

*The following supplement accompanies the article*

# **Marine bacterial, archaeal and eukaryotic diversity and community structure on the continental shelf of the western Antarctic Peninsula**

**Catherine M. Luria<sup>1,2</sup>, Hugh W. Ducklow<sup>3</sup>, Linda A. Amaral-Zettler<sup>1,2,4,\*</sup>**

<sup>1</sup>Department of Ecology and Evolutionary Biology, Brown University, Providence, Rhode Island 02912, USA

<sup>2</sup>The Josephine Bay Paul Center for Comparative Molecular Biology and Evolution, Marine Biological Laboratory, Woods Hole, Massachusetts 02543, USA

<sup>3</sup>Lamont-Doherty Earth Observatory of Columbia University, Palisades, New York 10964, USA

<sup>4</sup>Department of Earth, Environmental and Planetary Sciences, Brown University, Providence, Rhode Island 02912, USA

\*Corresponding author: amaral@mbl.edu

*Aquatic Microbial Ecology 73: 107–121 (2014)*

---

**Supplement 1.** Additional data to accompany main text

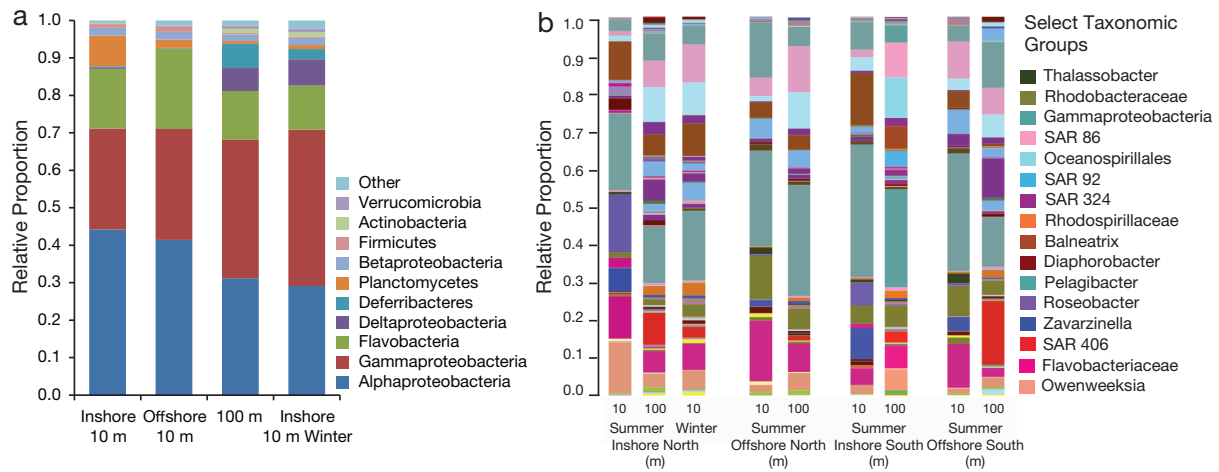


Fig. S1. Relative abundance of the most common bacterial taxa from (a) coarser taxonomic resolution for in-shore and offshore 10 m (north and south pooled), 100 m (north and south inshore and offshore pooled), and winter inshore surface (north only) samples. (b) Finer scaled taxonomic resolution; bar graphs for summer versus winter, inshore versus offshore, and north versus south. Both figures were generated in Qiime (Caporaso et al. 2010)

