

1 **SUPPLEMENTARY INFORMATION**

2 Table S1. 16S rDNA read information from the different sampling sites.

Station ID	Reads	Unique sequences	OTU (3%)
MC	26177	487	281
PO1	72436	768	363
PO3	69636	885	319
SA1	104893	1180	530
SA2	98852	1362	715
SA3	37991	746	407
SA4	55754	858	440
SA5	98552	1190	510
SA6	38323	522	233
SA7	58891	691	354
SA8	64970	867	379
TA1	151291	1155	436
TA2	143963	1189	421
TG1	62743	800	333
TG2	40506	601	312
VE3	83880	1076	354

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5 Table S2. Pairwise comparison of similarity (ANOSIM) among bacterial communities.

Cluster ID	R Statistic	P-Value
I- II	1	<i>P</i> <0.05
I- III	0.75	<i>P</i> ≥0.05
I- IV	1	<i>P</i> <0.05
I-MC	1	<i>P</i> >0.05
II-III	0.72	<i>P</i> >0.05
II-IV	0.47	<i>P</i> <0.05
II-MC	1	<i>P</i> >0.05
III-IV	0.4	<i>P</i> <0.05
III-MC	1	<i>P</i> <0.05
IV-MC	1	<i>P</i> >0.05

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20 Table S3. OTUs contributing the most to the Bray-Curtis similarity index in Group I (A), II+III (B), and IV (C).
 21 The cut-off for low contribution was set at a cumulative contribution of 90%. Note: Group II and III have been
 22 combined for this analysis as they were not significantly different ($P < 0.05$) according to ANOSIM test.

Higher taxonomic group	Phylum/class	OTU-ID (97%)	Contribution %	Cumulative %
SAR11	Alphaproteobacteria	1	9.02	66.67
SAR86	Gammaproteobacteria	3	3.31	69.99
NS5	Bacteroidetes	7	2.32	72.31
Rhodobacteraceae	Alphaproteobacteria	11	1.9	74.21
SAR11	Alphaproteobacteria	2	1.82	76.03
SAR406	Deferribacteres	25	1.6	77.63
Planctomycetaceae	Planctomycetes	42	1.44	79.07
NS4	Bacteroidetes	5	1.38	80.45
SAR116	Alphaproteobacteria	9	1.17	81.62
NS4	Bacteroidetes	13	1.07	82.69
SAR86	Gammaproteobacteria	14	0.87	83.55
Rhodobacteraceae	Alphaproteobacteria	4	0.82	84.37
Flavobacteraceae	Bacteroidetes	63	0.75	85.12
Unclassified	Bacteroidetes	44	0.71	85.82
Alteromonadaceae	Gammaproteobacteria	19	0.69	86.52
<i>Synechococcus</i>	Cyanobacteria	24	0.6	87.12
SAR92	Gammaproteobacteria	22	0.59	87.7
NS5	Bacteroidetes	15	0.54	88.25
Unclassified	Proteobacteria	46	0.47	88.71
Aeromonadaceae	Gammaproteobacteria	73	0.41	89.12
Puniceicoccaceae	Verrucomicrobia	57	0.4	89.52
(Rickettsiales)	Alphaproteobacteria	33	0.39	89.91
<i>Pseudospirillum</i>	Gammaproteobacteria	30	0.36	90.27

23 **A:** Group I (Average similarity=88.69%)

Higher taxonomic group	Phylum/class	OTU-ID (97%)	Contribution %	Cumulative %
Rhodobacteraceae	Alphaproteobacteria	11	5.50	63.21
SAR11	Alphaproteobacteria	10	2.89	66.10
Owenweeksia	Bacteroidetes	6	2.10	70.77
Flavobacteraceae	Bacteroidetes	26	2.08	72.84
Glaciecola	Gammaproteobacteria	8	1.79	74.64
SAR11	Alphaproteobacteria	1	1.71	76.35
Flavobacteraceae	Bacteroidetes	63	1.55	75.90
Roseobacter clade	Alphaproteobacteria	21	1.37	79.27
Rhodobacteraceae	Alphaproteobacteria	4	1.24	80.51
NS5	Bacteroidetes	15	1.19	81.70
NS4	Bacteroidetes	13	1.12	82.81
Flavobacteraceae	Bacteroidetes	29	1.05	83.86
NS5	Bacteroidetes	7	0.97	84.83
NS4	Bacteroidetes	5	0.95	85.78
Roseobacter clade	Alphaproteobacteria	37	0.93	86.71
SAR86	Gammaproteobacteria	3	0.90	83.60
Planctomycetaceae	Planctomycetes	42	0.82	88.43
Flavobacteraceae	Bacteroidetes	32	0.78	89.21
Rhodobacteraceae	Alphaproteobacteria	162	0.69	89.90
Pseudospirillum	Gammaproteobacteria	30	0.63	90.53

