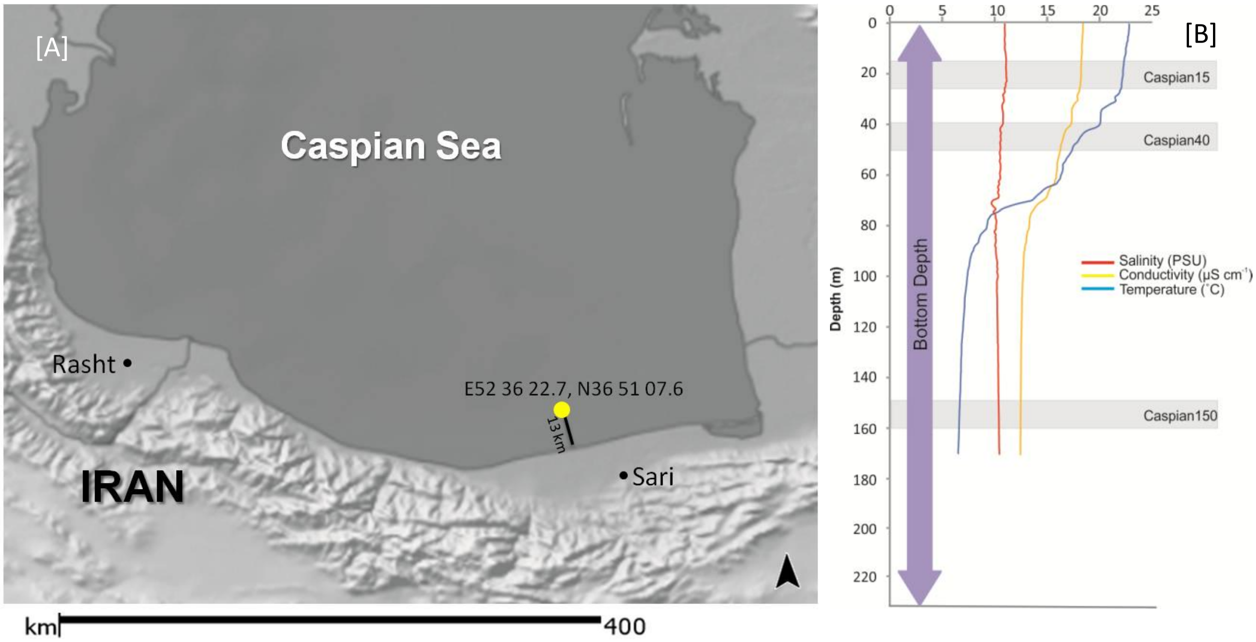
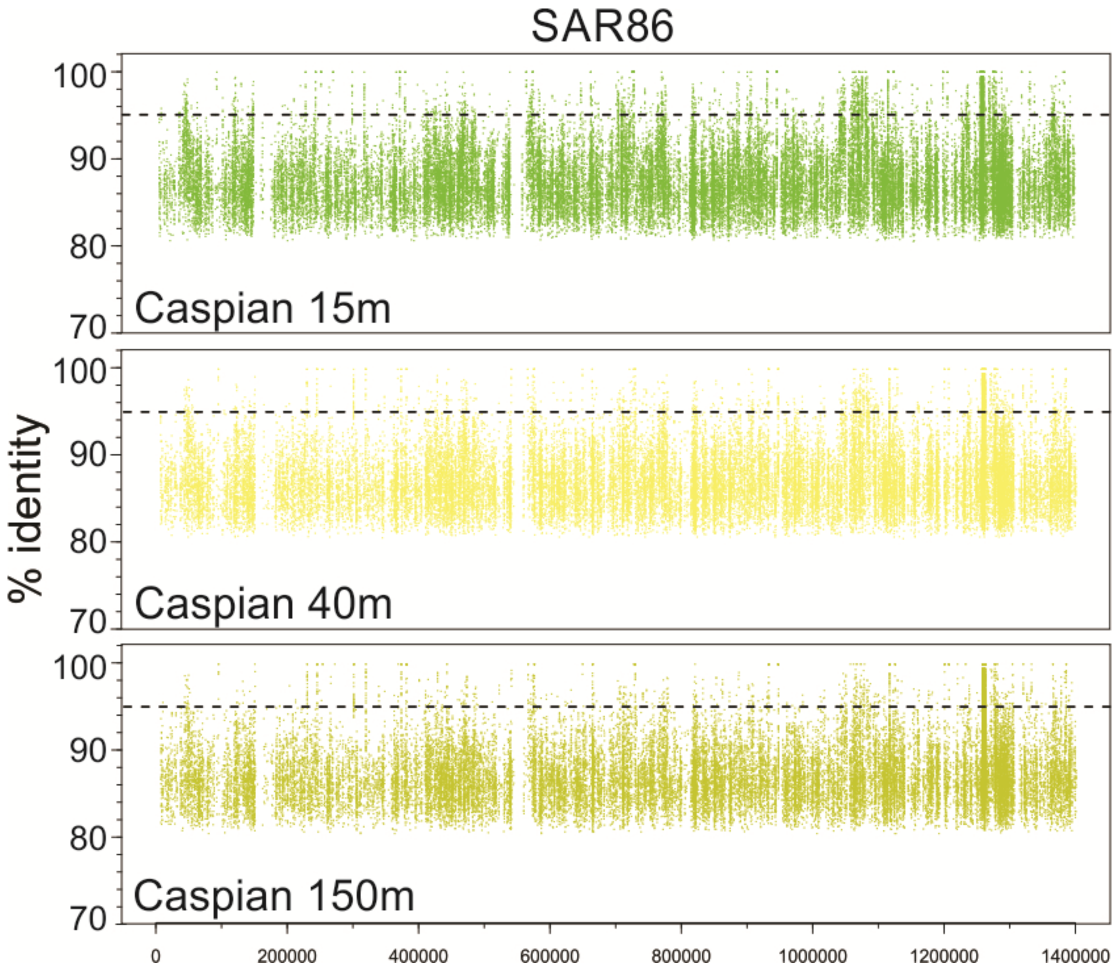