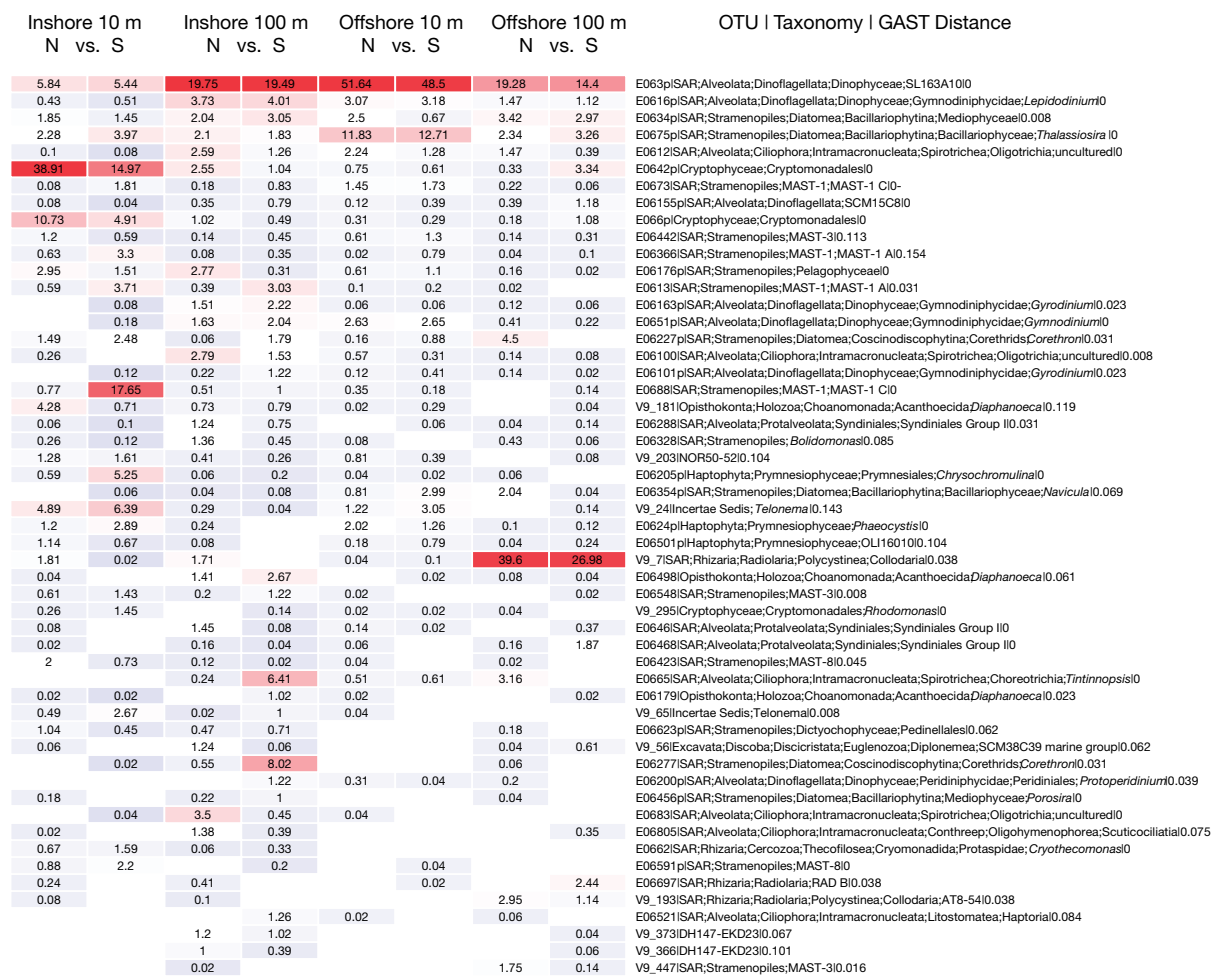


Fig. S2. Heatmap of eukaryotic operational taxonomic units recovered at a frequency of >1% at a given station. Hot colors indicate higher percentages, while cooler colors indicate lower percentages, with actual values superimposed over colors. Data shown are normalized by randomly resampling data to the lowest sampling effort. The depth of taxonomic resolution available in the V9 region varied by taxon and is displayed to the right along with Global Alignment for Sequence Taxonomy (Huse et al. 2008) distance values to the nearest relative in GenBank

Table S1. MIMARKS table with associated contextual data for the sequenced samples (in Supplement 2 at [www.int-res.com/articles/suppl/a073p107\\_supp.xls](http://www.int-res.com/articles/suppl/a073p107_supp.xls))

Table S2. Axis summary statistics for canonical correspondence analysis. OTU: operational taxonomic units

	Axis 1	Axis 2	Axis 3
Bacterial Analysis Eigenvalue	0.4344	0.2296	0.1707
Variance in Bacterial OTU data			
Cumulative % explained	21.7	33.2	41.8
Variance of Bacterial OTU-environment-relation			
Cumulative % explained	33.6	51.5	64.6
Eukaryotic Analysis Eigenvalue	0.3815	0.2952	0.2429
Variance of Eukaryotic OTU data			
Cumulative % explained	13.3	23.6	32.0
Variance of Eukaryotic OTU-environment-relation			
Cumulative % explained	22.3	39.3	53.4