Supplementary Material

Figure S1. Moraine pavement sampling location at New Harbour, Lower Taylor Valley, East Antarctica.
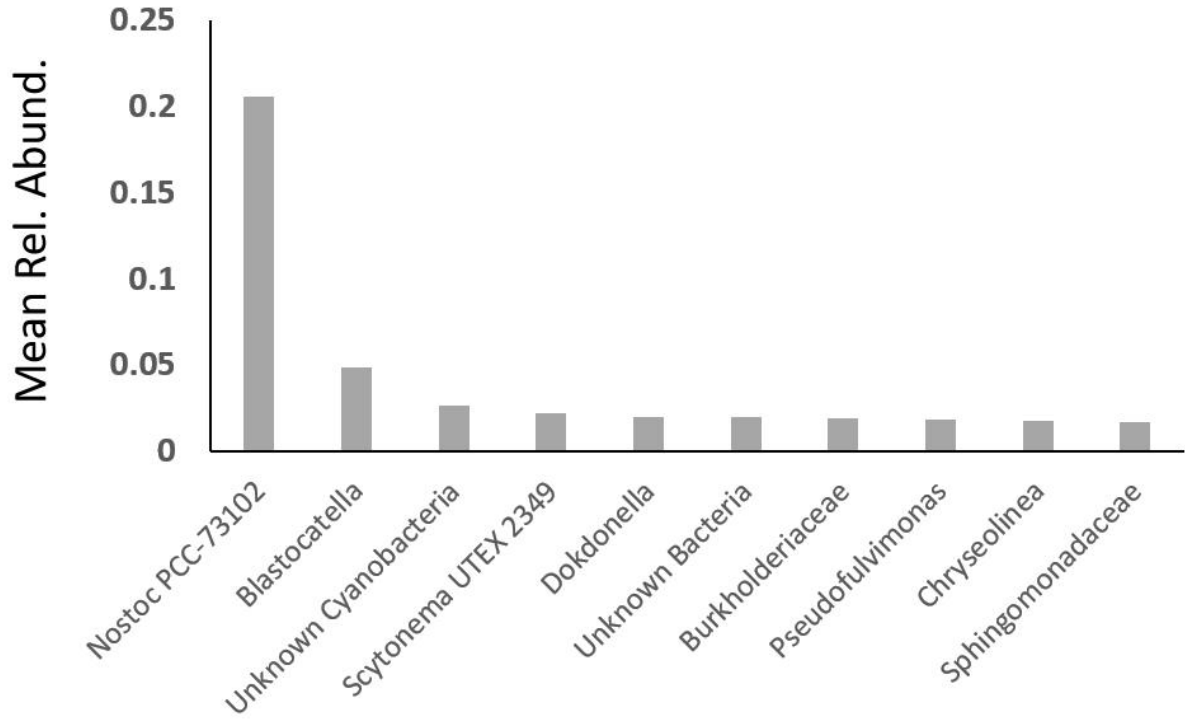
Figure S2. Barplot of mean relative abundance of the 10 most abundant genera the hypolith communities.
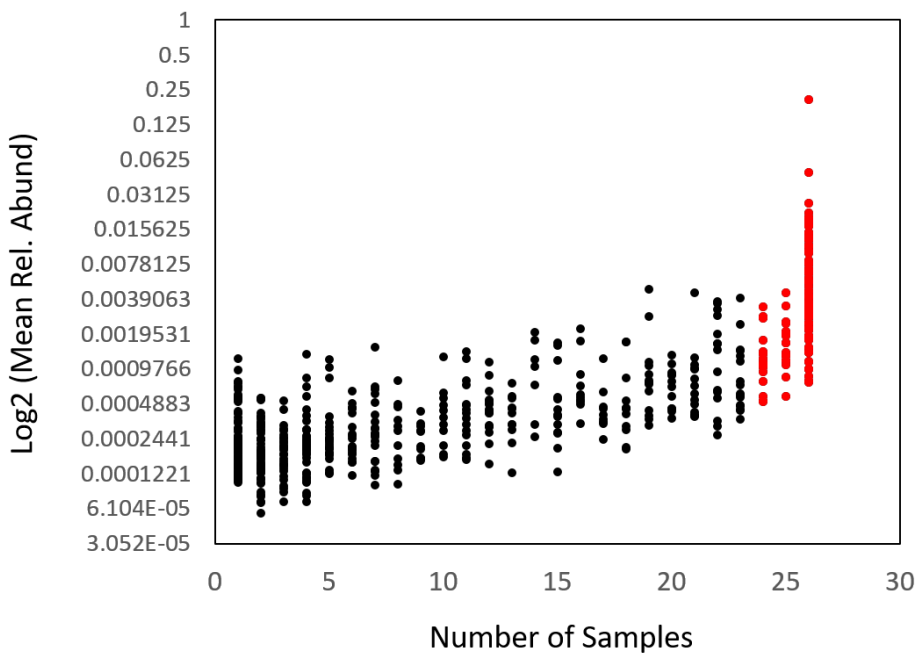

