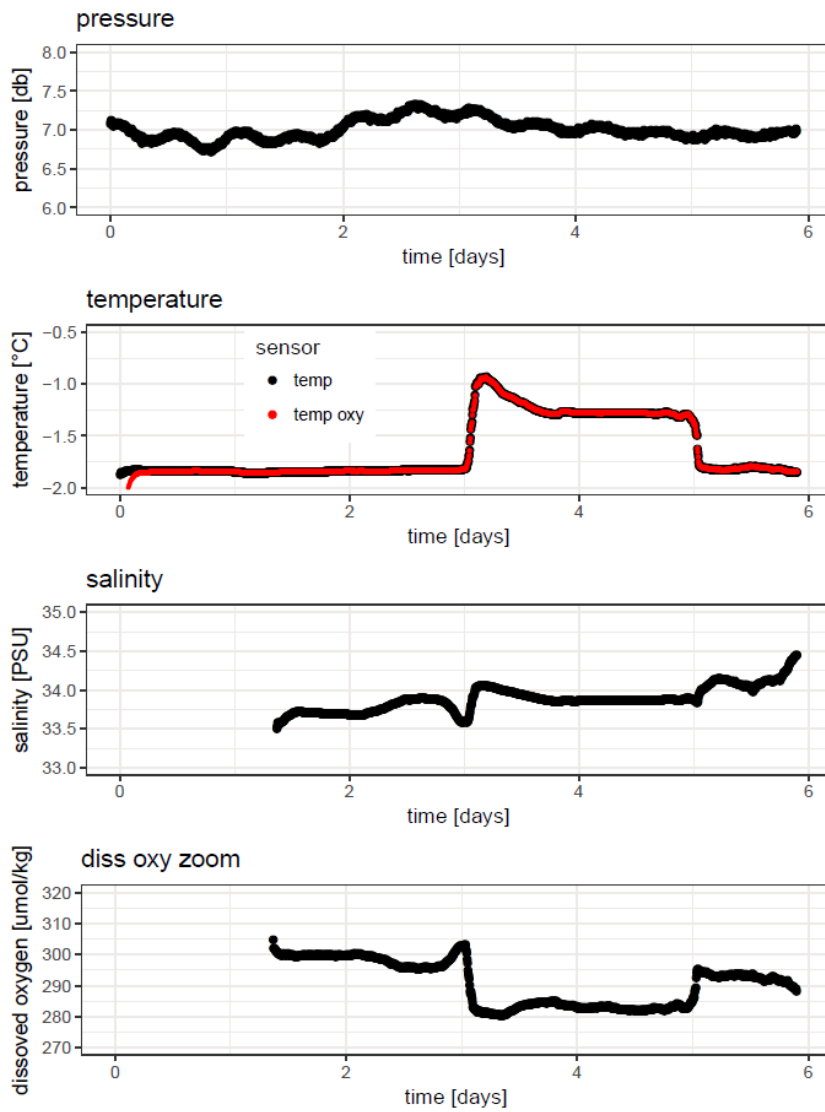
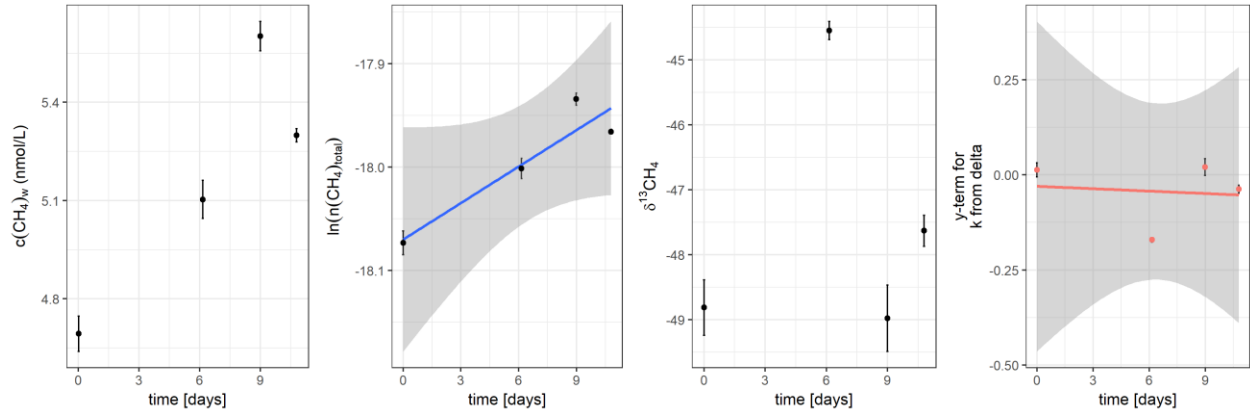
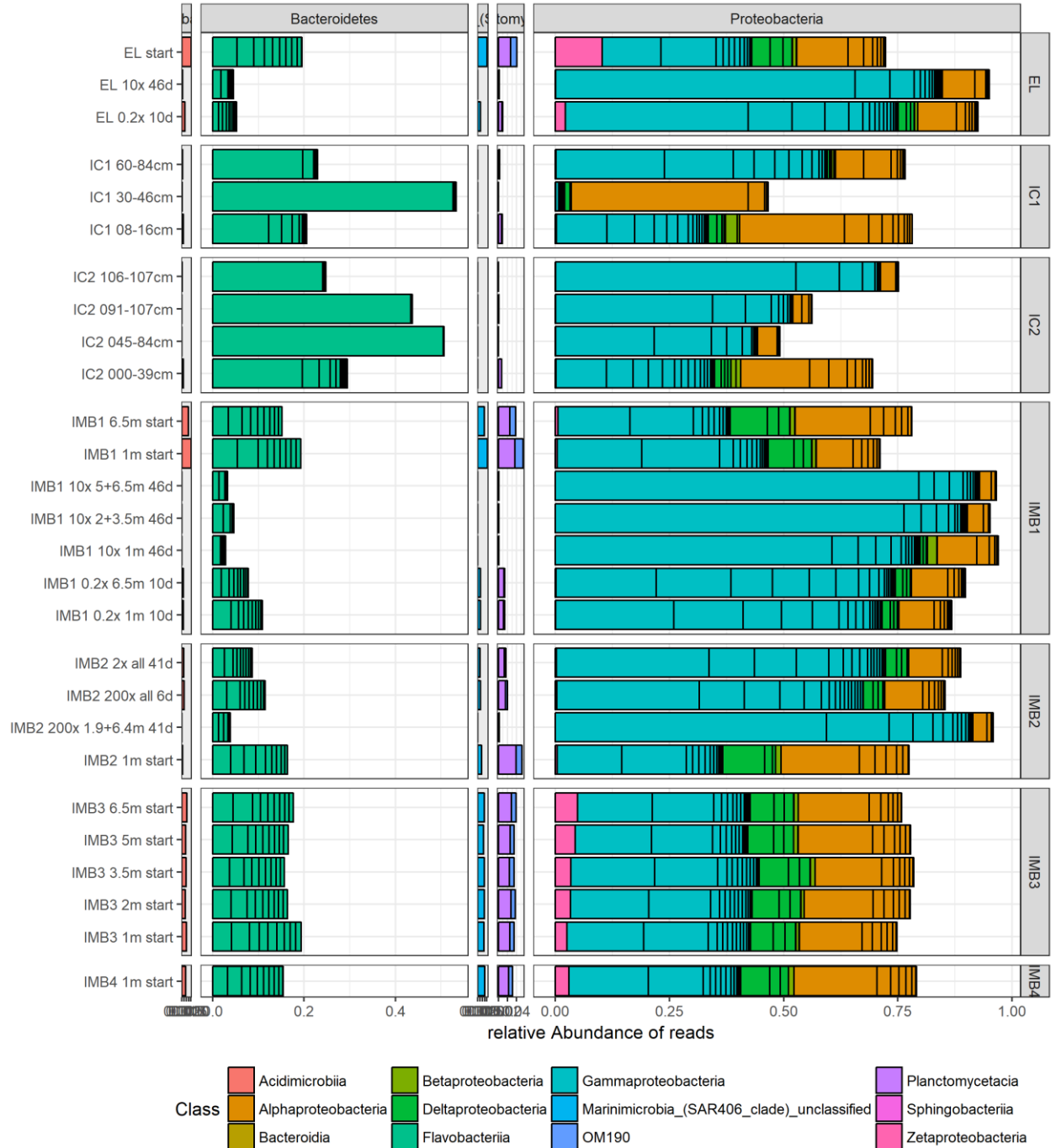
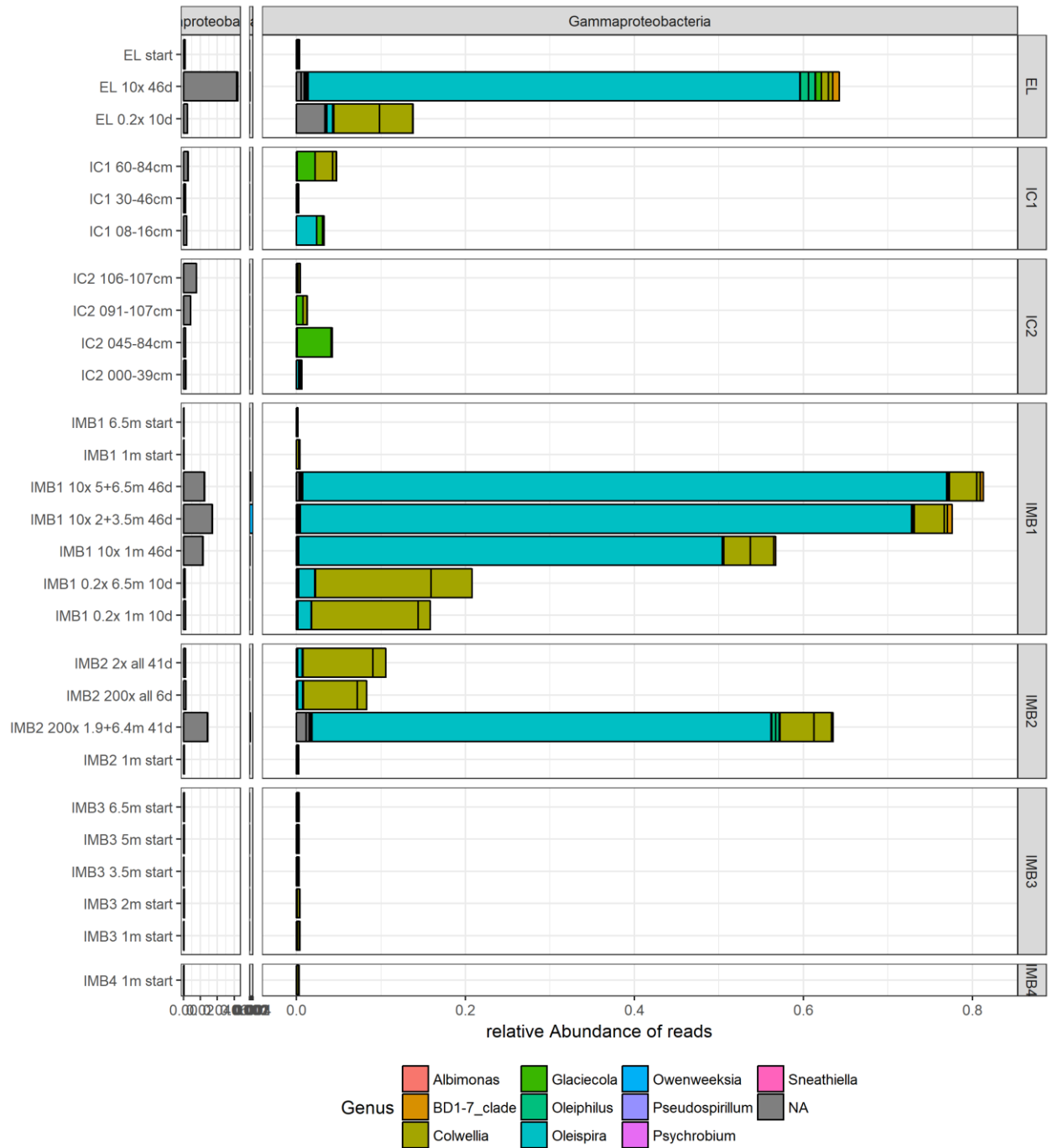
Supplementary Figure 1: ADCP data (Aquadopp Profiler, Nortek AS, Norway) between April 9 and 15 April at site IMB

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

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: 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, Bacteriodetes, Marinimicrobia_SAR406, Planctomycetes, Proteobacteria. Not-normalized data was used to calculate relative abundances. X-axis scaling is identical for all panels. *Note: IC1 30-46cm had sediment layer, IC2 106-107cm was biomass/algae rich bottom.*

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, Flavobacteriia < 4%, Gammaproteobacteria. X-axis scaling is identical for all panels. Not-normalized data was used to calculate relative abundances.

Supplementary Table 1: Sequencing statistics

	V4V5	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: Relative sequence read abundances of microbial groups atypical for sea ice and found in an anoxic Antartic ice core (Eronen-Rasimus et al., 2017) **:**

class	genus	IC1 mean ± standard deviation	IC2 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	$2.13 \times 10^{-4} \pm 1.51 \times 10^{-4}$	$1.14 \times 10^{-4} \pm 2.28 \times 10^{-4}$

References:

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.