

Figure S1. Isolates compositional differences and diversity across culture media. Sampling effort across culture media and in the site of study. A. PCoA showing compositional differences (β -diversity) across culture media computed from the normalized iOTU table. **B.** Boxplots showing α -diversity indices: Chao1 richness estimator, Shannon index, Pielou evenness and FPD. Significance values: . = $p < 0.1$, * = $p < 0.05$, ** = $p < 0.01$. **C.** Rarefaction curves computed using the non-normalized iOTU table subdivided by culture medium. **D.** General rarefaction curve of all isolates computed using the non-normalized iOTU table.

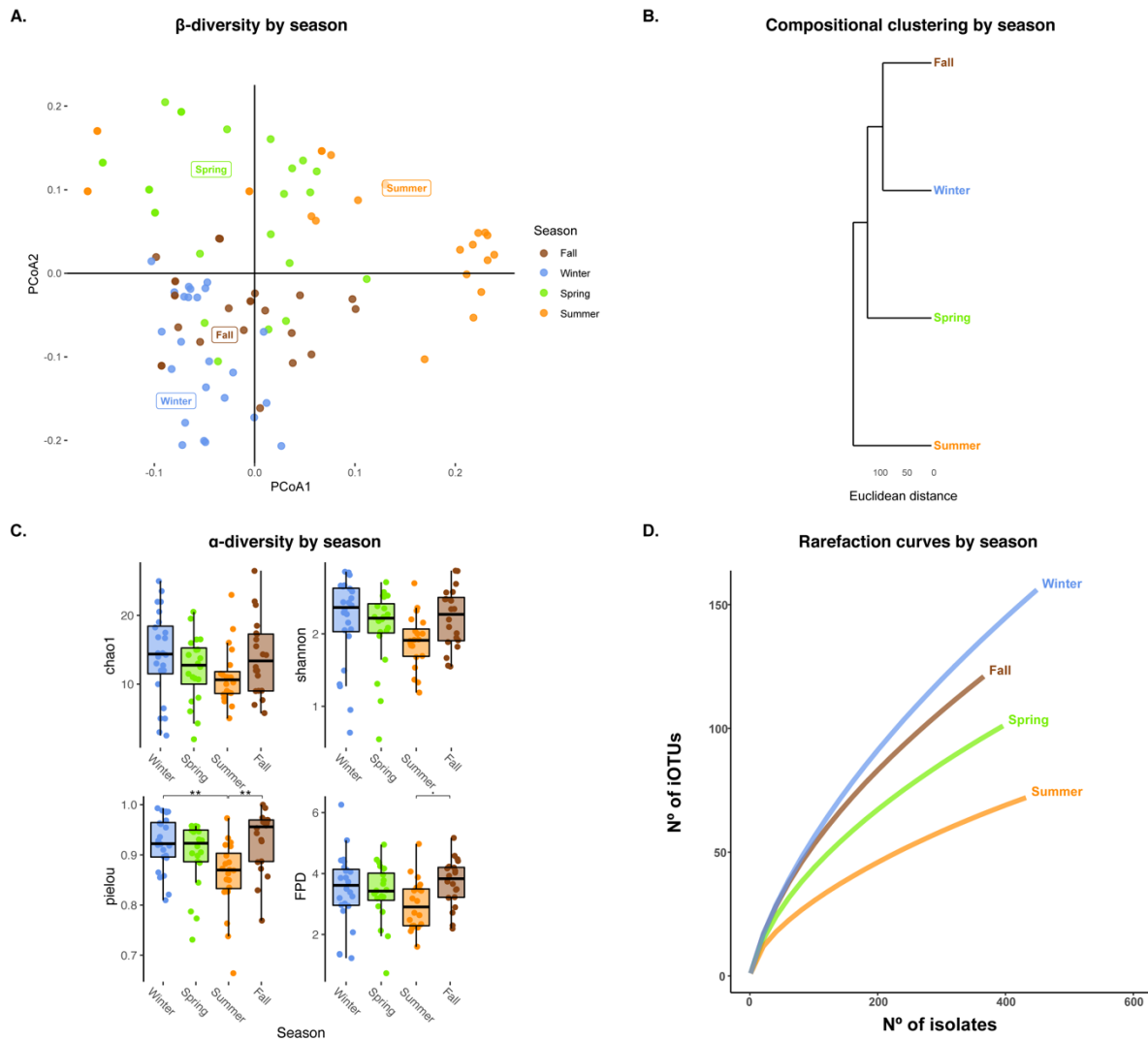


Figure S2. Isolates compositional differences, diversity and sampling effort across seasons. A. PCoA showing compositional differences (β -diversity) across seasons computed from the normalized iOTU table. Centroids were scaled by 0.2. **B.** Dendrogram showing the compositional similarity (euclidean distances) between seasons calculated from the iOTU table. **C.** Boxplots showing α -diversity indices: Chao1 richness estimator, Shannon index, Pielou evenness and FPD. Significance values: . = $p < 0.1$, * = $p < 0.05$, ** = $p < 0.01$. **D.** Rarefaction curves computed using the non-normalized iOTU table subdivided by season.