Figure S3. Distribution of genera as a function of number of samples in which they are present. Red dots represent taxa that are present in more than 90% of samples and are therefore considered "generalist" taxa.
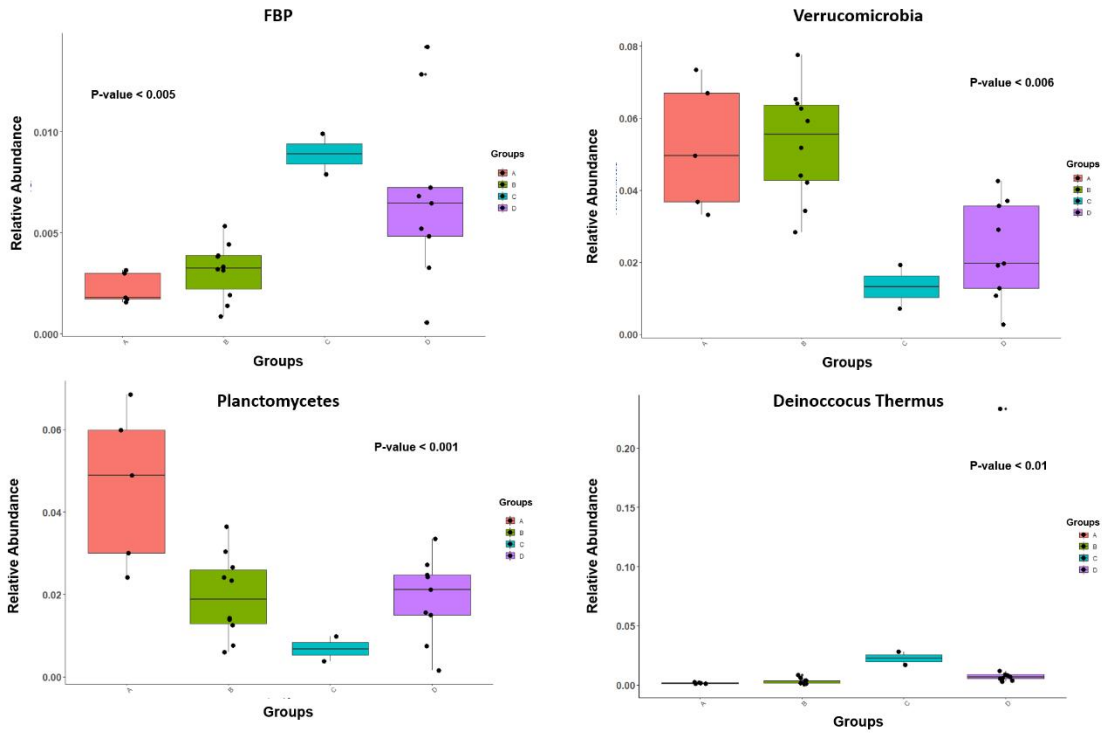
Figure S4. Significant differences in relative abundances of phyla across hypolith communities. Community clusters are colored according to the color-coding used throughout this study: Red- Group A; Green – Group B; Blue – Group C; Purple – Group D.
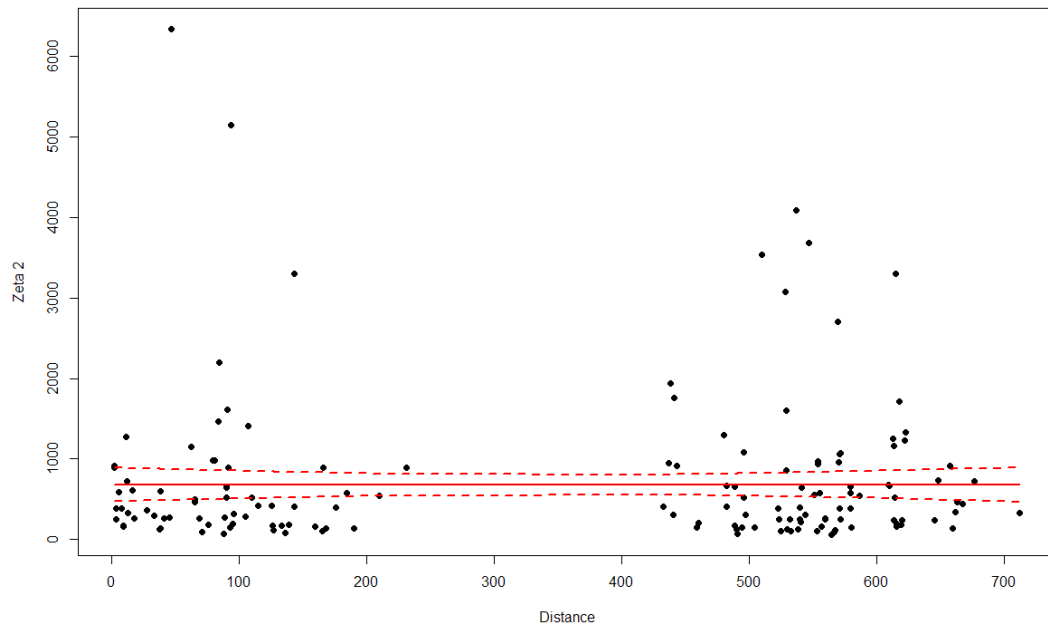