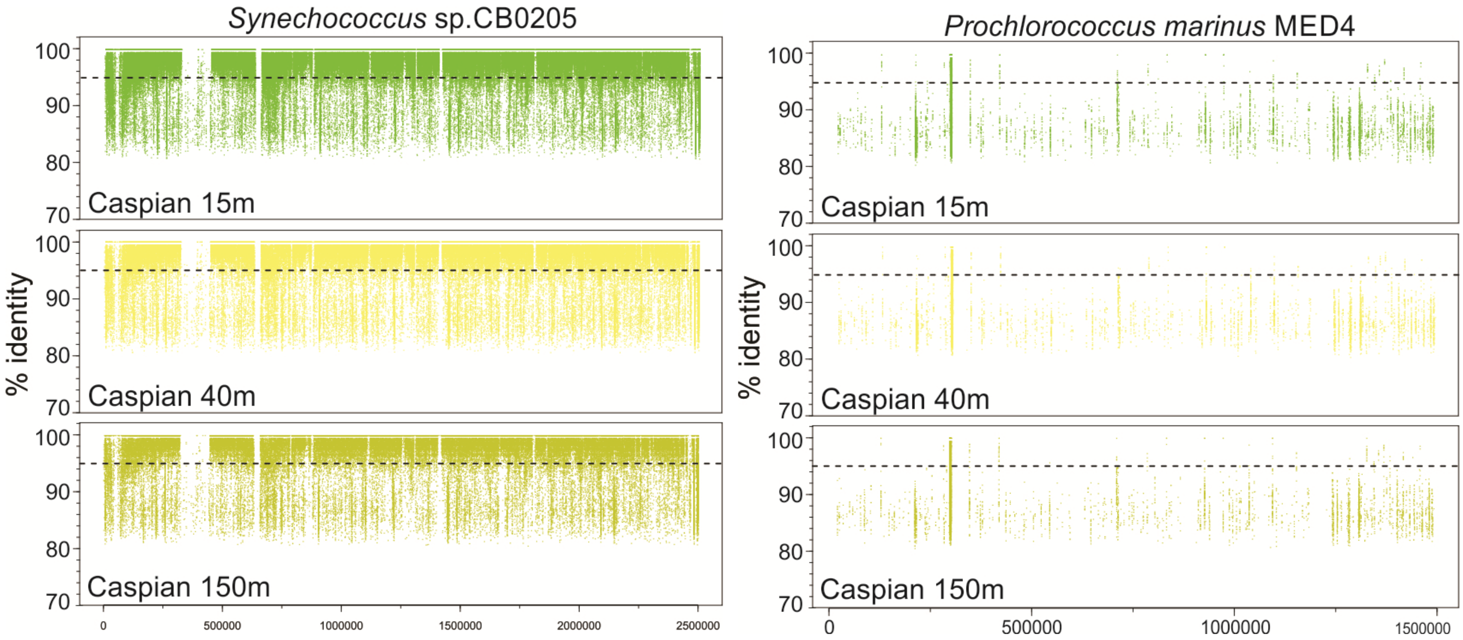


