**Methods**

*Sequence data processing*

*Statistical analyses of sequence data*

**Results**

*Summary of sequence data pre-processing*

Following pre-processing, X% of total raw reads were retained, for a mean sample read depth of 8,020. Dada2 ASV assignments produced 1,337 ASVs. Within sample proportional abundances were calculated as sum of reads assigned to each taxa divided by the total reads for that sample. Upon rarefaction to 1,100 reads, the dataset consisted of 851 ASVs. Rarefaction at 1,100 reads sufficiently captured richness as demonstrated in by plots of rarefaction curves (figure S1). For subsequent analyses, we report independent 69 samples in the rarefied dataset and 72 for the within sample proportional abundances dataset.

*Alpha (α) diversity*

ANOVA showed sampling location to be a significant predictor of species richness, Shannon diversity (H`), and Chao1 (p < 0.05, F < 2.702) (Figure S2). The interaction of sampling timepoint x sampling location was a significant of species richness and Chao1 (p < 0.05, F < 2.871), while sampling location x treatment was significant for Shannon diversity (H`) (p < 0.05, F < 2.718). No clear trends in directionality were observed for alpha diversity metrics across sampling locations, treatments, or sampling timepoints.

*Beta (β) diversity*

We show sampling location to be the dominate predictor of β-diversity for both weighted and unweighted unifrac distances (p < 0.001, R2 = 0.31, F5,36 = 8.149, p < 0.001, R2 = 0.15, F5,36 = 2.768, respectively). When controlling for variability within sampling locations (e.g., strata = sampling location), we show sampling timepoint (e.g., before and after treatment) to be a significant predictor of community composition (p < 0.05, R2 = 0.03, F1,36 = 4.256, p < 0.001, R2 = 0.03, F1,36 = 2.959, respectively).

Figures:

Figure 1. Descriptive map of sampling locations

Figure 2. 4 panel, 3 ordinations and a plot of beta disper

Figure 3. Prevalence and abundance histogram

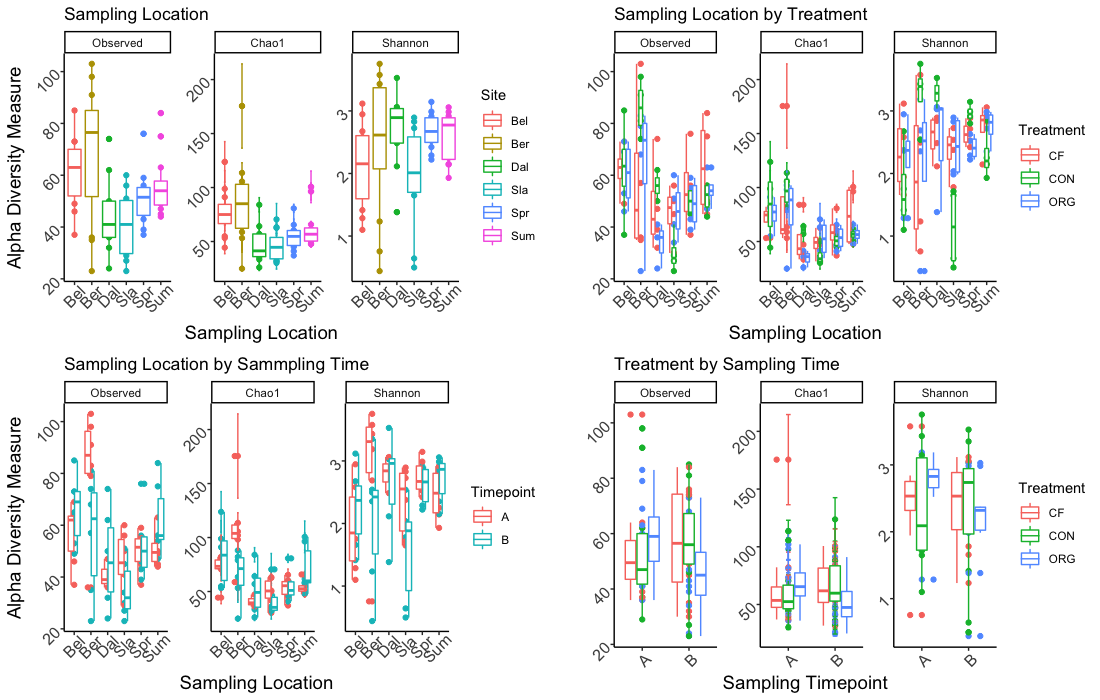
Supplementary Figures:

SFigure1. Rarefaction curves depicting leveling off at approximately 1,000 reads.

A picture containing diagram

Description automatically generated

SFigure2. Boxplots of alpha diversity metrics.

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