Figure S5. Decay of shared taxa between two or more samples as a function of physical distance (in metres). Points represent pair-wise comparisons between. Number of shared taxa is expressed as the zeta score. The trend line of the regression of points according to distance is represented by the

solid red line, while the 95% confidence interval is represented by the dashed red lines. The trend line shows no significant decay in the number of shared taxa as distance increases between samples.
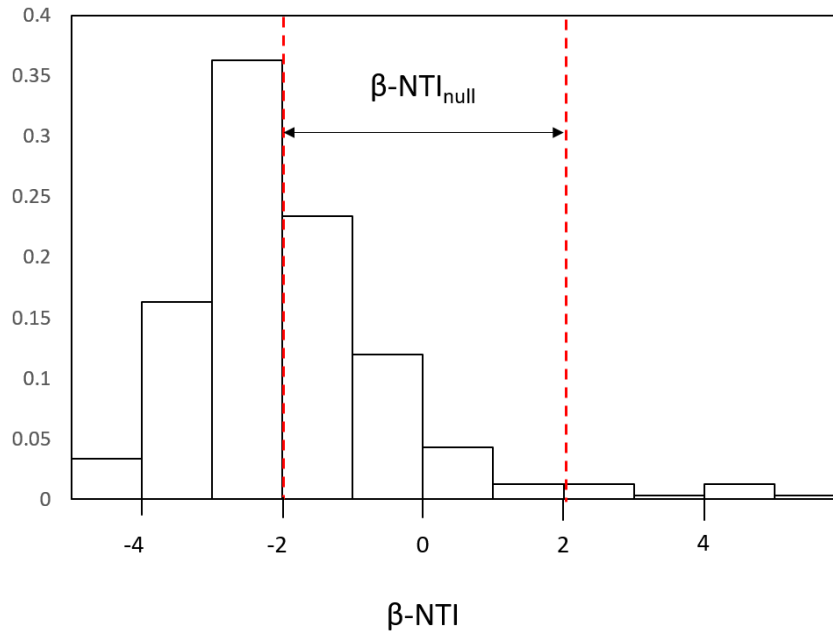

Figure S6. Distribution of β-NTIs across all pair-wise comparisons between hypolith communities, expressed as percentage of total comparisons. Values expected if only stochastic processes drive phylogenetic turnover of communities are represented within the red trace lines (β-NTI$_{null}$).

Tables

Table S1. GPS coordinated of the hypolith samples used in this study.

Table S2. Main topological features of the taxa used to generate the interaction network, together with their functional predictions according to the FAPROTAX database.

Table S3. RC$_{bray}$ values for pairwise comparisons with | β-NTI| <2, together with the significance of the results. The groups to which each sample in the comparison belong to are shown in the 'Groups' column, with letters in bold representing comparisons within the same group.