739	1817	1821	99.7	99.7	658818	669763	1729	2331
Bacteria;Cyanobacteria;Oxyphotobacteria;Thermosynechococcales	6.1	84.0	3	42	49	50	99.5	99.4	660586	671534	3426	4028
Bacteria;Cyanobacteria;Melainabacteria	0	0.4	0	2	506	510	0	99.4	660129	671074	3429	4068
Bacteria;Cyanobacteria;Oxyphotobacteria	26.6	31.6	3422	4062	12846	12874	100	100	647789	658710	7	8
Bacteria;Cyanobacteria;Oxyphotobacteria;Chloroplast	0	9.4	0	565	6031	6040	0	99.5	654604	665544	3429	3505
Bacteria;Cyanobacteria;Oxyphotobacteria;Eurycoccales	0	26.7	0	12	45	45	0	99.4	660590	671539	3429	4058
Bacteria;Cyanobacteria;Oxyphotobacteria;Fr127	0	100.0	0	4	4	4	0	99.4	660631	671580	3429	4066
Bacteria;Cyanobacteria;Oxyphotobacteria;Leptolyngbyales	5.1	93.4	10	184	196	197	99.5	99.4	660439	671387	3419	3886
Bacteria;Cyanobacteria;Oxyphotobacteria;Limnotrichales	5.9	82.4	1	14	17	17	99.5	99.4	660618	671567	3428	4056
Bacteria;Cyanobacteria;Oxyphotobacteria;Neosynechococcales	0	100.0	0	1	1	1	0	99.4	660634	671583	3429	4069
Bacteria;Cyanobacteria;Oxyphotobacteria;Nostocales	45	19.7	1690	741	3757	3768	99.7	99.5	656878	667816	1739	3329
Bacteria;Cyanobacteria;Oxyphotobacteria;Oxyphotobacteria Incertae Sedis	2.6	92.5	13	458	493	495	99.5	99.5	660142	671089	3416	3612
Bacteria;Cyanobacteria;Oxyphotobacteria;Phormidesmiales	0.3	91.4	1	266	291	291	99.5	99.4	660344	671293	3428	3804
Bacteria;Cyanobacteria;Oxyphotobacteria;Pseudanabaenales	2	4.9	2	5	102	102	99.5	99.4	660533	671482	3427	4065
Bacteria;Cyanobacteria;Oxyphotobacteria;RD011	0	87.5	0	7	8	8	0	99.4	660627	671576	3429	4063
Bacteria;Cyanobacteria;Oxyphotobacteria;RD017	8.3	91.7	1	11	12	12	99.5	99.4	660623	671572	3428	4059
Bacteria;Cyanobacteria;Oxyphotobacteria;SepB-3	12.5	100.0	1	8	8	8	99.5	99.4	660627	671576	3428	4062
Bacteria;Cyanobacteria;Oxyphotobacteria;uncultured	0	75.0	0	3	4	4	0	99.4	660631	671580	3429	4067
Bacteria;Patescibacteria	0	0.1	2	5	8956	4521	99.5	99.4	651679	667063	3427	4065
Bacteria;Proteobacteria	0	0.0	1	1	228791	229791	99.2	99.1	431844	441793	3428	4069
Bacteria;Verrucomicrobia	0	0.0	2	0	4385	4411	99.5	0	656250	667173	3427	4070

a= SILVA taxonomy, SSU r132 database; RefNR Sequence Collection
b=(match/elegible)*100
c=number of match hits in the taxa path.
d=number of hits whith sequence data at the primers position in the taxa path
e=100-(outgroup_matches/outgroup_matchable)*100
f=number of matched hits outside the taxonomic path
g=number of matchable hits outside the taxonomic path

Table S3: *In silico* evaluation of specificity and coverage rate of primer pairs designed in this work compared with those designed by Nübel et al. (13) allowing two mismatches.

	coverage (%)[b]		Match[c]		Eligible[d]		specificity (%)[e]		outgroup_matched[f]		outgroup_matchable[g]	
Taxonomy[a]	This work	Nübel al., (13)	This work	Nübel al., (13)	This work	Nübel al., (13)	This work	Nübel al., (13)	This work	Nübel al., (13)	This work	Nübel al., (13)
SILVA(only NR);Bacteria;	1.2	3.7	7053	21417	572584	575243	100	100	0	0	88051	96341
SILVA(only NR);Bacteria;Acetothermia;	0	12.7	0	21	165	165	0	96.8	7053	21391	660470	671419
SILVA(only NR);Bacteria;Acidobacteria;	1.7	30.4	250	4412	14486	14532	98.9	97.4	6803	17000	646149	657052
SILVA(only NR);Bacteria;Actinobacteria;	0	0	3	5	59305	59486	98.8	96.5	7050	21407	601330	612098
SILVA(only NR);Bacteria;Armatimonadetes;	1.3	1.3	10	10	748	750	98.9	96.8	7043	21402	659887	670834
SILVA(only NR);Bacteria;Atribacteria;	0	83.4	0	481	572	577	0	96.9	7053	20931	660063	671007
SILVA(only NR);Bacteria;BHI80-139;	0	39	0	16	41	41	0	96.8	7053	21396	660594	671543
SILVA(only NR);Bacteria;BRC1;	0	2.1	0	8	377	380	0	96.8	7053	21404	660258	671204
SILVA(only NR);Bacteria;Chloroflexi;	2.1	3.3	192	307	9183	9226	98.9	96.8	6861	21105	651452	662358
SILVA(only NR);Bacteria;Coprothermobacteraeota;	8.1	1.4	6	1	74	74	98.9	96.8	7047	21411	660561	671510
SILVA(only NR);Bacteria;Cyanobacteria;	38.1	83.9	5116	11297	13434	13466	99.7	98.5	1937	10115	647201	658118
SILVA(only NR);Bacteria;Cyanobacteria;Oxyphotobacteria;Synechococcales;Cyanobiaceae;	96.2	97.5	1714	1740	1781	1785	99.2	97.1	5339	19672	658854	669799
SILVA(only NR);Bacteria;Cyanobacteria;Oxyphotobacteria;Synechococcales;Cyanobiaceae;Cyanobium PCC-6307;	97.1	97.7	628	635	647	650	99	96.9	6425	20777	659988	670934
SILVA(only NR);Bacteria;Cyanobacteria;Oxyphotobacteria;Synechococcales;Cyanobiaceae;Prochlorococcus MIT9313;	95.8	97.6	431	440	450	451	99	96.9	6622	20972	660185	671133
SILVA(only NR);Bacteria;Cyanobacteria;Oxyphotobacteria;Synechococcales;Cyanobiaceae;Synechococcus CC9902;	95.6	97.2	608	618	636	636	99	96.9	6445	20794	659999	670948
SILVA(only NR);Bacteria;Cyanobacteria;Oxyphotobacteria;Synechococcales;Cyanobiaceae;Synechococcus MBIC10613;	100	100	5	5	5	5	98.9	96.8	7048	21407	660630	671579
SILVA(only NR);Bacteria;Cyanobacteria;Oxyphotobacteria;Synechococcales;Cyanobiaceae;[Synechococcus] spongiarum group;	97.6	97.6	41	41	42	42	98.9	96.8	7012	21371	660593	671542
SILVA(only NR);Bacteria;Cyanobacteria;Oxyphotobacteria;Synechococcales;	95.7	97.4	1738	1773	1817	1821	99.2	97.1	5315	19639	658818	669763
SILVA(only NR);Bacteria;Cyanobacteria;Oxyphotobacteria;Synechococcales;Prochlorotrichaceae;	63.6	100	7	11	11	11	98.9	96.8	7046	21401	660624	671573
SILVA(only NR);Bacteria;Cyanobacteria;Oxyphotobacteria;Synechococcales;Synechococcaceae;	60	80	9	12	15	15	98.9	96.8	7044	21400	660620	671569
SILVA(only NR);Bacteria;Cyanobacteria;Oxyphotobacteria;Thermosynechococcales;	67.3	96	33	48	49	50	98.9	96.8	7020	21364	660586	671534
SILVA(only NR);Bacteria;Cyanobacteria;Melainabacteria;	7.1	77.6	36	396	506	510	98.9	96.9	7017	21016	660129	671074
SILVA(only NR);Bacteria;Cyanobacteria;Oxyphotobacteria;	39.5	84.4	5080	10869	12846	12874	99.7	98.4	1973	10543	647789	658710
SILVA(only NR);Bacteria;Cyanobacteria;Oxyphotobacteria;Chloroplast;	0.6	72.5	37	4377	6031	6040	98.9	97.4	7016	17035	654604	665544
SILVA(only NR);Bacteria;Cyanobacteria;Oxyphotobacteria;Eurycoccales;	68.9	93.3	31	42	45	45	98.9	96.8	7022	21370	660590	671539
SILVA(only NR);Bacteria;Cyanobacteria;Oxyphotobacteria;Fr127;	100	100	4	4	4	4	98.9	96.8	7049	21408	660631	671580
SILVA(only NR);Bacteria;Cyanobacteria;Oxyphotobacteria;Geitlerinematales;	100	100	1	1	1	1	98.9	96.8	7052	21411	660634	671583
SILVA(only NR);Bacteria;Cyanobacteria;Oxyphotobacteria;Gloeobacterales;	12.5	100	1	8	8	8	98.9	96.8	7052	21404	660627	671576
SILVA(only NR);Bacteria;Cyanobacteria;Oxyphotobacteria;Leptolyngbyales;	78.1	95.9	153	189	196	197	99	96.8	6900	21223	660439	671387
SILVA(only NR);Bacteria;Cyanobacteria;Oxyphotobacteria;Limnotrichales;	11.8	94.1	2	16	17	17	98.9	96.8	7051	21396	660618	671567
SILVA(only NR);Bacteria;Cyanobacteria;Oxyphotobacteria;Neosynechococcales;	100	100	1	1	1	1	98.9	96.8	7052	21411	660634	671583
SILVA(only NR);Bacteria;Cyanobacteria;Oxyphotobacteria;Nostocales;	65.3	93.4	2455	3521	3757	3768	99.3	97.3	4598	17891	656878	667816
SILVA(only NR);Bacteria;Cyanobacteria;Oxyphotobacteria;Oxyphotobacteria Incertae Sedis;	79.7	96	393	475	493	495	99	96.9	6660	20937	660142	671089
SILVA(only NR);Bacteria;Cyanobacteria;Oxyphotobacteria;Phormidesmiales;	62.5	96.9	182	282	291	291	99	96.9	6871	21130	660344	671293
SILVA(only NR);Bacteria;Cyanobacteria;Oxyphotobacteria;Pseudanabaenales;	16.7	97.1	17	99	102	102	98.9	96.8	7036	21313	660533	671482
SILVA(only NR);Bacteria;Cyanobacteria;Oxyphotobacteria;RD011;	100	87.5	8	7	8	8	98.9	96.8	7045	21405	660627	671576
SILVA(only NR);Bacteria;Cyanobacteria;Oxyphotobacteria;RD017;	100	100	12	12	12	12	98.9	96.8	7041	21400	660623	671572
SILVA(only NR);Bacteria;Cyanobacteria;Oxyphotobacteria;SepB-3;	100	100	8	8	8	8	98.9	96.8	7045	21404	660627	671576
SILVA(only NR);Bacteria;Cyanobacteria;Oxyphotobacteria;uncultured;	75	100	3	4	4	4	98.9	96.8	7050	21408	660631	671580
SILVA(only NR);Bacteria;Cyanobacteria;Sericytochromatia;	0	39	0	32	82	82	0	96.8	7053	21380	660553	671502
SILVA(only NR);Bacteria;Deferribacteres;	0	0.8	0	1	129	130	0	96.8	7053	21411	660506	671454
SILVA(only NR);Bacteria;Dependentiae;	0	1.2	0	7	575	580	0	96.8	7053	21405	660060	671004
SILVA(only NR);Bacteria;Dictyoglomi;	0	100	0	9	9	9	0	96.8	7053	21403	660626	671575
SILVA(only NR);Bacteria;Elusimicrobia;	0	0.2	0	1	431	435	0	96.8	7053	21411	660204	671149
SILVA(only NR);Bacteria;FCPU426;	2.7	37.8	1	14	37	37	98.9	96.8	7052	21398	660598	671547
SILVA(only NR);Bacteria;Firmicutes;	0.7	2.1	951	3025	143134	144049	98.8	96.5	6102	18387	517501	527535
SILVA(only NR);Bacteria;Fusobacteria;	0	0	1	0	2163	2177	98.9	0	7052	21412	658472	669407
SILVA(only NR);Bacteria;GN01;	0.9	0	1	0	115	120	98.9	0	7052	21412	660520	671464
SILVA(only NR);Bacteria;Halanaerobiaeota;	0	62.5	0	158	253	253	0	96.8	7053	21254	660382	671331
SILVA(only NR);Bacteria;Hydrogenedentes;	0.4	0.4	1	1	270	271	98.9	96.8	7052	21411	660365	671313
SILVA(only NR);Bacteria;Margulisbacteria;	0	14	0	12	86	86	0	96.8	7053	21400	660549	671498
SILVA(only NR);Bacteria;Marinimicrobia(SAR406 clade);	0	0.2	0	1	553	554	0	96.8	7053	21411	660082	671030
SILVA(only NR);Bacteria;Modulibacteria;	0	82.4	0	210	253	255	0	96.8	7053	21202	660382	671329
SILVA(only NR);Bacteria;Nitrospinae;	0.3	87.9	1	320	363	364	98.9	96.9	7052	21092	660272	671220
SILVA(only NR);Bacteria;Nitrospirae;	0	0.5	0	7	1288	1294	0	96.8	7053	21405	659347	670290
SILVA(only NR);Bacteria;Patescibacteria;	0.2	8.6	8	390	4507	4521	98.9	96.8	7045	21022	656128	667063
SILVA(only NR);Bacteria;Planctomycetes;	3.7	0.1	327	11	8956	9001	99	96.8	6726	21401	651679	662583
SILVA(only NR);Bacteria;Proteobacteria;	0	0.1	2	194	228791	229791	98.4	95.2	7051	21218	431844	441793
SILVA(only NR);Bacteria;Rokubacteria;	0.5	88.2	2	335	380	380	98.9	96.9	7051	21077	660255	671204
SILVA(only NR);Bacteria;Schekmanbacteria;	0	72.5	0	29	40	40	0	96.8	7053	21383	660595	671544
SILVA(only NR);Bacteria;Spirochaetes;	0	0	1	0	4181	4200	98.9	0	7052	21412	656454	667384
SILVA(only NR);Bacteria;Synergistetes;	0.2	5	2	57	1137	1138	98.9	96.8	7051	21355	659498	670446
SILVA(only NR);Bacteria;Tenericutes;	0	0.3	0	7	2480	2497	0	96.8	7053	21405	658155	669087
SILVA(only NR);Bacteria;Thermotogae;	0.3	4.5	1	13	291	292	98.9	96.8	7052	21399	660344	671292
SILVA(only NR);Bacteria;Verrucomicrobia;	4	0.1	176	4	4385	4411	99	96.8	6877	21408	656250	667173
SILVA(only NR);Bacteria;WOR-1;	0	79.4	0	27	34	34	0	96.8	7053	21385	660601	671550
SILVA(only NR);Bacteria;WPS-2;	2	49	1	25	51	51	98.9	96.8	7052	21387	660584	671533
SILVA(only NR);Bacteria;WS1;	0	1.1	0	1	93	93	0	96.8	7053	21411	660542	671491
SILVA(only NR);Eukaryota;	0	0	0	3	72786	72420	0	96.4	7053	21409	587849	599164

a= SILVA taxonomy, SSU r132 database; RefNR Sequence Collection
b=(match/elegible)*100
c=number of match hits in the taxa path.
d=number of hits whithsequence data at the primers position in the taxa path
e=100-(outgroup_matches/outgroup_matchable)*100
f=number of matched hits outside the taxonomic path
g=number of matchable hits outside the taxonomic path

Table S4: In silico evaluation of specificity and coverage rate of primer pairs proposed by Herlemann et al., (14) allowing zero mismatch.

Taxonomy [a]	**coverage (%)** [b]	**Match** [c]	**Eligible** [d]	**specificity (%)** [e]	**outgroup matched** [f]	**outgroup matchable**
Archaea;	0.6	136	23664	23	647372	498332
Bacteria;	86.6	498339	575236	99.9	95800	129
Bacteria;Acetothermia;	22.4	37	165	25.7	670871	498431
Bacteria;Acidobacteria;	92.0	13371	14532	26.1	656504	485097
Bacteria;Actinobacteria;	82.4	49010	59486	26.5	611550	449458
Bacteria;Aerophobetes;	3.0	2	66	25.7	670970	498466
Bacteria;AncK6;	4.8	1	21	25.7	671015	498467
Bacteria;Aquificae;	89.3	301	337	25.7	670699	498167
Bacteria;Armatimonadetes;	30.9	232	750	25.7	670286	498236
Bacteria;Bacteroidetes;	89.8	49639	55295	27.1	615741	448829
Bacteria;BHI80-139;	92.7	38	41	25.7	670995	498430
Bacteria;BRC1;	87.6	333	380	25.7	670656	498135
Bacteria;Caldiserica;	91.6	87	95	25.7	670941	498381
Bacteria;Calditrichaeota;	85.8	236	275	25.7	670761	498232
Bacteria;Chlamydiae;	82.8	323	390	25.7	670646	498145
Bacteria;Chloroflexi;	39.0	3595	9226	25.2	661810	494873
Bacteria;Chrysiogenetes;	90.0	9	10	25.7	671026	498459
Bacteria;CK-2C2-2;	81.0	17	21	25.7	671015	498451
Bacteria;Cloacimonetes;	82.3	247	300	25.7	670736	498221
Bacteria;Coprothermobacteraeota;	82.4	61	74	25.7	670962	498407
Bacteria;Cyanobacteria;	76.2	10255	13465	25.8	657571	488213
Bacteria;Cyanobacteria;Melainabacteria;	84.7	432	510	25.7	670526	498036
Bacteria;Cyanobacteria;Oxyphotobacteria;	75.8	9764	12873	25.7	658163	488704
Bacteria;Cyanobacteria;Oxyphotobacteria;Chloroplast;	57.3	3462	6039	25.6	664997	495006
Bacteria;Cyanobacteria;Oxyphotobacteria;Eurycoccales;	86.7	39	45	25.7	670991	498429
Bacteria;Cyanobacteria;Oxyphotobacteria;Eurycoccales;Leptococcaceae;	93.8	15	16	25.7	671020	498453
Bacteria;Cyanobacteria;Oxyphotobacteria;Eurycoccales;uncultured;	90.0	9	10	25.7	671026	498459
Bacteria;Cyanobacteria;Oxyphotobacteria;Fr127;	75.0	3	4	25.7	671032	498465
Bacteria;Cyanobacteria;Oxyphotobacteria;Geitlerinematales;	100.0	1	1	25.7	671035	498467
Bacteria;Cyanobacteria;Oxyphotobacteria;Gloeobacterales;	100.0	8	8	25.7	671028	498460
Bacteria;Cyanobacteria;Oxyphotobacteria;Leptolyngbyales;	93.4	184	197	25.7	670839	498284
Bacteria;Cyanobacteria;Oxyphotobacteria;Limnotrichales;	94.1	16	17	25.7	671019	498452
Bacteria;Cyanobacteria;Oxyphotobacteria;Neosynechococcales;	100.0	1	1	25.7	671035	498467
Bacteria;Cyanobacteria;Oxyphotobacteria;Nostocales;	91.8	3460	3768	25.8	667268	495008
Bacteria;Cyanobacteria;Oxyphotobacteria;Oxyphotobacteria Incertae Sedis;	90.9	450	495	25.7	670541	498018
Bacteria;Cyanobacteria;Oxyphotobacteria;Phormidesmiales;	91.8	267	291	25.7	670745	498201
Bacteria;Cyanobacteria;Oxyphotobacteria;Pseudanabaenales;	95.1	97	102	25.7	670934	498371
Bacteria;Cyanobacteria;Oxyphotobacteria;RD011;	87.5	7	8	25.7	671028	498461
Bacteria;Cyanobacteria;Oxyphotobacteria;RD017;	83.3	10	12	25.7	671024	498458
Bacteria;Cyanobacteria;Oxyphotobacteria;SepB-3;	87.5	7	8	25.7	671028	498461
Bacteria;Cyanobacteria;Oxyphotobacteria;Synechococcales;	93.4	1700	1821	25.8	669215	496768
Bacteria;Cyanobacteria;Oxyphotobacteria;Synechococcales;Cyanobiaceae;	93.4	1667	1785	25.8	669251	496801
Bacteria;Cyanobacteria;Oxyphotobacteria;Synechococcales;Cyanobiaceae;Cyanobium PCC-6307;	**93.5**	**608**	**650**	**25.7**	**670386**	**497860**
Bacteria;Cyanobacteria;Oxyphotobacteria;Synechococcales;Cyanobiaceae;Prochlorococcus MIT9313;	**95.1**	**429**	**451**	**25.7**	**670585**	**498039**
Bacteria;Cyanobacteria;Oxyphotobacteria;Synechococcales;Cyanobiaceae;Synechococcus CC9902;	**93.1**	**592**	**636**	**25.7**	**670400**	**497876**
Bacteria;Cyanobacteria;Oxyphotobacteria;Synechococcales;Cyanobiaceae;Synechococcus MBIC10613;	**80.0**	**4**	**5**	**25.7**	**671031**	**498464**
Bacteria;Cyanobacteria;Oxyphotobacteria;Synechococcales;Cyanobiaceae;[Synechococcus] spongiarum group;	78.6	33	42	25.7	670994	498435
Bacteria;Cyanobacteria;Oxyphotobacteria;Synechococcales;Prochlorotrichaceae;	100.0	11	11	25.7	671025	498457
Bacteria;Cyanobacteria;Oxyphotobacteria;Synechococcales;Synechococcaceae;	80.0	12	15	25.7	671021	498456
Bacteria;Cyanobacteria;Oxyphotobacteria;Thermosynechococcales;	94.0	47	50	25.7	670986	498421
Bacteria;Cyanobacteria;Oxyphotobacteria;uncultured;	100.0	4	4	25.7	671032	498464
Bacteria;Cyanobacteria;Sericytochromatia;	72.0	59	82	25.7	670954	498409
Bacteria;Dadabacteria;	90.5	153	169	25.7	670867	498315
Bacteria;Deferribacteres;	93.1	121	130	25.7	670906	498347
Bacteria;Deinococcus-Thermus;	92.9	849	914	25.7	670122	497619
Bacteria;Dependentiae;	93.3	541	580	25.7	670456	497927
Bacteria;Desantisbacteria;	100.0	2	2	25.7	671034	498466
Bacteria;Dictyoglomi;	100.0	9	9	25.7	671027	498459
Bacteria;Edwardsbacteria;	25.0	1	4	25.7	671032	498467
Bacteria;Elusimicrobia;	84.8	369	435	25.7	670601	498099
Bacteria;Entotheonellaeota;	88.1	148	168	25.7	670868	498320
Bacteria;Epsilonbacteraeota;	93.9	4852	5167	25.9	665869	493616
Bacteria;FBP;	85.8	133	155	25.7	670881	498335
Bacteria;FCPU426;	83.8	31	37	25.7	670999	498437
Bacteria;Fervidibacteria;	100.0	4	4	25.7	671032	498464
Bacteria;Fibrobacteres;	82.9	619	747	25.7	670289	497849
Bacteria;Firestonebacteria;	100.0	3	3	25.7	671033	498465
Bacteria;Firmicutes;	88.2	127119	144048	29.5	526988	371349
Bacteria;Fusobacteria;	87.1	1896	2177	25.8	668859	496572
Bacteria;Fusobacteria;Fusobacteriia;	87.1	1896	2177	25.8	668859	496572
Bacteria;GAL15;	90.7	39	43	25.7	670993	498429
Bacteria;GBS-1;	100.0	2	2	25.7	671034	498466
Bacteria;Gemmatimonadetes;	89.6	1957	2184	25.8	668852	496511
Bacteria;GN01;	3.3	4	120	25.7	670916	498464
Bacteria;Halanaerobiaeota;	75.5	191	253	25.7	670783	498277
Bacteria;Hydrogenedentes;	87.5	237	271	25.7	670765	498231
Bacteria;Hydrothermae;	44.7	17	38	25.7	670998	498451
Bacteria;Kiritimatiellaeota;	79.4	774	975	25.7	670061	497694
Bacteria;Latescibacteria;	85.9	426	496	25.7	670540	498042
Bacteria;LCP-89;	82.6	38	46	25.7	670990	498430
Bacteria;Lentisphaerae;	81.0	380	469	25.7	670567	498088
Bacteria;Margulisbacteria;	87.2	75	86	25.7	670950	498393
Bacteria;Marinimicrobia (SAR406 clade);	59.9	332	554	25.7	670482	498136
Bacteria;MAT-CR-M4-B07;	56.0	14	25	25.7	671011	498454
Bacteria;Modulibacteria;	85.1	217	255	25.7	670781	498251
Bacteria;Nitrospinae;	67.0	244	364	25.7	670672	498224
Bacteria;Omnitrophicaeota;	61.7	313	507	25.7	670529	498155
Bacteria;Patescibacteria;	58.5	2647	4521	25.6	666515	495821
Bacteria;PAUC34f;	1.1	1	88	25.7	670948	498467
Bacteria;Planctomycetes;	73.5	6617	9001	25.7	662035	491851
Bacteria;Poribacteria;	42.9	21	49	25.7	670987	498447
Bacteria;Proteobacteria;	90.0	206746	229787	33.9	441249	291722
Bacteria;Rokubacteria;	90.3	343	380	25.7	670656	498125
Bacteria;RsaHF231;	100.0	8	8	25.7	671028	498460
Bacteria;Schekmanbacteria;	92.5	37	40	25.7	670996	498431
Bacteria;Spirochaetes;	75.7	3179	4200	25.7	666836	495289
Bacteria;Synergistetes;	90.1	1025	1138	25.7	669898	497443
Bacteria;TA06;	88.2	60	68	25.7	670968	498408
Bacteria;Tenericutes;	64.2	1604	2497	25.7	668539	496864
Bacteria;Thermosulfidibacteraeota;	100.0	3	3	25.7	671033	498465
Bacteria;Thermotogae;	91.8	268	292	25.7	670744	498200
Bacteria;uncultured;	100.0	5	5	25.7	671031	498463
Bacteria;Verrucomicrobia;	87.3	3852	4411	25.8	666625	494616
Bacteria;WOR-1;	91.2	31	34	25.7	671002	498437
Bacteria;WPS-2;	86.3	44	51	25.7	670985	498424
Bacteria;WS1;	3.2	3	93	25.7	670943	498465
Bacteria;WS2;	77.6	45	58	25.7	670978	498423
Bacteria;WS4;	37.5	6	16	25.7	671020	498462
Bacteria;Zixibacteria;	88.7	180	203	25.7	670833	498288
Eukaryota;	0.0	2	72163	16.8	598873	498466

