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Supplement of

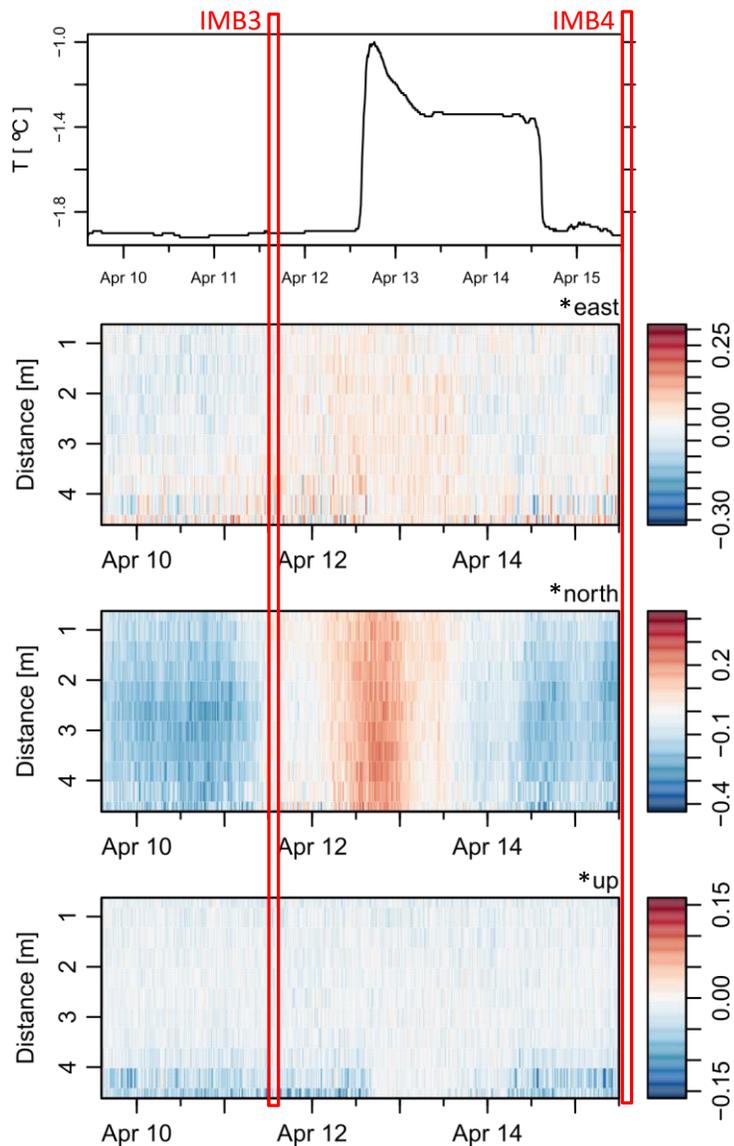
Methane-oxidizing seawater microbial communities from an Arctic shelf

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Supplementary Figure 1



Sampling times at station IMB in AKST (UTC-8)

