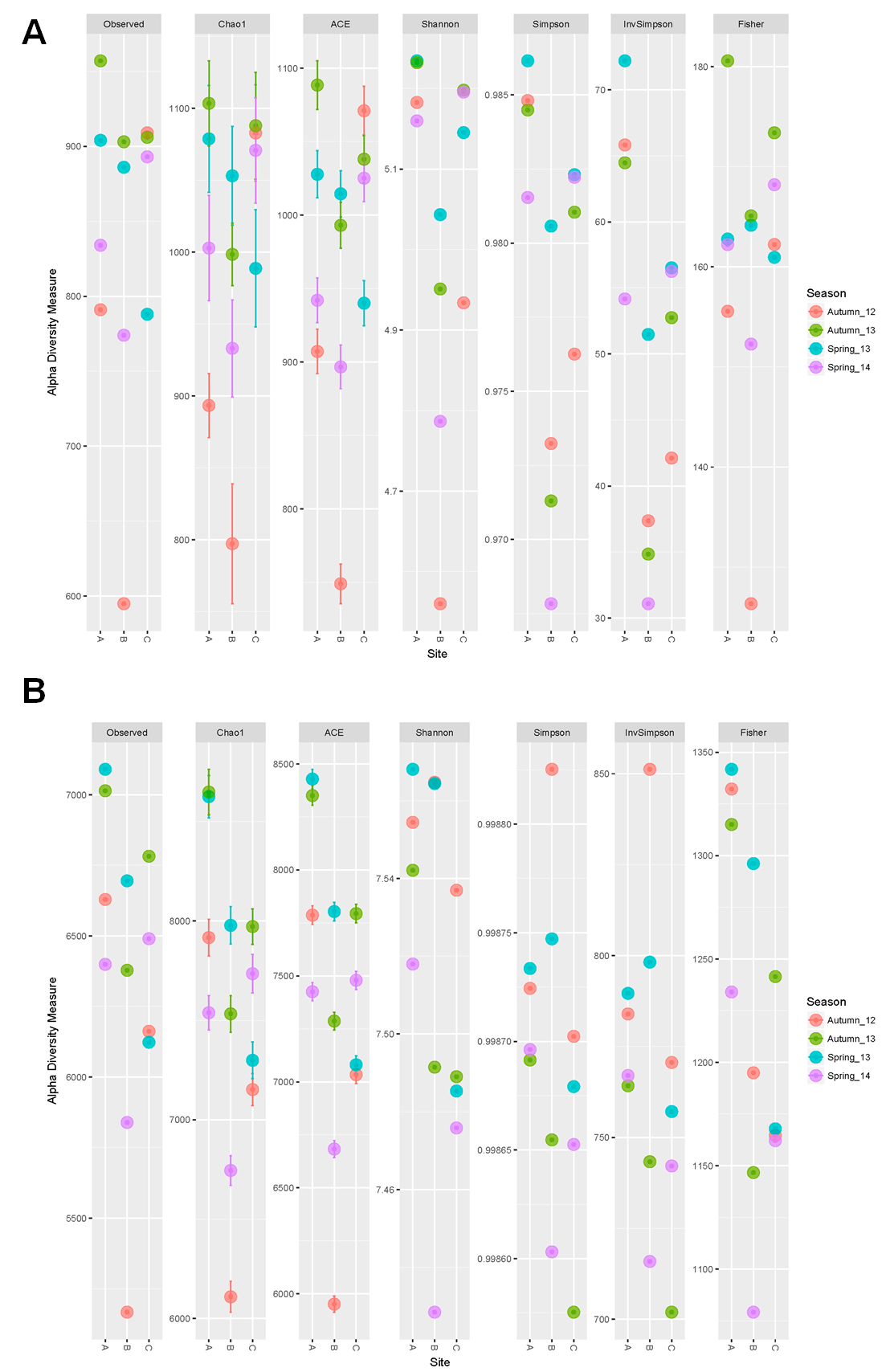
***Supplementary Material***

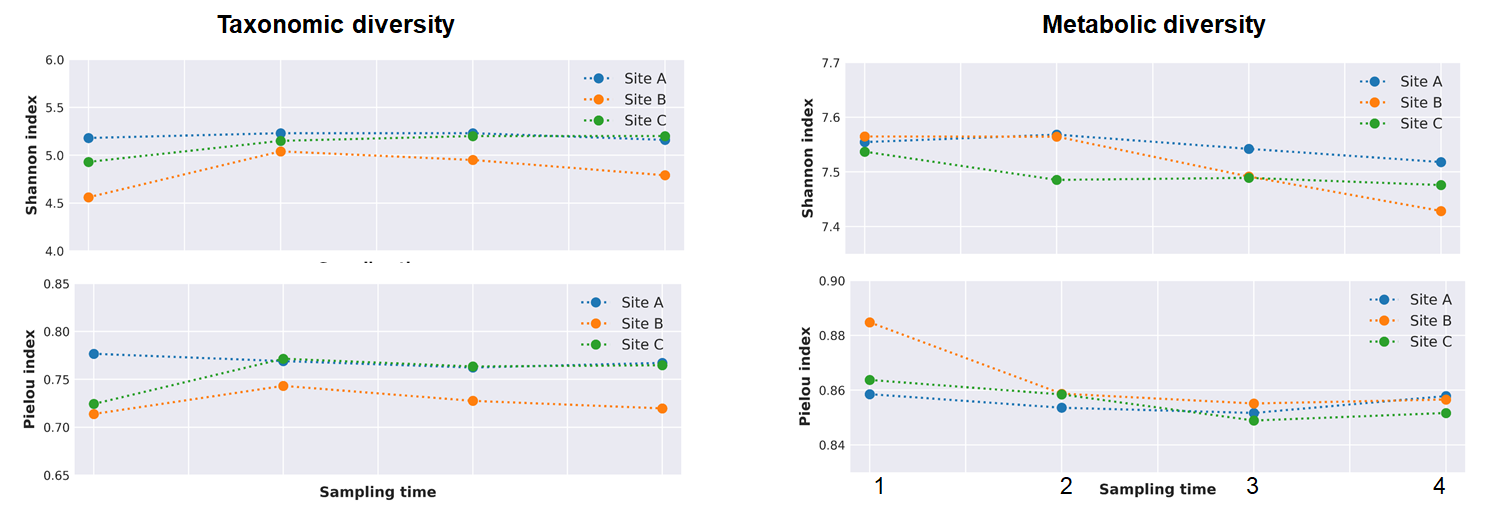
**Understanding the mechanisms behind the response of environmental perturbation in microbial