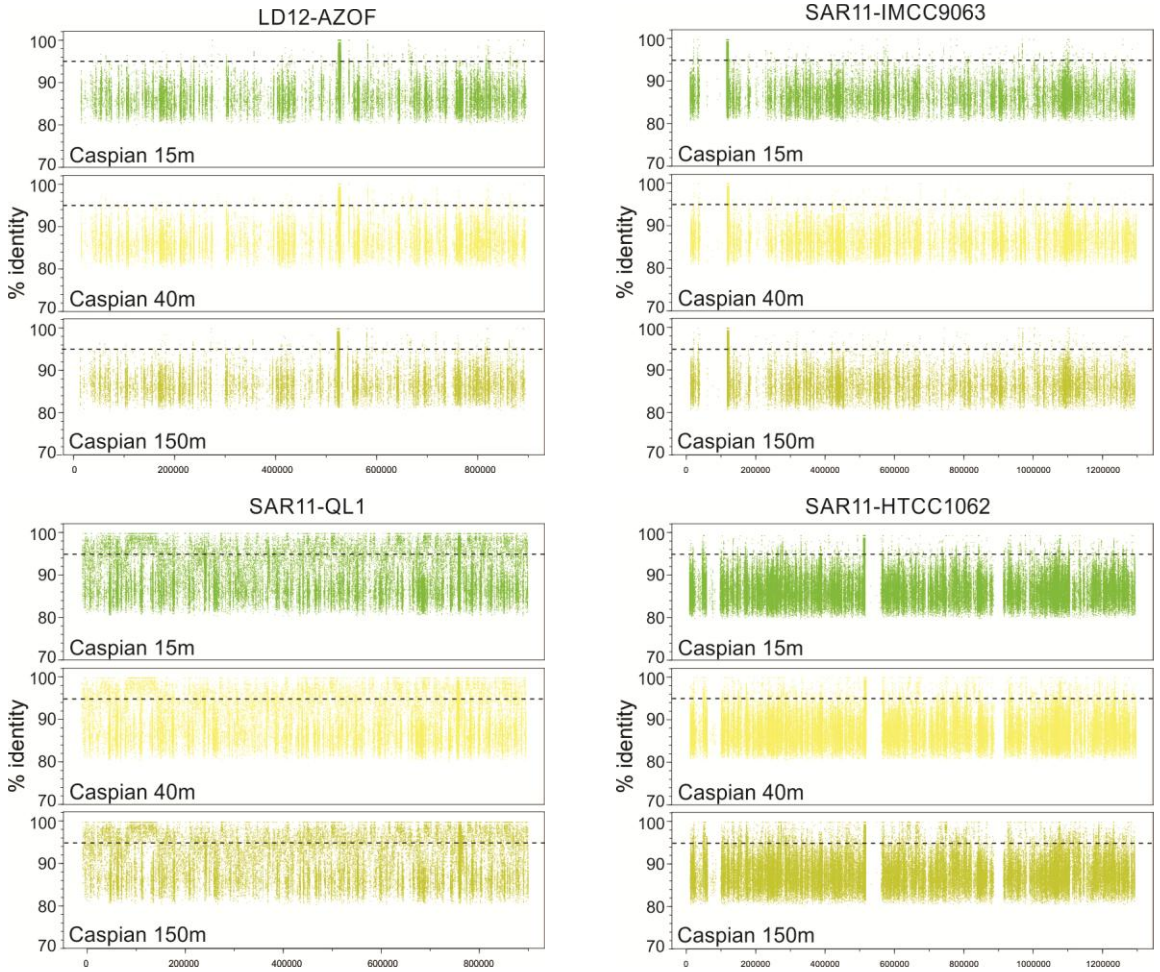
Supplementary Figure 1- [A] the map shows the location of the sampling site. The site is indicated by a yellow marker. The geographical coordinates (latitude, longitude) and the distance from the shore are also shown. A scale (km) is displayed below. The map is a modified version of a map freely available from www.naturalearthdata.com. [B] CTD profile of Caspian Sea datasets. Salinity, conductivity and temperature along the depth profile are shown.



