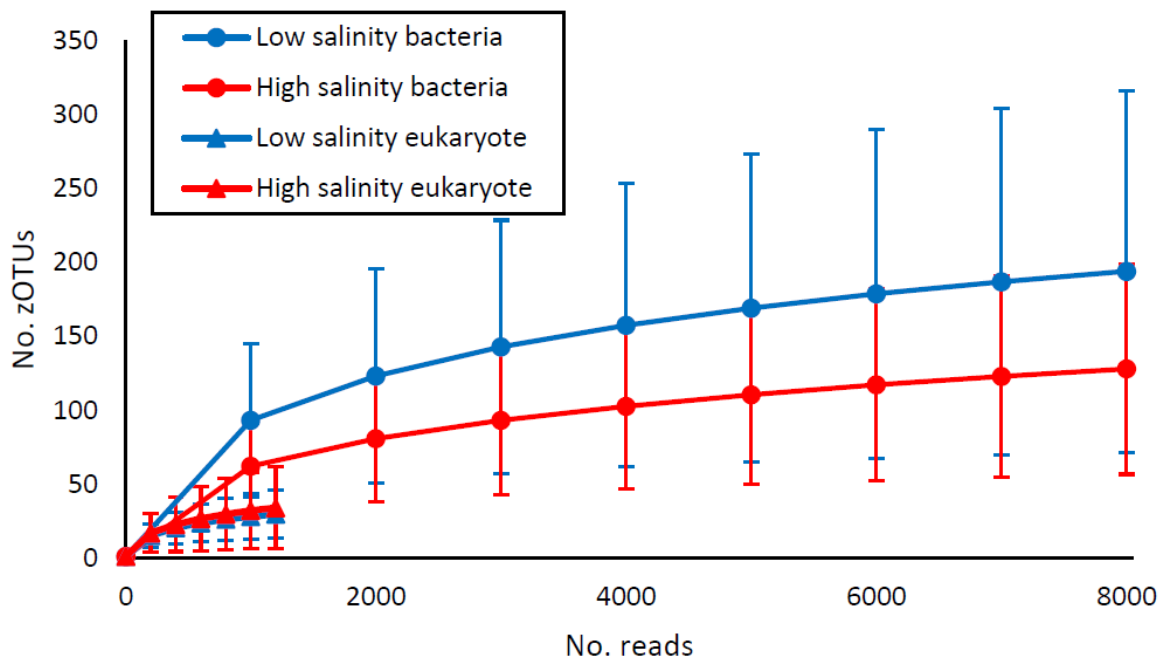


**Supplementary material for ‘Extremophile hypolithic communities in the Vestfold Hills, East Antarctica’**

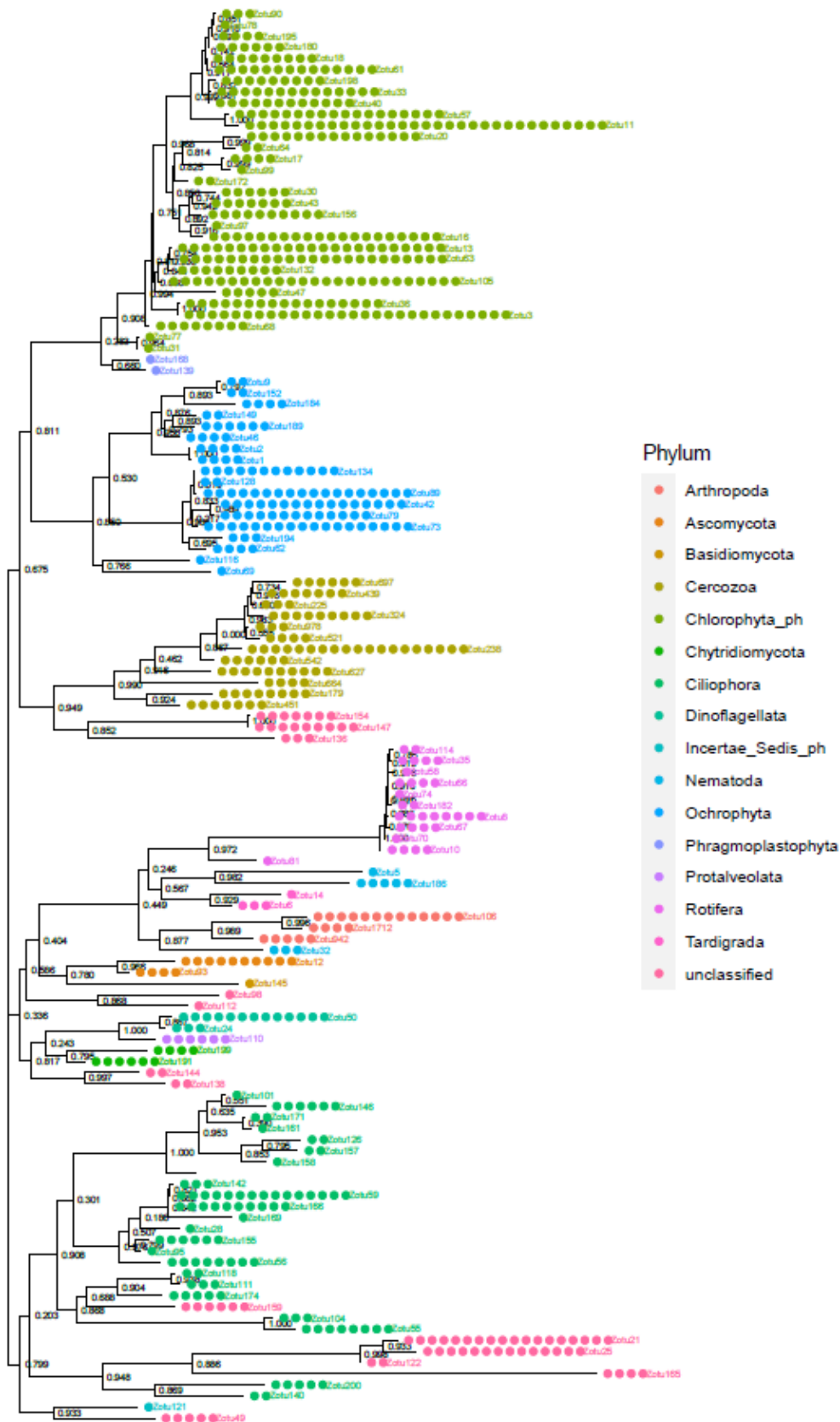
Laurence J. Clarke, Eric J. Raes, Toby Travers, Patti Virtue, Dana M. Bergstrom