mats: a metagenomic-network approach**

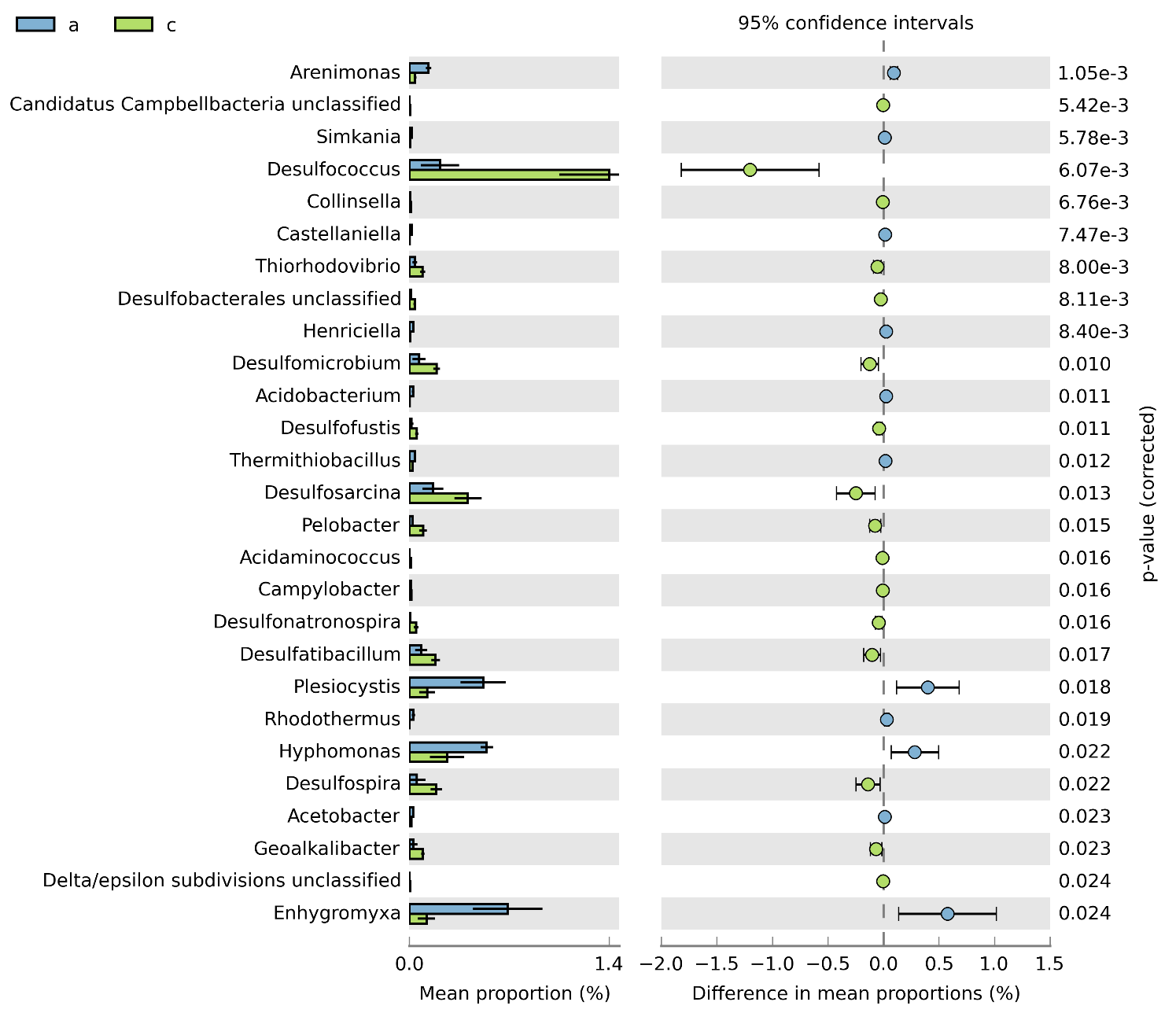
***Valerie De Anda1, Icoquih Zapata-Peñasco 2, Jazmín Blaz3, Augusto Cesar Poot-Hernández4, Bruno Contreras Moreira5,6,Marcos