IMB1: April 7, 3:20 pm

IMB2: April 9, 5:00 pm

IMB3: April 11, 12:30 pm

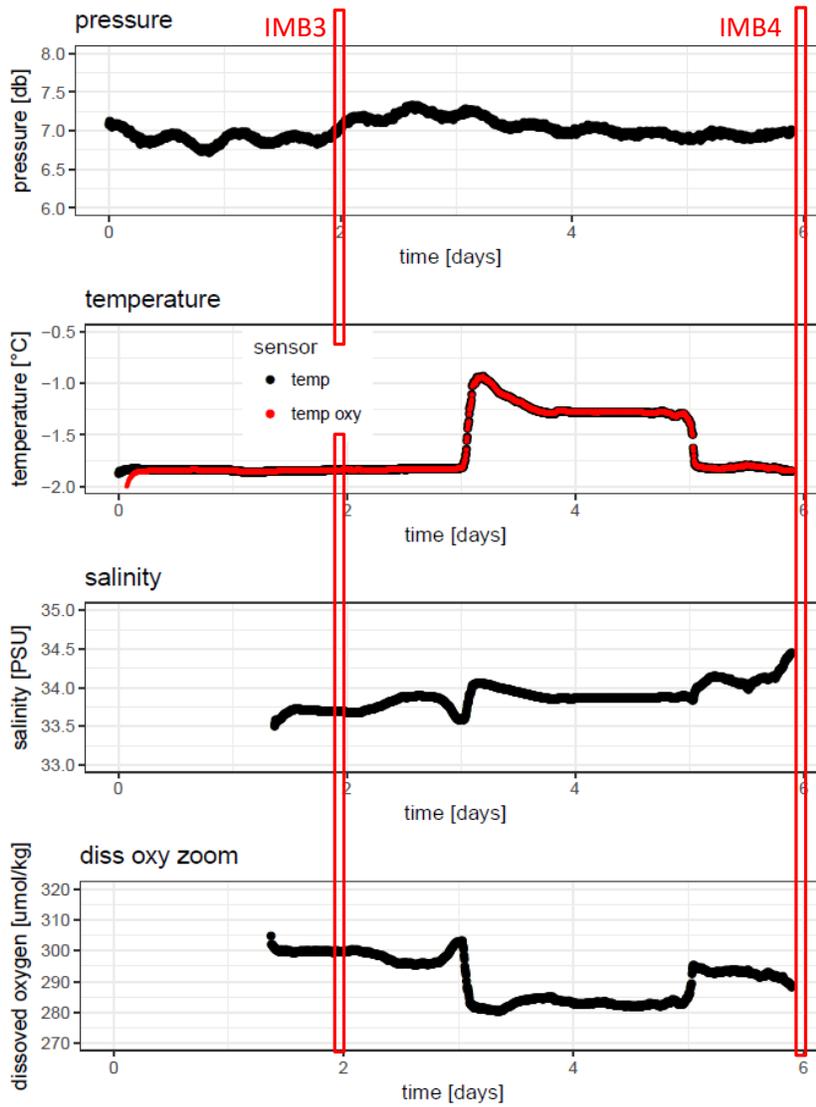
IMB4: April 15, 12:00 pm

Supplementary Figure 1: ADCP data (Aquadopp Profiler, Nortek AS, Norway) between April 9 and 15 April at site IMB. Approximate sampling time for IMB3 and IMB4 are shown as red vertical box, while the other sampling times are outside the recorded time.

*Note on current directions: The more frequent current direction along Barrow Canyon is northeastward transporting cold Chuckchi Sea resident water (Aagaard and Roach, 1990; Woodgate et al., 2005). The flow reversal leads to a southwest direction combined with upwelling of warmer Arctic Intermediate water (Atlantic Layer). Local current directions indicated in Supplementary Figure 1 are very likely influenced by small scale local conditions and may not reflect the general transport through Barrow Canyon (pers. comm. Andy Mahony, University Fairbanks, AK). Factors that might be causing this disturbance are (i) seawater swirling around Point Barrow or (ii) grounded fast ice at the shallow deployment site beneath the sea ice local. The current direction indicated by the ADCP does thus likely not reflect the general flow directions