a= SILVAtaxonomy, SSU r132 database; RefNR Sequence Collection
b=(match/elegible)*100
c=number of match hits in the taxa path.
d=number of hits whithsequence data at the primers position in the taxa path
e=100-(outgroup_matches/outgroup_matchable)*100
f=number of matched hits outside the taxonomic path
g=number of matchable hits outside the taxonomic path

Table S5: In silico evaluation of specificity and coverage rate of primer pairs proposed by Herlemann et al., (14) allowing one mismatch**.**

Taxonomy [a]	**coverage (%)** [b]	**Match** [c]	**Eligible** [d]	**specificity (%)** [e]	**outgroup matched** [f]	**outgroup matchable**
Archaea;	66.8	15806	23664	15.9	647372	544446
Bacteria;	94.6	544429	575236	83.5	95800	15823
Bacteria;Acetothermia;	95.2	157	165	16.5	670871	560095
Bacteria;Acidobacteria;	96.0	13944	14532	16.8	656504	546308
Bacteria;Actinobacteria;	95.8	56981	59486	17.7	611550	503271
Bacteria;Aegiribacteria;	94.2	49	52	16.5	670984	560203
Bacteria;Aerophobetes;	92.4	61	66	16.5	670970	560191
Bacteria;AncK6;	100.0	21	21	16.5	671015	560231
Bacteria;Aquificae;	95.5	322	337	16.5	670699	559930
Bacteria;Armatimonadetes;	77.3	580	750	16.5	670286	559672
Bacteria;Atribacteria;	93.9	542	577	16.5	670459	559710
Bacteria;Bacteroidetes;	95.4	52766	55295	17.6	615741	507486
Bacteria;BHI80-139;	95.1	39	41	16.5	670995	560213
Bacteria;BRC1;	96.1	365	380	16.5	670656	559887
Bacteria;Caldiserica;	95.8	91	95	16.5	670941	560161
Bacteria;Calditrichaeota;	89.5	246	275	16.5	670761	560006
Bacteria;Calescamantes;	100.0	3	3	16.5	671033	560249
Bacteria;Chlamydiae;	86.7	338	390	16.5	670646	559914
Bacteria;Chloroflexi;	81.8	7548	9226	16.5	661810	552704
Bacteria;Chrysiogenetes;	100.0	10	10	16.5	671026	560242
Bacteria;CK-2C2-2;	90.5	19	21	16.5	671015	560233
Bacteria;Cloacimonetes;	94.0	282	300	16.5	670736	559970
Bacteria;Coprothermobacteraeota;	85.1	63	74	16.5	670962	560189
Bacteria;Cyanobacteria;	89.1	12000	13465	16.6	657571	548252
Bacteria;Cyanobacteria;Melainabacteria;	88.2	450	510	16.5	670526	559802
Bacteria;Cyanobacteria;Oxyphotobacteria;	89.2	11487	12873	16.6	658163	548765
Bacteria;Cyanobacteria;Oxyphotobacteria;Chloroplast;	81.2	4906	6039	16.5	664997	555346
Bacteria;Cyanobacteria;Oxyphotobacteria;Eurycoccales;	97.8	44	45	16.5	670991	560208
Bacteria;Cyanobacteria;Oxyphotobacteria;Fr127;	100.0	4	4	16.5	671032	560248
Bacteria;Cyanobacteria;Oxyphotobacteria;Geitlerinematales;	100.0	1	1	16.5	671035	560251
Bacteria;Cyanobacteria;Oxyphotobacteria;Gloeobacterales;	100.0	8	8	16.5	671028	560244
Bacteria;Cyanobacteria;Oxyphotobacteria;Leptolyngbyales;	97.0	191	197	16.5	670839	560061
Bacteria;Cyanobacteria;Oxyphotobacteria;Limnotrichales;	94.1	16	17	16.5	671019	560236
Bacteria;Cyanobacteria;Oxyphotobacteria;Neosynechococcales;	100.0	1	1	16.5	671035	560251
Bacteria;Cyanobacteria;Oxyphotobacteria;Nostocales;	95.3	3592	3768	16.6	667268	556660
Bacteria;Cyanobacteria;Oxyphotobacteria;Oxyphotobacteria Incertae Sedis;	96.2	476	495	16.5	670541	559776
Bacteria;Cyanobacteria;Oxyphotobacteria;Phormidesmiales;	97.3	283	291	16.5	670745	559969
Bacteria;Cyanobacteria;Oxyphotobacteria;Pseudanabaenales;	99.0	101	102	16.5	670934	560151
Bacteria;Cyanobacteria;Oxyphotobacteria;RD011;	87.5	7	8	16.5	671028	560245
Bacteria;Cyanobacteria;Oxyphotobacteria;RD017;	100.0	12	12	16.5	671024	560240
Bacteria;Cyanobacteria;Oxyphotobacteria;SepB-3;	100.0	8	8	16.5	671028	560244
Bacteria;Cyanobacteria;Oxyphotobacteria;Synechococcales;	98.0	1784	1821	16.5	669215	558468
Bacteria;Cyanobacteria;Oxyphotobacteria;Synechococcales;Cyanobiaceae;	**98.0**	**1749**	**1785**	**16.5**	**669251**	**558503**
Bacteria;Cyanobacteria;Oxyphotobacteria;Synechococcales;Cyanobiaceae;Cyanobium PCC-6307;	**97.8**	**636**	**650**	**16.5**	**670386**	**559616**
Bacteria;Cyanobacteria;Oxyphotobacteria;Synechococcales;Cyanobiaceae;Prochlorococcus MIT9313;	**98.2**	**443**	**451**	**16.5**	**670585**	**559809**
Bacteria;Cyanobacteria;Oxyphotobacteria;Synechococcales;Cyanobiaceae;Synechococcus CC9902;	**98.0**	**623**	**636**	**16.5**	**670400**	**559629**
Bacteria;Cyanobacteria;Oxyphotobacteria;Synechococcales;Cyanobiaceae;Synechococcus MBIC10613;	**100.0**	**5**	**5**	**16.5**	**671031**	**560247**
Bacteria;Cyanobacteria;Oxyphotobacteria;Synechococcales;Cyanobiaceae;[Synechococcus] spongiarum group;	97.6	41	42	16.5	670994	560211
Bacteria;Cyanobacteria;Oxyphotobacteria;Synechococcales;Prochlorotrichaceae;	100.0	11	11	16.5	671025	560241
Bacteria;Cyanobacteria;Oxyphotobacteria;Synechococcales;Synechococcaceae;	93.3	14	15	16.5	671021	560238
Bacteria;Cyanobacteria;Oxyphotobacteria;Thermosynechococcales;	96.0	48	50	16.5	670986	560204
Bacteria;Cyanobacteria;Oxyphotobacteria;uncultured;	100.0	4	4	16.5	671032	560248
Bacteria;Cyanobacteria;Sericytochromatia;	76.8	63	82	16.5	670954	560189
Bacteria;Dadabacteria;	94.7	160	169	16.5	670867	560092
Bacteria;Deferribacteres;	96.2	125	130	16.5	670906	560127
Bacteria;Deinococcus-Thermus;	96.3	880	914	16.5	670122	559372
Bacteria;Dependentiae;	97.1	563	580	16.5	670456	559689
Bacteria;Desantisbacteria;	100.0	2	2	16.5	671034	560250
Bacteria;Dictyoglomi;	100.0	9	9	16.5	671027	560243
Bacteria;Edwardsbacteria;	25.0	1	4	16.5	671032	560251
Bacteria;Elusimicrobia;	94.5	411	435	16.5	670601	559841
Bacteria;Entotheonellaeota;	94.0	158	168	16.5	670868	560094
Bacteria;Epsilonbacteraeota;	96.8	5002	5167	16.6	665869	555250
Bacteria;FBP;	91.0	141	155	16.5	670881	560111
Bacteria;FCPU426;	89.2	33	37	16.5	670999	560219
Bacteria;Fervidibacteria;	100.0	4	4	16.5	671032	560248
Bacteria;Fibrobacteres;	93.0	695	747	16.5	670289	559557
Bacteria;Firestonebacteria;	100.0	3	3	16.5	671033	560249
Bacteria;Firmicutes;	94.7	136458	144048	19.6	526988	423794
Bacteria;Fusobacteria;	95.2	2073	2177	16.5	668859	558179
Bacteria;GAL15;	93.0	40	43	16.5	670993	560212
Bacteria;GBS-1;	100.0	2	2	16.5	671034	560250
Bacteria;Gemmatimonadetes;	93.7	2047	2184	16.5	668852	558205
Bacteria;GN01;	5.8	7	120	16.5	670916	560245
Bacteria;Halanaerobiaeota;	90.1	228	253	16.5	670783	560024
Bacteria;Hydrogenedentes;	93.0	252	271	16.5	670765	560000
Bacteria;Hydrothermae;	94.7	36	38	16.5	670998	560216
Bacteria;Kiritimatiellaeota;	93.9	916	975	16.5	670061	559336
Bacteria;Latescibacteria;	96.6	479	496	16.5	670540	559773
Bacteria;LCP-89;	93.5	43	46	16.5	670990	560209
Bacteria;Lentisphaerae;	95.3	447	469	16.5	670567	559805
Bacteria;Lindowbacteria;	100.0	1	1	16.5	671035	560251
Bacteria;Margulisbacteria;	93.0	80	86	16.5	670950	560172
Bacteria;Marinimicrobia (SAR406 clade);	93.3	517	554	16.5	670482	559735
Bacteria;MAT-CR-M4-B07;	68.0	17	25	16.5	671011	560235
Bacteria;Modulibacteria;	92.9	237	255	16.5	670781	560015
Bacteria;Nitrospinae;	97.0	353	364	16.5	670672	559899
Bacteria;Omnitrophicaeota;	70.8	359	507	16.5	670529	559893
Bacteria;Patescibacteria;	83.8	3787	4521	16.5	666515	556465
Bacteria;PAUC34f;	86.4	76	88	16.5	670948	560176
Bacteria;Planctomycetes;	81.9	7369	9001	16.5	662035	552883
Bacteria;Poribacteria;	98.0	48	49	16.5	670987	560204
Bacteria;Proteobacteria;	95.8	220097	229787	22.9	441249	340155
Bacteria;Rokubacteria;	94.5	359	380	16.5	670656	559893
Bacteria;RsaHF231;	100.0	8	8	16.5	671028	560244
Bacteria;Schekmanbacteria;	97.5	39	40	16.5	670996	560213
Bacteria;Spirochaetes;	94.5	3968	4200	16.6	666836	556284
Bacteria;Synergistetes;	93.7	1066	1138	16.5	669898	559186
Bacteria;TA06;	98.5	67	68	16.5	670968	560185
Bacteria;Tenericutes;	93.5	2335	2497	16.5	668539	557917
Bacteria;Thermosulfidibacteraeota;	100.0	3	3	16.5	671033	560249
Bacteria;Thermotogae;	95.9	280	292	16.5	670744	559972
Bacteria;uncultured;	100.0	5	5	16.5	671031	560247
Bacteria;Verrucomicrobia;	94.1	4149	4411	16.6	666625	556103
Bacteria;WOR-1;	97.1	33	34	16.5	671002	560219
Bacteria;WPS-2;	90.2	46	51	16.5	670985	560206
Bacteria;WS1;	3.2	3	93	16.5	670943	560249
Bacteria;WS2;	82.8	48	58	16.5	670978	560204
Bacteria;WS4;	93.8	15	16	16.5	671020	560237
Bacteria;Zixibacteria;	94.1	191	203	16.5	670833	560061
Eukaryota;	0.1	6.5	72163	6.5	598873	560215

a= SILVA taxonomy, SSU r132 database; RefNR Sequence Collection
b=(match/elegible)*100
c=number of match hits in the taxa path.
d=number of hits whithsequence data at the primers position in the taxa path
e=100-(outgroup_matches/outgroup_matchable)*100
f=number of matched hits outside the taxonomic path
g=number of matchable hits outside the taxonomic path

Table S6: In silico evaluation of specificity and coverage rate of primer pairs proposed by Herlemann et al., (14) allowing two mismatch.

Taxonomy [a]	coverage (%) [b]	Match [c]	Eligible [d]	specificity (%) [e]	outgroup matched [f]	outgroup matchable
Archaea;	89.9	21263	23664	14.5	647372	553259
Bacteria;	96.2	553118	575236	77.7	95800	21404
Bacteria;Acetothermia;	99.4	164	165	14.4	670871	574358
Bacteria;Acidobacteria;	96.5	14029	14532	14.6	656504	560493
Bacteria;Actinobacteria;	96.9	57670	59486	15.5	611550	516852
Bacteria;Aegiribacteria;	98.1	51	52	14.4	670984	574471
Bacteria;Aerophobetes;	97.0	64	66	14.4	670970	574458
Bacteria;AncK6;	100.0	21	21	14.4	671015	574501
Bacteria;Aquificae;	95.5	322	337	14.4	670699	574200
Bacteria;Armatimonadetes;	90.4	678	750	14.4	670286	573844
Bacteria;Atribacteria;	96.4	556	577	14.4	670459	573966
Bacteria;Atribacteria;JS1;	96.2	511	531	14.4	670505	574011
Bacteria;Bacteroidetes;	96.8	53533	55295	15.4	615741	520989
Bacteria;BHI80-139;	95.1	39	41	14.4	670995	574483
Bacteria;BRC1;	96.6	367	380	14.4	670656	574155
Bacteria;Caldiserica;	97.9	93	95	14.4	670941	574429
Bacteria;Calditrichaeota;	93.5	257	275	14.4	670761	574265
Bacteria;Calescamantes;	100.0	3	3	14.4	671033	574519
Bacteria;Chlamydiae;	98.2	383	390	14.4	670646	574139
Bacteria;Chloroflexi;	91.8	8468	9226	14.5	661810	566054
Bacteria;Chrysiogenetes;	100.0	10	10	14.4	671026	574512
Bacteria;CK-2C2-2;	95.2	20	21	14.4	671015	574502
Bacteria;Cloacimonetes;	95.7	287	300	14.4	670736	574235
Bacteria;Cyanobacteria;	94.5	12719	13465	14.6	657571	561803
Bacteria;Cyanobacteria;Melainabacteria;	96.5	492	510	14.4	670526	574030
Bacteria;Cyanobacteria;Oxyphotobacteria;	94.4	12149	12873	14.6	658163	562373
Bacteria;Cyanobacteria;Oxyphotobacteria;Chloroplast;	91.5	5528	6039	14.4	664997	568994
Bacteria;Cyanobacteria;Oxyphotobacteria;Eurycoccales;	97.8	44	45	14.4	670991	574478
Bacteria;Cyanobacteria;Oxyphotobacteria;Fr127;	100.0	4	4	14.4	671032	574518
Bacteria;Cyanobacteria;Oxyphotobacteria;Geitlerinematales;	100.0	1	1	14.4	671035	574521
Bacteria;Cyanobacteria;Oxyphotobacteria;Gloeobacterales;	100.0	8	8	14.4	671028	574514
Bacteria;Cyanobacteria;Oxyphotobacteria;Leptolyngbyales;	97.5	192	197	14.4	670839	574330
Bacteria;Cyanobacteria;Oxyphotobacteria;Limnotrichales;	94.1	16	17	14.4	671019	574506
Bacteria;Cyanobacteria;Oxyphotobacteria;Neosynechococcales;	100.0	1	1	14.4	671035	574521
Bacteria;Cyanobacteria;Oxyphotobacteria;Nostocales;	96.1	3621	3768	14.4	667268	570901
Bacteria;Cyanobacteria;Oxyphotobacteria;Oxyphotobacteria Incertae Sedis;	96.4	477	495	14.4	670541	574045
Bacteria;Cyanobacteria;Oxyphotobacteria;Phormidesmiales;	97.9	285	291	14.4	670745	574237
Bacteria;Cyanobacteria;Oxyphotobacteria;Pseudanabaenales;	99.0	101	102	14.4	670934	574421
Bacteria;Cyanobacteria;Oxyphotobacteria;RD011;	87.5	7	8	14.4	671028	574515
Bacteria;Cyanobacteria;Oxyphotobacteria;RD017;	100.0	12	12	14.4	671024	574510
Bacteria;Cyanobacteria;Oxyphotobacteria;SepB-3;	100.0	8	8	14.4	671028	574514
Bacteria;Cyanobacteria;Oxyphotobacteria;Synechococcales;	98.3	1790	1821	14.4	669215	572732
Bacteria;Cyanobacteria;Oxyphotobacteria;Synechococcales;Cyanobiaceae;	**98.3**	**1755**	**1785**	**14.4**	**669251**	**572767**
Bacteria;Cyanobacteria;Oxyphotobacteria;Synechococcales;Cyanobiaceae;Cyanobium PCC-6307;	**98.5**	**640**	**650**	**14.4**	**670386**	**573882**
Bacteria;Cyanobacteria;Oxyphotobacteria;Synechococcales;Cyanobiaceae;Prochlorococcus MIT9313;	**98.4**	**444**	**451**	**14.4**	**670585**	**574078**
Bacteria;Cyanobacteria;Oxyphotobacteria;Synechococcales;Cyanobiaceae;Synechococcus CC9902;	**98.1**	**624**	**636**	**14.4**	**670400**	**573898**
Bacteria;Cyanobacteria;Oxyphotobacteria;Synechococcales;Cyanobiaceae;Synechococcus MBIC10613;	**100.0**	**5**	**5**	**14.4**	**671031**	**574517**
Bacteria;Cyanobacteria;Oxyphotobacteria;Synechococcales;Cyanobiaceae;[Synechococcus] spongiarum group;	97.6	41	42	14.4	670994	574481
Bacteria;Cyanobacteria;Oxyphotobacteria;Synechococcales;Prochlorotrichaceae;	100.0	11	11	14.4	671025	574511
Bacteria;Cyanobacteria;Oxyphotobacteria;Synechococcales;Synechococcaceae;	93.3	14	15	14.4	671021	574508
Bacteria;Cyanobacteria;Oxyphotobacteria;Thermosynechococcales;	98.0	49	50	14.4	670986	574473
Bacteria;Cyanobacteria;Oxyphotobacteria;uncultured;	100.0	4	4	14.4	671032	574518
Bacteria;Cyanobacteria;Sericytochromatia;	95.1	78	82	14.4	670954	574444
Bacteria;Dadabacteria;	94.7	160	169	14.4	670867	574362
Bacteria;Deferribacteres;	96.9	126	130	14.4	670906	574396
Bacteria;Deinococcus-Thermus;	97.5	891	914	14.4	670122	573631
Bacteria;Dependentiae;	97.4	565	580	14.4	670456	573957
Bacteria;Desantisbacteria;	100.0	2	2	14.4	671034	574520
Bacteria;Dictyoglomi;	100.0	9	9	14.4	671027	574513
Bacteria;Edwardsbacteria;	100.0	4	4	14.4	671032	574518
Bacteria;Elusimicrobia;	96.8	421	435	14.4	670601	574101
Bacteria;Entotheonellaeota;	95.2	160	168	14.4	670868	574362
Bacteria;Epsilonbacteraeota;	97.3	5026	5167	14.5	665869	569496
Bacteria;FBP;	94.8	147	155	14.4	670881	574375
Bacteria;FCPU426;	89.2	33	37	14.4	670999	574489
Bacteria;Fervidibacteria;	100.0	4	4	14.4	671032	574518
Bacteria;Fibrobacteres;	94.5	706	747	14.4	670289	573816
Bacteria;Firestonebacteria;	100.0	3	3	14.4	671033	574519
Bacteria;Firmicutes;	96.2	138553	144048	17.3	526988	435969
Bacteria;Fusobacteria;	96.9	2109	2177	14.4	668859	572413
Bacteria;GAL15;	93.0	40	43	14.4	670993	574482
Bacteria;GBS-1;	100.0	2	2	14.4	671034	574520
Bacteria;Gemmatimonadetes;	94.6	2067	2184	14.4	668852	572455
Bacteria;GN01;	5.8	7	120	14.4	670916	574515
Bacteria;Halanaerobiaeota;	93.3	236	253	14.4	670783	574286
Bacteria;Hydrogenedentes;	94.1	255	271	14.4	670765	574267
Bacteria;Hydrothermae;	94.7	36	38	14.4	670998	574486
Bacteria;Kiritimatiellaeota;	95.7	933	975	14.4	670061	573589
Bacteria;Latescibacteria;	97.4	483	496	14.4	670540	574039
Bacteria;LCP-89;	97.8	45	46	14.4	670990	574477
Bacteria;Lentisphaerae;	97.2	456	469	14.4	670567	574066
Bacteria;Lindowbacteria;	100.0	1	1	14.4	671035	574521
Bacteria;Margulisbacteria;	94.2	81	86	14.4	670950	574441
Bacteria;Marinimicrobia (SAR406 clade);	95.3	528	554	14.4	670482	573994
Bacteria;MAT-CR-M4-B07;	100.0	25	25	14.4	671011	574497
Bacteria;Modulibacteria;	94.1	240	255	14.4	670781	574282
Bacteria;Nitrospinae;	97.8	356	364	14.4	670672	574166
Bacteria;Omnitrophicaeota;	96.6	490	507	14.4	670529	574032
Bacteria;Patescibacteria;	88.0	3977	4521	14.4	666515	570545
Bacteria;PAUC34f;	94.3	83	88	14.4	670948	574439
Bacteria;Planctomycetes;	86.7	7803	9001	14.4	662035	566719
Bacteria;Poribacteria;	98.0	48	49	14.4	670987	574474
Bacteria;Proteobacteria;	96.7	222097	229787	20.1	441249	352425
Bacteria;Rokubacteria;	94.7	360	380	14.4	670656	574162
Bacteria;RsaHF231;	100.0	8	8	14.4	671028	574514
Bacteria;Spirochaetes;	96.1	4036	4200	14.4	666836	570486
Bacteria;Synergistetes;	96.5	1098	1138	14.4	669898	573424
Bacteria;TA06;	98.5	67	68	14.4	670968	574455
Bacteria;Tenericutes;	97.5	2435	2497	14.4	668539	572087
Bacteria;Thermosulfidibacteraeota;	100.0	3	3	14.4	671033	574519
Bacteria;Thermotogae;	97.6	285	292	14.4	670744	574237
Bacteria;uncultured;	100.0	5	5	14.4	671031	574517
Bacteria;Verrucomicrobia;	95.2	4199	4411	14.4	666625	570323
Bacteria;WOR-1;	97.1	33	34	14.4	671002	574489
Bacteria;WPS-2;	90.2	46	51	14.4	670985	574476
Bacteria;WS1;	3.2	3	93	14.4	670943	574519
Bacteria;WS2;	84.5	49	58	14.4	670978	574473
Bacteria;WS4;	93.8	15	16	14.4	671020	574507
Bacteria;Zixibacteria;	95.6	194	203	14.4	670833	574328
Eukaryota;	0.2	163	72163	4.1	598873	574359

a= SILVA taxonomy, SSU r132 database; RefNR Sequence Collection
b=(match/elegible)*100
c=number of match hits in the taxa path.
d=number of hits whithsequence data at the primers position in the taxa path
e=100-(outgroup_matches/outgroup_matchable)*100
f=number of matched hits outside the taxonomic path
g=number of matchable hits outside the taxonomic path

Table S7: In silico evaluation of specificity and coverage rate of primer pairs proposed by Parada et al., (15) allowing zero mismatch.