González Laffitte7, Niza Gámez Tamariz1, Maribel Hernández Rosales7, Luis E. Eguiarte1 and Valeria Souza\****

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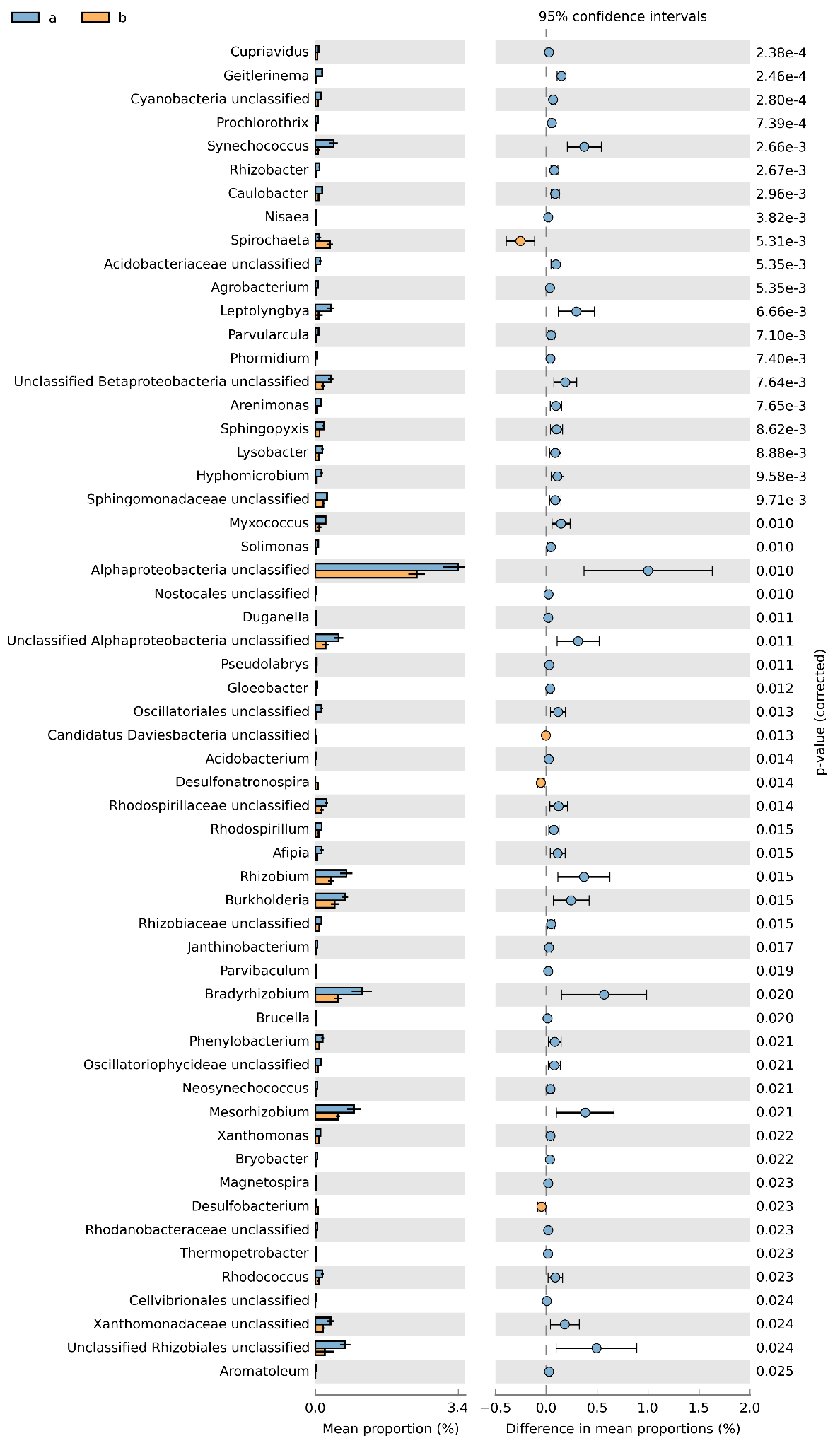
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**Supplementary Figure 1**. Several estimators of Alpha-richness in the microbial mats samples at taxonomic (panel A), and metabolic level (panel B).