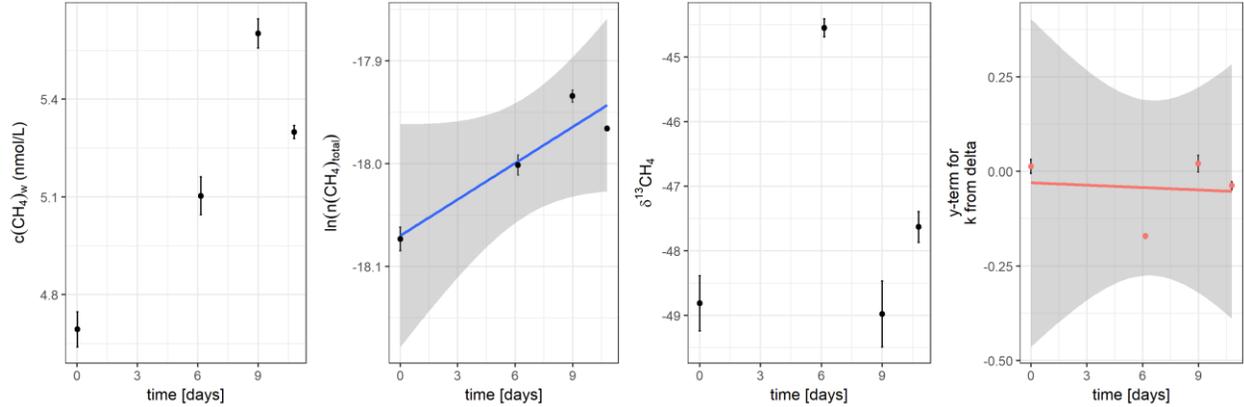
along Barrow Canyon. We thus interpret the temperature signature with given literature to determine the general source region of the advected water.

Supplementary Figure 2



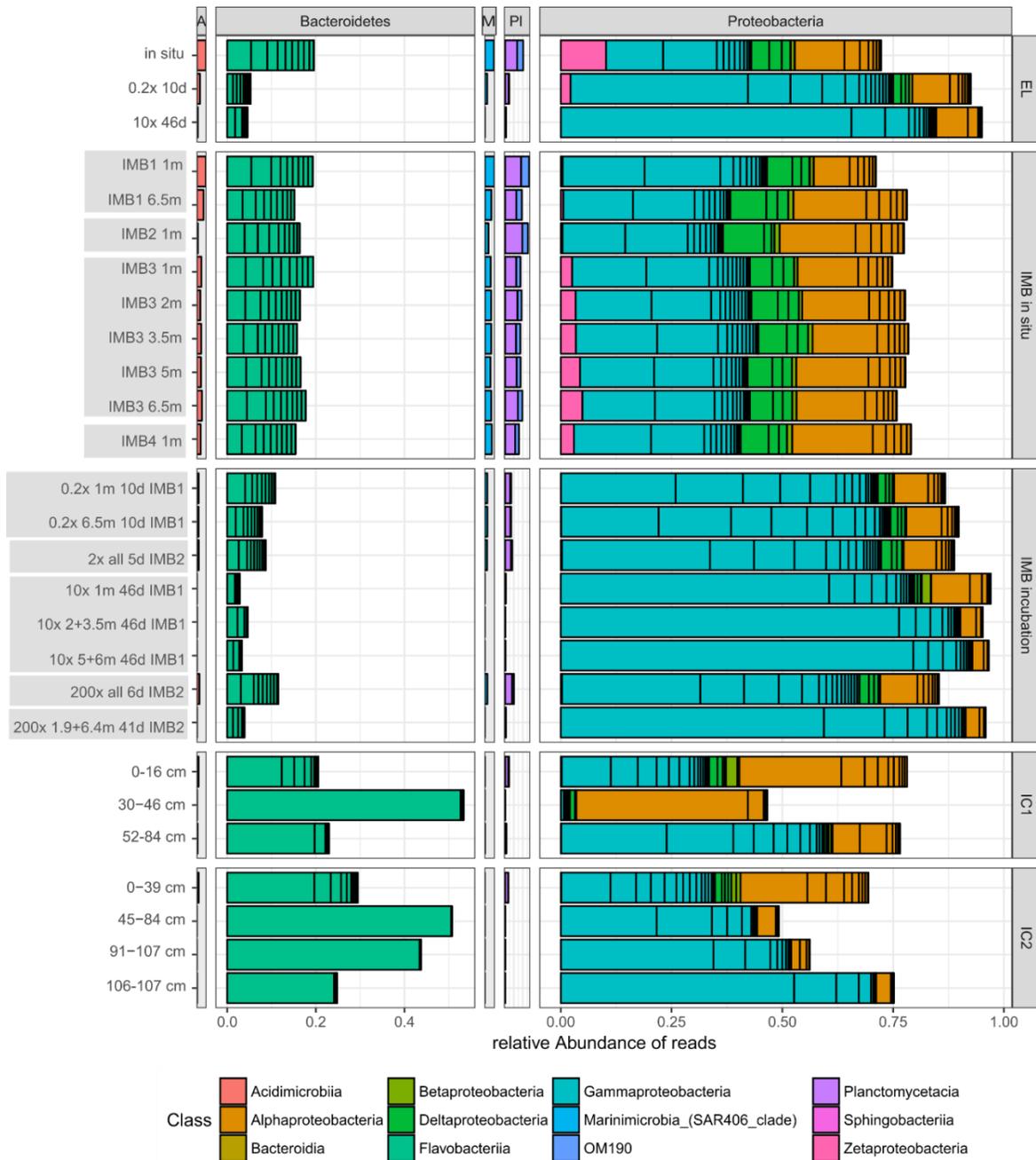
Supplementary Figure 2: SBE37 data (SBE37SMP, Sea-Bird Scientific, Washington, USA) between April 9 and 15 April at site IMB

