Supplementary File for

**A dataset of glacier microbiomes for the Three Poles**

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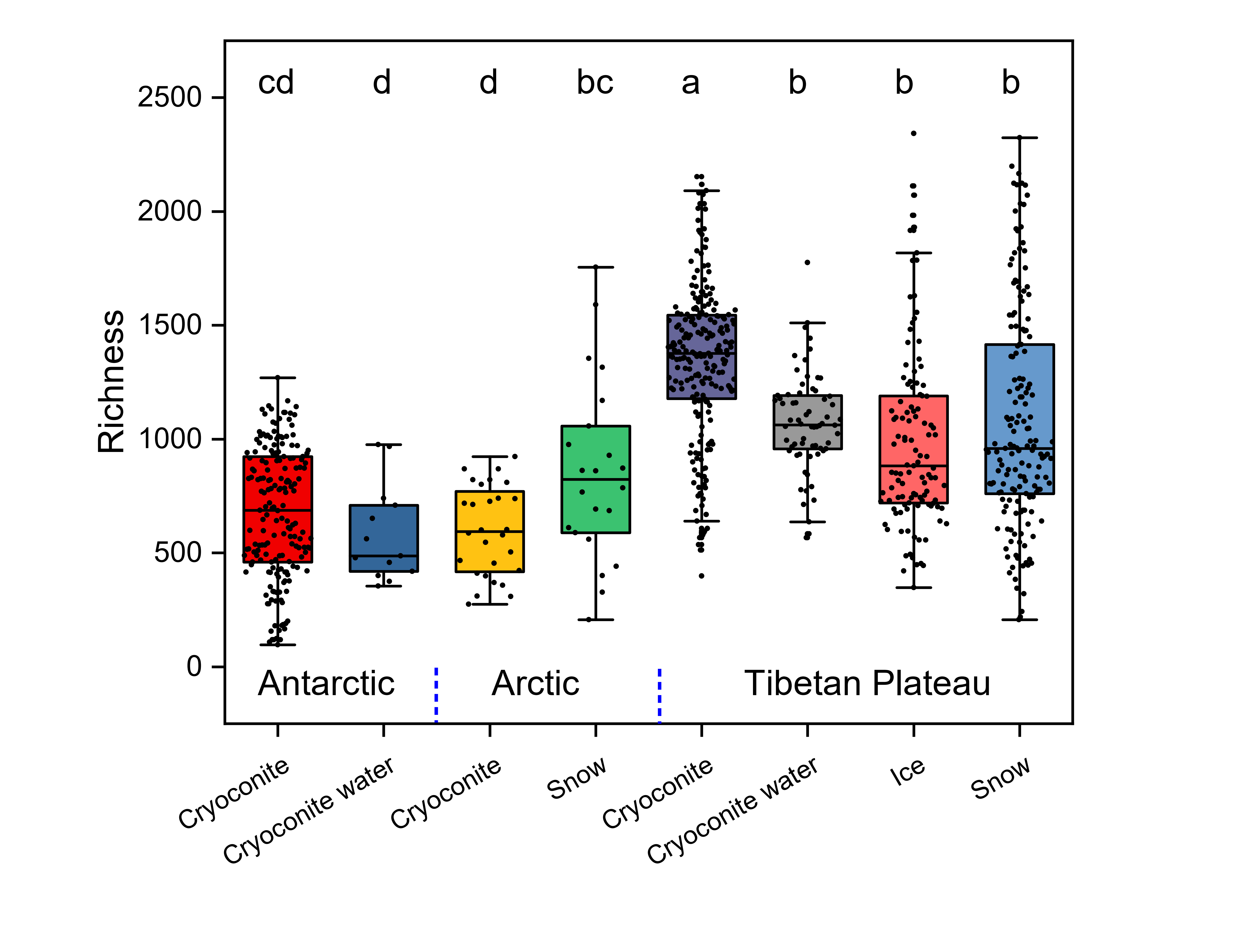


Fig. S1 Comparison of microbial (bacteria and archaea) richness across different habitat-region combinations. Letters indicate significance at *P* < 0.05, significance is based on Dunn’s post-hoc test with Bonfferoni’s correction.