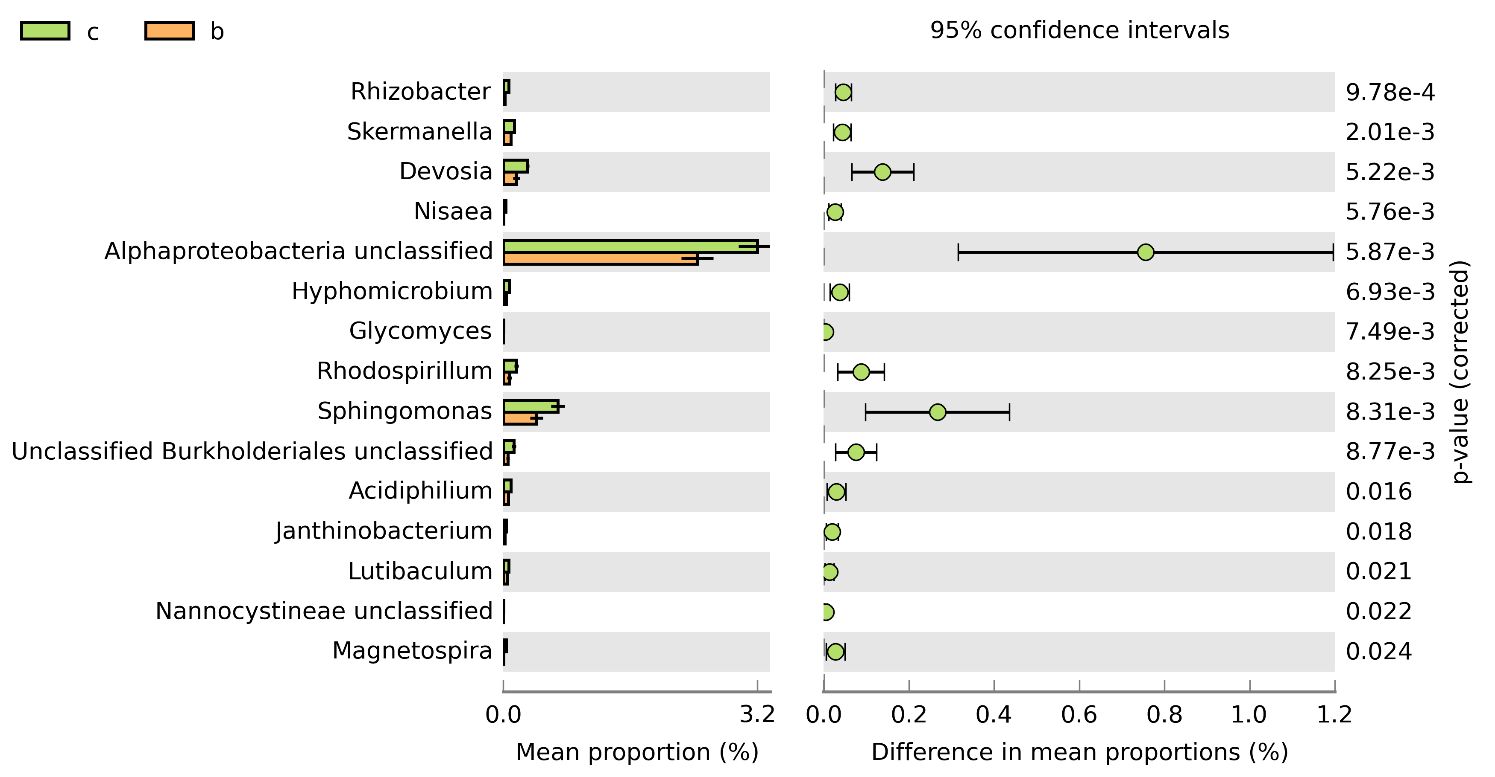
**Supplementary Figure 2.** Variation through time of Shannon and Pielou diversity across sites at taxonomic (A) and metabolic (B), level.

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**Supplementary Figure 3.**  Extender error bar indicating all genera where Welch’s t-test with confidence interval method DP welch’ inverted of 0.95 produces a p-value (>0.025). The difference in mean proportion between the microbial mats from site A and C are shown in blue and green colors respectively.

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**Supplementary figure 4.**  Extender error bar indicating all genera where Welch’s t-test with confidence interval method DP welch’ inverted of 0.95 produces a p-value (>0.025). The difference in mean proportion between the microbial mats from site A and B are shown in blue and orange colors respectively.

****

**Supplementary figure 5.**  Extender error bar indicating all genera where Welch’s t-test with confidence interval method DP welch’ inverted of 0.95 produces a p-value (>0.025). The difference in mean proportion between the microbial mats from site B and C are shown in orange and green colors respectively.