Taxonomy [a]	coverage (%) [b]	Match [c]	Eligible [d]	specificity (%) [e]	outgroup matched [f]	outgroup matchable
Archaea;	84.6	20824	24615	12	649163	571167
Bacteria;	88.4	508457	575261	15.2	98517	83534
Bacteria;Acetothermia;	0.6	1	165	12.1	673613	591990
Bacteria;Acidobacteria;	93.4	13575	14532	12.3	659246	578416
Bacteria;Actinobacteria;	85.5	50887	59486	11.9	614292	541104
Bacteria;Aegiribacteria;	88.5	46	52	12.1	673726	591945
Bacteria;Aerophobetes;	1.5	1	66	12.1	673712	591990
Bacteria;AncK6;	90.5	19	21	12.1	673757	591972
Bacteria;Aquificae;	78.9	266	337	12.1	673441	591725
Bacteria;Armatimonadetes;	89.5	671	750	12.1	673028	591320
Bacteria;Atribacteria;	91.2	527	578	12.1	673200	591464
Bacteria;Bacteroidetes;	90.0	49754	55295	12.3	618483	542237
Bacteria;BHI80-139;	90.2	37	41	12.1	673737	591954
Bacteria;BRC1;	89.7	341	380	12.1	673398	591650
Bacteria;Caldiserica;	5.3	5	95	12.1	673683	591986
Bacteria;Calditrichaeota;	87.3	240	275	12.1	673503	591751
Bacteria;Chlamydiae;	17.4	68	390	12.1	673388	591923
Bacteria;Chloroflexi;	79.6	7344	9226	12	664552	584647
Bacteria;Chrysiogenetes;	80.0	8	10	12.1	673768	591983
Bacteria;CK-2C2-2;	100.0	21	21	12.1	673757	591970
Bacteria;Coprothermobacteraeota;	94.6	70	74	12.1	673704	591921
Bacteria;Cyanobacteria;	88.4	11904	13467	12.1	660311	580087
Bacteria;Cyanobacteria;Melainabacteria;	92.4	471	510	12.1	673268	591520
Bacteria;Cyanobacteria;Oxyphotobacteria;	88.2	11355	12875	12.1	660903	580636
Bacteria;Cyanobacteria;Oxyphotobacteria;Chloroplast;	84.3	5094	6041	12.1	667737	586897
Bacteria;Cyanobacteria;Oxyphotobacteria;Eurycoccales;	95.6	43	45	12.1	673733	591948
Bacteria;Cyanobacteria;Oxyphotobacteria;Fr127;	75.0	3	4	12.1	673774	591988
Bacteria;Cyanobacteria;Oxyphotobacteria;Geitlerinematales;	100.0	1	1	12.1	673777	591990
Bacteria;Cyanobacteria;Oxyphotobacteria;Gloeobacterales;	100.0	8	8	12.1	673770	591983
Bacteria;Cyanobacteria;Oxyphotobacteria;Leptolyngbyales;	91.4	180	197	12.1	673581	591811
Bacteria;Cyanobacteria;Oxyphotobacteria;Limnotrichales;	100.0	17	17	12.1	673761	591974
Bacteria;Cyanobacteria;Oxyphotobacteria;Neosynechococcales;	100.0	1	1	12.1	673777	591990
Bacteria;Cyanobacteria;Oxyphotobacteria;Nostocales;	91.7	3454	3768	12.2	670010	588537
Bacteria;Cyanobacteria;Oxyphotobacteria;Oxyphotobacteria Incertae Sedis;	87.5	433	495	12.1	673283	591558
Bacteria;Cyanobacteria;Oxyphotobacteria;Phormidesmiales;	91.8	267	291	12.1	673487	591724
Bacteria;Cyanobacteria;Oxyphotobacteria;Pseudanabaenales;	99.0	101	102	12.1	673676	591890
Bacteria;Cyanobacteria;Oxyphotobacteria;RD011;	75.0	6	8	12.1	673770	591985
Bacteria;Cyanobacteria;Oxyphotobacteria;RD017;	91.7	11	12	12.1	673766	591980
Bacteria;Cyanobacteria;Oxyphotobacteria;SepB-3;	87.5	7	8	12.1	673770	591984
Bacteria;Cyanobacteria;Oxyphotobacteria;Synechococcales;	92.0	1676	1821	12.1	671957	590315
Bacteria;Cyanobacteria;Oxyphotobacteria;Synechococcales;Cyanobiaceae;	**91.9**	**1641**	**1785**	**12.1**	**671993**	**590350**
Bacteria;Cyanobacteria;Oxyphotobacteria;Synechococcales;Cyanobiaceae;Cyanobium PCC-6307;	**94.5**	**614**	**650**	**12.1**	**673128**	**591377**
Bacteria;Cyanobacteria;Oxyphotobacteria;Synechococcales;Cyanobiaceae;Prochlorococcus MIT9313;	**83.8**	**378**	**451**	**12.1**	**673327**	**591613**
Bacteria;Cyanobacteria;Oxyphotobacteria;Synechococcales;Cyanobiaceae;Synechococcus CC9902;	**94.5**	**601**	**636**	**12.1**	**673142**	**591390**
Bacteria;Cyanobacteria;Oxyphotobacteria;Synechococcales;Cyanobiaceae;Synechococcus MBIC10613;	**100.0**	**5**	**5**	**12.1**	**673773**	**591986**
Bacteria;Cyanobacteria;Oxyphotobacteria;Synechococcales;Cyanobiaceae;[Synechococcus] spongiarum group;	100.0	42	42	12.1	673736	591949
Bacteria;Cyanobacteria;Oxyphotobacteria;Synechococcales;Prochlorotrichaceae;	100.0	11	11	12.1	673767	591980
Bacteria;Cyanobacteria;Oxyphotobacteria;Synechococcales;Synechococcaceae;	93.3	14	15	12.1	673763	591977
Bacteria;Cyanobacteria;Oxyphotobacteria;Thermosynechococcales;	94.0	47	50	12.1	673728	591944
Bacteria;Cyanobacteria;Sericytochromatia;	95.1	78	82	12.1	673696	591913
Bacteria;Dadabacteria;	91.1	154	169	12.1	673609	591837
Bacteria;Deferribacteres;	93.1	121	130	12.1	673648	591870
Bacteria;Deinococcus-Thermus;	92.3	844	914	12.1	672864	591147
Bacteria;Dependentiae;	86.9	504	580	12.1	673198	591487
Bacteria;Dictyoglomi;	88.9	8	9	12.1	673769	591983
Bacteria;Edwardsbacteria;	50.0	2	4	12.1	673774	591989
Bacteria;Elusimicrobia;	88.7	386	435	12.1	673343	591605
Bacteria;Entotheonellaeota;	71.4	120	168	12.1	673610	591871
Bacteria;Epsilonbacteraeota;	1.6	83	5167	11.5	668611	591908
Bacteria;FBP;	91.0	141	155	12.1	673623	591850
Bacteria;FCPU426;	78.4	29	37	12.1	673741	591962
Bacteria;Fibrobacteres;	83.9	627	747	12.1	673031	591364
Bacteria;Firestonebacteria;	33.3	1	3	12.1	673775	591990
Bacteria;Firmicutes;	87.9	126673	144050	12.2	529728	465318
Bacteria;Fusobacteria;	84.1	1831	2177	12.1	671601	590160
Bacteria;GAL15;	95.3	41	43	12.1	673735	591950
Bacteria;GBS-1;	100.0	2	2	12.1	673776	591989
Bacteria;Gemmatimonadetes;	92.0	2010	2184	12.2	671594	589981
Bacteria;GN01;	65.0	78	120	12.1	673658	591913
Bacteria;Halanaerobiaeota;	86.6	219	253	12.1	673525	591772
Bacteria;Hydrogenedentes;	95.6	259	271	12.1	673507	591732
Bacteria;Hydrothermae;	73.7	28	38	12.1	673740	591963
Bacteria;Kiritimatiellaeota;	88.3	861	975	12.1	672803	591130
Bacteria;Latescibacteria;	90.9	452	497	12.1	673281	591539
Bacteria;LCP-89;	89.1	41	46	12.1	673732	591950
Bacteria;Lentisphaerae;	90.6	425	469	12.1	673309	591566
Bacteria;Lindowbacteria;	100.0	1	1	12.1	673777	591990
Bacteria;Margulisbacteria;	96.5	83	86	12.1	673692	591908
Bacteria;Marinimicrobia (SAR406 clade);	94.0	521	554	12.1	673224	591470
Bacteria;MAT-CR-M4-B07;	88.0	22	25	12.1	673753	591969
Bacteria;Modulibacteria;	78.8	201	255	12.1	673523	591790
Bacteria;Nitrospinae;	96.2	350	364	12.1	673414	591641
Bacteria;Nitrospirae;	91.5	1184	1294	12.1	672484	590807
Bacteria;Omnitrophicaeota;	91.3	463	507	12.1	673271	591528
Bacteria;Patescibacteria;	4.2	189	4521	11.6	669257	591802
Bacteria;PAUC34f;	97.7	86	88	12.1	673690	591905
Bacteria;Planctomycetes;	85.9	7734	9002	12.1	664776	584257
Bacteria;Proteobacteria;	93.1	213874	229805	14.8	443973	378117
Bacteria;Rokubacteria;	93.7	356	380	12.1	673398	591635
Bacteria;RsaHF231;	75.0	6	8	12.1	673770	591985
Bacteria;Schekmanbacteria;	95.0	38	40	12.1	673738	591953
Bacteria;Spirochaetes;	88.5	3718	4200	12.1	669578	588273
Bacteria;Synergistetes;	92.7	1055	1138	12.1	672640	590936
Bacteria;TA06;	85.3	58	68	12.1	673710	591933
Bacteria;Tenericutes;	78.9	1971	2497	12.1	671281	590020
Bacteria;Thermosulfidibacteraeota;	66.7	2	3	12.1	673775	591989
Bacteria;Thermotogae;	91.1	266	292	12.1	673486	591725
Bacteria;Verrucomicrobia;	88.9	3923	4411	12.1	669367	588068
Bacteria;WOR-1;	23.5	8	34	12.1	673744	591983
Bacteria;WPS-2;	98.0	50	51	12.1	673727	591941
Bacteria;WS1;	76.3	71	93	12.1	673685	591920
Bacteria;WS2;	82.8	48	58	12.1	673720	591943
Bacteria;WS4;	100.0	16	16	12.1	673762	591975
Bacteria;Zixibacteria;	86.7	176	203	12.1	673575	591815
Eukaryota;	84.9	62731	73929	11.8	599849	529260
Eukaryota;uncultured;	72.7	8	11	12.1	673767	591983

a= SILVA taxonomy, SSU r132 database; RefNR Sequence Collection
b=(match/elegible)*100
c=number of match hits in the taxa path.
d=number of hits whithsequence data at the primers position in the taxa path
e=100-(outgroup_matches/outgroup_matchable)*100
f=number of matched hits outside the taxonomic path
g=number of matchable hits outside the taxonomic path

Table S8: In silico evaluation of specificity and coverage rate of primer pairs proposed by Parada et al., (15) allowing one mismatch.

Taxonomy [a]	**coverage (%)** [b]	**Match** [c]	**Eligible** [d]	**specificity (%)** [e]	**outgroup matched** [f]	**outgroup matchable**
Archaea;	92.9	22858	24615	4.8	649163	617934
Bacteria;	95.5	549190	575261	7	98517	91602
Bacteria;Acetothermia;	56.4	93	165	4.9	673613	640699
Bacteria;Acidobacteria;	97.4	14160	14532	4.9	659246	626632
Bacteria;Actinobacteria;	95.0	56525	59486	4.9	614292	584267
Bacteria;Aegiribacteria;	96.2	50	52	4.9	673726	640742
Bacteria;Aerophobetes;	97.0	64	66	4.9	673712	640728
Bacteria;AncK6;	95.2	20	21	4.9	673757	640772
Bacteria;Aquificae;	95.3	321	337	4.9	673441	640471
Bacteria;Armatimonadetes;	95.7	718	750	4.9	673028	640074
Bacteria;Atribacteria;	97.2	562	578	4.9	673200	640230
Bacteria;Bacteroidetes;	95.7	52895	55295	4.9	618483	587897
Bacteria;BHI80-139;	95.1	39	41	4.9	673737	640753
Bacteria;BRC1;	94.7	360	380	4.9	673398	640432
Bacteria;Caldiserica;	91.6	87	95	4.9	673683	640705
Bacteria;Calditrichaeota;	92.4	254	275	4.9	673503	640538
Bacteria;Calescamantes;	100.0	3	3	4.9	673775	640789
Bacteria;Chlamydiae;	94.1	367	390	4.9	673388	640425
Bacteria;Chloroflexi;	94.8	8743	9226	4.9	664552	632049
Bacteria;Chrysiogenetes;	80.0	8	10	4.9	673768	640784
Bacteria;CK-2C2-2;	100.0	21	21	4.9	673757	640771
Bacteria;Cloacimonetes;	92.0	276	300	4.9	673478	640516
Bacteria;Coprothermobacteraeota;	97.3	72	74	4.9	673704	640720
Bacteria;Cyanobacteria;	93.9	12648	13467	4.9	660311	628144
Bacteria;Cyanobacteria;Melainabacteria;	96.7	493	510	4.9	673268	640299
Bacteria;Cyanobacteria;Oxyphotobacteria;	93.8	12074	12875	4.9	660903	628718
Bacteria;Cyanobacteria;Oxyphotobacteria;Chloroplast;	91.3	5514	6041	4.9	667737	635278
Bacteria;Cyanobacteria;Oxyphotobacteria;Eurycoccales;	97.8	44	45	4.9	673733	640748
Bacteria;Cyanobacteria;Oxyphotobacteria;Fr127;	75.0	3	4	4.9	673774	640789
Bacteria;Cyanobacteria;Oxyphotobacteria;Geitlerinematales;	100.0	1	1	4.9	673777	640791
Bacteria;Cyanobacteria;Oxyphotobacteria;Gloeobacterales;	100.0	8	8	4.9	673770	640784
Bacteria;Cyanobacteria;Oxyphotobacteria;Leptolyngbyales;	95.9	189	197	4.9	673581	640603
Bacteria;Cyanobacteria;Oxyphotobacteria;Limnotrichales;	100.0	17	17	4.9	673761	640775
Bacteria;Cyanobacteria;Oxyphotobacteria;Neosynechococcales;	100.0	1	1	4.9	673777	640791
Bacteria;Cyanobacteria;Oxyphotobacteria;Nostocales;	95.9	3612	3768	4.9	670010	637180
Bacteria;Cyanobacteria;Oxyphotobacteria;Oxyphotobacteria Incertae Sedis;	94.1	466	495	4.9	673283	640326
Bacteria;Cyanobacteria;Oxyphotobacteria;Phormidesmiales;	95.2	277	291	4.9	673487	640515
Bacteria;Cyanobacteria;Oxyphotobacteria;Pseudanabaenales;	99.0	101	102	4.9	673676	640691
Bacteria;Cyanobacteria;Oxyphotobacteria;Pseudanabaenales;Pseudanabaenaceae;	99.0	101	102	4.9	673676	640691
Bacteria;Cyanobacteria;Oxyphotobacteria;Pseudanabaenales;Pseudanabaenaceae;Pseudanabaena PCC-6802;	100.0	4	4	4.9	673774	640788
Bacteria;Cyanobacteria;Oxyphotobacteria;Pseudanabaenales;Pseudanabaenaceae;Pseudanabaena PCC-7367;	100.0	8	8	4.9	673770	640784
Bacteria;Cyanobacteria;Oxyphotobacteria;Pseudanabaenales;Pseudanabaenaceae;Pseudanabaena PCC-7403;	100.0	3	3	4.9	673775	640789
Bacteria;Cyanobacteria;Oxyphotobacteria;Pseudanabaenales;Pseudanabaenaceae;Pseudanabaena PCC-7429;	100.0	37	37	4.9	673741	640755
Bacteria;Cyanobacteria;Oxyphotobacteria;Pseudanabaenales;Pseudanabaenaceae;Synechococcus PCC-7502;	100.0	14	14	4.9	673764	640778
Bacteria;Cyanobacteria;Oxyphotobacteria;Pseudanabaenales;Pseudanabaenaceae;uncultured;	97.1	34	35	4.9	673743	640758
Bacteria;Cyanobacteria;Oxyphotobacteria;RD011;	100.0	8	8	4.9	673770	640784
Bacteria;Cyanobacteria;Oxyphotobacteria;RD017;	91.7	11	12	4.9	673766	640781
Bacteria;Cyanobacteria;Oxyphotobacteria;SepB-3;	100.0	8	8	4.9	673770	640784
Bacteria;Cyanobacteria;Oxyphotobacteria;Synechococcales;	96.7	1761	1821	4.9	671957	639031
Bacteria;Cyanobacteria;Oxyphotobacteria;Synechococcales;Cyanobiaceae;	**96.6**	**1725**	**1785**	**4.9**	**671993**	**639067**
Bacteria;Cyanobacteria;Oxyphotobacteria;Synechococcales;Cyanobiaceae;Cyanobium PCC-6307;	**98.0**	**637**	**650**	**4.9**	**673128**	**640155**
Bacteria;Cyanobacteria;Oxyphotobacteria;Synechococcales;Cyanobiaceae;Prochlorococcus MIT9313;	**91.1**	**411**	**451**	**4.9**	**673327**	**640381**
Bacteria;Cyanobacteria;Oxyphotobacteria;Synechococcales;Cyanobiaceae;Synechococcus CC9902;	**98.9**	**629**	**636**	**4.9**	**673142**	**640163**
Bacteria;Cyanobacteria;Oxyphotobacteria;Synechococcales;Cyanobiaceae;Synechococcus MBIC10613;	**100.0**	**5**	**5**	**4.9**	**673773**	**640787**
Bacteria;Cyanobacteria;Oxyphotobacteria;Synechococcales;Cyanobiaceae;[Synechococcus] spongiarum group;	100.0	42	42	4.9	673736	640750
Bacteria;Cyanobacteria;Oxyphotobacteria;Synechococcales;Prochlorotrichaceae;	100.0	11	11	4.9	673767	640781
Bacteria;Cyanobacteria;Oxyphotobacteria;Synechococcales;Synechococcaceae;	100.0	15	15	4.9	673763	640777
Bacteria;Cyanobacteria;Oxyphotobacteria;Thermosynechococcales;	94.0	47	50	4.9	673728	640745
Bacteria;Cyanobacteria;Oxyphotobacteria;Thermosynechococcales;Acaryochloridaceae;	86.7	13	15	4.9	673763	640779
Bacteria;Cyanobacteria;Oxyphotobacteria;Thermosynechococcales;Acaryochloridaceae;Acaryochloris MBIC1101	86.7	13	15	4.9	673763	640779
Bacteria;Cyanobacteria;Oxyphotobacteria;Thermosynechococcales;Thermosynechococcaceae;	97.1	34	35	4.9	673743	640758
Bacteria;Cyanobacteria;Oxyphotobacteria;Thermosynechococcales;Thermosynechococcaceae;Cyanothece PCC 7	100.0	8	8	4.9	673770	640784
Bacteria;Cyanobacteria;Oxyphotobacteria;Thermosynechococcales;Thermosynechococcaceae;Loriellopsis LF-B5;	83.3	5	6	4.9	673772	640787
Bacteria;Cyanobacteria;Oxyphotobacteria;Thermosynechococcales;Thermosynechococcaceae;Synechococcus IR	100.0	6	6	4.9	673772	640786
Bacteria;Cyanobacteria;Oxyphotobacteria;Thermosynechococcales;Thermosynechococcaceae;Synechococcus PC	100.0	2	2	4.9	673776	640790
Bacteria;Cyanobacteria;Oxyphotobacteria;Thermosynechococcales;Thermosynechococcaceae;Thermosynechoco	100.0	9	9	4.9	673769	640783
Bacteria;Cyanobacteria;Oxyphotobacteria;Thermosynechococcales;Thermosynechococcaceae;uncultured;	100.0	3	3	4.9	673775	640789
Bacteria;Cyanobacteria;Oxyphotobacteria;uncultured;	100.0	4	4	4.9	673774	640788
Bacteria;Cyanobacteria;Sericytochromatia;	98.8	81	82	4.9	673696	640711
Bacteria;Dadabacteria;	98.2	166	169	4.9	673609	640626
Bacteria;Deferribacteres;	97.7	127	130	4.9	673648	640665
Bacteria;Deinococcus-Thermus;	97.0	887	914	4.9	672864	639905
Bacteria;Dependentiae;	96.6	560	580	4.9	673198	640232
Bacteria;Desantisbacteria;	100.0	2	2	4.9	673776	640790
Bacteria;Dictyoglomi;	88.9	8	9	4.9	673769	640784
Bacteria;Edwardsbacteria;	75.0	3	4	4.9	673774	640789
Bacteria;Elusimicrobia;	96.8	421	435	4.9	673343	640371
Bacteria;Entotheonellaeota;	99.4	167	168	4.9	673610	640625
Bacteria;Epsilonbacteraeota;	95.2	4921	5167	4.9	668611	635871
Bacteria;FBP;	98.7	153	155	4.9	673623	640639
Bacteria;FCPU426;	91.9	34	37	4.9	673741	640758
Bacteria;Fibrobacteres;	93.3	697	747	4.9	673031	640095
Bacteria;Firestonebacteria;	100.0	3	3	4.9	673775	640789
Bacteria;Firmicutes;	94.6	136341	144050	4.8	529728	504451
Bacteria;Fusobacteria;	91.0	1980	2177	4.9	671601	638812
Bacteria;GAL15;	100.0	43	43	4.9	673735	640749
Bacteria;GBS-1;	100.0	2	2	4.9	673776	640790
Bacteria;Gemmatimonadetes;	96.4	2106	2184	4.9	671594	638686
Bacteria;GN01;	80.8	97	120	4.9	673658	640695
Bacteria;Halanaerobiaeota;	92.9	235	253	4.9	673525	640557
Bacteria;Hydrogenedentes;	98.5	267	271	4.9	673507	640525
Bacteria;Hydrothermae;	97.4	37	38	4.9	673740	640755
Bacteria;Kiritimatiellaeota;	94.7	923	975	4.9	672803	639869
Bacteria;Latescibacteria;	96.2	478	497	4.9	673281	640314
Bacteria;LCP-89;	97.8	45	46	4.9	673732	640747
Bacteria;Lentisphaerae;	96.4	452	469	4.9	673309	640340
Bacteria;Lindowbacteria;	100.0	1	1	4.9	673777	640791
Bacteria;Margulisbacteria;	98.8	85	86	4.9	673692	640707
Bacteria;Marinimicrobia (SAR406 clade);	97.3	539	554	4.9	673224	640253
Bacteria;MAT-CR-M4-B07;	92.0	23	25	4.9	673753	640769
Bacteria;Modulibacteria;	85.9	219	255	4.9	673523	640573
Bacteria;Nitrospinae;	98.6	359	364	4.9	673414	640433
Bacteria;Nitrospirae;	96.2	1245	1294	4.9	672484	639547
Bacteria;Omnitrophicaeota;	96.3	488	507	4.9	673271	640304
Bacteria;Patescibacteria;	65.6	2964	4521	4.7	669257	637828
Bacteria;PAUC34f;	98.9	87	88	4.9	673690	640705
Bacteria;Poribacteria;	10.2	5	49	4.9	673729	640787
Bacteria;Proteobacteria;	96.8	222363	229805	5.8	443973	418429
Bacteria;Rokubacteria;	98.4	374	380	4.9	673398	640418
Bacteria;RsaHF231;	100.0	8	8	4.9	673770	640784
Bacteria;Schekmanbacteria;	97.5	39	40	4.9	673738	640753
Bacteria;Spirochaetes;	95.3	4001	4200	4.9	669578	636791
Bacteria;Synergistetes;	97.6	1111	1138	4.9	672640	639681
Bacteria;TA06;	98.5	67	68	4.9	673710	640725
Bacteria;Tenericutes;	88.1	2199	2497	4.9	671281	638593
Bacteria;Thermosulfidibacteraeota;	100.0	3	3	4.9	673775	640789
Bacteria;Thermotogae;	95.9	280	292	4.9	673486	640512
Bacteria;uncultured;	100.0	5	5	4.9	673773	640787
Bacteria;Verrucomicrobia;	95.0	4189	4411	4.9	669367	636603
Bacteria;WOR-1;	100.0	34	34	4.9	673744	640758
Bacteria;WPS-2;	98.0	50	51	4.9	673727	640742
Bacteria;WS1;	95.7	89	93	4.9	673685	640703
Bacteria;WS2;	93.1	54	58	4.9	673720	640738
Bacteria;WS4;	100.0	16	16	4.9	673762	640776
Bacteria;Zixibacteria;	97.0	197	203	4.9	673575	640595
Eukaryota;	93.0	68767	73929	4.6	599849	572025