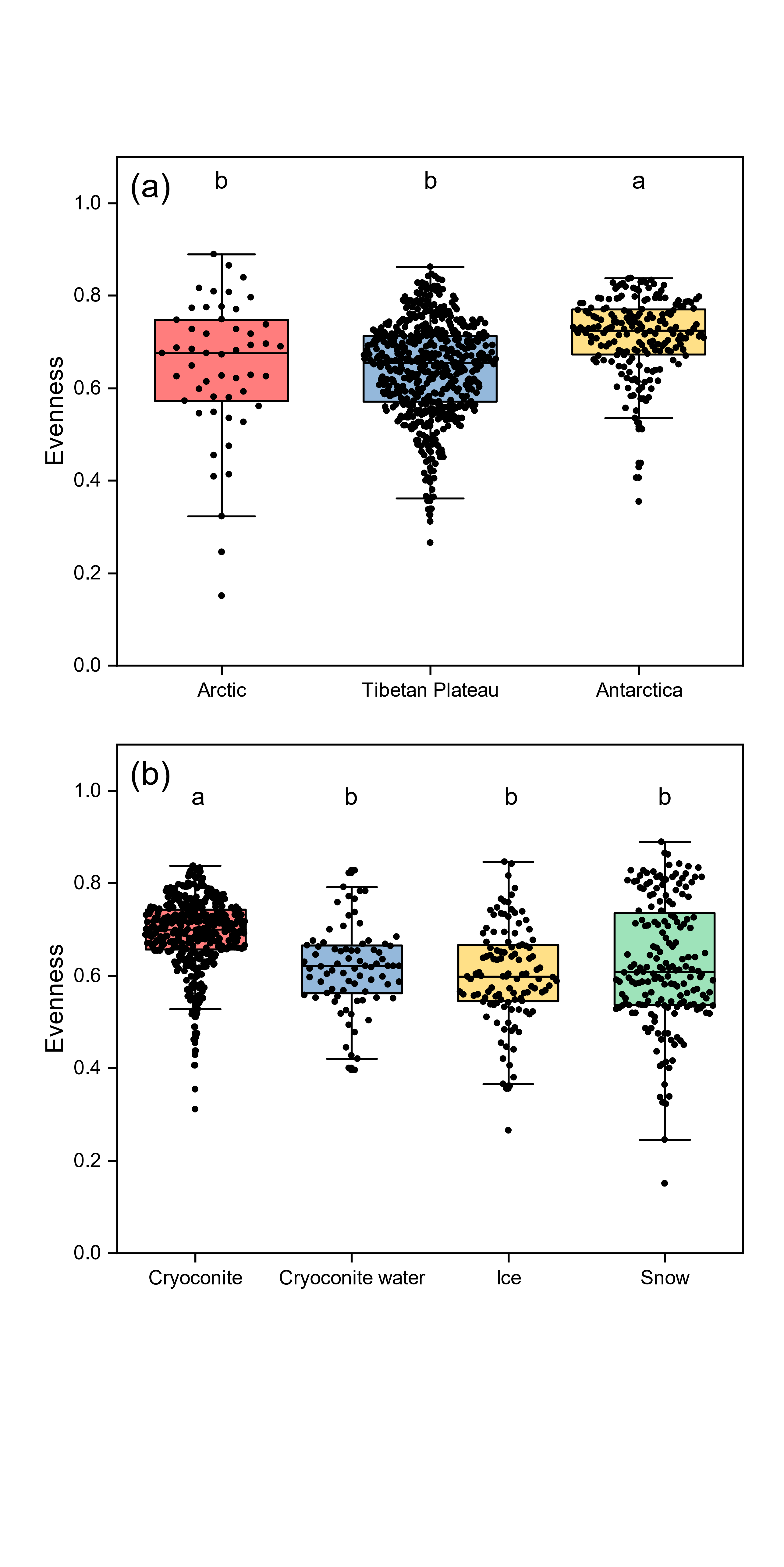


Fig. S2 Microbial (bacteria and archaea) evenness comparison by region (a) and habitats (b). Letters indicate significance at *P* < 0.05, significance is based on Dunn’s post-hoc test with Bonfferoni’s correction.

