

## **Supporting Information**

# **THE ECOLOGICAL ASSEMBLY OF BACTERIAL COMMUNITIES IN ANTARCTIC WETLANDS VARIES ACROSS LEVELS OF PHYLOGENETIC RESOLUTION**

María V Quiroga<sup>†</sup>; Angel Valverde<sup>†</sup>; Gabriela Mataloni; Valeria Casa; James C Stegen;

Don Cowan

<sup>†</sup> These authors contributed equally to this work

Corresponding author contact: mvquiroga@iib.unsam.edu.ar

**Supporting Table S1**

**Supporting Figures S1-S7**

**Supporting References**

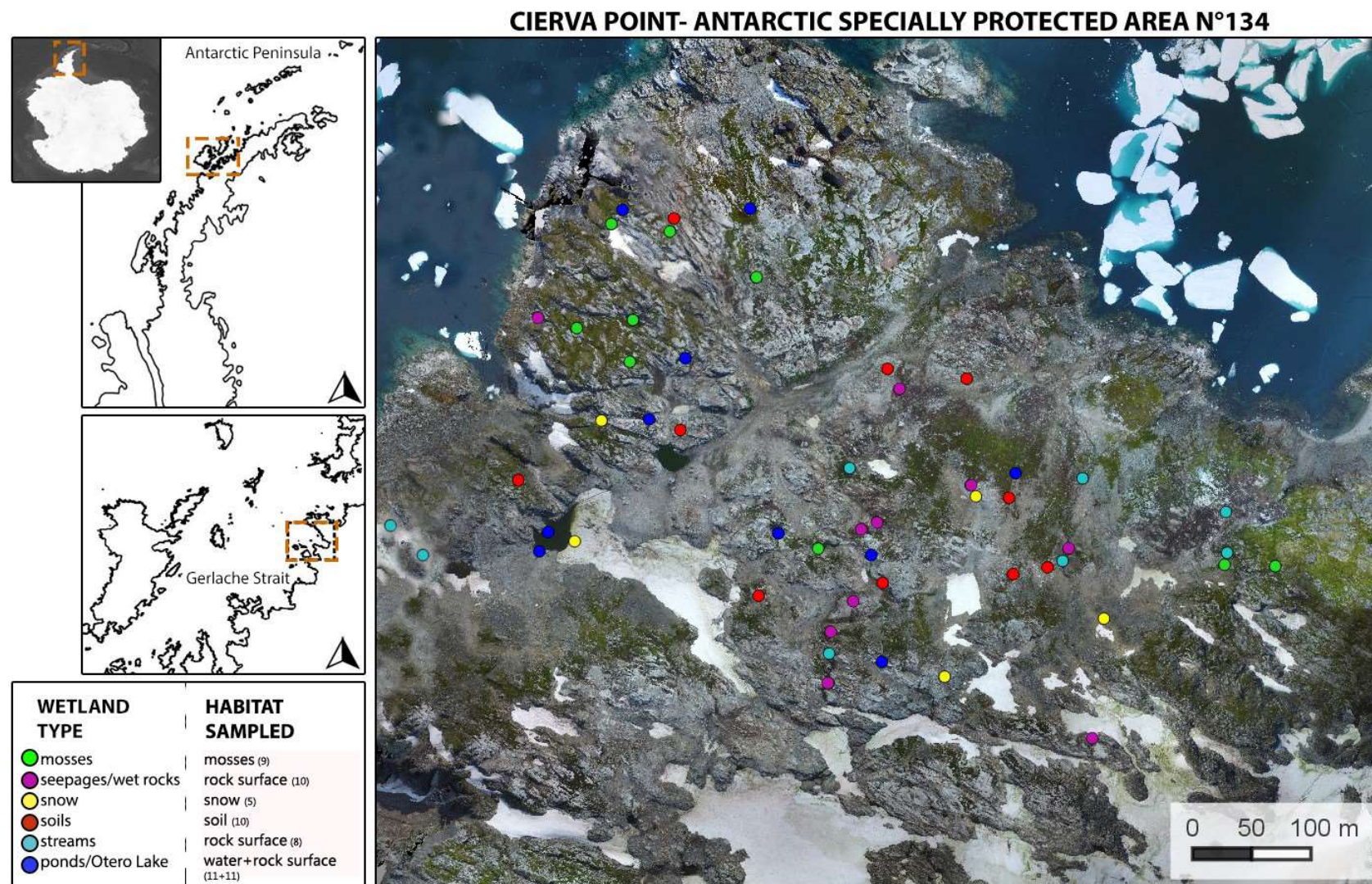
Ramos Marín (2018) Master Thesis. Universidade de Lisboa.