**Table S4.** Two-way Permutational Analysis of Variance (PERMANOVA) results for microbial and inferred functional hypolithic composition. No other variable tested (elevation, rock size) explained as great a proportion of community variation as soil salinity or water availability.

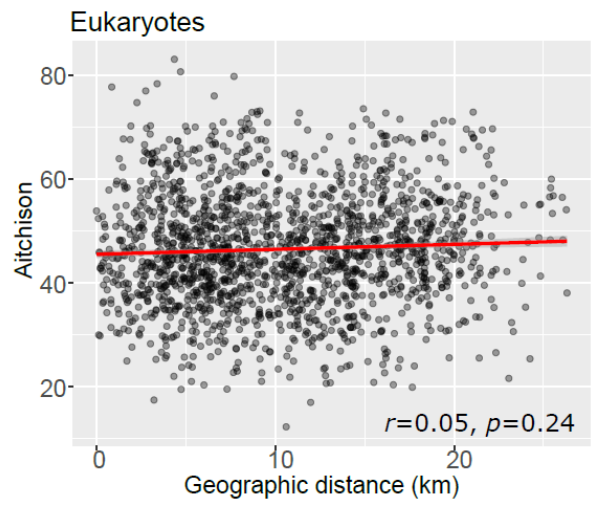
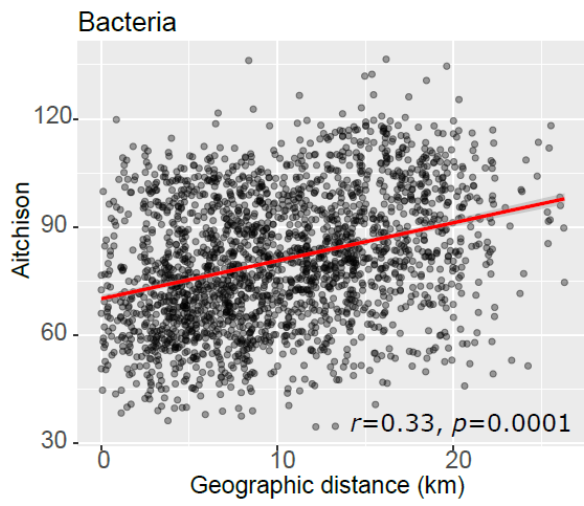
	Eukaryote $R^2$	$p$ -value	Bacterial $R^2$	$p$ -value	Pathways $R^2$	$p$ -value
Water availability	0.080	0.003	0.087	0.001	0.106	0.001
High vs. low salinity	0.050	0.001	0.067	0.001	0.053	0.001
Interaction	0.018	0.30	0.046	0.022	0.03	0.22



**Fig. S1.** Number of zOTUs (bacterial or eukaryote) at different sequencing depths in hypolithic communities from the Vestfold Hills, showing whether the sequencing depth per sample was adequate to assess alpha-diversity. Error bars are standard deviations.



**Fig. S2.** Phylogenetic tree of 150 most abundant eukaryotic zOTUs. The number of dots at each tip is the number of samples each zOTU was detected in. Several unclassified zOTUs (zotu21, 25, 122, 159 and 165) are most closely related to ciliates (Ciliophora, near the bottom of the tree), which can have massive SSU rDNA copy number variation, explaining the high relative abundance of unclassified reads in some samples.



**Supplementary Fig. S3.** Geographic vs. ecological (Aitchison) distance for bacterial or eukaryote hypolithic communities.