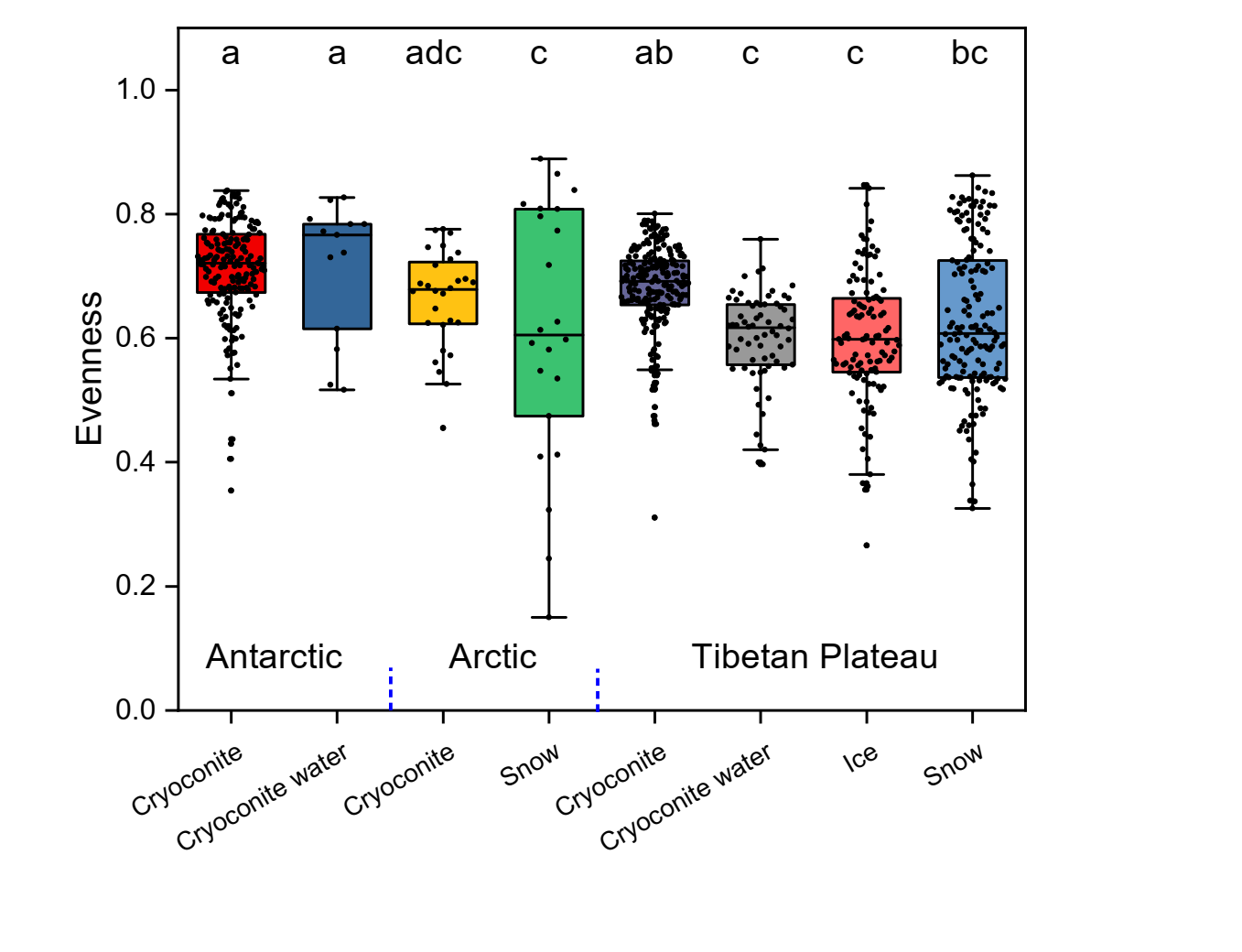


Fig. S3 Microbial evenness (bacteria and archaea) comparison among different habitat-region combinations. Letters indicate significance at *P* < 0.05, significance is based on Dunn’s post-hoc test with Bonfferoni’s correction.