**Supporting Table S1** Bacterial community sampled.

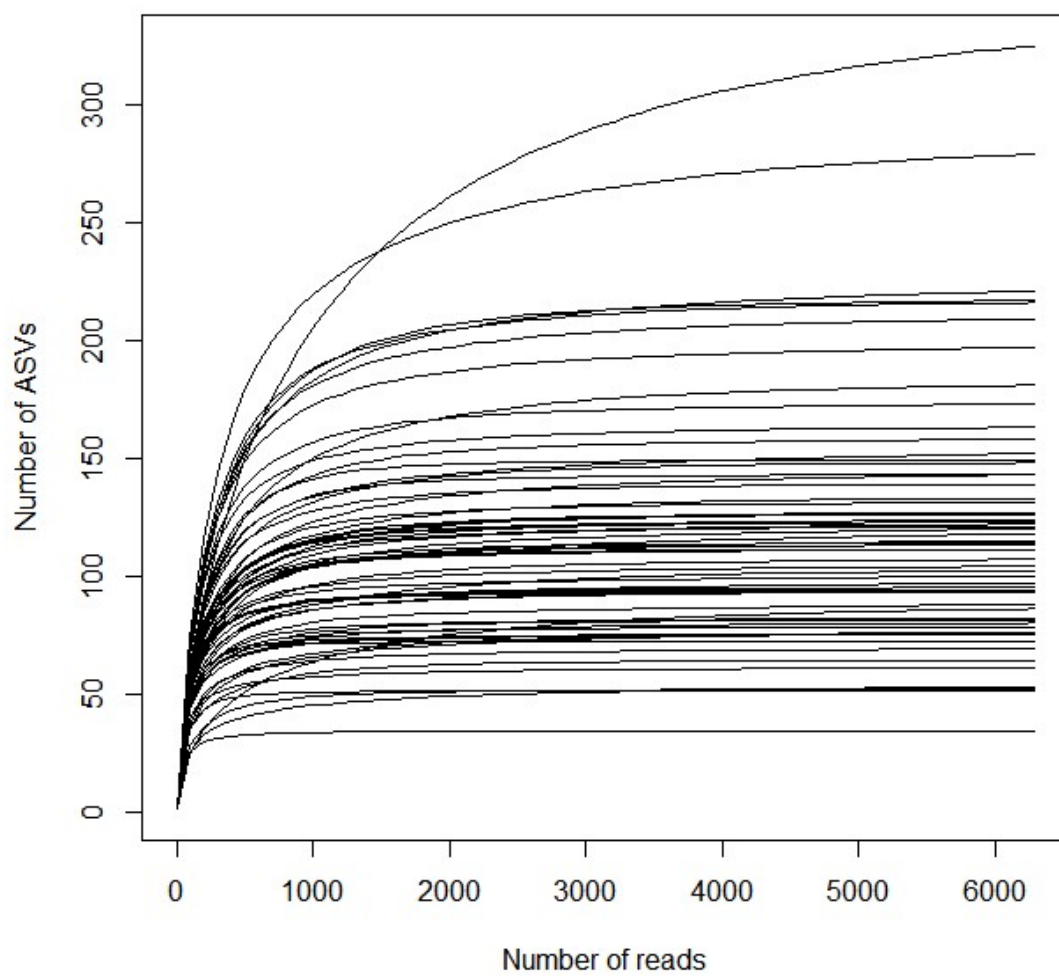
Type of environment	Wetland type	No. of wetlands sampled	No. of samples per wetland	Habitat sampled
Lotic	Stream	4	2 (upstream, downstream)	Rock surface
Lotic	Seepages	5	1	Rock surface
Lotic	Wet rocks	5	1	Rock surface
Lentic	Pond	9	2 (paired)	Water / Rock surface
Lentic	Otero lake	1	4 (two shores: paired samples)	Water / Rock surface
Terrestrial	Soil	10	1	Soil
Terrestrial	Mosses	9	1	Interstitial water
Terrestrial	Snow	5	1	Snow

