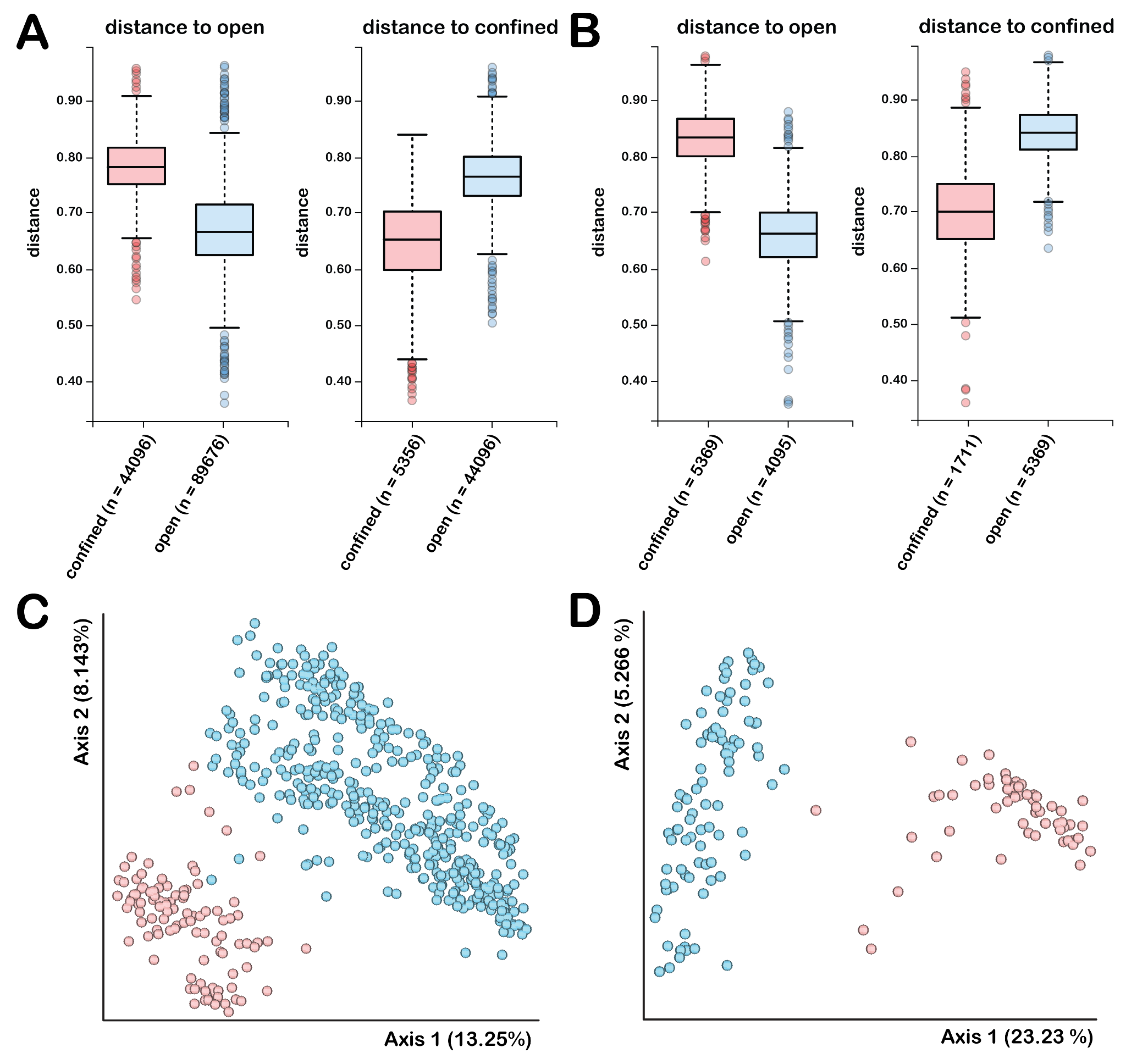
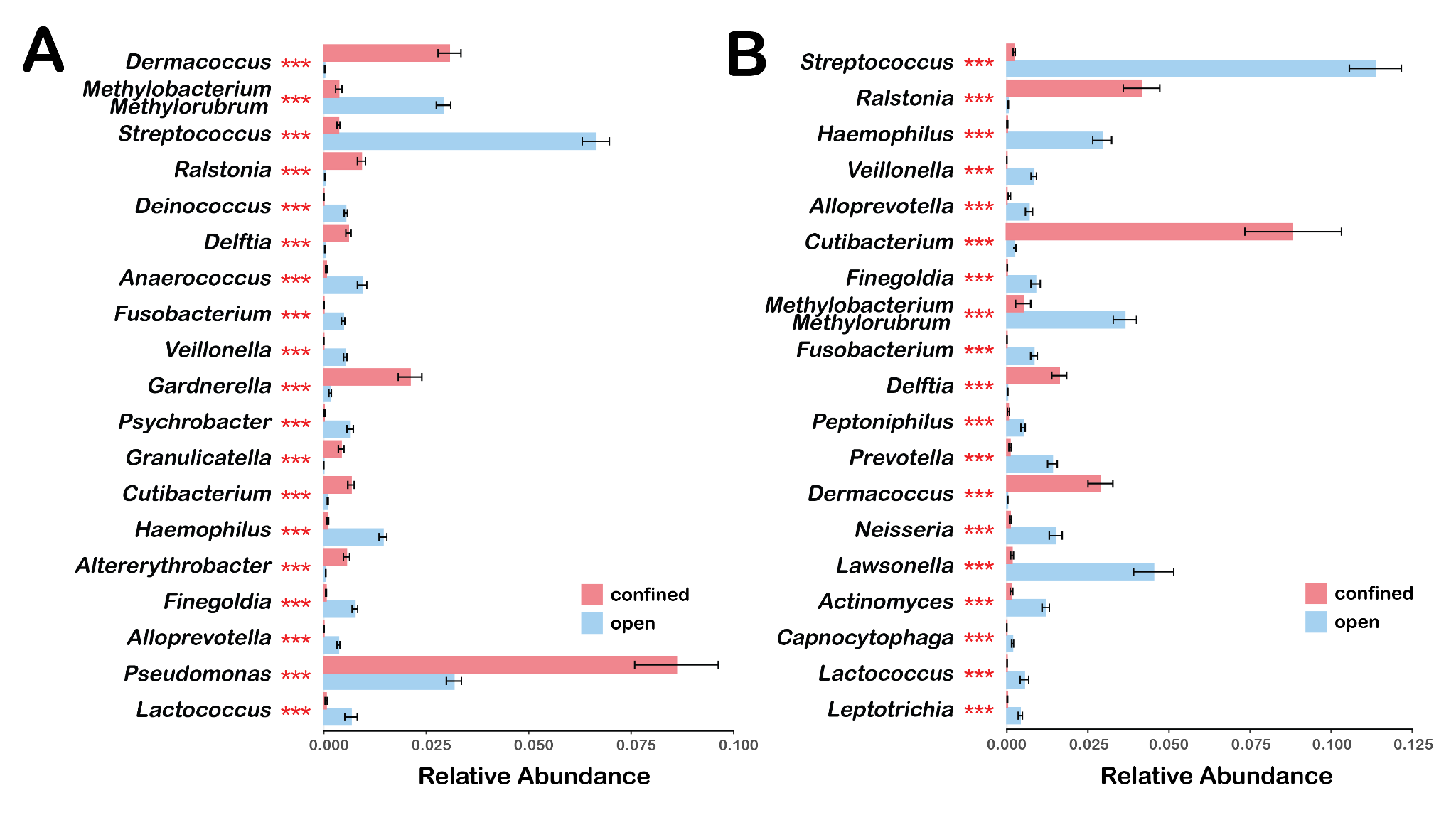
**SUPPLEMENTAL MATERIALS**

** Supplemental Figure 1. Open and confined environments have different microbiome diversity.** Unweighted UniFrac analysis of **(A)** abiotic (p = 0.001, q = 0.001) and **(B)** biotic (p = 0.001, q = 0.001) surfaces in the confined (red) and open (blue) environments were conducted. Box plots and error bars represent mean ± SEM. Statistical analysis was performed via the permutational multivariate analysis of variance (PERMANOVA). Principal coordinates analysis (PCoA) plot of beta diversity (Unweighted Unifrac) distances across the hiseas and dorms datasets for **(C)** abiotic and **(D)** biotic surfaces.

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**Supplemental Figure 2. *Pseudomonas* sp. and *Cutibacterium* sp. are more abundant in confined environments relative to open environments, while *Streptococcus* sp. are more abundant in open environments relative to confined environments.** Relative abundance analysis was conducted using the RandomForest/Microeco pipeline for both **(A)** abiotic and **(B)** biotic surfaces in the confined (red) and open (blue) environment. Statistical analysis via the Wald Chi-Squared Test. \*\*\* p < 0.005.