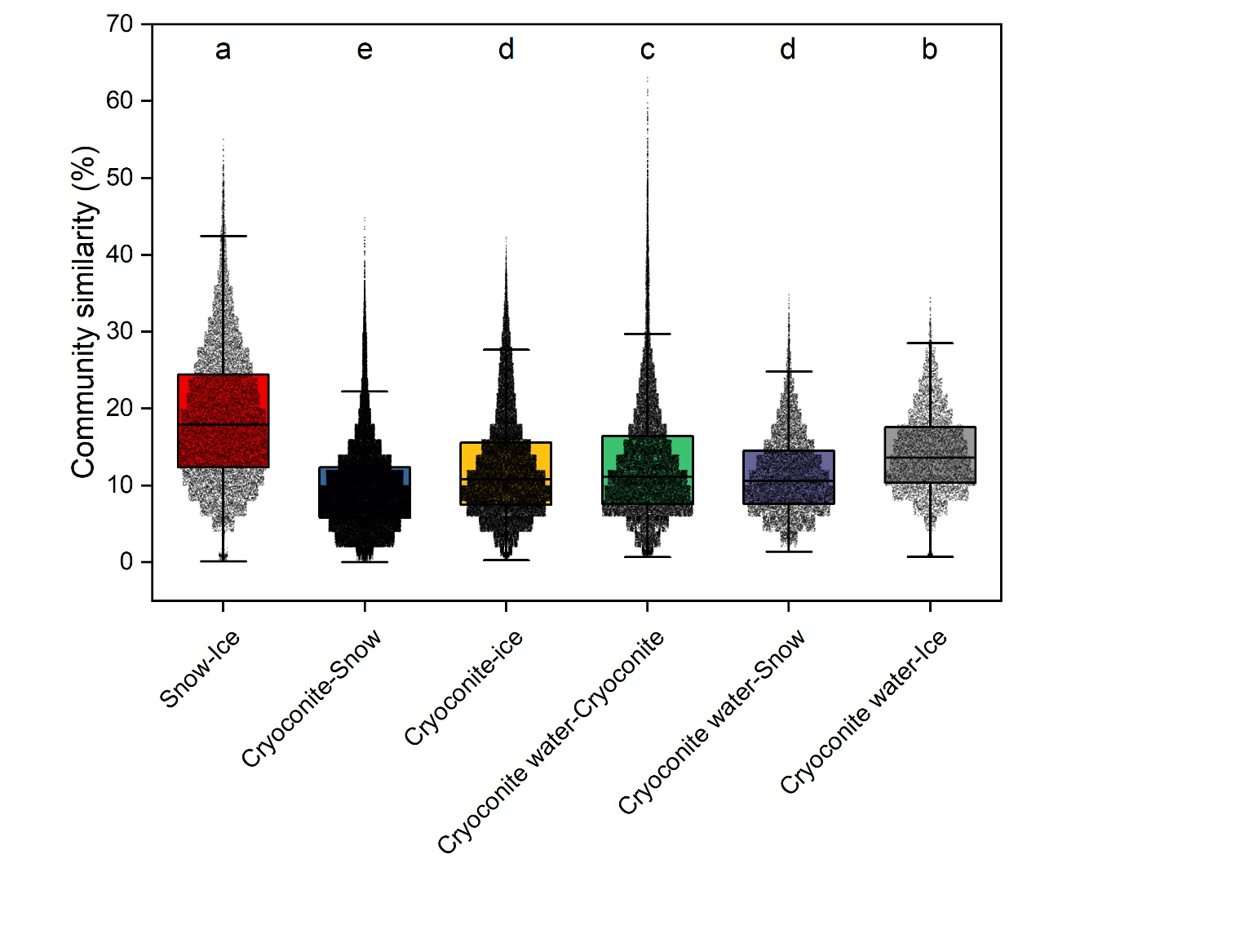


Fig. S4 Within group community similarity comparison among different habitat-region pairs. For box plot, minimum value, lower quartile, median value, mean value, upper quartile, and max value are shown. Significance is based one PERMANOVA pairwise test.