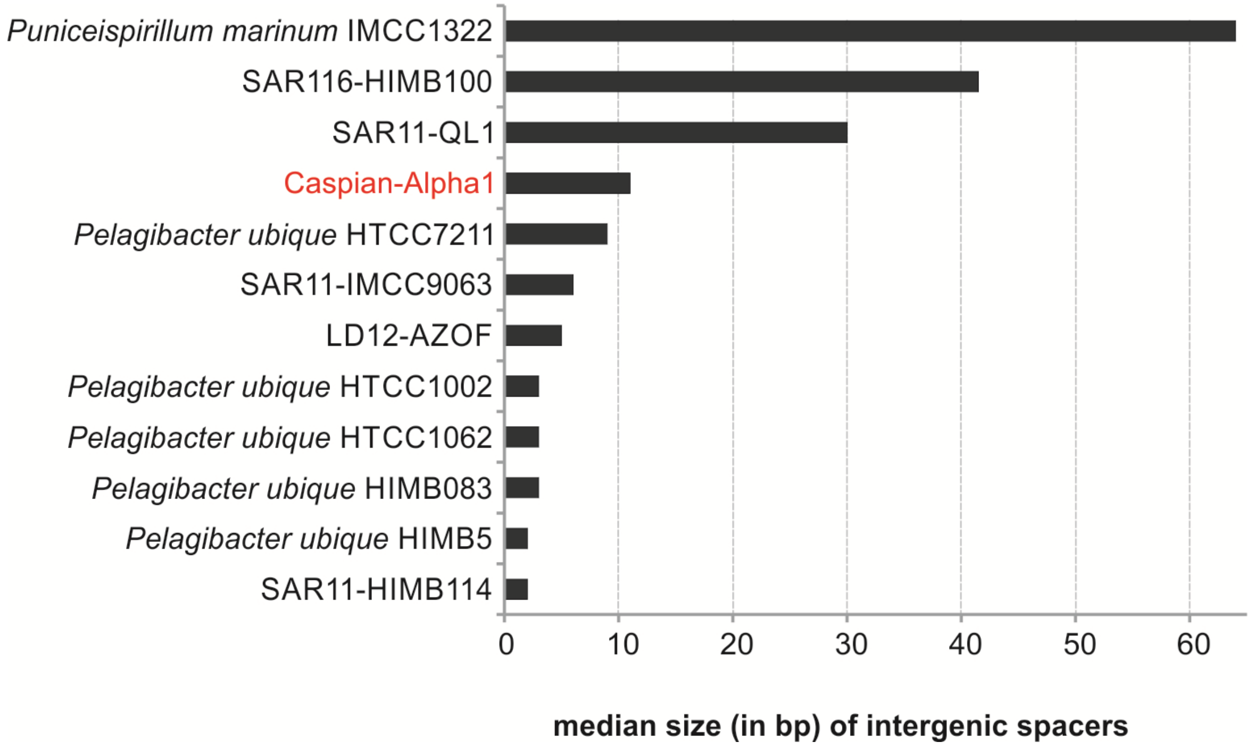
Supplementary Figure 2- Recruitment plot for SAR86E (NCBI Reference Sequence: NZ_AMWX00000000.1) a single cell genome of the 16S clade SAR86 subgroup IIIa from class *Gammaproteobacteria* against different depth datasets of Caspian Sea.