a= SILVA taxonomy, SSU r132 database; RefNR Sequence Collection
b=(match/elegible)*100
c=number of match hits in the taxa path.
d=number of hits whithsequence data at the primers position in the taxa path
e=100-(outgroup_matches/outgroup_matchable)*100
f=number of matched hits outside the taxonomic path
g=number of matchable hits outside the taxonomic path

Table S9: In silico evaluation of specificity and coverage rate of primer pairs proposed by Parada et al., (15) allowing two mismatch.

Taxonomy [a]	coverage (%) [b]	Match [c]	Eligible [d]	specificity (%) [e]	outgroup matched [f]	outgroup matchable
Archaea;	94.0	23132	24615	3.6	649163	625721
Bacteria;	96.6	555910	575261	5.7	98517	92943
Bacteria;Acetothermia;	95.8	158	165	3.7	673613	648695
Bacteria;Acidobacteria;	97.8	14215	14532	3.7	659246	634638
Bacteria;Actinobacteria;	96.4	57368	59486	3.7	614292	591485
Bacteria;Aegiribacteria;	96.2	50	52	3.7	673726	648803
Bacteria;Aerophobetes;	100.0	66	66	3.7	673712	648787
Bacteria;AncK6;	95.2	20	21	3.7	673757	648833
Bacteria;Aquificae;	97.6	329	337	3.7	673441	648524
Bacteria;Armatimonadetes;	96.4	723	750	3.7	673028	648130
Bacteria;Atribacteria;	97.8	565	578	3.7	673200	648288
Bacteria;Bacteroidetes;	96.6	53424	55295	3.7	618483	595429
Bacteria;BHI80-139;	97.6	40	41	3.7	673737	648813
Bacteria;BRC1;	95.8	364	380	3.7	673398	648489
Bacteria;Caldiserica;	93.7	89	95	3.7	673683	648764
Bacteria;Calditrichaeota;	94.5	260	275	3.7	673503	648593
Bacteria;Calescamantes;	100.0	3	3	3.7	673775	648850
Bacteria;Chlamydiae;	95.9	374	390	3.7	673388	648479
Bacteria;Chloroflexi;	96.4	8891	9226	3.7	664552	639962
Bacteria;Chrysiogenetes;	90.0	9	10	3.7	673768	648844
Bacteria;CK-2C2-2;	100.0	21	21	3.7	673757	648832
Bacteria;Cloacimonetes;	94.3	283	300	3.7	673478	648570
Bacteria;Coprothermobacteraeota;	98.6	73	74	3.7	673704	648780
Bacteria;Cyanobacteria;	95.4	12850	13467	3.7	660311	636003
Bacteria;Cyanobacteria;Melainabacteria;	97.5	497	510	3.7	673268	648356
Bacteria;Cyanobacteria;Oxyphotobacteria;	95.3	12271	12875	3.7	660903	636582
Bacteria;Cyanobacteria;Oxyphotobacteria;Chloroplast;	93.6	5656	6041	3.7	667737	643197
Bacteria;Cyanobacteria;Oxyphotobacteria;Eurycoccales;	97.8	44	45	3.7	673733	648809
Bacteria;Cyanobacteria;Oxyphotobacteria;Fr127;	100.0	4	4	3.7	673774	648849
Bacteria;Cyanobacteria;Oxyphotobacteria;Geitlerinematales;	100.0	1	1	3.7	673777	648852
Bacteria;Cyanobacteria;Oxyphotobacteria;Gloeobacterales;	100.0	8	8	3.7	673770	648845
Bacteria;Cyanobacteria;Oxyphotobacteria;Leptolyngbyales;	96.4	190	197	3.7	673581	648663
Bacteria;Cyanobacteria;Oxyphotobacteria;Limnotrichales;	100.0	17	17	3.7	673761	648836
Bacteria;Cyanobacteria;Oxyphotobacteria;Neosynechococcales;	100.0	1	1	3.7	673777	648852
Bacteria;Cyanobacteria;Oxyphotobacteria;Nostocales;	96.9	3651	3768	3.7	670010	645202
Bacteria;Cyanobacteria;Oxyphotobacteria;Oxyphotobacteria Incertae Sedis;	95.4	472	495	3.7	673283	648381
Bacteria;Cyanobacteria;Oxyphotobacteria;Phormidesmiales;	95.2	277	291	3.7	673487	648576
Bacteria;Cyanobacteria;Oxyphotobacteria;Pseudanabaenales;	99.0	101	102	3.7	673676	648752
Bacteria;Cyanobacteria;Oxyphotobacteria;RD011;	100.0	8	8	3.7	673770	648845
Bacteria;Cyanobacteria;Oxyphotobacteria;RD017;	91.7	11	12	3.7	673766	648842
Bacteria;Cyanobacteria;Oxyphotobacteria;SepB-3;	100.0	8	8	3.7	673770	648845
Bacteria;Cyanobacteria;Oxyphotobacteria;Synechococcales;	97.0	1767	1821	3.7	671957	647086
Bacteria;Cyanobacteria;Oxyphotobacteria;Synechococcales;Cyanobiaceae;	**97.0**	**1731**	**1785**	**3.7**	**671993**	**647122**
Bacteria;Cyanobacteria;Oxyphotobacteria;Synechococcales;Cyanobiaceae;Cyanobium PCC-6307;	**98.5**	**640**	**650**	**3.7**	**673128**	**648213**
Bacteria;Cyanobacteria;Oxyphotobacteria;Synechococcales;Cyanobiaceae;Prochlorococcus MIT9313;	**91.6**	**413**	**451**	**3.7**	**673327**	**648440**
Bacteria;Cyanobacteria;Oxyphotobacteria;Synechococcales;Cyanobiaceae;Synechococcus CC9902;	**99.1**	**630**	**636**	**3.7**	**673142**	**648223**
Bacteria;Cyanobacteria;Oxyphotobacteria;Synechococcales;Cyanobiaceae;Synechococcus MBIC10613;	100.0	5	5	3.7	673773	648848
Bacteria;Cyanobacteria;Oxyphotobacteria;Synechococcales;Cyanobiaceae;[Synechococcus] spongiarum group;	100.0	42	42	3.7	673736	648811
Bacteria;Cyanobacteria;Oxyphotobacteria;Synechococcales;Prochlorotrichaceae;	100.0	11	11	3.7	673767	648842
Bacteria;Cyanobacteria;Oxyphotobacteria;Synechococcales;Synechococcaceae;	100.0	15	15	3.7	673763	648838
Bacteria;Cyanobacteria;Oxyphotobacteria;Thermosynechococcales;	98.0	49	50	3.7	673728	648804
Bacteria;Cyanobacteria;Oxyphotobacteria;uncultured;	100.0	4	4	3.7	673774	648849
Bacteria;Cyanobacteria;Sericytochromatia;	100.0	82	82	3.7	673696	648771
Bacteria;Dadabacteria;	98.2	166	169	3.7	673609	648687
Bacteria;Deferribacteres;	97.7	127	130	3.7	673648	648726
Bacteria;Deinococcus-Thermus;	97.2	888	914	3.7	672864	647965
Bacteria;Dependentiae;	97.1	563	580	3.7	673198	648290
Bacteria;Desantisbacteria;	100.0	2	2	3.7	673776	648851
Bacteria;Dictyoglomi;	88.9	8	9	3.7	673769	648845
Bacteria;Edwardsbacteria;	75.0	3	4	3.7	673774	648850
Bacteria;Elusimicrobia;	96.8	421	435	3.7	673343	648432
Bacteria;Entotheonellaeota;	100.0	168	168	3.7	673610	648685
Bacteria;Epsilonbacteraeota;	97.8	5054	5167	3.7	668611	643799
Bacteria;FBP;	99.4	154	155	3.7	673623	648699
Bacteria;FCPU426;	91.9	34	37	3.7	673741	648819
Bacteria;Fervidibacteria;	100.0	4	4	3.7	673774	648849
Bacteria;Fibrobacteres;	94.5	706	747	3.7	673031	648147
Bacteria;Firestonebacteria;	100.0	3	3	3.7	673775	648850
Bacteria;Firmicutes;	96.0	138350	144050	3.6	529728	510503
Bacteria;Fusobacteria;	92.4	2012	2177	3.7	671601	646841
Bacteria;GAL15;	100.0	43	43	3.7	673735	648810
Bacteria;GBS-1;	100.0	2	2	3.7	673776	648851
Bacteria;Gemmatimonadetes;	96.9	2117	2184	3.7	671594	646736
Bacteria;GN01;	85.8	103	120	3.7	673658	648750
Bacteria;Halanaerobiaeota;	93.7	237	253	3.7	673525	648616
Bacteria;Hydrogenedentes;	98.5	267	271	3.7	673507	648586
Bacteria;Hydrothermae;	100.0	38	38	3.7	673740	648815
Bacteria;Kiritimatiellaeota;	96.4	940	975	3.7	672803	647913
Bacteria;Latescibacteria;	97.0	482	497	3.7	673281	648371
Bacteria;LCP-89;	97.8	45	46	3.7	673732	648808
Bacteria;Lentisphaerae;	97.4	457	469	3.7	673309	648396
Bacteria;Lindowbacteria;	100.0	1	1	3.7	673777	648852
Bacteria;Margulisbacteria;	98.8	85	86	3.7	673692	648768
Bacteria;Marinimicrobia (SAR406 clade);	97.7	541	554	3.7	673224	648312
Bacteria;MAT-CR-M4-B07;	96.0	24	25	3.7	673753	648829
Bacteria;Modulibacteria;	89.8	229	255	3.7	673523	648624
Bacteria;Nitrospinae;	98.6	359	364	3.7	673414	648494
Bacteria;Omnitrophicaeota;	96.6	490	507	3.7	673271	648363
Bacteria;Patescibacteria;	86.9	3930	4521	3.6	669257	644923
Bacteria;PAUC34f;	98.9	87	88	3.7	673690	648766
Bacteria;Planctomycetes;	96.7	8709	9002	3.7	664776	640144
Bacteria;Poribacteria;	81.6	40	49	3.7	673729	648813
Bacteria;Proteobacteria;	97.4	223752	229805	4.3	443973	425101
Bacteria;Rokubacteria;	98.4	374	380	3.7	673398	648479
Bacteria;RsaHF231;	100.0	8	8	3.7	673770	648845
Bacteria;Schekmanbacteria;	97.5	39	40	3.7	673738	648814
Bacteria;Spirochaetes;	96.1	4038	4200	3.7	669578	644815
Bacteria;Synergistetes;	98.4	1120	1138	3.7	672640	647733
Bacteria;TA06;	100.0	68	68	3.7	673710	648785
Bacteria;Tenericutes;	89.1	2224	2497	3.7	671281	646629
Bacteria;Thermosulfidibacteraeota;	100.0	3	3	3.7	673775	648850
Bacteria;Thermotogae;	96.9	283	292	3.7	673486	648570
Bacteria;uncultured;	100.0	5	5	3.7	673773	648848
Bacteria;Verrucomicrobia;	96.0	4236	4411	3.7	669367	644617
Bacteria;WOR-1;	100.0	34	34	3.7	673744	648819
Bacteria;WPS-2;	98.0	50	51	3.7	673727	648803
Bacteria;WS1;	98.9	92	93	3.7	673685	648761
Bacteria;WS2;	93.1	54	58	3.7	673720	648799
Bacteria;WS4;	100.0	16	16	3.7	673762	648837
Bacteria;Zixibacteria;	98.0	199	203	3.7	673575	648654
Eukaryota;	94.5	69836	73929	3.5	599849	579017

a= SILVA taxonomy, SSU r132 database; RefNR Sequence Collection
b=(match/elegible)*100
c=number of match hits in the taxa path.
d=number of hits whith sequence data at the primers position in the taxa path
e=100-(outgroup_matches/outgroup_matchable)*100
f=number of matched hits outside the taxonomic path
g=number of matchable hits outside the taxonomic path

Table S10: zOTU list with taxonomic affiliation (based on the SILVA database SSU r132) and sequence abundance in each sample.