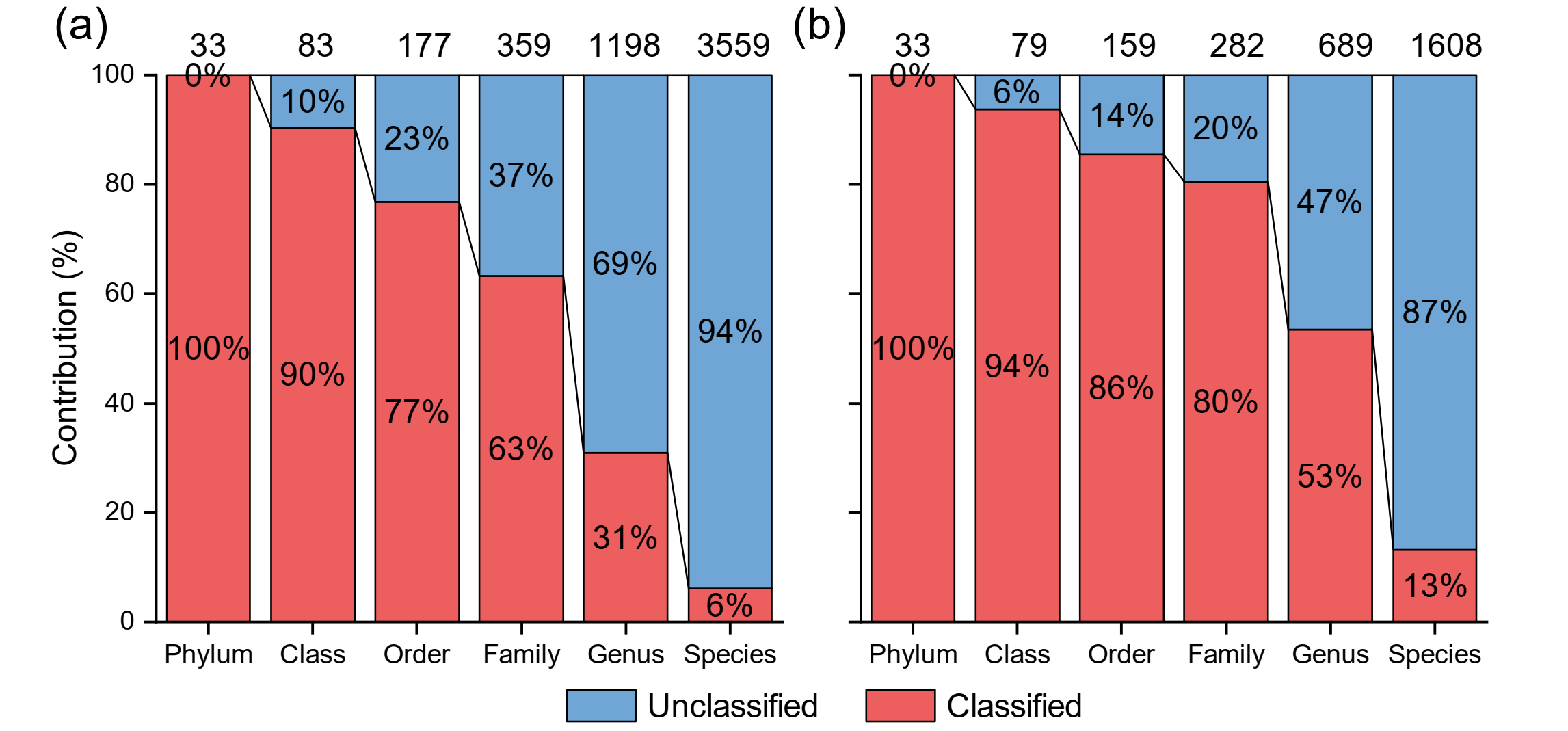


Fig. S5 phylotype numbers and novelty percentage.