Supplementary Figure 3



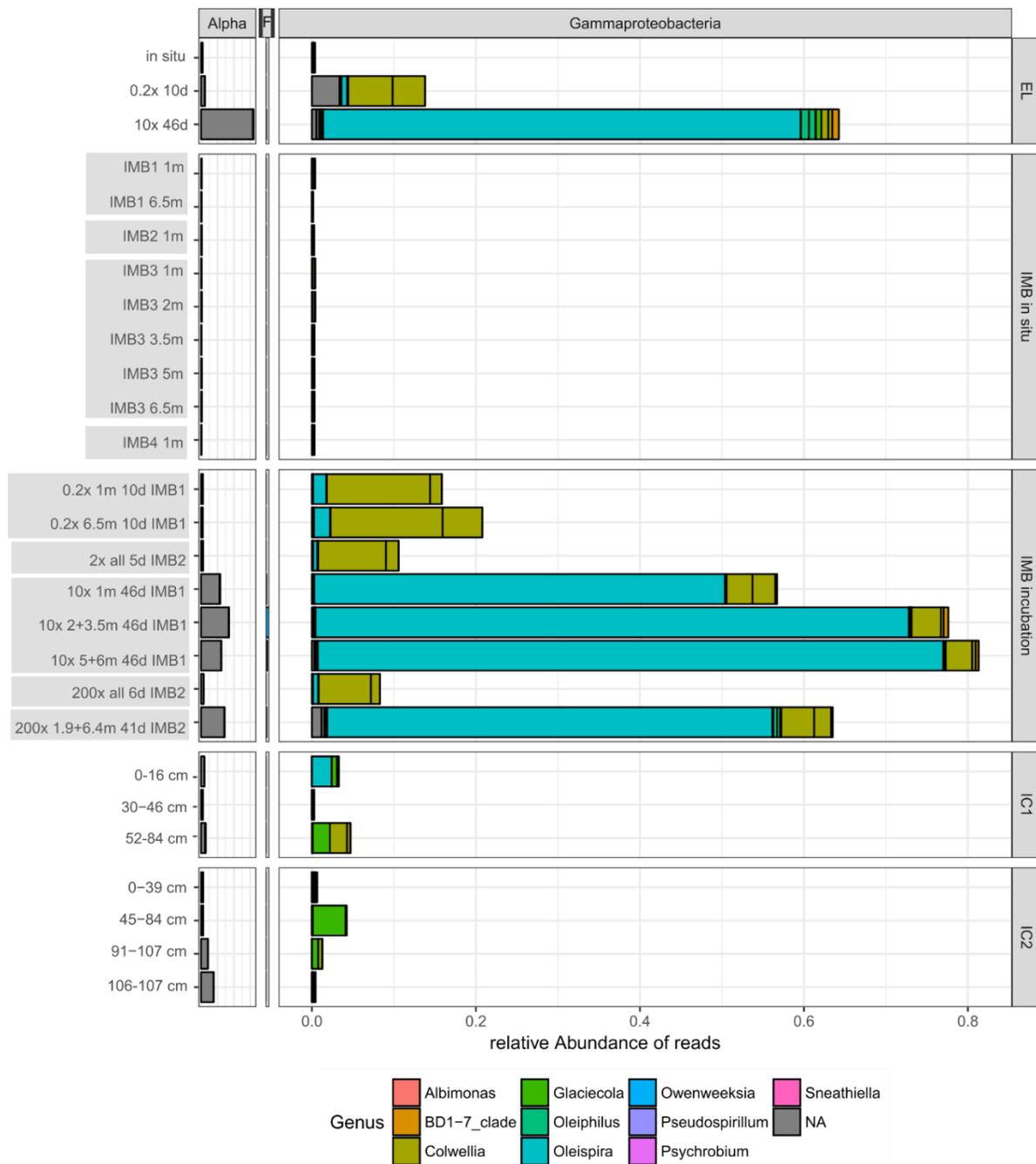
Supplementary Figure 3: Example of 0.2x incubation experiment. Error bars show standard deviation on duplicate measurement. Gray shaded area indicates the 95% confidence interval of the linear model.