zOTUId	Blanes Spring (Apr-13)	Blanes Summer (Aug-13)	Chascomús Spring (Oct-12)	Chascomús Winter (Jun-13)	Chascomús Spring (Nov-13)	Chascomús Summer (Feb-14)	Chascomús Autumn (May-14)	El Carpinc Spring (Dic-09)	Bragado Spring (Dic-09)	Monte Spring (Dic-09)	Taxonomy	Similarity (%)	Alignment Length(pb)
zOTU_17	9	445	0	0	0	0	0	0	0	0	KF271075_Bacteria;Cyanobacteria;Oxyphotobacteria;Synechococcales;Cyanobiaceae;Synechococcus CC9902;uncultured bacterium	100.000	542
zOTU_9	1813	5884	0	0	0	0	0	0	0	0	KM520687_Bacteria;Cyanobacteria;Oxyphotobacteria;Synechococcales;Cyanobiaceae;Synechococcus CC9902;uncultured bacterium	100.000	542
zOTU_37	241	37	0	0	0	0	0	0	0	0	KM520687_Bacteria;Cyanobacteria;Oxyphotobacteria;Synechococcales;Cyanobiaceae;Synechococcus CC9902;uncultured bacterium	99.815	542
zOTU_3	157	1313	0	0	0	0	0	0	0	0	KX937164_Bacteria;Cyanobacteria;Oxyphotobacteria;Synechococcales;Cyanobiaceae;Synechococcus CC9902;uncultured marine cyanobacterium	100.000	542
zOTU_18	70	1064	0	0	0	0	0	0	0	0	KX937164_Bacteria;Cyanobacteria;Oxyphotobacteria;Synechococcales;Cyanobiaceae;Synechococcus CC9902;uncultured marine cyanobacterium	99.815	542
zOTU_25	46	1270	0	0	0	0	0	0	0	0	GU119191_Bacteria;Cyanobacteria;Oxyphotobacteria;Synechococcales;Cyanobiaceae;Synechococcus CC9902;uncultured bacterium	99.815	542
zOTU_13	11	799	0	0	0	0	0	0	0	0	KC000289_Bacteria;Cyanobacteria;Oxyphotobacteria;Synechococcales;Cyanobiaceae;Synechococcus CC9902;unidentified marine bacterioplankt…	100.000	542
zOTU_50	4	93	0	0	0	0	0	0	0	0	KC000289_Bacteria;Cyanobacteria;Oxyphotobacteria;Synechococcales;Cyanobiaceae;Synechococcus CC9902;unidentified marine bacterioplankt…	99.815	542
zOTU_100	3	161	0	0	0	0	0	0	0	0	KC000289_Bacteria;Cyanobacteria;Oxyphotobacteria;Synechococcales;Cyanobiaceae;Synechococcus CC9902;unidentified marine bacterioplankt…	99.631	542
zOTU_105	3	152	0	0	0	0	0	0	0	0	GU119191_Bacteria;Cyanobacteria;Oxyphotobacteria;Synechococcales;Cyanobiaceae;Synechococcus CC9902;uncultured bacterium	99.631	542
zOTU_101	130	5	0	0	0	0	0	0	0	0	KM520687_Bacteria;Cyanobacteria;Oxyphotobacteria;Synechococcales;Cyanobiaceae;Synechococcus CC9902;uncultured bacterium	99.631	542
zOTU_38	5	445	0	0	0	0	0	0	0	0	AAOK01000002_Bacteria;Cyanobacteria;Oxyphotobacteria;Synechococcales;Cyanobiaceae;Synechococcus CC9902;Synechococcus sp. WH 7805	100.000	542
zOTU_54	4	284	0	0	0	0	0	0	0	0	GU061474_Bacteria;Cyanobacteria;Oxyphotobacteria;Synechococcales;Cyanobiaceae;uncultured bacterium	99.446	542
zOTU_1	150	1997	0	0	0	0	0	0	0	0	KX934805_Bacteria;Cyanobacteria;Oxyphotobacteria;Synechococcales;Cyanobiaceae;uncultured marine cyanobacterium	100.000	542
zOTU_31	37	403	0	0	0	0	0	0	0	0	KX934805_Bacteria;Cyanobacteria;Oxyphotobacteria;Synechococcales;Cyanobiaceae;Synechococcus CC9902;uncultured marine cyanobacterium	99.631	542
zOTU_4	51	2150	0	0	0	0	0	0	0	0	GU119191_Bacteria;Cyanobacteria;Oxyphotobacteria;Synechococcales;Cyanobiaceae;Synechococcus CC9902;uncultured bacterium	100.000	542
zOTU_21	20	648	0	0	0	0	0	0	0	0	GU119191_Bacteria;Cyanobacteria;Oxyphotobacteria;Synechococcales;Cyanobiaceae;Synechococcus CC9902;uncultured bacterium	99.815	542
zOTU_110	15	441	0	0	0	0	0	0	0	0	KX934805_Bacteria;Cyanobacteria;Oxyphotobacteria;Synechococcales;Cyanobiaceae;Synechococcus CC9902;uncultured marine cyanobacterium	99.631	542
zOTU_67	12	315	0	0	0	0	0	0	0	0	KX937164_Bacteria;Cyanobacteria;Oxyphotobacteria;Synechococcales;Cyanobiaceae;Synechococcus CC9902;uncultured marine cyanobacterium	99.631	542
zOTU_56	6	108	0	0	0	0	0	0	0	0	GU119191_Bacteria;Cyanobacteria;Oxyphotobacteria;Synechococcales;Cyanobiaceae;Synechococcus CC9902;uncultured bacterium	99.631	542
zOTU_91	4	81	0	0	0	0	0	0	0	0	KC000289_Bacteria;Cyanobacteria;Oxyphotobacteria;Synechococcales;Cyanobiaceae;Synechococcus CC9902;unidentified marine bacterioplankt…	99.631	542
zOTU_104	0	0	67	0	74	12	9	3	0	0	KU841560_Bacteria;Cyanobacteria;Oxyphotobacteria;Synechococcales;Cyanobiaceae;uncultured Cyanobium sp.	99.631	542
zOTU_108	0	0	63	0	76	12	13	3	0	0	KU841560_Bacteria;Cyanobacteria;Oxyphotobacteria;Synechococcales;Cyanobiaceae;uncultured Cyanobium sp.	99.631	542
zOTU_109	0	0	2	0	1	0	0	26	0	4	KU841560_Bacteria;Cyanobacteria;Oxyphotobacteria;Synechococcales;Cyanobiaceae;uncultured Cyanobium sp.	98.893	542
zOTU_11	0	0	15	0	9	8	11	850	0	40	KU841560_Bacteria;Cyanobacteria;Oxyphotobacteria;Synechococcales;Cyanobiaceae;uncultured Cyanobium sp.	99.262	542
zOTU_118	0	0	3	1	1	3	1	2	3	3	AB935892_Bacteria;Cyanobacteria;Oxyphotobacteria;Synechococcales;Cyanobiaceae;Cyanobium PCC-6307;uncultured cyanobacterium	99.631	542
zOTU_20	0	0	51	73	56	19	83	234	126	1216	AB935892_Bacteria;Cyanobacteria;Oxyphotobacteria;Synechococcales;Cyanobiaceae;Cyanobium PCC-6307;uncultured cyanobacterium	100.000	542
zOTU_24	0	0	285	0	189	51	54	5	0	0	KU841560_Bacteria;Cyanobacteria;Oxyphotobacteria;Synechococcales;Cyanobiaceae;uncultured Cyanobium sp.	99.815	542
zOTU_32	0	0	8	0	5	4	141	511	24	66	DQ275599_Bacteria;Cyanobacteria;Oxyphotobacteria;Synechococcales;Cyanobiaceae;Cyanobium PCC-6307;Synechococcus sp. B9801	100.000	542
zOTU_43	0	0	9	0	4	2	2	266	1	8	KU841560_Bacteria;Cyanobacteria;Oxyphotobacteria;Synechococcales;Cyanobiaceae;uncultured Cyanobium sp.	99.077	542
zOTU_45	0	0	78	0	396	81	128	7	2	0	GU061634_Bacteria;Cyanobacteria;Oxyphotobacteria;Synechococcales;Cyanobiaceae;uncultured bacterium	99.077	542
zOTU_62	0	0	14	24	9	2	9	32	19	136	AB935892_Bacteria;Cyanobacteria;Oxyphotobacteria;Synechococcales;Cyanobiaceae;Cyanobium PCC-6307;uncultured cyanobacterium	99.815	542
zOTU_75	0	0	5	0	7	1	4	79	0	4	KU841560_Bacteria;Cyanobacteria;Oxyphotobacteria;Synechococcales;Cyanobiaceae;uncultured Cyanobium sp.	98.893	542
zOTU_76	0	0	11	43	7	8	6	166	15	8	DQ300610_Bacteria;Cyanobacteria;Oxyphotobacteria;Synechococcales;Cyanobiaceae;Uncultured bacterium	99.262	542
zOTU_77	0	0	6	3	2	3	2	36	2	1	KU841560_Bacteria;Cyanobacteria;Oxyphotobacteria;Synechococcales;Cyanobiaceae;uncultured Cyanobium sp.	98.893	542
zOTU_85	0	0	197	1	294	66	139	4	0	0	KU841560_Bacteria;Cyanobacteria;Oxyphotobacteria;Synechococcales;Cyanobiaceae;uncultured Cyanobium sp.	99.262	542
zOTU_89	0	0	52	0	70	12	12	2	0	0	KU841560_Bacteria;Cyanobacteria;Oxyphotobacteria;Synechococcales;Cyanobiaceae;uncultured Cyanobium sp.	99.262	543
zOTU_93	0	0	7	1	7	1	10	120	2	5	KU841560_Bacteria;Cyanobacteria;Oxyphotobacteria;Synechococcales;Cyanobiaceae;uncultured Cyanobium sp.	98.893	542
zOTU_114	0	0	0	0	1	1	0	1	0	0	KU841569_Bacteria;Cyanobacteria;Oxyphotobacteria;Synechococcales;Cyanobiaceae;Cyanobium PCC-6307;uncultured Synechococcus sp.	99.446	542
zOTU_23	0	0	26	101	43	32	84	123	236	195	KU841569_Bacteria;Cyanobacteria;Oxyphotobacteria;Synechococcales;Cyanobiaceae;Cyanobium PCC-6307;uncultured Synechococcus sp.	99.815	542
zOTU_26	0	0	12	45	13	7	31	40	103	85	KU841569_Bacteria;Cyanobacteria;Oxyphotobacteria;Synechococcales;Cyanobiaceae;Cyanobium PCC-6307;uncultured Synechococcus sp.	99.815	542
zOTU_27	0	0	25	63	20	27	55	74	204	141	KU841569_Bacteria;Cyanobacteria;Oxyphotobacteria;Synechococcales;Cyanobiaceae;Cyanobium PCC-6307;uncultured Synechococcus sp.	99.815	542
zOTU_29	0	0	13	42	12	15	34	66	133	132	KU841569_Bacteria;Cyanobacteria;Oxyphotobacteria;Synechococcales;Cyanobiaceae;Cyanobium PCC-6307;uncultured Synechococcus sp.	99.815	542
zOTU_5	0	0	126	274	121	137	330	459	943	815	KU841569_Bacteria;Cyanobacteria;Oxyphotobacteria;Synechococcales;Cyanobiaceae;Cyanobium PCC-6307;uncultured Synechococcus sp.	100.000	542
zOTU_83	0	0	4	19	4	6	24	39	68	77	KU841569_Bacteria;Cyanobacteria;Oxyphotobacteria;Synechococcales;Cyanobiaceae;Cyanobium PCC-6307;uncultured Synechococcus sp.	99.631	542
zOTU_94	0	0	11	4	3	5	17	43	41	23	KU841569_Bacteria;Cyanobacteria;Oxyphotobacteria;Synechococcales;Cyanobiaceae;Cyanobium PCC-6307;uncultured Synechococcus sp.	99.631	542
zOTU_95	0	0	14	38	18	27	31	64	114	106	KU841569_Bacteria;Cyanobacteria;Oxyphotobacteria;Synechococcales;Cyanobiaceae;Cyanobium PCC-6307;uncultured Synechococcus sp.	99.631	542
zOTU_96	0	0	2	0	0	1	0	0	3	0	KU841564_Bacteria;Cyanobacteria;Oxyphotobacteria;Synechococcales;Cyanobiaceae;Cyanobium PCC-6307;uncultured Cyanobium sp.	99.815	542
zOTU_78	65	125	0	0	0	0	0	0	0	0	BX548174_Bacteria;Cyanobacteria;Oxyphotobacteria;Synechococcales;Cyanobiaceae;Prochlorococcus MIT9313;	99.631	542
zOTU_74	2	50	0	0	0	0	0	0	0	0	BX548174_Bacteria;Cyanobacteria;Oxyphotobacteria;Synechococcales;Cyanobiaceae;Prochlorococcus MIT9313;	99.231	542
zOTU_68	0	0	3	0	8	2	18	36	9	4	KU841563_Bacteria;Cyanobacteria;Oxyphotobacteria;Synechococcales;Cyanobiaceae;Cyanobium PCC-6307;uncultured Synechococcus sp.	99.446	542
zOTU_106	0	0	17	0	2	6	4	55	6	2	EF630354_Bacteria;Cyanobacteria;Oxyphotobacteria;Synechococcales;Cyanobiaceae;Synechococcus sp. MLCB	99.262	542
zOTU_113	0	0	2	1	1	5	3	97	12	0	EF630354_Bacteria;Cyanobacteria;Oxyphotobacteria;Synechococcales;Cyanobiaceae;Synechococcus sp. MLCB	99.262	542
zOTU_121	0	0	7	1	0	4	1	166	16	6	EF630354_Bacteria;Cyanobacteria;Oxyphotobacteria;Synechococcales;Cyanobiaceae;Synechococcus sp. MLCB	99.262	542
zOTU_35	0	0	17	4	5	6	4	488	51	3	EF630354_Bacteria;Cyanobacteria;Oxyphotobacteria;Synechococcales;Cyanobiaceae;Synechococcus sp. MLCB	99.446	542
zOTU_51	0	0	23	6	5	6	20	238	20	4	AY151245_Bacteria;Cyanobacteria;Oxyphotobacteria;Synechococcales;Cyanobiaceae;Cyanobium PCC-6307;Synechococcus sp. MW76B2	99.631	542
zOTU_53	0	0	261	0	8	313	0	0	7	6	KU841560_Bacteria;Cyanobacteria;Oxyphotobacteria;Synechococcales;Cyanobiaceae;uncultured Cyanobium sp.	96.125	542
zOTU_7	0	0	89	17	19	30	40	2674	281	53	EF630354_Bacteria;Cyanobacteria;Oxyphotobacteria;Synechococcales;Cyanobiaceae;Synechococcus sp. MLCB	99.631	542
zOTU_116	0	0	6	0	0	2	0	1	1	0	KU841564_Bacteria;Cyanobacteria;Oxyphotobacteria;Synechococcales;Cyanobiaceae;Cyanobium PCC-6307;uncultured Cyanobium sp.	99.815	542
zOTU_34	0	0	276	354	103	85	121	361	240	157	KC358198_Bacteria;Cyanobacteria;Oxyphotobacteria;Synechococcales;Cyanobiaceae;Cyanobium PCC-6307;uncultured bacterium	100.000	542
zOTU_99	0	0	4	1	0	2	0	1	1	2	KC358198_Bacteria;Cyanobacteria;Oxyphotobacteria;Synechococcales;Cyanobiaceae;Cyanobium PCC-6307;uncultured bacterium	99.815	542
zOTU_102	0	0	23	2	1	7	2	2	1	1	KU841564_Bacteria;Cyanobacteria;Oxyphotobacteria;Synechococcales;Cyanobiaceae;Cyanobium PCC-6307;uncultured Cyanobium sp.	99.815	542
zOTU_120	0	0	32	26	32	9	39	148	65	25	KU841564_Bacteria;Cyanobacteria;Oxyphotobacteria;Synechococcales;Cyanobiaceae;Cyanobium PCC-6307;uncultured Cyanobium sp.	99.815	542
zOTU_122	0	0	2	0	0	1	0	0	0	0	KU841564_Bacteria;Cyanobacteria;Oxyphotobacteria;Synechococcales;Cyanobiaceae;Cyanobium PCC-6307;uncultured Cyanobium sp.	99.815	542
zOTU_48	0	0	180	236	188	56	223	527	333	127	KU841564_Bacteria;Cyanobacteria;Oxyphotobacteria;Synechococcales;Cyanobiaceae;Cyanobium PCC-6307;uncultured Cyanobium sp.	99.815	542
zOTU_59	0	0	12	17	30	9	14	40	13	11	KU841564_Bacteria;Cyanobacteria;Oxyphotobacteria;Synechococcales;Cyanobiaceae;Cyanobium PCC-6307;uncultured Cyanobium sp.	99.815	542
zOTU_60	0	0	18	36	23	4	27	77	22	11	KU841564_Bacteria;Cyanobacteria;Oxyphotobacteria;Synechococcales;Cyanobiaceae;Cyanobium PCC-6307;uncultured Cyanobium sp.	99.815	542
zOTU_63	0	0	19	49	38	8	28	74	45	23	KU841564_Bacteria;Cyanobacteria;Oxyphotobacteria;Synechococcales;Cyanobiaceae;Cyanobium PCC-6307;uncultured Cyanobium sp.	99.631	542
zOTU_65	0	0	22	48	56	12	28	94	34	17	KU841564_Bacteria;Cyanobacteria;Oxyphotobacteria;Synechococcales;Cyanobiaceae;Cyanobium PCC-6307;uncultured Cyanobium sp.	99.815	542
zOTU_81	0	0	2	7	2	2	3	9	2	2	KU841564_Bacteria;Cyanobacteria;Oxyphotobacteria;Synechococcales;Cyanobiaceae;Cyanobium PCC-6307;uncultured Cyanobium sp.	99.815	542
zOTU_82	0	0	4	2	5	2	5	4	2	1	KU841564_Bacteria;Cyanobacteria;Oxyphotobacteria;Synechococcales;Cyanobiaceae;Cyanobium PCC-6307;uncultured Cyanobium sp.	99.815	542
zOTU_86	0	0	1	1	1	2	1	4	1	0	KU841564_Bacteria;Cyanobacteria;Oxyphotobacteria;Synechococcales;Cyanobiaceae;Cyanobium PCC-6307;uncultured Cyanobium sp.	99.815	542
zOTU_87	0	0	5	0	2	0	1	1	1	0	KU841564_Bacteria;Cyanobacteria;Oxyphotobacteria;Synechococcales;Cyanobiaceae;Cyanobium PCC-6307;uncultured Cyanobium sp.	99.815	542
zOTU_98	0	0	2	0	0	1	0	2	3	0	KU841564_Bacteria;Cyanobacteria;Oxyphotobacteria;Synechococcales;Cyanobiaceae;Cyanobium PCC-6307;uncultured Cyanobium sp.	99.815	542
zOTU_14	0	0	48	636	75	68	139	380	395	406	KU841588_Bacteria;Cyanobacteria;Oxyphotobacteria;Synechococcales;Cyanobiaceae;Cyanobium PCC-6307;uncultured Synechococcus sp.	100.000	542
zOTU_42	0	0	9	4	6	1	4	77	3	9	KU841588_Bacteria;Cyanobacteria;Oxyphotobacteria;Synechococcales;Cyanobiaceae;Cyanobium PCC-6307;uncultured Synechococcus sp.	99.815	542
zOTU_47	0	0	30	572	45	31	68	254	134	156	KU841588_Bacteria;Cyanobacteria;Oxyphotobacteria;Synechococcales;Cyanobiaceae;Cyanobium PCC-6307;uncultured Synechococcus sp.	99.815	542
zOTU_52	0	0	15	291	26	14	36	102	100	98	KU841588_Bacteria;Cyanobacteria;Oxyphotobacteria;Synechococcales;Cyanobiaceae;Cyanobium PCC-6307;uncultured Synechococcus sp.	99.815	542
zOTU_69	0	0	21	424	54	31	55	157	102	93	KU841588_Bacteria;Cyanobacteria;Oxyphotobacteria;Synechococcales;Cyanobiaceae;Cyanobium PCC-6307;uncultured Synechococcus sp.	99.815	542
zOTU_30	0	0	35	162	56	36	140	529	139	186	EU703329_Bacteria;Cyanobacteria;Oxyphotobacteria;Synechococcales;Cyanobiaceae;Cyanobium PCC-6307;uncultured Synechococcus sp.	99.815	542
zOTU_16	0	0	40	1203	126	163	212	852	132	190	EU703481_Bacteria;Cyanobacteria;Oxyphotobacteria;Synechococcales;Cyanobiaceae;Cyanobium PCC-6307;uncultured Synechococcus sp.	99.815	542
zOTU_119	0	0	1	2	0	1	1	1	0	1	KM205485_Bacteria;Cyanobacteria;Oxyphotobacteria;Synechococcales;Cyanobiaceae;Cyanobium PCC-6307;uncultured soil bacterium	99.815	542
zOTU_10	0	0	63	29	360	75	214	832	82	56	KU841563_Bacteria;Cyanobacteria;Oxyphotobacteria;Synechococcales;Cyanobiaceae;Cyanobium PCC-6307;uncultured Synechococcus sp.	99.815	542
zOTU_115	0	0	12	0	2	4	3	1	1	1	KU841563_Bacteria;Cyanobacteria;Oxyphotobacteria;Synechococcales;Cyanobiaceae;Cyanobium PCC-6307;uncultured Synechococcus sp.	99.446	542
zOTU_12	0	0	43	20	329	45	185	678	81	31	KU841563_Bacteria;Cyanobacteria;Oxyphotobacteria;Synechococcales;Cyanobiaceae;Cyanobium PCC-6307;uncultured Synechococcus sp.	99.815	542
zOTU_15	0	0	31	217	132	142	124	312	628	76	GQ091396_Bacteria;Cyanobacteria;Oxyphotobacteria;Synechococcales;Cyanobiaceae;Cyanobium PCC-6307;GQ091396	100.000	542
zOTU_2	0	0	157	7	1093	251	836	3258	220	116	KU841563_Bacteria;Cyanobacteria;Oxyphotobacteria;Synechococcales;Cyanobiaceae;Cyanobium PCC-6307;uncultured Synechococcus sp.	100.000	542
zOTU_49	0	0	22	24	168	19	52	184	28	18	KU841563_Bacteria;Cyanobacteria;Oxyphotobacteria;Synechococcales;Cyanobiaceae;Cyanobium PCC-6307;uncultured Synechococcus sp.	99.631	542
zOTU_57	0	0	22	13	236	19	113	229	45	25	KU841585_Bacteria;Cyanobacteria;Oxyphotobacteria;Synechococcales;Cyanobiaceae;Cyanobium PCC-6307;uncultured Synechococcus sp.	99.631	542
zOTU_6	0	0	47	1	944	54	588	714	134	135	KU841585_Bacteria;Cyanobacteria;Oxyphotobacteria;Synechococcales;Cyanobiaceae;Cyanobium PCC-6307;uncultured Synechococcus sp.	100.000	542
zOTU_8	0	0	93	20	557	98	351	1158	130	96	KU841563_Bacteria;Cyanobacteria;Oxyphotobacteria;Synechococcales;Cyanobiaceae;Cyanobium PCC-6307;uncultured Synechococcus sp.	99.815	542
zOTU_80	0	0	32	0	76	21	43	64	6	12	KU841563_Bacteria;Cyanobacteria;Oxyphotobacteria;Synechococcales;Cyanobiaceae;Cyanobium PCC-6307;uncultured Synechococcus sp.	99.446	542
zOTU_36	0	0	1	19	13	3	24	54	86	63	KU841569_Bacteria;Cyanobacteria;Oxyphotobacteria;Synechococcales;Cyanobiaceae;Cyanobium PCC-6307;uncultured Synechococcus sp.	99.631	542
zOTU_44	0	0	30	16	30	20	38	631	15	29	DQ300610_Bacteria;Cyanobacteria;Oxyphotobacteria;Synechococcales;Cyanobiaceae;Uncultured bacterium	99.446	542
zOTU_46	0	0	2	0	4	2	52	1	173	1	KU841589_Bacteria;Cyanobacteria;Oxyphotobacteria;Synechococcales;Cyanobiaceae;Cyanobium PCC-6307;uncultured Cyanobium sp.	99.815	542
zOTU_112	0	0	2	0	0	2	2	28	22	8	KX504417_Bacteria;Cyanobacteria;Oxyphotobacteria;Synechococcales;Cyanobiaceae;Cyanobium PCC-6307;uncultured bacterium	99.077	542
zOTU_28	0	0	33	3	13	11	29	406	260	164	KX504417_Bacteria;Cyanobacteria;Oxyphotobacteria;Synechococcales;Cyanobiaceae;Cyanobium PCC-6307;uncultured bacterium	99.262	542
zOTU_55	0	0	11	5	1	3	2	71	70	40	KX504417_Bacteria;Cyanobacteria;Oxyphotobacteria;Synechococcales;Cyanobiaceae;Cyanobium PCC-6307;uncultured bacterium	99.077	542
zOTU_70	0	0	10	18	1	1	3	163	68	46	GU305837_Bacteria;Cyanobacteria;Oxyphotobacteria;Synechococcales;Cyanobiaceae;Cyanobium PCC-6307;uncultured bacterium	99.446	542
zOTU_71	0	0	10	3	2	2	5	126	78	38	KX504417_Bacteria;Cyanobacteria;Oxyphotobacteria;Synechococcales;Cyanobiaceae;Cyanobium PCC-6307;uncultured bacterium	99.077	542
zOTU_107	0	0	0	0	0	10	2	1	0	0	HAFO01014186_Bacteria;Cyanobacteria;Oxyphotobacteria;Synechococcales;Cyanobiaceae;Cyanobium PCC-6307;Uroglena sp. WA34KE	99.815	542
zOTU_19	0	0	10	0	93	240	60	76	1	4	KU841571_Bacteria;Cyanobacteria;Oxyphotobacteria;Synechococcales;Cyanobiaceae;Cyanobium PCC-6307;uncultured Cyanobium sp.	100.000	542
zOTU_61	0	0	2	1	17	30	16	12	2	0	KU841571_Bacteria;Cyanobacteria;Oxyphotobacteria;Synechococcales;Cyanobiaceae;Cyanobium PCC-6307;uncultured Cyanobium sp.	99.815	542
zOTU_64	0	0	3	0	26	58	22	27	0	0	KU841571_Bacteria;Cyanobacteria;Oxyphotobacteria;Synechococcales;Cyanobiaceae;Cyanobium PCC-6307;uncultured Cyanobium sp.	99.815	542
zOTU_79	0	0	1	1	15	58	16	16	0	0	KU841571_Bacteria;Cyanobacteria;Oxyphotobacteria;Synechococcales;Cyanobiaceae;Cyanobium PCC-6307;uncultured Cyanobium sp.	99.815	542
zOTU_97	0	0	5	1	5	13	4	0	0	0	HAFO01014186_Bacteria;Cyanobacteria;Oxyphotobacteria;Synechococcales;Cyanobiaceae;Cyanobium PCC-6307;Uroglena sp. WA34KE	99.631	542
zOTU_92	0	0	1	0	1	9	3	0	12	0	FJ612247_Bacteria;Cyanobacteria;Oxyphotobacteria;Synechococcales;Cyanobiaceae;Cyanobium PCC-6307;uncultured bacterium	100.000	542
zOTU_84	0	0	1	34	3	0	0	1	3	7	KF799725_Bacteria;Cyanobacteria;Oxyphotobacteria;Synechococcales;Cyanobiaceae;Cyanobium PCC-6307;uncultured bacterium	99.815	542
zOTU_90	0	0	0	31	0	0	1	5	7	9	KF799725_Bacteria;Cyanobacteria;Oxyphotobacteria;Synechococcales;Cyanobiaceae;Cyanobium PCC-6307;uncultured bacterium	99.815	542
zOTU_88	2	147	0	0	0	0	0	0	0	0	CT971583_Bacteria;Cyanobacteria;Oxyphotobacteria;Synechococcales;Cyanobiaceae;Synechococcus CC9902;Synechococcus sp. WH 7804	99.815	542
zOTU_117	0	75	0	0	0	0	0	0	0	0	CT971583_Bacteria;Cyanobacteria;Oxyphotobacteria;Synechococcales;Cyanobiaceae;Synechococcus CC9902;Synechococcus sp. WH 7803	99.815	542
zOTU_123	0	50	0	0	0	0	0	0	0	0	GU119191_Bacteria;Cyanobacteria;Oxyphotobacteria;Synechococcales;Cyanobiaceae;Synechococcus CC9902;uncultured bacterium	99.631	542
zOTU_103	0	0	0	0	0	0	0	15	0	0	BX294802_Bacteria;Planctomycetes;Planctomycetacia;Planctomycetales;Rubinisphaeraceae;uncultured;uncultured bacterium	98.532	545
zOTU_111	0	0	0	0	0	0	0	60	2	0	FJ543008_Bacteria;Verrucomicrobia;Verrucomicrobiae;Verrucomicrobiales;Rubritaleaceae;Luteolibacter;uncultured Verrucomicrobiaceae bacterium	99.077	542
zOTU_22	0	0	831	0	0	177	1	0	1	1	ACYA01000016_Bacteria;Cyanobacteria;Oxyphotobacteria;Nostocales;Nostocaceae;Cylindrospermopsis CRJ1;Cylindrospermopsis raciborskii CS-505	99.445	541
zOTU_33	0	0	0	0	0	0	0	147	0	0	JN868793_Bacteria;Verrucomicrobia;Verrucomicrobiae;Verrucomicrobiales;DEV007;unidentified marine bacterioplankt…	94.872	546
zOTU_39	0	0	37	0	4	195	24	0	55	0	KU841591_Bacteria;Cyanobacteria;Oxyphotobacteria;Phormidesmiales;Nodosilineaceae;Nodosilinea PCC-7104;uncultured Leptolyngbya sp.	98.716	543
zOTU_40	0	0	1	0	0	2	0	174	6	0	KF003214_Bacteria;Verrucomicrobia;Verrucomicrobiae;Verrucomicrobiales;DEV007;uncultured bacterium	99.083	545
zOTU_41	0	0	3	0	0	1	1	139	0	9	FPLP01002477_Bacteria;Verrucomicrobia;Verrucomicrobiae;Verrucomicrobiales;DEV007;uncultured metagenome	99.083	545
zOTU_58	0	0	3	0	1	0	0	25	0	2	FJ542920_Bacteria;Verrucomicrobia;Verrucomicrobiae;Verrucomicrobiales;Verrucomicrobiaceae;uncultured Verrucomicrobiaceae bacterium	99.267	546
zOTU_66	0	0	0	0	0	0	0	25	0	0	FPLP01002477_Bacteria;Verrucomicrobia;Verrucomicrobiae;Verrucomicrobiales;DEV007;uncultured metagenome	98.899	545
zOTU_72	0	0	0	0	0	0	0	65	0	0	FPLP01013433_Bacteria;Verrucomicrobia;Verrucomicrobiae;Verrucomicrobiales;Verrucomicrobiaceae;uncultured;uncultured metagenome	96.337	546
zOTU_73	0	0	0	0	0	0	0	64	0	0	JN868793_Unclassified;unidentified marine bacterioplankton	94.689	546

Table S11: Main biotic and abiotic variables of the studied systems.