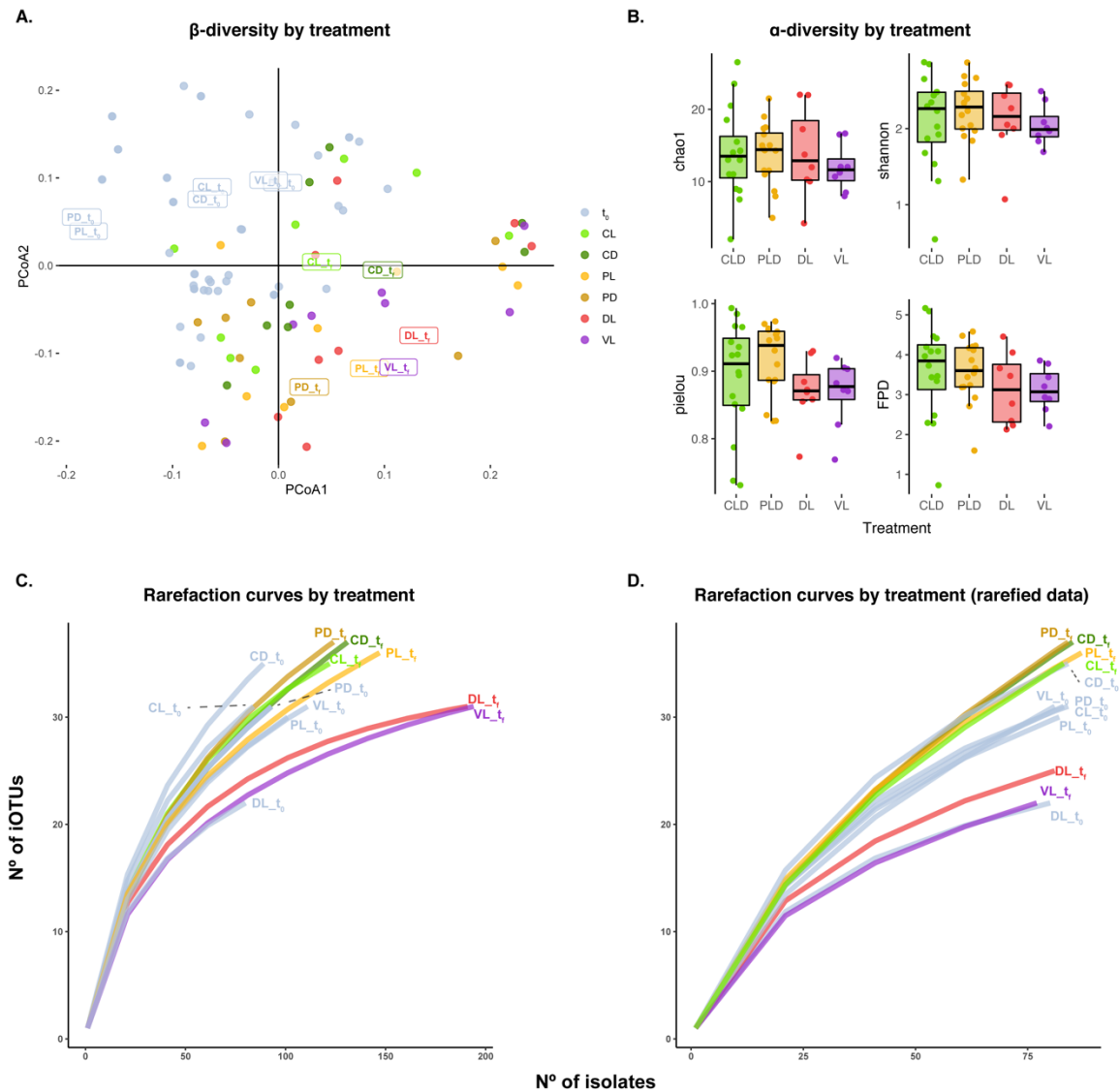


Figure S3. Isolates compositional differences, diversity and sampling effort across treatments. **A.** PCoA showing compositional differences (β -diversity) across treatments computed from the normalized iOTU table. Centroids were scaled by 0.2. In the legend: Category t_0 takes into account all treatments at initial time; CL, CD, PL, PD, DL and VL correspond to t_f of each treatment. **B.** Boxplots showing α -diversity indices in the final times of the light treatments: Chao1 richness estimator, Shannon index, Pielou evenness and FPD. Significance values: . = $p < 0.1$, * = $p < 0.05$, ** = $p < 0.01$. **C.** Rarefaction curves computed using the non-normalized iOTU table subdivided by treatment. **D.** Rarefaction curves calculated from rarefied iOTU table down to the lowest sampling effort by treatment and time (80, DL t_0)