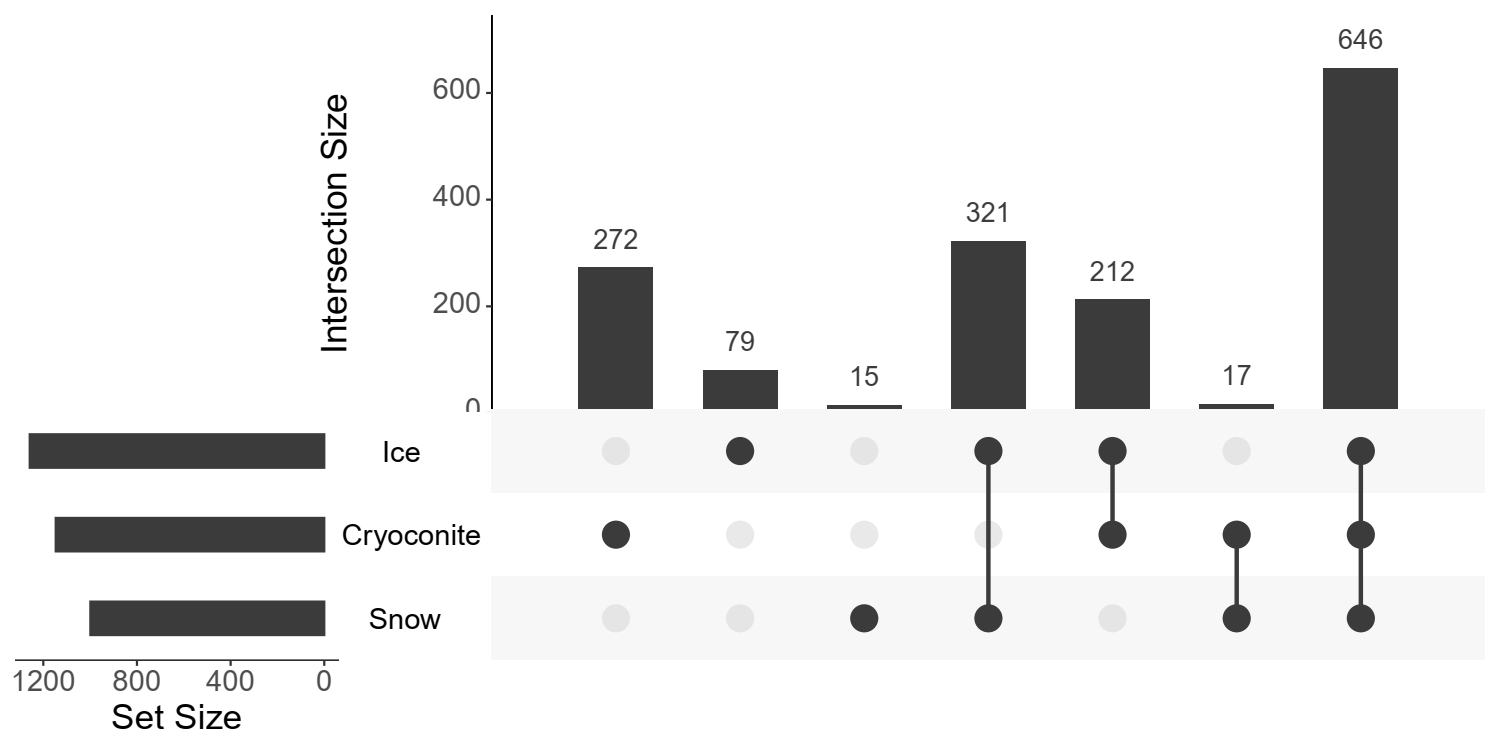
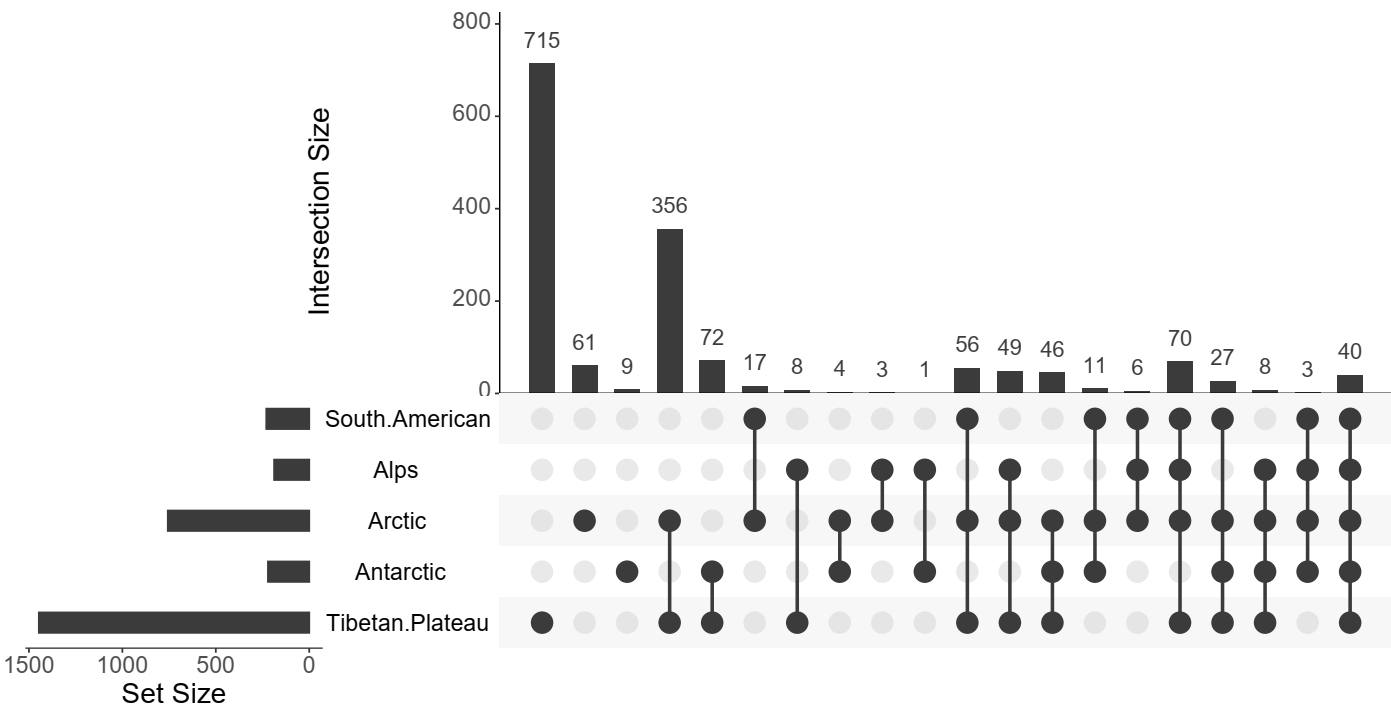


Fig. S6 The upset plot shows the distribution of the dereplicated microbial (bacterial and archaeal) genomes by region (A) and by habitat (B).