24 **B: Group II+III (Average similarity=86.64%)**

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Higher taxonomic group	Phylum/class	OUT-ID (97%)	Contribution %	Cumulative %
Glaciecola	Gammaproteobacteria	8	8.25	65.84
Rhodobacteraceae	Alphaproteobacteria	11	5.85	71.69
SAR11	Alphaproteobacteria	10	3.09	74.78
SAR11	Alphaproteobacteria	1	2.64	77.42

Owenweeksia	Bacteroidetes	6	2.48	79.9
Roseobacter clade	Alphaproteobacteria	21	2.21	82.1
Rhodobacteraceae	Alphaproteobacteria	4	1.37	83.48
SA86	Gammaproteobacteria	3	1.32	84.8
Flavobacteraceae	Bacteroidetes	26	0.95	85.75
Flavobacteraceae	Bacteroidetes	29	0.92	86.67
NS4	Bacteroidetes	13	0.9	87.57
Flavobacteraceae	Bacteroidetes	32	0.85	88.42
Roseobacter clade	Alphaproteobacteria	37	0.71	89.14
NS5	Bacteroidetes	7	0.68	89.82
Pseudospirillum	Gammaproteobacteria	30	0.66	90.48

27 **C: Group IV (Average similarity=88.80%)**

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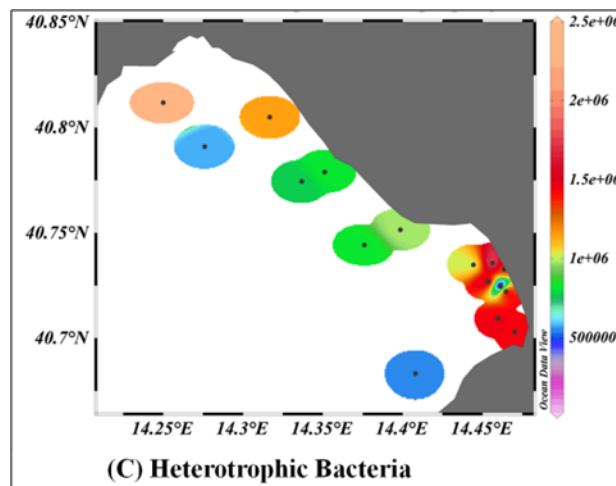
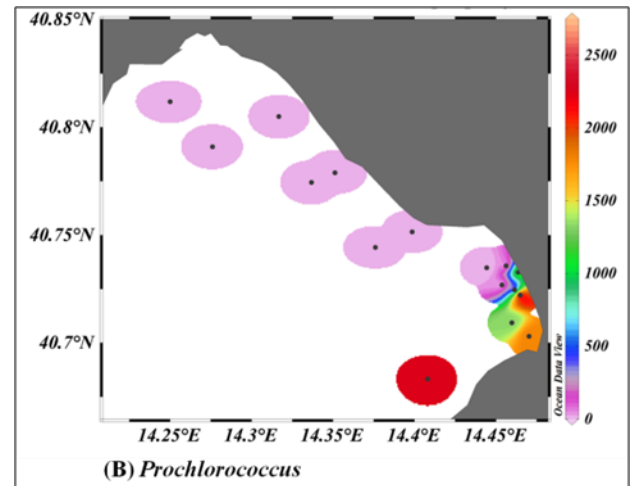
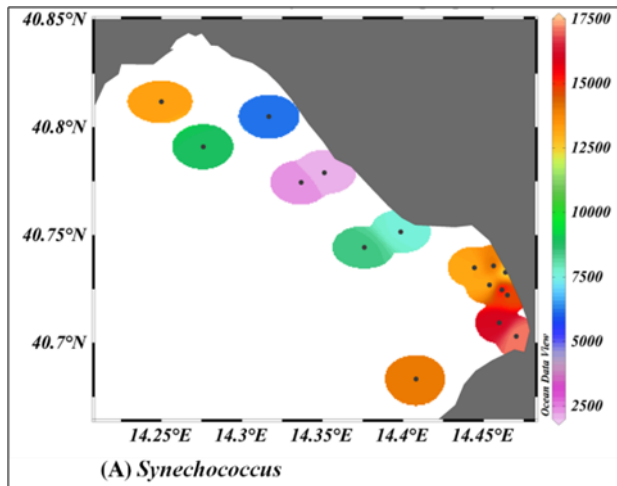
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42 Fig S1. Distribution of prokaryotic groups in surface waters of the GON as determined by flow cytometry. A)
43 *Synechococcus*, B) *Prochlorococcus*, C) Heterotrophic Bacteria. Cell abundance for each group is shown
44 as Cells ml⁻¹.



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54 Fig S2. Rarefaction curves of the observed OTUs (a), Chao I richness estimator (b), and Shannon diversity index
55 (c).