	Temporal							Spatial			
System	Blanes Bay	Blanes Bay	Chascomús	Chascomús	Chascomús	Chascomús	Chascomús	El Carpincho	Bragado	Monte	Chascomús
Sample date	Spring apr-13	Summer Aug-13	Spring oct-12	Winter jun-13	Spring nov-13	Summer feb-14	Autumn may-14	Spring dic-09	Spring dic-09	Spring dic-09	Spring nov-13
Vol.filtered (ml)	10000	10000	50	50	50	50	50	25	40	50	50
WaterT° (°C)	14,51	23,58	20	6	22	23	13	23	25	23	22
conductivity (mS cm^{-1})			1.69	1.92	2.03	2.03	2.01	2.8	6.4	18.8	2.03
TN (µg L^{-1})			4200	5768	5051	4883	4715	4402	4391	10058	5051
TP (µg L^{-1})			747	364	749	491	481	862	474	724	749
Clh *a* (µg L^{-1})	0,49	0,21	278	79	300	278	253	447	10	9	300
Turbity (NTU)			304	56	200	85	113	158	12	60	200
Kd$_{(PAR)}$^{a} (m^{-1})			24	25	22	11	14	23	4	4	22
KD$_{(red/green)}$^{b} (m^{-1})			0.93	0.99	1.06	1.12	1.12	1.2	0.8	0.9	1.06
pH	8.128	8.053	8.3	9.05	8.77	9.13	9.22	9.29	8.88	9.27	8.77
***Synechococcus* (org ml^{-1})^{c}**	7.91E+04	2.43E+04	2.00E+06	1.40E+07	4.90E+06	3.90E+06	6.20E+06	2.50E+06	2.00E+05	1.30E+05	4.90E+06
***Prochlorococcus* (org ml^{-1})^{c}**	885	32									

a) Vertical attenuation coefficient for PAR.

b) Vertical attenuation coefficient for red/green light ratio.

c) Number of cell per milliliter estimate by flow cytometry in Chascomús lake and Blanes Bay, and by epifluorescence microscopy in El Carpincho, Bragado and Monte lakes.

Table S12: Table showing sequence information used for the phylogenetic construction of reference trees: GenBank accession numbers, strain name, ecosystem/lake and country/continent isolation, clade assignment and sequence reference.

Reference Tree	Accession nº	Strain name	Place of isolation	Country/ Continent	Sub-cluster	Clade 16S rDNA	Sequence reference
Marine	**BX548174**	MED4	Mediterranean Sea			HLI	Biller et al.(12)
Marine	**AF001468**	MIT 9107	Tropical Pacific			HLII	Biller et al.(12)
Marine	**AF115268**	MIT 9201	Tropical Pacific			HLII	Biller et al.(12)
Marine	**CP000576**	MIT 9301	Atlantic Ocean			HLII	Biller et al.(12)
Marine	JNAV01000002	MIT0602	Station ALOHA/ North Pacific			LLII-III	Biller et al.(12)
Marine	**AE017126**	SS120				LLII-III	Biller et al.(12)
Freshwater	HE805929	1G10	Nahuel Huapi	Argentina		Nahuel Huapi	Callieri et al.(9)
Freshwater	HE805928	1F8	Nahuel Huapi	Argentina		Nahuel Huapi	Callieri et al.(9)
Freshwater	HE805927	1E+11	Nahuel Huapi	Argentina		Nahuel Huapi	Callieri et al.(9)
Freshwater	HE805924	1D8	Moreno	Argentina		Moreno/Morenito	Callieri et al.(9)
Freshwater	HE805923	1C8	Moreno	Argentina		Moreno/Morenito	Callieri et al.(9)
Freshwater	HE805920	9A8	Morenito	Argentina		Moreno/Morenito	Callieri et al.(9)
Freshwater	HE805919	9A2	Morenito	Argentina		Moreno/Morenito	Callieri et al.(9)
Freshwater	HE805945	5F7	Orta	Italy		A	Callieri et al.(9)
Marine	**AF053396**	MIT 9302	Atlantic Ocean			HLII	Coleman et al.(16)
Freshwater	AF216951	PS 680	Biwa	Japan		N	Crosbie et al. (8)
Freshwater	AF448063	UBR	brackish mangrove. Iriomote	Japan		PVIII	Crosbie et al. (8)
Freshwater	AF330250	LB B3	Biwa	Japan		PVIII	Crosbie et al. (8)
Freshwater	AF330249	LB G2	Biwa	Japan		PVIII	Crosbie et al. (8)
Freshwater	AF448065	NAN	brackish marshland. Nagasaki	Japan		N	Crosbie et al. (8)
Freshwater	AY151249	MW 100C3	Mondsee	Austria		I	Crosbie et al. (8)
Freshwater	AY151247	MW99B6	Mondsee	Austria		I	Crosbie et al. (8)
Freshwater	AF330251	BO 0014	Constance	Cent. Europe		I	Crosbie et al. (8)
Freshwater	AF098373	P 211	Bylot island tundra pond	Arctic		I	Crosbie et al. (8)
Freshwater	AY151243	MW 6C6	Mondsee	Austria		H	Crosbie et al. (8)
Freshwater	AY151239	MW 6B4	Mondsee	Austria		H	Crosbie et al. (8)
Freshwater	AY151234	MW 26A5	Mondsee	Austria		H	Crosbie et al. (8)
Freshwater	AY151233	MW 25B5	Mondsee	Austria		H	Crosbie et al. (8)
Freshwater	AF330248	LM 94	Maggiore	Italy		H	Crosbie et al. (8)
Freshwater	AF317074	BO 8807	Constance	Cent. Europe		H	Crosbie et al. (8)
Freshwater	AF216955	PS723	Biwa	Japan		E	Crosbie et al. (8)
Freshwater	AF216954	PS721	Biwa	Japan		E	Crosbie et al. (8)
Freshwater	AF216953	PS 717	Biwa	Japan		E	Crosbie et al. (8)
Freshwater	AM710383	JJ27STR	Machovo	Czech Rep.		Cz	Crosbie et al. (8)
Freshwater	AF330253	BS 5	Bornholm Sea	Europe		Bornholm	Crosbie et al. (8)
Freshwater	AF330252	BS 4	Bornholm Sea	Europe		Bornholm	Crosbie et al. (8)
Freshwater	AY151250	MW 73B4	Hallstättersee	Austria		B	Crosbie et al. (8)
Freshwater	AY151248	MW 10#1	Mondsee	Austria		B	Crosbie et al. (8)
Freshwater	AY151245	MW 76B2	Hallstattersee	Austria		B	Crosbie et al. (8)
Freshwater	AY151242	MW 74D6	Hallstättersee	Austria		B	Crosbie et al. (8)
Freshwater	AY151241	MW 73D5	Hallstattersee	Austria		B	Crosbie et al. (8)
Freshwater	AY151232	MW 15#2	Austria	Mondsee		B	Crosbie et al. (8)
Freshwater	AF317076	SAG 3.81	Zurich	Switzerland		B	Crosbie et al. (8)
Freshwater	AF317075	BO 9404	Constance	Cent. Europe		B	Crosbie et al. (8)
Freshwater	AF448072	PCC 8966	Brackish marshland	France		A	Crosbie et al. (8)
Freshwater	AF330254	BS20				A	Crosbie et al. (8)
Freshwater	AF330246	BGS171	Balaton	Hungary		A	Crosbie et al. (8)
Freshwater	AF317078	BO983115	Constance	Central Europe		A	Crosbie et al. (8)
Freshwater	AF317072	BO8806	Constance	Central Europe		A	Crosbie et al. (8)
Freshwater	AF317071	BO8801	Constance	Central Europe		A	Crosbie et al. (8)
Freshwater	AF216944	PCC 6904	Stream	USA		A	Crosbie et al. (8)
Freshwater	AJ133176	GL 150636	GrandLieu	France		A	Crosbie et al. (8)
Freshwater	AF448071	PCC 8916	brackish marshland	France		A	Crosbie et al. (8)
Freshwater	AF317077	BO 981502	Constance	Cent. Europe		A	Crosbie et al. (8)
Freshwater	AF216952	PS 715	Akan	Japan		A	Crosbie et al. (8)
Freshwater	AF216948	PCC 7920	pond. Tolsa	Finland		A	Crosbie et al. (8)
Freshwater	AF216947	PCC 7918	pond	Finland		A	Crosbie et al. (8)
Freshwater	AF216945	PCC 7009	low salinity brine pond. CA	USA		A	Crosbie et al. (8)
Freshwater	AF098374	P 212	Bylot island tundra pond	Arctic		A	Crosbie et al. (8)
Freshwater	AF001477	PCC 6307	lake water Wisconsin	USA		A	Crosbie et al. (8)
Marine	AATZ01000004	BL107	Mediterranean Sea		5.1	IV	Dufresne et al.(17)
Marine	CP000097	CC9902	Pacific Ocean		5.1	IV	Dufresne et al.(17)
Marine	CT978603	RCC307	Mediterranean Sea		5.3		Dufresne et al.(17)
Marine	**ALPB01000050**	W2				HLIV	Dufresne et al.(17)
Marine	AF330247	LPB1	Lake Biwa		5.3		Ernst et al. (18)
Marine	AY172801	CC9311	Pacific Ocean		5.1	I	Fuller et al. (19)
Marine	**AY172803**	DIM(UW01)			5.1	V	Fuller et al. (19)
Marine	AY172811	RS9901	Gulf of Aqaba		5.1	IX	Fuller et al. (19)
Marine	**AY172812**	RS9902	Gulf of Aqaba		5.1	II	Fuller et al. (19)
Marine	**AY172814**	RS9904	Gulf of Aqaba		5.1	II	Fuller et al. (19)
Marine	**AY172815**	RS9905	Gulf of Aqaba		5.1	III	Fuller et al. (19)
Marine	**AY172816**	RS9906	Gulf of Aqaba		5.1	VIII	Fuller et al. (19)
Marine	**AY172817**	RS9907	Gulf of Aqaba		5.1	II	Fuller et al. (19)
Marine/Freshwater	**AY172818**	RS9908	Gulf of Aqaba		5.1	II	Fuller et al. (19)
Marine/Freshwater	**AY172819**	RS9909	Gulf of Aqaba		5.1	VIII	Fuller et al. (19)
Marine/Freshwater	**AY172820**	RS9910	Gulf of Aqaba		5.1	II	Fuller et al. (19)

Table S12 cont.

Reference Tree	Accession nº	Strain name	Place of isolation	Country/ Continent	Sub-cluster	Clade 16S rDNA	Sequence reference
Marine	**AY172821**	RS9911	Gulf of Aqaba		5.1	II	Fuller et al. (19)
Marine	**AY172822**	RS9912	Gulf of Aqaba		5.1	II	Fuller et al. (19)
Marine	**AY172823**	RS9913	Gulf of Aqaba		5.1	VIII	Fuller et al. (19)
Marine	**AY172824**	RS9914	Gulf of Aqaba		5.1	VIII	Fuller et al. (19)
Marine	**AY172825**	RS9915	Gulf of Aqaba		5.1	III	Fuller et al. (19)
Marine	**AY172829**	RS9919	Gulf of Aqaba		5.1	II	Fuller et al. (19)
Marine	**AY172831**	RS9921	Gulf of Aqaba		5.1	IX	Fuller et al. (19)
Freshwater	KU841621	Env. clone CH62	Chascomús	Argentina		PVIII	Huber et al. (4)
Freshwater	KU841610	Env. clone CH51	Chascomús	Argentina		PV	Huber et al. (4)
Freshwater	KU841616	Env. clone CH57	Chascomús	Argentina		PV	Huber et al. (4)
Freshwater	KU841566	Env. clone CH07	Chascomús	Argentina		PIV	Huber et al. (4)
Freshwater	KU841572	Env. clone CH13	Chascomús	Argentina		PIV	Huber et al. (4)
Freshwater	KU841579	Env. clone CH20	Chascomús	Argentina		PIV	Huber et al. (4)
Freshwater	KU841580	Env. clone CH21	Chascomús	Argentina		PIV	Huber et al. (4)
Freshwater	KU841581	Env. clone CH22	Chascomús	Argentina		PIV	Huber et al. (4)
Freshwater	KU841582	Env. clone CH23	Chascomús	Argentina		PIV	Huber et al. (4)
Freshwater	KU841592	Env. clone CH33	Chascomús	Argentina		PIV	Huber et al. (4)
Freshwater	KU841593	Env. clone CH34	Chascomús	Argentina		PIV	Huber et al. (4)
Freshwater	KU841596	Env. clone CH37	Chascomús	Argentina		PIV	Huber et al. (4)
Freshwater	KU841599	Env. clone CH40	Chascomús	Argentina		PIV	Huber et al. (4)
Freshwater	KU841614	Env. clone CH55	Chascomús	Argentina		PIV	Huber et al. (4)
Freshwater	KU841570	Env. clone CH11	Chascomús	Argentina		PIII	Huber et al. (4)
Freshwater	KU841642	Env. clone CH83	Chascomús	Argentina		PIII	Huber et al. (4)
Freshwater	KU841653	Env. clone CH94	Chascomús	Argentina		PIII	Huber et al. (4)
Freshwater	KU841655	Env. clone CH96	Chascomús	Argentina		PIII	Huber et al. (4)
Freshwater	KU841567	Env. clone CH08	Chascomús	Argentina		PII	Huber et al. (4)
Freshwater	KU841542	Env. clone CH83	Chascomús	Argentina		PI	Huber et al. (4)
Freshwater	KU841562	Env. clone CH03	Chascomús	Argentina		PI	Huber et al. (4)
Freshwater	KU841565	Env. clone CH06	Chascomús	Argentina		PI	Huber et al. (4)
Freshwater	KU841578	Env. clone CH19	Chascomús	Argentina		PI	Huber et al. (4)
Freshwater	KU841583	Env. clone CH24	Chascomús	Argentina		PI	Huber et al. (4)
Freshwater	KU841585	Env. clone CH26	Chascomús	Argentina		PI	Huber et al. (4)
Freshwater	KU841597	Env. clone CH38	Chascomús	Argentina		PI	Huber et al. (4)
Freshwater	KU841598	Env. clone CH39	Chascomús	Argentina		PI	Huber et al. (4)
Freshwater	KU841600	Env. clone CH41	Chascomús	Argentina		PI	Huber et al. (4)
Freshwater	KU841601	Env. clone CH42	Chascomús	Argentina		PI	Huber et al. (4)
Freshwater	KU841606	Env. clone CH47	Chascomús	Argentina		PI	Huber et al. (4)
Freshwater	KU841608	Env. clone CH49	Chascomús	Argentina		PI	Huber et al. (4)
Freshwater	KU841612	Env. clone CH53	Chascomús	Argentina		PI	Huber et al. (4)
Freshwater	KU841613	Env. clone CH54	Chascomús	Argentina		PI	Huber et al. (4)
Freshwater	KU841624	Env. clone CH65	Chascomús	Argentina		PI	Huber et al. (4)
Freshwater	KU841625	Env. clone CH66	Chascomús	Argentina		PI	Huber et al. (4)
Freshwater	KU841632	Env. clone CH73	Chascomús	Argentina		PI	Huber et al. (4)
Freshwater	KU841633	Env. clone CH74	Chascomús	Argentina		PI	Huber et al. (4)
Freshwater	KU841636	Env. clone CH77	Chascomús	Argentina		PI	Huber et al. (4)
Freshwater	KU841639	Env. clone CH80	Chascomús	Argentina		PI	Huber et al. (4)
Freshwater	KU841640	Env. clone CH81	Chascomús	Argentina		PI	Huber et al. (4)
Freshwater	KU841645	Env. clone CH86	Chascomús	Argentina		PI	Huber et al. (4)
Freshwater	KU841647	Env. clone CH88	Chascomús	Argentina		PI	Huber et al. (4)
Freshwater	KU841648	Env. clone CH89	Chascomús	Argentina		PI	Huber et al. (4)
Freshwater	KU841649	Env. clone CH90	Chascomús	Argentina		PI	Huber et al. (4)
Freshwater	KU841651	Env. clone CH92	Chascomús	Argentina		PI	Huber et al. (4)
Freshwater	KU841658	Env. clone CH99	Chascomús	Argentina		PI	Huber et al. (4)
Freshwater	KU841672	Env. clone CH113	Chascomús	Argentina		PI	Huber et al. (4)
Freshwater	KU841673	Env. clone CH114	Chascomús	Argentina		PI	Huber et al. (4)
Freshwater	MG844481	Env. clone SA37	Salada de Monasterio	Argentina		PI	Huber et al. (4)
Freshwater	KU841564	Env. clone CH05	Chascomús	Argentina		CZ	Huber et al. (4)
Freshwater	KU841568	Env. clone CH09	Chascomús	Argentina		CZ	Huber et al. (4)
Freshwater	KU841569	Env. clone CH10	Chascomús	Argentina		CZ	Huber et al. (4)
Freshwater	KU841586	Env. clone CH27	Chascomús	Argentina		CZ	Huber et al. (4)
Freshwater	KU841587	Env. clone CH28	Chascomús	Argentina		CZ	Huber et al. (4)
Freshwater	KU841588	Env. clone CH29	Chascomús	Argentina		CZ	Huber et al. (4)
Freshwater	KU841615	Env. clone CH56	Chascomús	Argentina		CZ	Huber et al. (4)
Freshwater	KU841629	Env. clone CH70	Chascomús	Argentina		CZ	Huber et al. (4)
Freshwater	KU841635	Env. clone CH76	Chascomús	Argentina		CZ	Huber et al. (4)
Freshwater	KU841560	Env. clone CH01	Chascomús	Argentina		A	Huber et al. (4)
Freshwater	KU841561	Env. clone CH02	Chascomús	Argentina		A	Huber et al. (4)
Freshwater	FJ763779	MA 0607 K	Majcz	Poland		PVIII	Jasser et al. (10)
Freshwater	GQ130156	MA 0607 B	Majcz	Poland		M	Jasser et al. (10)
Freshwater	GQ130153	MI 0607 B	Mikołajske	Poland		M	Jasser et al. (10)
Freshwater	GQ130150	MI 0607 D	Mikołajske	Poland		M	Jasser et al. (10)
Freshwater	GQ130146	MI 0608 G	Mikołajskie	Poland		M	Jasser et al. (10)
Freshwater	GQ130143	MA 0607 E	Majcz	Poland		M	Jasser et al. (10)
Freshwater	FJ763787	MA 0607 A	Majcz	Poland		M	Jasser et al. (10)
Freshwater	FJ763786	MA 0607 I	Majcz	Poland		M	Jasser et al. (10)

Table S12 cont.