## Supporting Figures

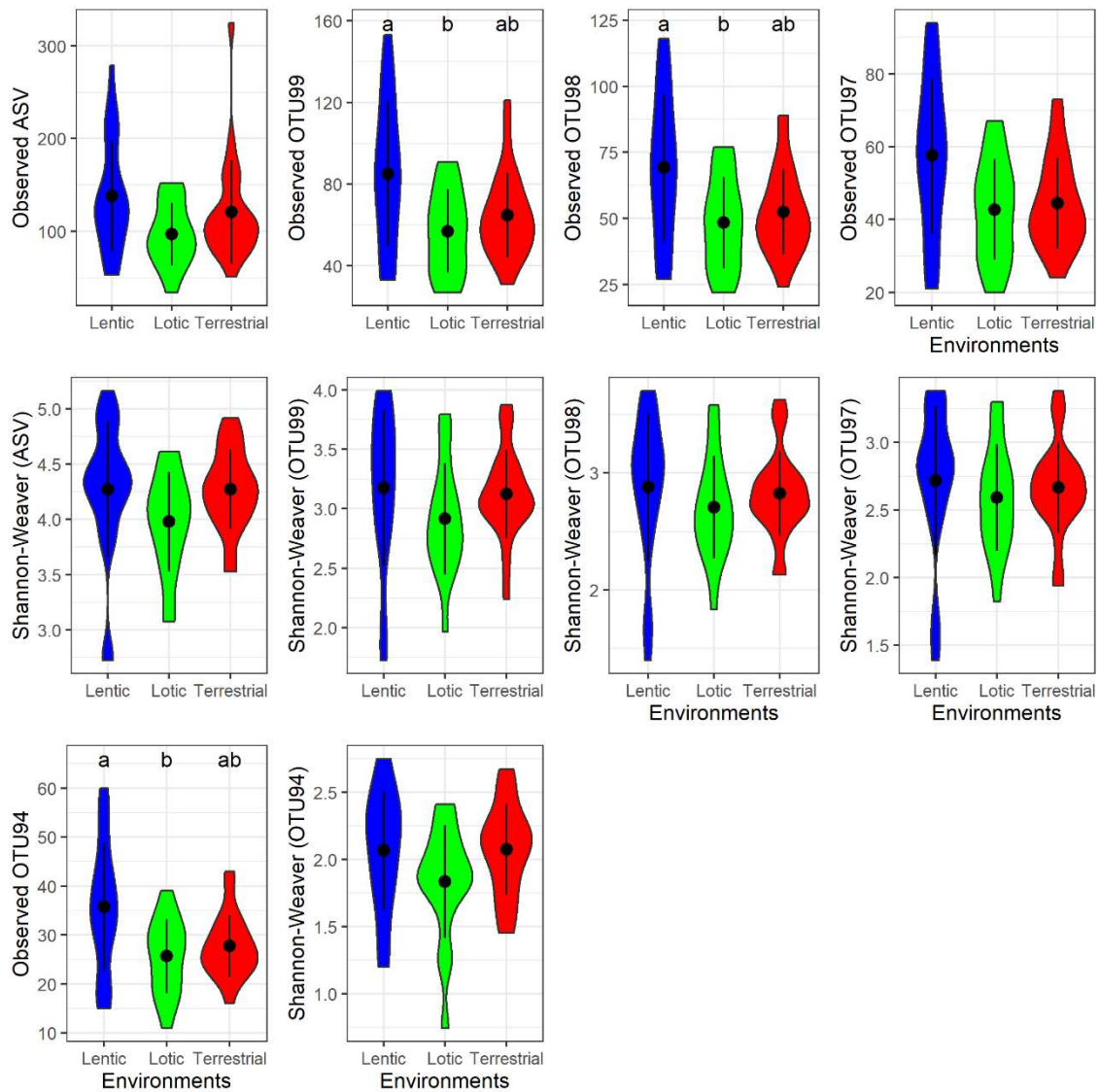
Fig. S1 Location of sampled sites within the Cierva Point Wetland Complex. Modified from Ramos Marín (2018).