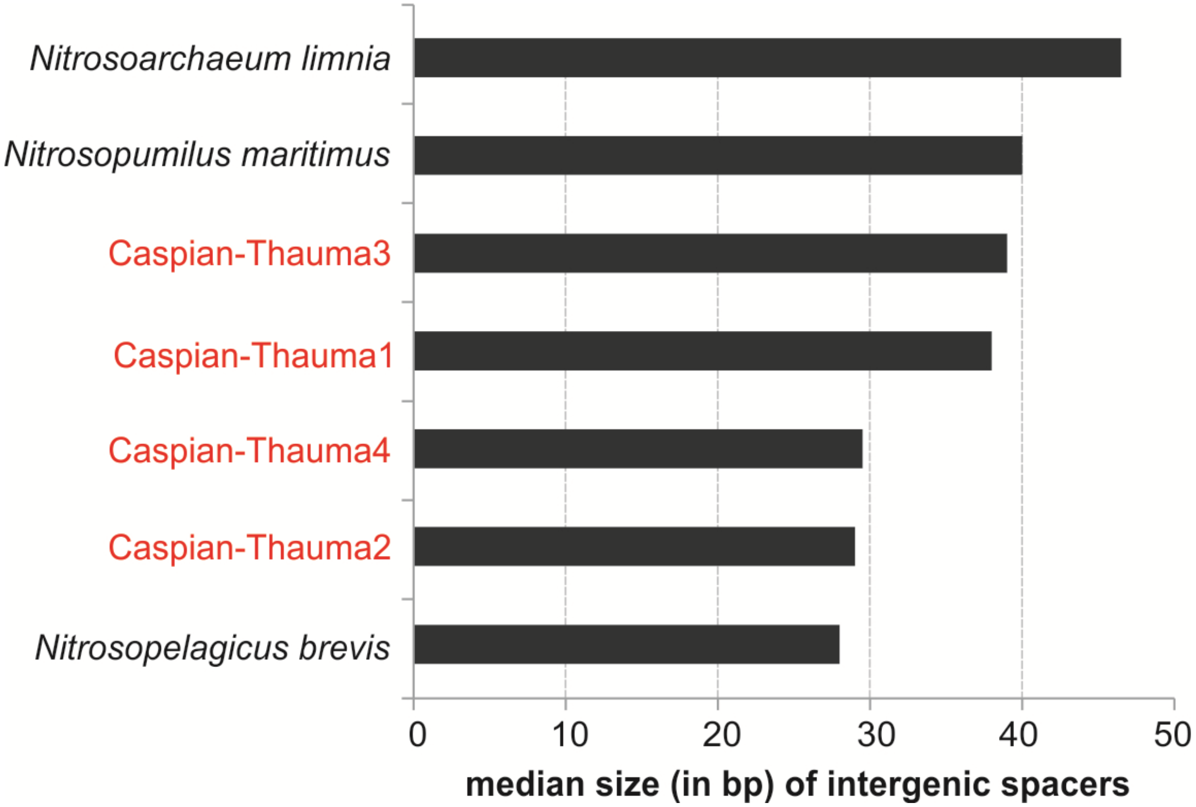
Supplementary Figure 3- Recruitment plot for representatives from phylum *Cyanobacteria* against different depth datasets of Caspian Sea. *Prochlorococcus marinus* MED4 does not exist in Caspian datasets as it is shown in the plot. *Synechococcus* sp.CB0205 is present in Caspian datasets although it was not present in contigs larger than 10Kb which have been assembled from Caspian Datasets.