Reference Tree	Accession nº	Strain name	Place of isolation	Country/ Continent	Sub-cluster	Clade 16S rDNA	Sequence reference
Freshwater	FJ763785	MI 0607 I	Mikołajske	Poland		M	Jasser et al. (10)
Freshwater	FJ763784	MA 0607 G	Majcz	Poland		M	Jasser et al. (10)
Freshwater	FJ763783	MI 0608 A	Mikołajske	Poland		M	Jasser et al. (10)
Freshwater	FJ763781	MA 0607 C	Majcz	Poland		M	Jasser et al. (10)
Freshwater	FJ763780	MA 0607 F	Majcz	Poland		M	Jasser et al. (10)
Freshwater	FJ763776	MA 0607 H	Majcz	Poland		M	Jasser et al. (10)
Freshwater	FJ763775	MA 0607 J	Majcz	Poland		M	Jasser et al. (10)
Freshwater	FJ763768	MA 0607 L	Majcz	Poland		M	Jasser et al. (10)
Freshwater	FJ763778	BE 0807 L	Bełdany	Poland		Cz	Jasser et al. (10)
Freshwater	FJ763772	BE 0807 G	Bełdany	Poland		Cz	Jasser et al. (10)
Freshwater	FJ763770	BE 0807 F	Bełdany	Poland		Cz	Jasser et al. (10)
Freshwater	FJ763769	MA 0607	Majcz	Poland		B	Jasser et al. (10)
Freshwater	FJ763767	MI 0507 B	Mikołajske	Poland		B	Jasser et al. (10)
Freshwater	GQ130155	MA 0607 N	Majcz	Poland		A	Jasser et al. (10)
Freshwater	GQ130149	SN 0807	Śniardwy	Poland		A	Jasser et al. (10)
Freshwater	GQ130148	BE 0807 J	Bełdany	Poland		A	Jasser et al. (10)
Freshwater	GQ130147	MI 0608 H	Mikołajskie	Poland		A	Jasser et al. (10)
Freshwater	GQ130145	MI 0407	Mikołajskie	Poland		A	Jasser et al. (10)
Freshwater	GQ130144	MA 0607 M	Majcz	Poland		A	Jasser et al. (10)
Freshwater	GQ130142	MA 0607 D	Majcz	Poland		A	Jasser et al. (10)
Freshwater	FJ763777	BE 0807 K	Bełdany	Poland		A	Jasser et al. (10)
Freshwater	FJ763774	MI 0608 F	Mikołajskie	Poland		A	Jasser et al. (10)
Freshwater	FJ763773	MA 0707 A	Majcz	Poland		A	Jasser et al. (10)
Freshwater	FJ763771	MA 0707 B	Majcz	Poland		A	Jasser et al. (10)
Marine	**CP000551**	AS9601	Indian Ocean			HLII	Kettler et al.(20)
Marine	**AF001472**	GP2	Western Pacific			HLII	Kettler et al.(20)
Marine	**AF115269**	MIT 9202	Pacific Ocean			HLII	Kettler et al.(20)
Marine	**AF115271**	MIT 9215	Pacific Ocean			HLII	Kettler et al.(20)
Marine	**AF001471**	PAC1	Station ALOHA/ North Pacific			LLI	Kettler et al.(20)
Marine	**AF001473**	SB	Western Pacific			HLII	Kettler et al.(20)
Marine	**ALPI01000039**	W11				HLIV	Kettler et al.(20)
Marine	**ALPD01000082**	W4				HLIV	Kettler et al.(20)
Freshwater	AM710382	JJCD	Svet	Czech Rep.		PIII	Komarek et al. (21)
Freshwater	AM710381	JJR2A5	Rimov	Czech Rep.		A	Komarek et al. (21)
Freshwater	AM710380	JJM10D5	Machovojezero	Czech Rep.		A	Komarek et al. (21)
Freshwater	AM710351	JJNV	pond in Nova Rıse	Czech Rep.		A	Komarek et al. (21)
Freshwater	AJ639901	0BB21S01	Bubano Basin	Italy		A	Komarek et al. (21)
Marine	**JF306717**	Biosope_211	Pacific Ocean		5.1	I	Le Gall et al. (22)
Marine	**JF306719**	Biosope_45 C4Y	Pacific Ocean		5.1	CRD1	Le Gall et al. (22)
Marine	**JF306723**	Biosope_199	Pacific Ocean		5.1	CRD1	Le Gall et al. (22)
Marine	**JNAO01000008**	MIT 9314	Atlantic Ocean			HLII	Malmstrom et al. (23)
Marine	**JNAP01000007**	MIT 9321	Equatorial Pacific			HLII	Malmstrom et al. (23)
Marine	**CP000552**	MIT 9515	Pacific Ocean			HLI	Malmstrom et al. (23)
Marine	**CP000553**	NATL1A				LLI	Malmstrom et al. (23)
Marine/Freshwater	**AF001467**	NATL2A				LLI	Malmstrom et al. (23)
Marine	AY172807	Minos11	Mediterranean Sea		5.3		Mazard et al. (24)
Marine	**JF306652**	BL8	Mediterranean Sea		5.1	VI	Mazard et al. (24)
Marine	**JF306653**	PROSOPE_53-4	Mediterranean Sea		5.1	VI	Mazard et al. (24)
Marine	**JF306654**	BL48	Mediterranean Sea		5.1	VI	Mazard et al. (24)
Marine	**JF306655**	BL161	Mediterranean Sea		5.1	VI	Mazard et al. (24)
Marine	**JF306656**	PROSOPE_77-2	Mediterranean Sea		5.1	VI	Mazard et al. (24)
Marine	**JF306657**	BL164	Mediterranean Sea		5.1	VI	Mazard et al. (24)
Marine	**JF306659**	BL36	Mediterranean Sea		5.1	VI	Mazard et al. (24)
Marine	**JF306661**	PROSOPE_41-3	Mediterranean Sea		5.1	XVI	Mazard et al. (24)
Marine	**JF306662**	PROSOPE_32-1	Mediterranean Sea		5.1	II	Mazard et al. (24)
Marine	**JF306663**	PROSOPE_25	Mediterranean Sea		5.1	VI	Mazard et al. (24)
Marine	**JF306664**	Eum13	Atlantic Ocean		5.1	VI	Mazard et al. (24)
Marine	**JF306665**	PROSOPE_110	Mediterranean Sea		5.1	VI	Mazard et al. (24)
Marine	**JF306667**	PROSOPE_37-2	Mediterranean Sea		5.1	XVI	Mazard et al. (24)
Marine	**JF306668**	PROSOPE_117-1	Mediterranean Sea		5.1	VI	Mazard et al. (24)
Marine	**JF306669**	PROSOPE_97-4	Mediterranean Sea		5.1	VI	Mazard et al. (24)
Marine	**JF306670**	PROSOPE_153-3	Mediterranean Sea		5.1	VI	Mazard et al. (24)
Marine	**JF306671**	PROSOPE_53-19	Mediterranean Sea		5.1	VI	Mazard et al. (24)
Marine	**JF306672**	PROSOPE_25-2	Mediterranean Sea		5.1	II	Mazard et al. (24)
Marine	**JF306674**	PROSOPE_49-2	Mediterranean Sea		5.1	II	Mazard et al. (24)
Marine	**JF306675**	RA000711-27-14	English channel		5.1	VI	Mazard et al. (24)
Marine	**JF306676**	PROSOPE_157-13	Mediterranean Sea		5.1	VI	Mazard et al. (24)
Marine	**JF306677**	MED SN-5	Mediterranean Sea		5.1	VI	Mazard et al. (24)
Marine	**JF306678**	PROSOPE_157-21	Mediterranean Sea		5.1	VI	Mazard et al. (24)
Marine	**JF306680**	TAK 9802	Pacific Ocean		5.1	II	Mazard et al. (24)
Marine	**JF306684**	PROSOPE_85-6	Mediterranean Sea		5.1	XVI	Mazard et al. (24)
Marine	**JF306686**	BL3	Mediterranean Sea		5.3		Mazard et al. (24)
Marine	**JF306690**	A15-29	Atlantic Ocean		5.1	III	Mazard et al. (24)
Marine	**JF306691**	A15-45	Atlantic Ocean		5.1	V	Mazard et al. (24)
Marine	**JF306692**	A15-46	Atlantic Ocean		5.1	V	Mazard et al. (24)
Marine	**JF306695**	A15-22	Atlantic Ocean		5.1	III	Mazard et al. (24)
Marine	**JF306696**	A15-24.2	Atlantic Ocean		5.1	III	Mazard et al. (24)

Table S12 cont.

Reference Tree	Accession nº	Strain name	Place of isolation	Country/ Continent	Sub-cluster	Clade 16S rDNA	Sequence reference
Marine	**JF306697**	A15-30	Atlantic Ocean		5.1	III	Mazard et al. (24)
Marine	**JF306698**	A15-38	Atlantic Ocean		5.1	II	Mazard et al. (24)
Marine	**JF306702**	A15-127	Atlantic Ocean		5.1	WPC1	Mazard et al. (24)
Marine	**JF306703**	A15-130	Atlantic Ocean		5.1	WPC1	Mazard et al. (24)
Marine	**JF306705**	A15-146	Atlantic Ocean		5.1	II	Mazard et al. (24)
Marine	**JF306707**	A15-17	Atlantic Ocean		5.1	III	Mazard et al. (24)
Marine	**JF306709**	A15-19	Atlantic Ocean		5.1	II	Mazard et al. (24)
Marine	**JF306712**	A15-37	Atlantic Ocean		5.1	II	Mazard et al. (24)
Marine	**JF306714**	A15-61	Atlantic Ocean		5.1	II	Mazard et al. (24)
Marine	**JF306724**	PROSOPE_107	Mediterranean Sea		5.1	I	Mazard et al. (24)
Freshwater	AB610893	Suigetsu-CR5	Japan	Suigetsu		PVIII	Ohki *et al.* (25)
Freshwater	AB610889	Suigetsu-CR3	Japan	Suigetsu		PVIII	Ohki *et al.* (25)
Freshwater	AB610885	Suigetsu-CR4	Japan	Suigetsu		PVIII	Ohki *et al.* (25)
Freshwater	AB610886	Suigetsu-CR2	Japan	Suigetsu		PVIII	Ohki *et al.* (25)
Freshwater	AB610892	Suigetsu-CG3	Suigetsu	Japan		A	Ohki *et al.* (25)
Freshwater	AB610891	NIBB-1026	Suigetsu	Japan		A	Ohki *et al.* (25)
Freshwater	AB610890	Suigetsu-CG4	Suigetsu	Japan		A	Ohki *et al.* (25)
Freshwater	AB610888	Suigetsu-CG1	Suigetsu	Japan		A	Ohki *et al.* (25)
Freshwater	AB610887	Suigetsu-CG2	Suigetsu	Japan		A	Ohki *et al.* (25)
Marine	**ALPE01000097**	W7				HLIII	Rocap et al. (26)
Marine	**ALPG01000093**	W9				HLIII	Rocap et al. (26)
Freshwater	EF638719	Synechococcus sp. 19-3	New Zealand	Helensville Dam		PVIII	Rueckert *et al. (*27)
Freshwater	AY945300	clone EW7	Esthwaite Water	England		II	Sanchez-Baracaldo et al. (28)
Freshwater	AY945298	cloneCWP124.2.10	Cotswold Water Park 124	England		II	Sanchez-Baracaldo et al. (28)
Freshwater	AY945296	cloneCWP123.2.2	Cotswold Water Park 123	England		II	Sanchez-Baracaldo et al. (28)
Freshwater	AY945294	clone CWP9.2.7	Cotswold Water Park 9	England		II	Sanchez-Baracaldo et al. (28)
Freshwater	AY945293	clone CWP9.2.33	Cotswold Water Park 9	England		II	Sanchez-Baracaldo et al. (28)
Freshwater	AY945292	cloneAP10.8	Abbot's Pool	England		II	Sanchez-Baracaldo et al. (28)
Freshwater	AY943947	clone AP10.7	Abbot's Pool	England		II	Sanchez-Baracaldo et al. (28)
Freshwater	MG844502	Env. clone SA15	Salada de Monasterio	Argentina		SA I	this work
Freshwater	MG844509	Env. clone SA08	Salada de Monasterio	Argentina		PVII	this work
Freshwater	MG844492	Env. clone SA26	Salada de Monasterio	Argentina		PIX	this work
Freshwater	MG844458	Env. clone TR21	El Triunfo	Argentina		PVI	this work
Freshwater	MG844462	Env. clone TR17	El Triunfo	Argentina		PVI	this work
Freshwater	MG844470	Env. clone TR09	El Triunfo	Argentina		PVI	this work
Freshwater	MG844478	Env. clone TR01	El Triunfo	Argentina		PVI	this work
Freshwater	MG844484	Env. clone SA34	Salada de Monasterio	Argentina		PIII	this work
Freshwater	MG844493	Env. clone SA25	Salada de Monasterio	Argentina		PIII	this work
Freshwater	MG844495	Env. clone SA23	Salada de Monasterio	Argentina		PIII	this work
Freshwater	MG844496	Env. clone SA22	Salada de Monasterio	Argentina		PIII	this work
Freshwater	MG844510	Env. clone SA07	Salada de Monasterio	Argentina		PIII	this work
Freshwater	MG844437	Env. clone TR42	El Triunfo	Argentina		PIII	this work
Freshwater	MG844471	Env. clone TR08	El Triunfo	Argentina		PIII	this work
Freshwater	MG844497	Env. clone SA21	Salada de Monasterio	Argentina		PII	this work
Freshwater	MG844501	Env. clone SA17	Salada de Monasterio	Argentina		PII	this work
Freshwater	MG844451	Env. clone TR28	El Triunfo	Argentina		PII	this work
Freshwater	MG844454	Env. clone TR25	El Triunfo	Argentina		PII	this work
Freshwater	MG844466	Env. clone TR13	El Triunfo	Argentina		PII	this work
Freshwater	MG844474	Env. clone TR05	El Triunfo	Argentina		PII	this work
Freshwater	MG844482	Env. clone SA36	Salada de Monasterio	Argentina		PI	this work
Freshwater	MG844485	Env. clone SA33	Salada de Monasterio	Argentina		PI	this work
Freshwater	MG844486	Env. clone SA32	Salada de Monasterio	Argentina		PI	this work
Freshwater	MG844488	Env. clone SA30	Salada de Monasterio	Argentina		PI	this work
Freshwater	MG844487	Env. clone SA31	Salada de Monasterio	Argentina		PI	this work
Freshwater	MG844490	Env. clone SA28	Salada de Monasterio	Argentina		PI	this work
Freshwater	MG844491	Env. clone SA27	Salada de Monasterio	Argentina		PI	this work
Freshwater	MG844494	Env. clone SA24	Salada de Monasterio	Argentina		PI	this work
Freshwater	MG844498	Env. clone SA20	Salada de Monasterio	Argentina		PI	this work
Freshwater	MG844499	Env. clone SA19	Salada de Monasterio	Argentina		PI	this work
Freshwater	MG844503	Env. clone SA14	Salada de Monasterio	Argentina		PI	this work
Freshwater	MG844504	Env. clone SA13	Salada de Monasterio	Argentina		PI	this work
Freshwater	MG844505	Env. clone SA12	Salada de Monasterio	Argentina		PI	this work
Freshwater	MG844506	Env. clone SA11	Salada de Monasterio	Argentina		PI	this work
Freshwater	MG844507	Env. clone SA10	Salada de Monasterio	Argentina		PI	this work
Freshwater	MG844512	Env. clone SA05	Salada de Monasterio	Argentina		PI	this work
Freshwater	MG844514	Env. clone SA03	Salada de Monasterio	Argentina		PI	this work
Freshwater	MG844438	Env. clone TR41	El Triunfo	Argentina		PI	this work
Freshwater	MG844439	Env. clone TR40	El Triunfo	Argentina		PI	this work
Freshwater	MG844441	Env. clone TR38	El Triunfo	Argentina		PI	this work
Freshwater	MG844445	Env. clone TR34	El Triunfo	Argentina		PI	this work

Table S12 cont.

Reference Tree	Accession nº	Strain name	Place of isolation	Country/ Continent	Sub-cluster	Clade 16S rDNA	Sequence reference
Freshwater	MG844447	Env. clone TR32	El Triunfo	Argentina		PI	this work
Freshwater	MG844449	Env. clone TR30	El Triunfo	Argentina		PI	this work
Freshwater	MG844452	Env. clone TR27	El Triunfo	Argentina		PI	this work
Freshwater	MG844461	Env. clone TR18	El Triunfo	Argentina		PI	this work
Freshwater	MG844463	Env. clone TR16	El Triunfo	Argentina		PI	this work
Freshwater	MG844465	Env. clone TR14	El Triunfo	Argentina		PI	this work
Freshwater	MG844468	Env. clone TR11	El Triunfo	Argentina		PI	this work
Freshwater	MG844469	Env. clone TR10	El Triunfo	Argentina		PI	this work
Freshwater	MG844475	Env. clone TR04	El Triunfo	Argentina		PI	this work
Freshwater	MG844476	Env. clone TR03	El Triunfo	Argentina		PI	this work
Freshwater	MG844489	Env. clone SA29	Salada de Monasterio	Argentina		CZ	this work
Freshwater	MG844500	Env. clone SA18	Salada de Monasterio	Argentina		CZ	this work
Freshwater	MG844508	Env. clone SA09	Salada de Monasterio	Argentina		CZ	this work
Freshwater	MG844511	Env. clone SA06	Salada de Monasterio	Argentina		CZ	this work
Freshwater	MG844513	Env. clone SA04	Salada de Monasterio	Argentina		CZ	this work
Freshwater	MG844515	Env. clone SA02	Salada de Monasterio	Argentina		CZ	this work
Freshwater	MG844516	Env. clone SA01	Salada de Monasterio	Argentina		CZ	this work
Freshwater	MG844442	Env. clone TR37	El Triunfo	Argentina		CZ	this work
Freshwater	MG844443	Env. clone TR36	El Triunfo	Argentina		CZ	this work
Freshwater	MG844448	Env. clone TR31	El Triunfo	Argentina		CZ	this work
Freshwater	MG844453	Env. clone TR26	El Triunfo	Argentina		CZ	this work
Freshwater	MG844455	Env. clone TR24	El Triunfo	Argentina		CZ	this work
Freshwater	MG844456	Env. clone TR23	El Triunfo	Argentina		CZ	this work
Freshwater	MG844457	Env. clone TR22	El Triunfo	Argentina		CZ	this work
Freshwater	MG844459	Env. clone TR20	El Triunfo	Argentina		CZ	this work
Freshwater	MG844464	Env. clone TR15	El Triunfo	Argentina		CZ	this work
Freshwater	MG844467	Env. clone TR12	El Triunfo	Argentina		CZ	this work
Freshwater	MG844472	Env. clone TR07	El Triunfo	Argentina		CZ	this work
Freshwater	MG844473	Env. clone TR06	El Triunfo	Argentina		CZ	this work
Freshwater	MG844477	Env. clone TR02	El Triunfo	Argentina		CZ	this work
Freshwater	HQ380799	CENA118	Praia dos Namorados	Brazil		A	unpublished
Freshwater	GU935366	Sai005	drinking reservoir Saidenbach	Germany		A	Unpublished
Freshwater	GU935365	Sai004	drinking reservoir Saidenbach	Germany		A	Unpublished
Freshwater	GU935362	Sai001	drinking reservoir Saidenbach	Germany		A	Unpublished
Freshwater	FM177488	2LT34S03	Trasimeno	Italy		A	unpublished
Freshwater	AF448067	TAGS	Finland	Brackish marshland		2	Unpublished
Marine	AF448068	PS838			5.2		Unpublished
Marine	AM709626	PCC7001	Atlantic Ocean		5.2		Unpublished
Marine	AY172832	WH5701	Atlantic Ocean		5.2		Waterbury et al. (29)
Marine	**AY172835**	WH8020	Sargasso Sea		5.1	I	Waterbury et al. (29)
Marine	CT971583	WH7803	Atlantic Ocean		5.1	V	Waterbury et al. (29)

Figure S1: Mean Pearson correlation (Mantel test) of patristic distances among trees constructed for each SLS in triplicates. In all cases p <0.05.

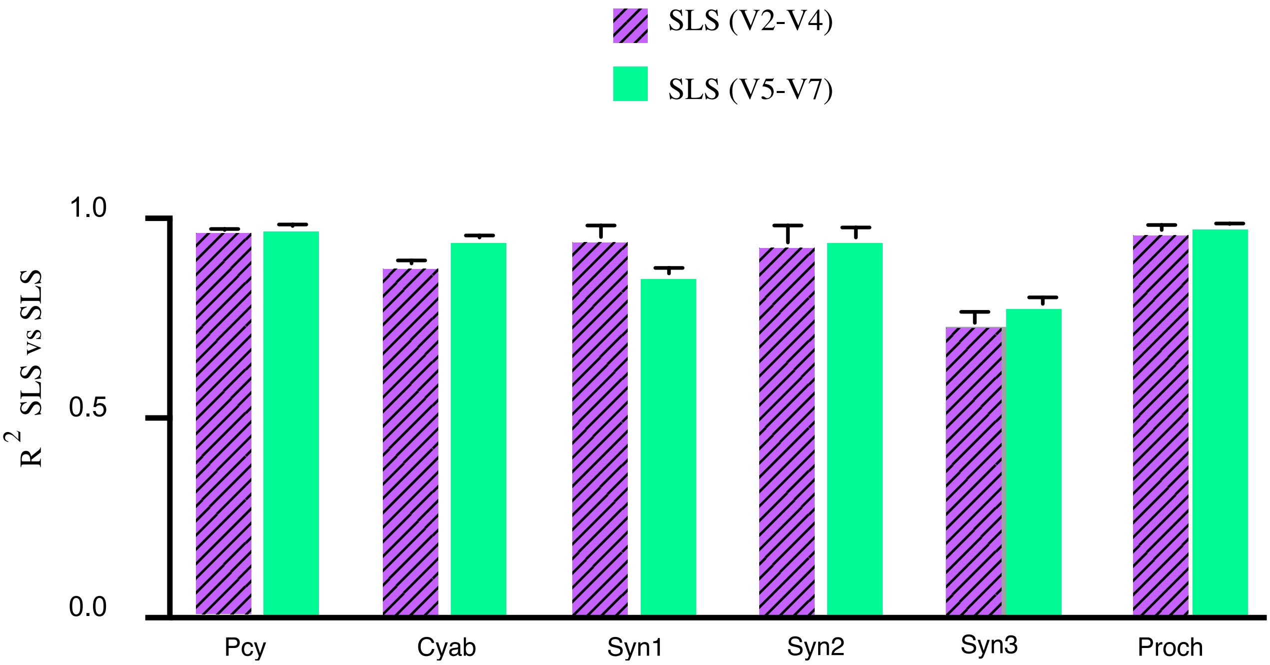


Figure S2: *In silico* evaluation of specificity and coverage rate for picocyanobacteria genera of primer pairs designed in this work compared with those proposed by Nübel et al. (13), Herlemann et al., (14) and Parada et al., (15) allowing zero, one and two mismatches.

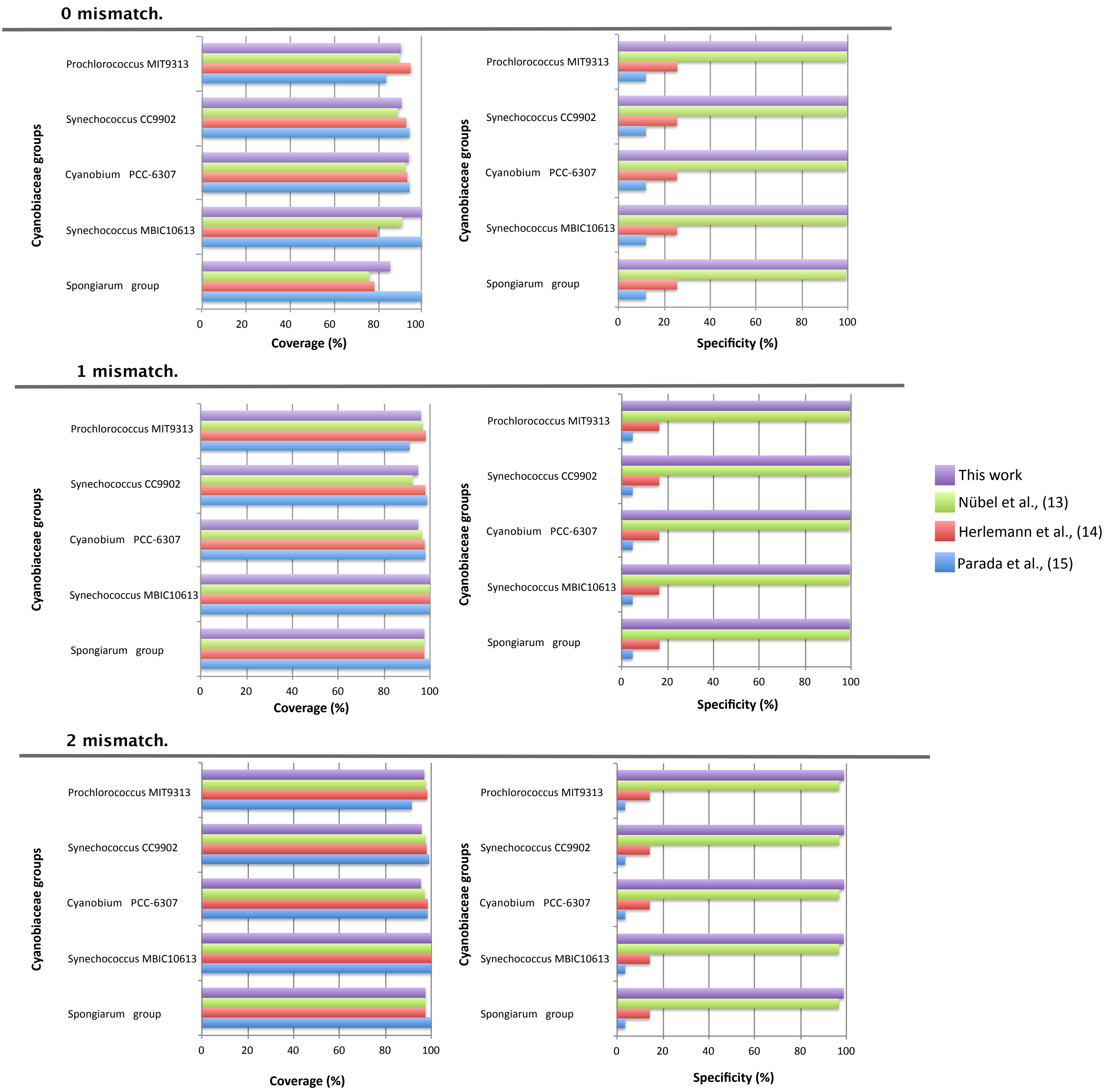


Figure S3: Rarefaction curves for the picocyanobacteria diversity in the ten samples studied.