Supplementary Figure 4



Supplementary Figure 4: Relative abundances of phylogenetic groups of the top 50 OTUs. The graph is subset for each sampling site or experiment in vertical direction and for the different phyla in horizontal direction; panels from left to right: Actinobacteria (A), Bacteroidetes, Marinimicrobia_SAR406 (M), Planctomycetes (PI), Proteobacteria. Not-normalized data was used to calculate relative abundances. X-axis scaling is identical for all panels. In addition to the sampling site and methane concentration, the sample names indicate sampling depth (m or cm) and the duration of incubation (d). *Note: IC1 30-46cm had sediment layer, IC2 106-107cm was biomass/algae rich bottom.*

Supplementary Figure 5



Supplementary Figure 5: Relative abundances of differentially more abundant OTUs. The graph is subset for each sampling site or experiment in vertical direction and for the different phylogenetic classes in horizontal direction; panels from left to right: Alphaproteobacteria (Alpha), Flavobacteriia (F) < 4%, Gammaproteobacteria. X-axis scaling is identical for all panels. Not-normalized data was used to calculate relative abundances. In addition to the sampling site and methane concentration, the sample names indicate sampling depth (m or cm) and the duration of incubation (d).

Supplementary Table 1: Sequencing statistics

	V4-V5	pmoA
Number of samples	27	15
Number of sequences after quality control	1,810,329	375,448
Number of unique sequences	158,540	2,776
Number of OTUs without rare (n≤2)	8,877 (97% similarity)	59 (93% similarity)
Mean length of analyzed amplicon in base pairs	407	219

Supplementary Table 2: landscape, see next page**Supplementary Table 3: Relative sequence read abundances of microbial groups atypical for sea ice and found in an anoxic Antarctic ice core (Eronen-Rasimus et al., 2017) :**

class	genus	IC1	IC2
		mean ± standard deviation	mean ± standard deviation
Deltaproteobacteria	Desulforhopalus	0	0
Deltaproteobacteria	Desulfofrigus	$6.39 \times 10^{-5} \pm 7.33 \times 10^{-5}$	$3.92 \times 10^{-5} \pm 5.38 \times 10^{-5}$
Epsilonproteobacteria	Sulfurospirillum	$6.92 \times 10^{-6} \pm 1.20 \times 10^{-5}$	0
Epsilonproteobacteria	Arcobacter	$4.88 \times 10^{-4} \pm 4.81 \times 10^{-4}$	$4.80 \times 10^{-4} \pm 2.97 \times 10^{-4}$
Bacteroidia	Marinifilum	$2.13 \times 10^{-4} \pm 1.51 \times 10^{-4}$	$1.14 \times 10^{-4} \pm 2.28 \times 10^{-4}$

Supplementary References:

Aagaard, K. and Roach, A. T.: Arctic ocean-shelf exchange: Measurements in Barrow Canyon, *J. Geophys. Res.*, 95(C10), 18163, doi:10.1029/JC095iC10p18163, 1990.