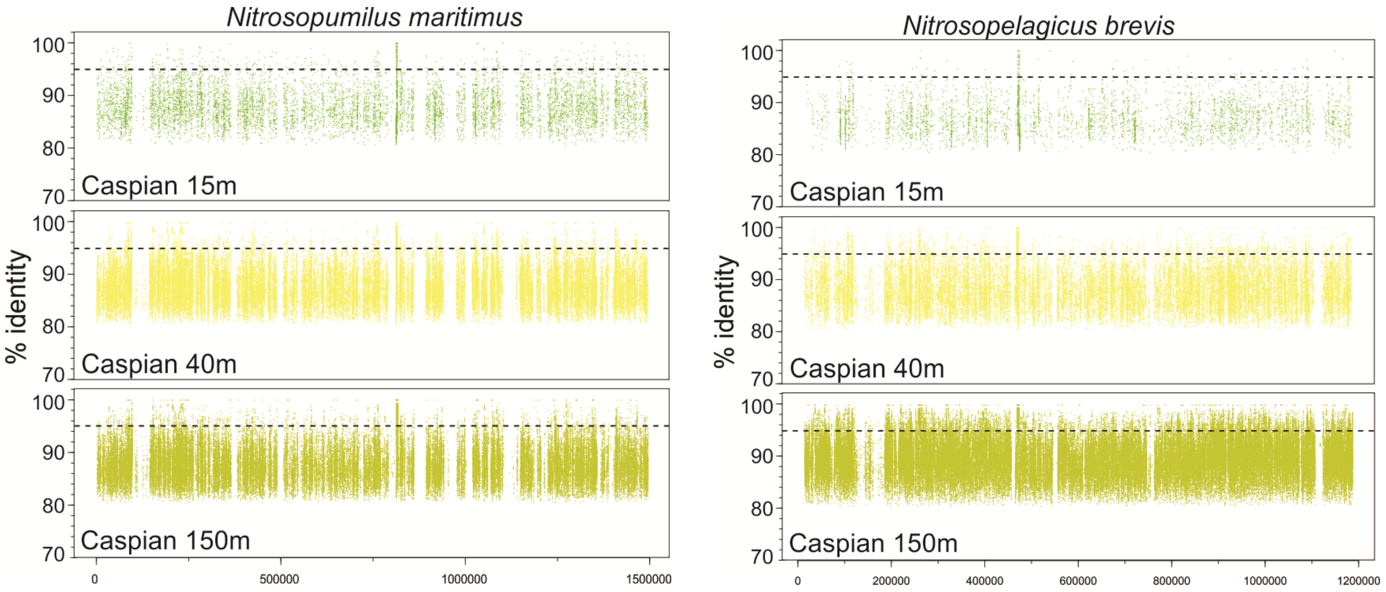
Supplementary Figure 4- recruitment plot for LD12 and 3 SAR11 representatives from phylum *Alphaproteobacteria* against different depth datasets of Caspian Sea. SAR11-QL1 is the isolated strain from brackish lake in china which shows 100% recruitment from Caspian Sea datasets.