**Fig. S2** Rarefaction curves for the 64 samples sequenced.

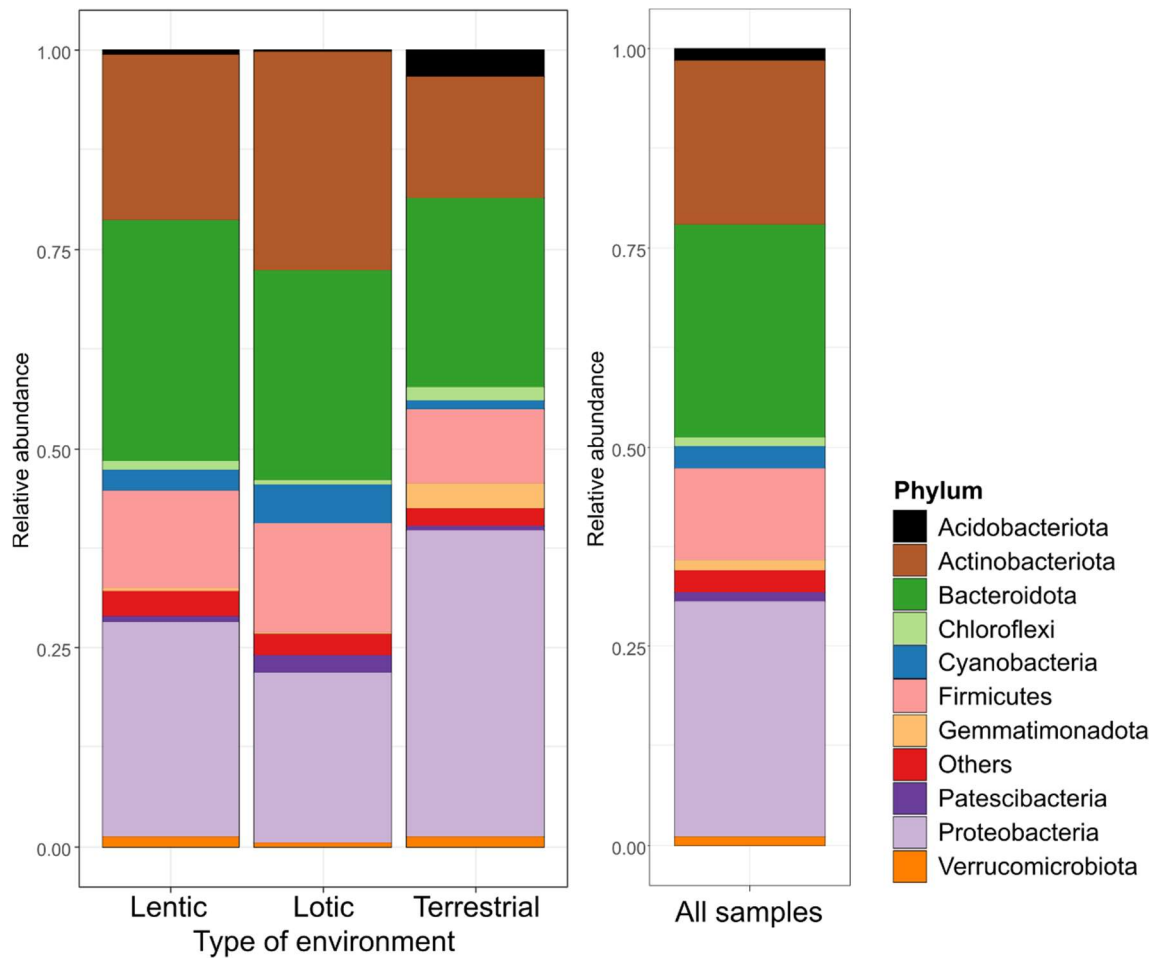


**Fig. S3** Diversity measures for the different environments. Black points indicate the mean value; bars represent  $\pm 1$  standard deviation. Differences between types of environments were evaluated with global Kruskal–Wallis test and Mann–Whitney *post-hoc* pairwise comparisons applying Bonferroni correction. Different letters indicate significant differences in mean between environments ( $P < 0.05$ ).