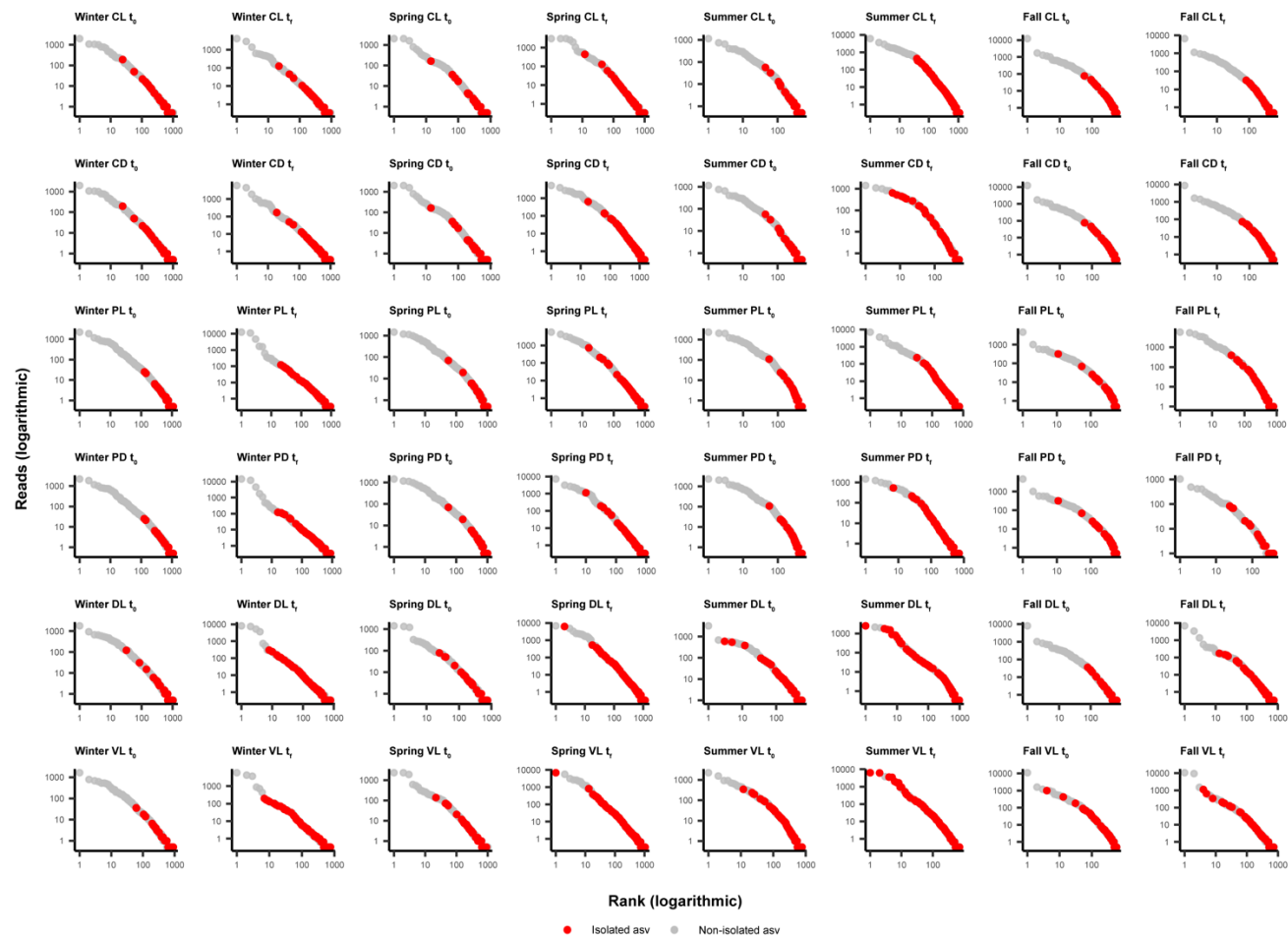


Fig. S4. Rank-abundance plots of ASVs indicating which ones had the same V4-V5 16S rRNA gene than our isolates for all samples. These ASVs are labelled as "isolated" (red) and "non-isolated" (grey) according to that criteria.