Supplementary Figure 5- Median size of intergenic spacers for selected microbial genomes in *Rickettsiales* order in Phylum *Alphaprotebacteria*. Caspian-Alpha1 is shown in red.



Supplementary Figure 6- Median size of intergenic spacers for selected microbial genomes in Phylum *Thaumarchaeota*. Caspian genomes are shown in red.



Supplementary Figure 7- recruitment plot for *ca.* Nitrosopelagicus brevis and *Nitrosopumilus maritimus* from phylum *Thaumarchaeota* against different depth datasets of Caspian Sea.

Supplementary Table1- Caspian physicochemical features

Feature	**Caspian Sea**	**Bermuda Atlantic Time-Series**	**Baltic SeaGS695**[f]
Salinity (%)	1.1	3.5	33.05
pH	8	7.9[b]	NA
Chlorophyll (µg/L)	2.29	0.15 (at Deep Chlorophyll Maximum)[c]	NA
Secchi Depth (m)	6.5	NA	NA
NO3- (µM)	1.64 ± 0.95[a]	≤ 0.01 [d]	0.495
NH4+ (µM)	1.01 ± 0.79[a]	<0.01 to sporadic observations of >0.08 [d]	0.472 **(µm/kg)**
Dissolved Inorganic Nitrogen (DIN) (µM)	2.65 ± 1.29[a]	0.6 [e]	NA
Dissolved Inorganic Phosphate (DIP) (µM)	0.70 ± 0.36[a]	0.012[e]	0.027 **(µm/kg)**
K^+(mg/L)	119.2	NA	NA
Ca^{2+} (mg/L)	330.3	NA	NA
Mg^{2+} (mg/L)	799	NA	NA
Fe (mg/L)	0.05	NA	NA
Na^+ (mg/L)	3045	NA	NA

Alphabetic symbols are showing archived data: a (1) b (2) c (3) d (4) e (5) f (6)

Not Available (NA)

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Supplementary table2- Prokaryotic community structure based on 16S rRNA reads from unassembled datasets of Caspian Sea depth profile in comparison with freshwater, marine and brackish datasets (Chesapeake Bay, an estuary, and the Baltic Sea salinity gradient).

	Alphaproteobacteria	*Actinobacteria*	*Gammaproteobacteria*	*Bacteroidetes*	*Cyanobacteria*	*Betaproteobacteria*	*Deltaproteobacteria*	*Chloroflexi*	*Planctomycetes*	*Verrucomicrobia*	*Acidobacteria*	*Euryarchaeota*	*Thaumarchaeota*	Other
Lake Lanier	6.37	26.09	1.68	3.79	6.73	20.76	6.45	0.42	1.68	13.46	0.7	0	0	11.22
Lake Amadorio	12.84	36.22	2.27	17.36	4.34	8.1	0.34	0.83	0.56	5.59	0.08	0.18	0	10.46
Lake Gatun	15.81	46.45	1.61	4.84	1.61	2.26	0.97	0	0.32	2.26	9.35	0	4.84	8.39
Amazon River	19.39	23.8	8.53	3.58	1.38	22.42	0.83	0.14	0.41	2.06	4.13	0.55	2.48	8.54
Chesapeake Bay GS012	26.42	39.62	2.52	8.18	0	13.84	0	0	0	1.26	0	0	0	8.18
Baltic GS666	16.85	24.64	4.71	14.86	8.15	14.86	0.36	0	2.17	5.98	0.72	0	0	6.7
Baltic GS677	34.18	22.53	5.57	8.86	14.68	6.84	1.27	0	0.51	2.28	0	0	0	3.29
Caspian 15m	25.24	22.94	15.05	11.97	11.1	3.87	1.69	0.2	0.47	1.38	0.06	0.16	0.14	5.61
Caspian 40m	24.54	21.76	13.82	10.21	9.23	3.38	2.26	1.66	1.22	1.55	0.51	0.12	1.62	7.77
Caspian 150m	21.13	19.14	13.97	9.15	7.55	3.88	1.82	3.96	1.95	2.02	1.33	0.38	2.46	10.36
Baltic GS684	28.29	2.45	22.27	21.16	12.25	1.11	0.22	0	1.78	5.57	0	1.56	0	3.24
Baltic GS688	35.21	2.54	20.56	13.24	5.07	3.66	1.13	0	0.85	2.25	0	4.51	0.56	10.43
Pacific HOTS	30.94	2.32	16.56	5.01	26	0.07	1.02	0.51	0.15	1.38	0	2.98	0	13
Atlantic BATS	45.42	1.64	16.39	5.01	13.69	0.29	0.39	0.19	0.19	1.45	0	1.25	0	14.08
Mediterranian DCM	41.06	2.92	15.41	10.01	11.47	1.01	0.11	0	0.11	1.12	0	4.5	0	12.14