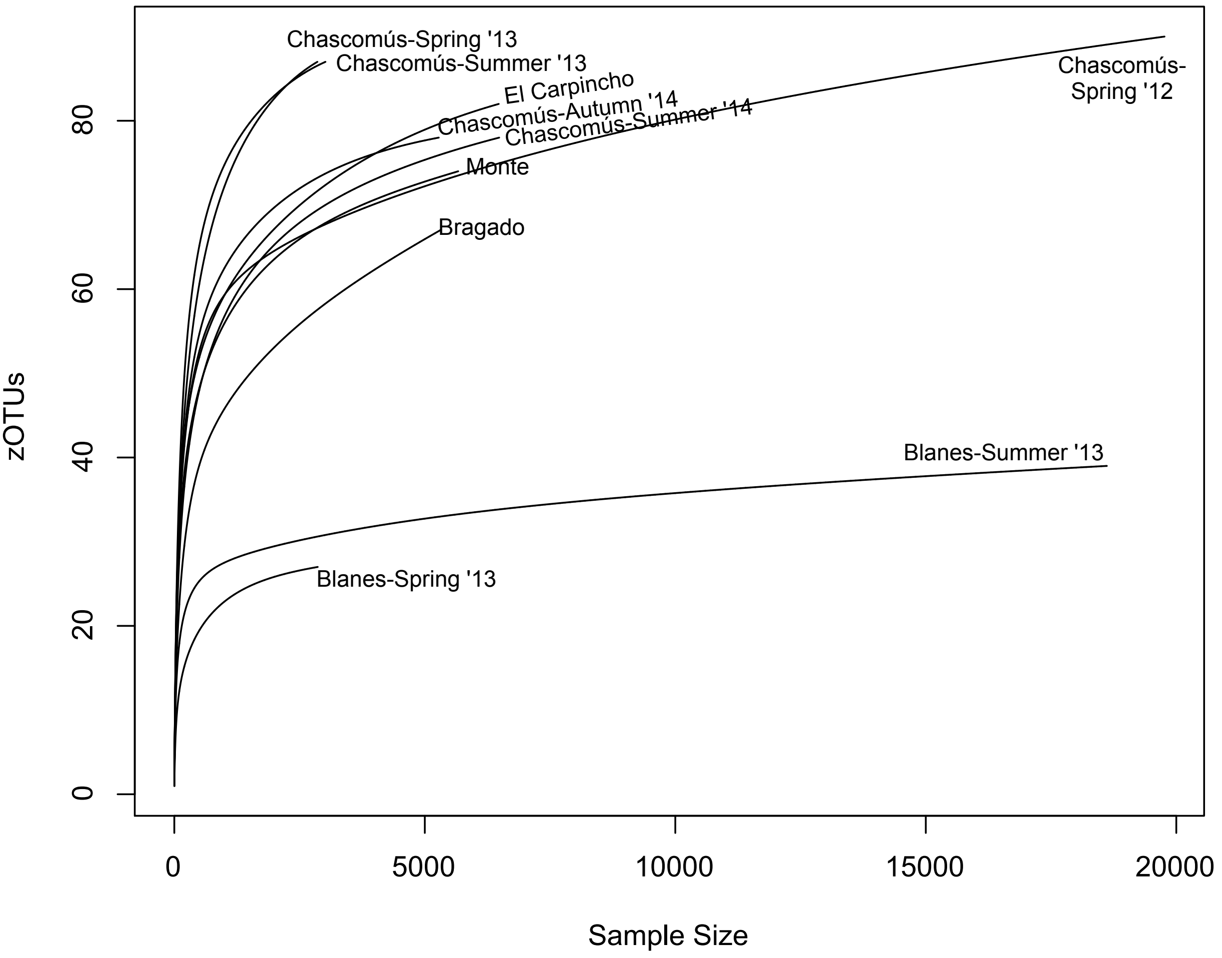


Figure S4: Phylogenetic tree based on the Reference Tree of marine picocyanobacteria showing the phyletic relationships of the zOTUs retrieved from Blanes Bay. Circle size in the nodes indicates the bootstrap values (1000 replicates of RT), values lower than 50 are not shown**.** The red circles represent the relative abundance of each zOTU.

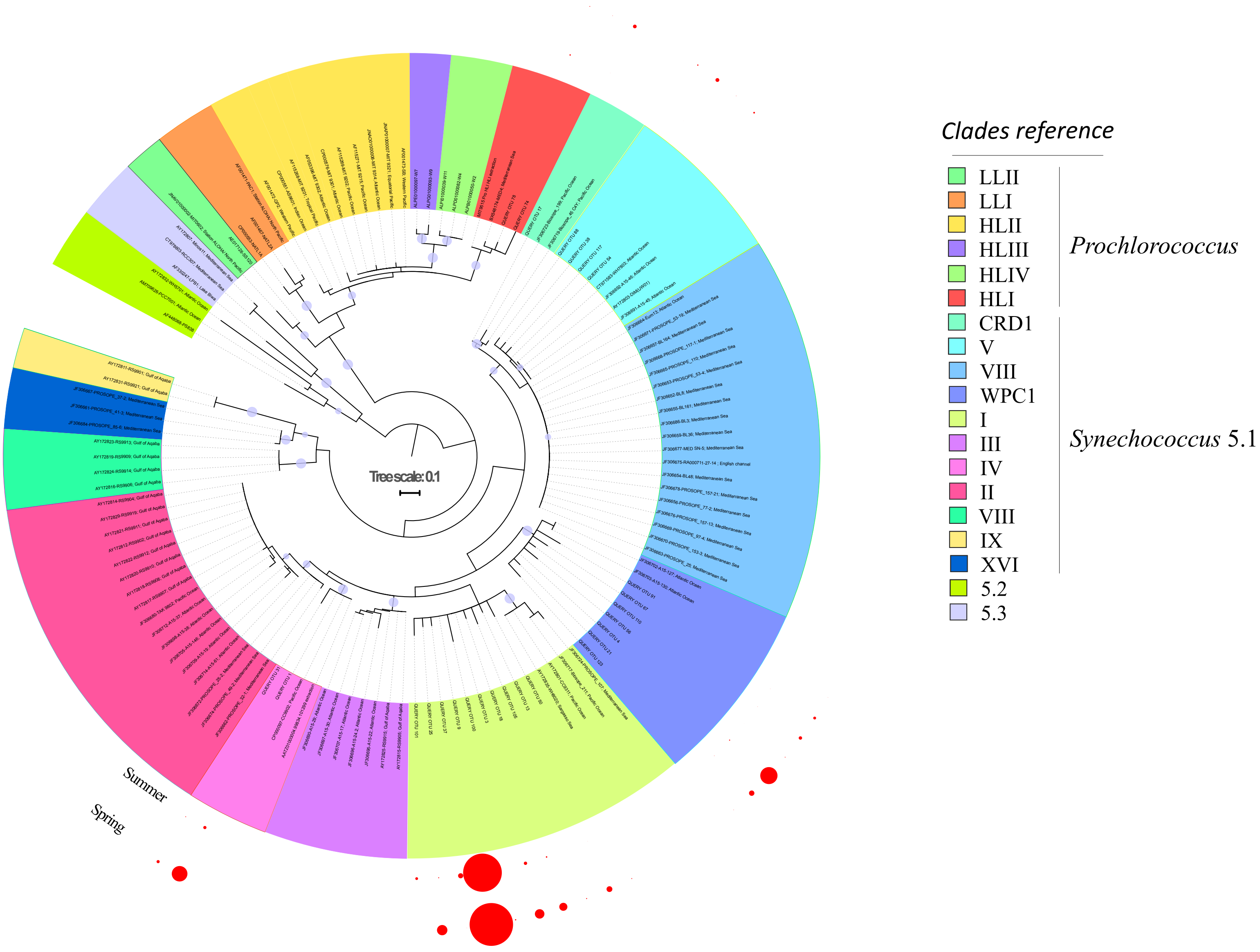


Figure S5: Phylogenetic tree based on the Reference Tree of freshwater picocyanobacteria showing the phyletic relationships of the zOTUs retrieved from Chascomús lake. Circle size in the nodes indicates the bootstrap values (1000 replicates of RT), values lower than 50 are not shown**.** The red circles represent the relative abundance of each zOTU. The numbers on the tree indicate the new clades represented exclusively by sequences presented here.

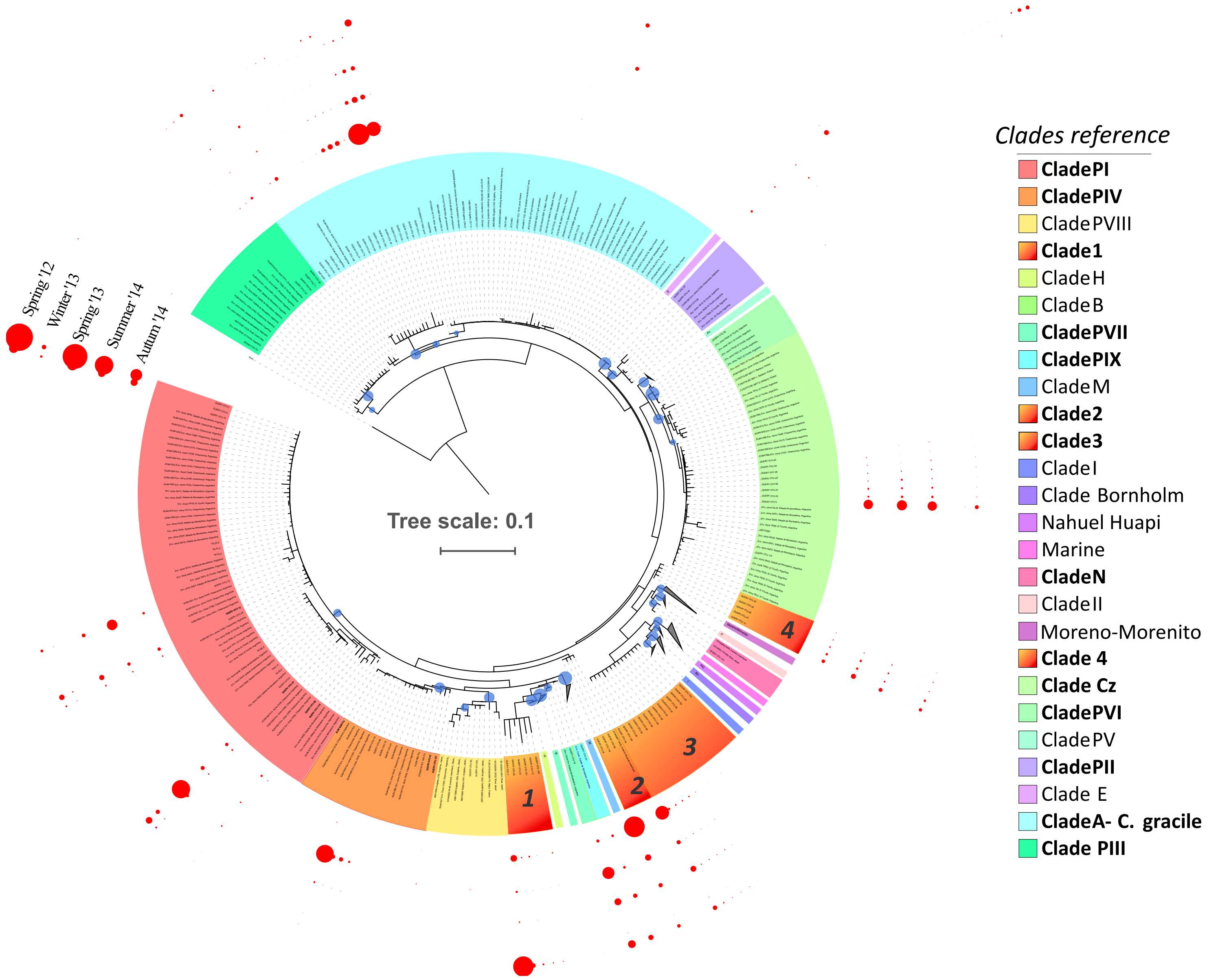
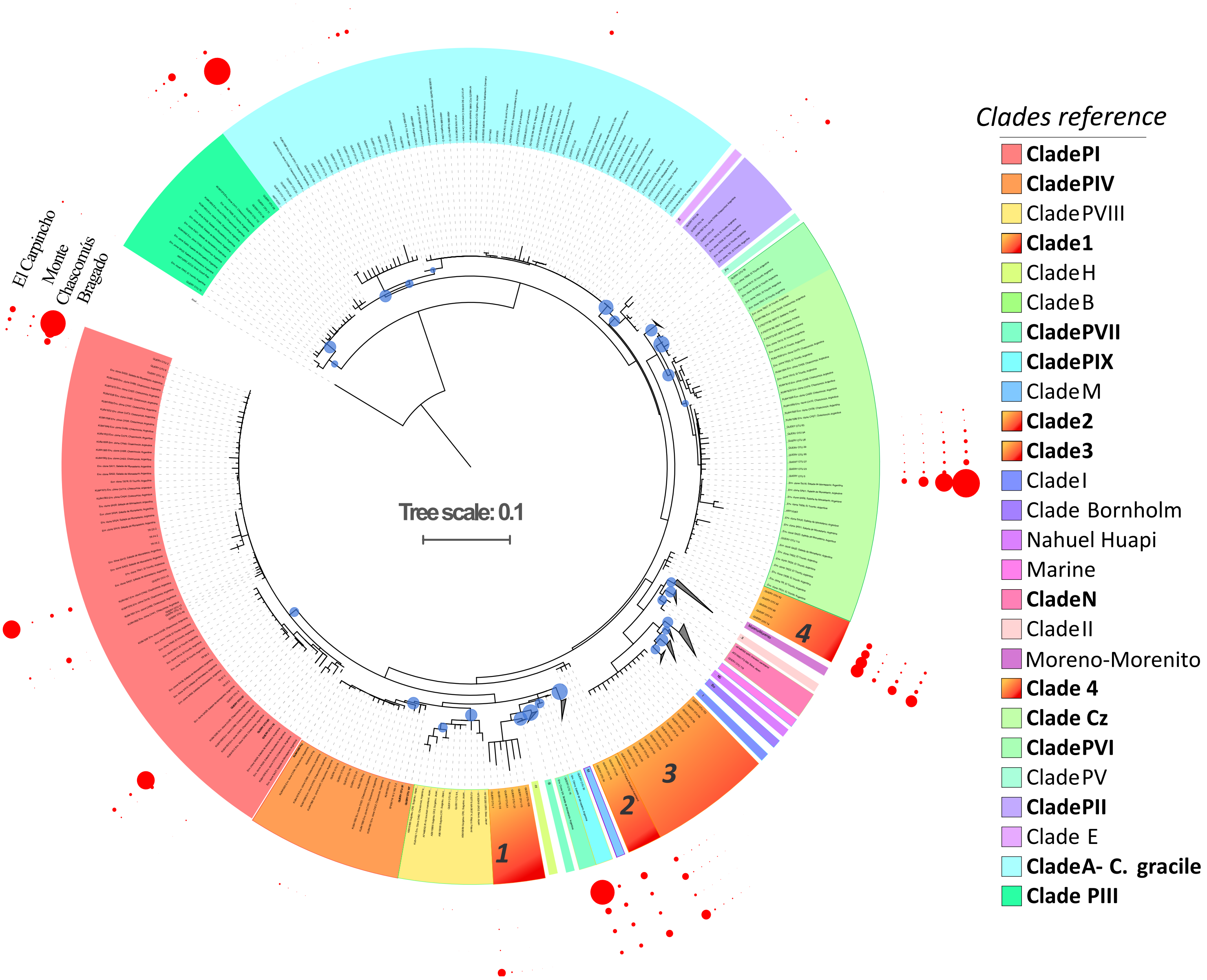


Figure S6: Phylogenetic tree based on the Reference tree of freshwater picocyanobacteria showing the phyletic relationships of the zOTUs retrieved from the Pampean lakes. Circle size in the nodes indicates the bootstrap values (1000 replicates of RT), values lower than 50 are not shown**.** The red circles represent the relative abundance of each zOTU. The numbers on the tree indicate the new clades represented exclusively by sequences presented here.



Literature

1. Izaguirre I, Sánchez ML, Schiaffino MR, O'Farrell I, Huber P, Ferrer N, Zunino J, Lagomarsino L, Mancini M. 2015. Which environmental factors trigger the dominance of phytoplankton species across a moisture gradient of shallow lakes? Hydrobiologia 752: 47-64

2. Fernandez Zenoff V, Sineriz F, Farias ME. 2006. Diverse Responses to UV-B Radiation and Repair Mechanisms of Bacteria Isolated from High-Altitude Aquatic Environments. Appl Environ Microbiol 72:7857–7863.

3. Llames ME, Giorgio PA, Zagarese H, Ferraro M, Izaguirre I. 2013. Alternative states drive the patterns in the bacterioplankton composition in shallow Pampean lakes (Argentina). Environ Microbiol Rep 5:310–321.

4. Huber P, Diovisalvi N, Ferraro M, Metz S, Lagomarsino L, Llames ME, Royo-Llonch M, Bustingorry J, Escaray R, Acinas SG, Gasol JM, Unrein F. 2017. Phenotypic plasticity in freshwater picocyanobacteria. Environ Microbiol 19:1120–1133.

5. Edgar RC. 2010. Search and clustering orders of magnitude faster than BLAST. Bioinformatics 26:2460–2461.

6. Edgar RC, Haas BJ, Clemente JC, Quince C, Knight R. 2011. UCHIME improves sensitivity and speed of chimera detection. Bioinformatics 27:2194–2200.

7. Kearse M, Moir R, Wilson A, Stones-Havas S, Cheung M, Sturrock S, Buxton S, Cooper A, Markowitz S, Duran C, Thierer T, Ashton B, Meintjes P, Drummond A. 2012. Geneious Basic: An integrated and extendable desktop software platform for the organization and analysis of sequence data. Bioinformatics 28:1647–1649.

8. Crosbie ND, Pöckl M, Weisse T. 2003. Dispersal and phylogenetic diversity of nonmarine picocyanobacteria, offered from 16S rRNA gene and cpcBA-intergenic spacer sequence analyses. Appl. Environ. Microbiol. 69(9):25716-5721.

9. Callieri C, Coci M, Corno G, Macek M, Modenutti B, Balseiro E, Bertoni R. 2013. Phylogenetic diversity of nonmarine picocyanobacteria. FEMS Microbiol. Ecol. 85(2): 293-301.

10. Jasser I, Krolicka A and Karnkowska-Ishikawa A. 2011. A novel phylogenetic clade of picocyanobacteria from the Mazurian lakes (Poland) realects the early ontogeny of glacial lakes. FEMS Microbiol. Ecol. 75(1):89-98.

11. Ahlgren NA and Rocap G. 2012. Diversity and distribution of marine *Synechococcus*: multiple gene phylogenies for consensus classification and development of qPCR assays for sensitive measurement of clades in the ocean. Front Microbiol 3: 213.

12. Biller SJ, Berube PM, Berta-Thompson JW, Kelly L, Roggensack SE, Awad L, … Chisholm SW. 2014. Genomes of diverse isolates of the marine cyanobacterium *Prochlorococcus*. *Scientific Data*, *1*, 140034. Retrieved from http://dx.doi.org/10.1038/sdata.2014.34

13. Nübel U, Garcia-Pichel F, Muyzer G. 1997. PCR primers to amplify 16S rRNA genes from cyanobacteria. Appl Environ Microbiol 63:3327–3332.

14. Herlemann DPR, Labrenz M, Jürgens K, Bertilsson S, Waniek JJ, Andersson AF. 2011. Transitions in bacterial communities along the 2000 km salinity gradient of the Baltic Sea. ISME J 5:1571–1579.Herlemann DPR, Labrenz M, Jürgens K, Bertilsson S, Waniek JJ,

Andersson AF. 2011. Transitions in bacterial communities along the 2000 km salinity gradient of the Baltic Sea. ISME J 5:1571–1579.

15. Parada AE, Needham DM, Fuhrman JA. 2016. Every base matters: Assessing small subunit rRNA primers for marine microbiomes with mock communities, time series and global field samples. Environ Microbiol 18:1403–1414.

16. Coleman ML, Chisholm SW. 2007. Code and context: *Prochlorococcus* as a model for cross-scale biology. Trends Microbiol 15(9): 398-407.

17. Dufresne A, Ostrowski M, Scanlan DJ, Garczarek L, Mazard S, Palenik BP, Paulsen IT, de Marsac NT, Wincker P, Dossat C, Ferriera S, Johnson J, Post AF, Hess WR, Partensky F. 2008. Unraveling the genomic mosaic of a ubiquitous genus of marine cyanobacteria. Genome Biol 9:R90.

18. Ernst A. 2003. Ecosystem-dependent adaptive radiations of picocyanobacteria inferred from 16S rRNA and ITS-1 sequence analysis. Microbiology 149:217–228.

19. Fuller NJ, Marie D, Vaulot D, Post AF, Scanlan DJ. 2003. Clade-Specific 16S Ribosomal DNA Oligonucleotides Reveal the Predominance of a Single Marine. Appl Environ Microbiol. 69(5):2430-2443.

20. Kettler GC, Martiny AC, Huang K, Zucker J, Coleman ML, Rodrigue S, Chen F, Lapidus A, Ferriera S, Johnson J, Steglich C, Church GM, Richardson P, Chisholm SW. 2007. Patterns and implications of gene gain and loss in the evolution of *Prochlorococcus*. PLoS Genet.

21. Komárek J, Kaštovský J, Jezberová J. 2011. Phylogenetic and taxonomic delimitation of the cyanobacterial genus *Aphanothece* and description of *Anathece* gen. nov. Eur J Phycol 46(3): 315-326.

22. Le Gall F, Rigaut-Jalabert F, Marie D, Garczarek L, Viprey M, Gobet A, Vaulot D. 2008. Picoplankton diversity in the South-East Pacific Ocean from cultures. Biogeosciences 5:203-214.

23. Malmstrom RR, Rodrigue S, Huang KH, Kelly L, Kern SE, Thompson A, Roggensack S, Berube PM, Henn MR, Chisholm SW. 2013. Ecology of uncultured *Prochlorococcus* clades revealed through single-cell genomics and biogeographic analysis. ISME J. 7(1):184-198

24. Mazard S, Ostrowski M, Partensky F, Scanlan DJ. 2012. Multi-locus sequence analysis, taxonomic resolution and biogeography of marine *Synechococcus*. Environ Microbiol 14:372–86.

25. Ohki K, Yamada K, Kamiya M, Yoshikawa S. 2012. Morphological, Phylogenetic and Physiological Studies of Pico-Cyanobacteria Isolated from the Halocline of a Saline Meromictic Lake, Lake Suigetsu, Japan. Microbes and Environments. 27(2):171-178.

26. Rocap G, Distel DL, Waterbury JB, Chisholm SW. 2002. Resolution of Prochlorococcus and Synechococcus ecotypes by using 16S-23S ribosomal DNA internal transcribed spacer sequences. Appl Environ Microbiol 68:1180–1191.

27. Rueckert A, Wood SA, Cary SC. 2007. Development and field assessment of a quantitative PCR for the detection and enumeration of the noxious bloom-former *Anabaena planktonica*. Limnolo and Oceano: Methods, 5, 474-483.

28. Sánchez-Baracaldo P, Handley BA, Hayes PK. 2008. Picocyanobacterial community structure of freshwater lakes and the Baltic Sea revealed by phylogenetic analyses and clade-speciaic quantitative PCR. Microbiol 154:3347-3357.

29. Waterbury JB, Watson SW, Valois FW, Franks DG. 1986. Biological and ecological characterization of the marine unicellular cyanobacterium *Synechococcus.* In: Photosynthetic Picoplankton. Platt T, Li WKW eds. Canad. Bull. Fish. Aquatic Sci. 214: 71–120.