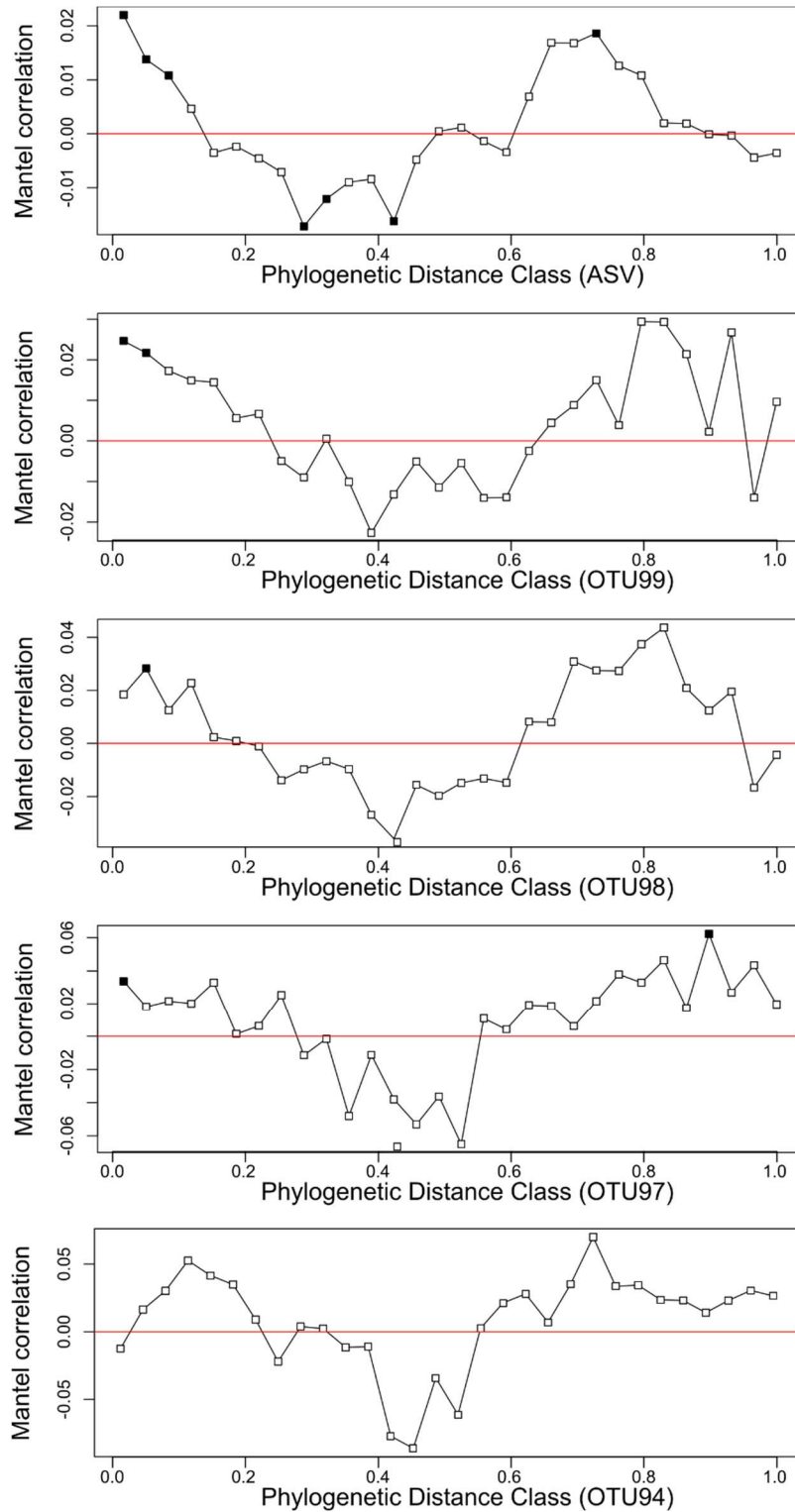




**Fig. S4** Relative abundance of the top 10 most abundant phyla.



**Fig. S5** Phylogenetic Mantel correlograms for each phylogenetic resolution. Solid symbols denote significant correlations at  $P < 0.05$ . Significantly positive correlations across short phylogenetic distances indicate that closely related taxa share environmental optima, but only across the phylogenetic distance class being evaluated. Phylogenetic distance class was normalized to vary between 0 and 1.



**Fig. S6** Violin plots of  $\beta$ MNTD indices across phylogenetic resolutions. Black points indicate the mean value; bars represent  $\pm 1$  standard deviation. Differences between taxonomic resolutions were evaluated with global Kruskal–Wallis test and Mann–Whitney post-hoc pairwise comparisons applying Bonferroni correction. Different letters indicate significant differences in mean between phylogenetic resolutions ( $P < 0.001$ ).