Eronen-Rasimus, E., Luhtanen, A.-M., Rintala, J.-M., Delille, B., Dieckmann, G., Karkman, A. and Tison, J.-L.: An active bacterial community linked to high chl-a concentrations in Antarctic winter-pack ice and evidence for the development of an anaerobic sea-ice bacterial community, *ISME J.*, doi:10.1038/ismej.2017.96, 2017.

Woodgate, R. A., Aagaard, K. and Weingartner, T. J.: A year in the physical oceanography of the Chukchi Sea: Moored measurements from autumn 1990–1991, *Deep Sea Res. Part II Top. Stud. Oceanogr.*, 52(24–26), 3116–3149, doi:10.1016/j.dsr2.2005.10.016, 2005.

Supplementary Table 2: Table of potential MOX OTUs

	in situ	oxi short	oxi long	Class	Family	Genus
# of Samples	10	5	5			
Otu000001	0.01%	1.09%	62.24%	Gammaproteobacteria	Oceanospirillaceae	Oleispira
Otu000006	0.17%	8.97%	2.58%	Gammaproteobacteria	Colwelliaceae	Colwellia
Otu000007	0.08%	2.86%	1.60%	Gammaproteobacteria	Colwelliaceae	Colwellia
Otu000013	0.08%	0.28%	3.45%	Alphaproteobacteria	Rhodobacteraceae	NA
Otu000064	0.01%	0.01%	0.17%	Gammaproteobacteria	Alteromonadaceae	Glaciecola
Otu000078	0.00%	0.02%	0.41%	Gammaproteobacteria	unclassified	NA
Otu000089	0.05%	0.70%	0.12%	Gammaproteobacteria	unclassified	NA
Otu000096	0.00%	0.03%	0.35%	Gammaproteobacteria	Oleiphilaceae	Oleiphilus
Otu000119	0.00%	0.01%	0.43%	Gammaproteobacteria	Spongiibacteraceae	BD1-7_clade
Otu000130	0.00%	0.01%	0.14%	Gammaproteobacteria	Cellvibrionaceae	NA
Otu000135	0.00%	0.02%	0.28%	Gammaproteobacteria	Oleiphilaceae	Oleiphilus
Otu000154	0.00%	0.00%	0.01%	Alphaproteobacteria	Sneathiellaceae	Sneathiella
Otu000160	0.01%	0.00%	0.15%	Flavobacteriia	Cryomorphaceae	Owenweeksia
Otu000306	0.00%	0.01%	0.12%	Gammaproteobacteria	Oceanospirillaceae	NA
Otu000316	0.00%	0.10%	0.01%	Gammaproteobacteria	Shewanellaceae	Psychrobium
Otu000369	0.00%	0.00%	0.08%	Gammaproteobacteria	Oceanospirillaceae	Pseudospirillum
Otu000474	0.00%	0.00%	0.04%	Alphaproteobacteria	Rhodobacteraceae	Albimonas
Otu000608	0.00%	0.00%	0.03%	Gammaproteobacteria	Oceanospirillaceae	NA
Otu000668	0.00%	0.00%	0.03%	Gammaproteobacteria	Oceanospirillaceae	Oleispira
Otu000698	0.00%	0.00%	0.03%	Gammaproteobacteria	Oceanospirillaceae	Oleispira
Otu000760	0.00%	0.01%	0.01%	Gammaproteobacteria	Cellvibrionaceae	NA
Otu000781	0.00%	0.00%	0.01%	Gammaproteobacteria	unclassified	NA
Otu000782	0.00%	0.00%	0.02%	Gammaproteobacteria	Oleiphilaceae	Oleiphilus
Otu000811	0.00%	0.01%	0.01%	Gammaproteobacteria	Oceanospirillaceae	Oleispira
Otu001155	0.00%	0.00%	0.01%	Gammaproteobacteria	Oceanospirillaceae	Oleispira