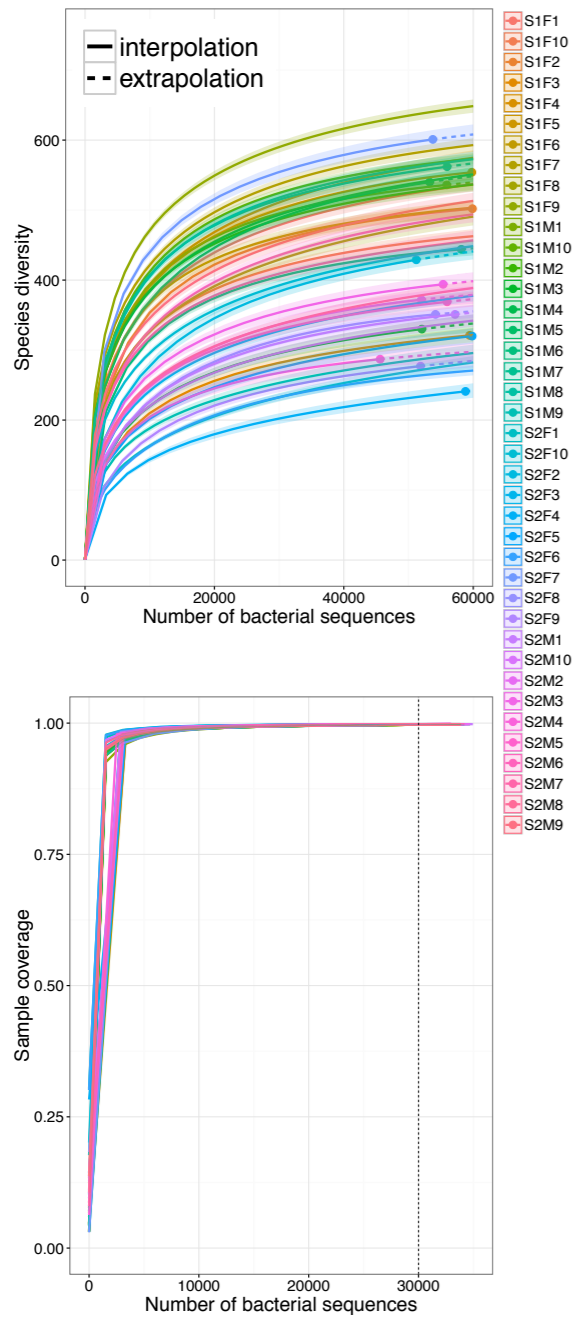
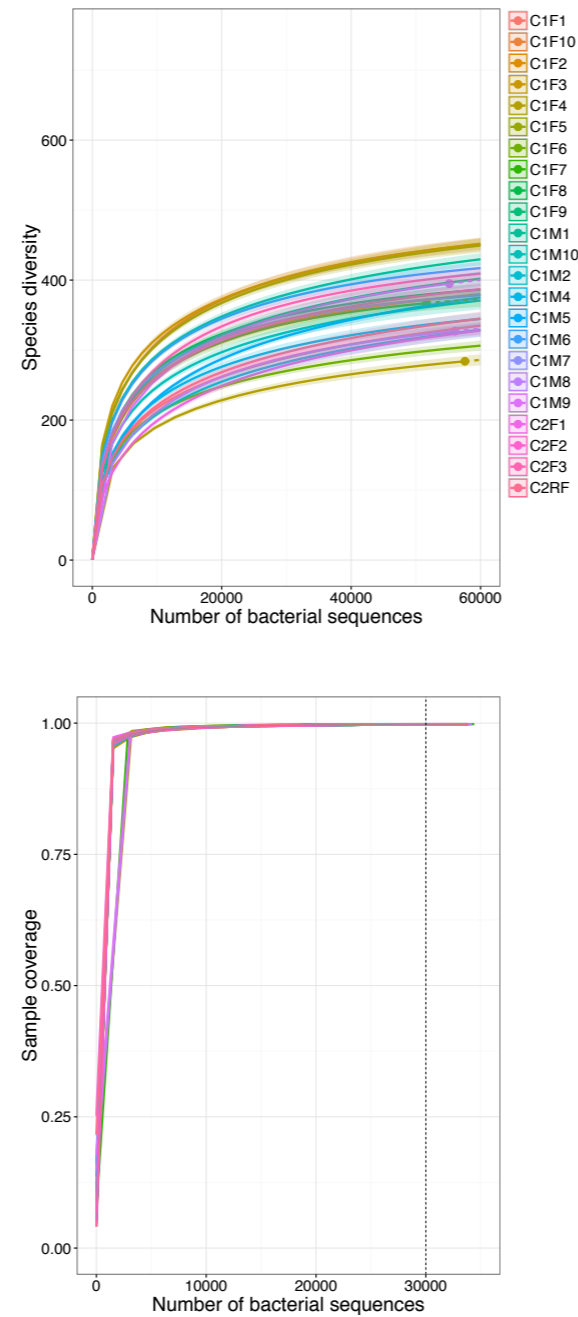


Figure S01. Collection localities of *D. nigrospiracula* individuals and necrotic cactus tissues. Map of the approximate range information for cardón and saguaro cactus and collection sites. Distribution boundaries modified from previous work (Turner *et al.* 1995; Pfeiler & Markow 2011). Map created in snazzymaps.com with the “lazzylazzy shuzhou super lazy” style.

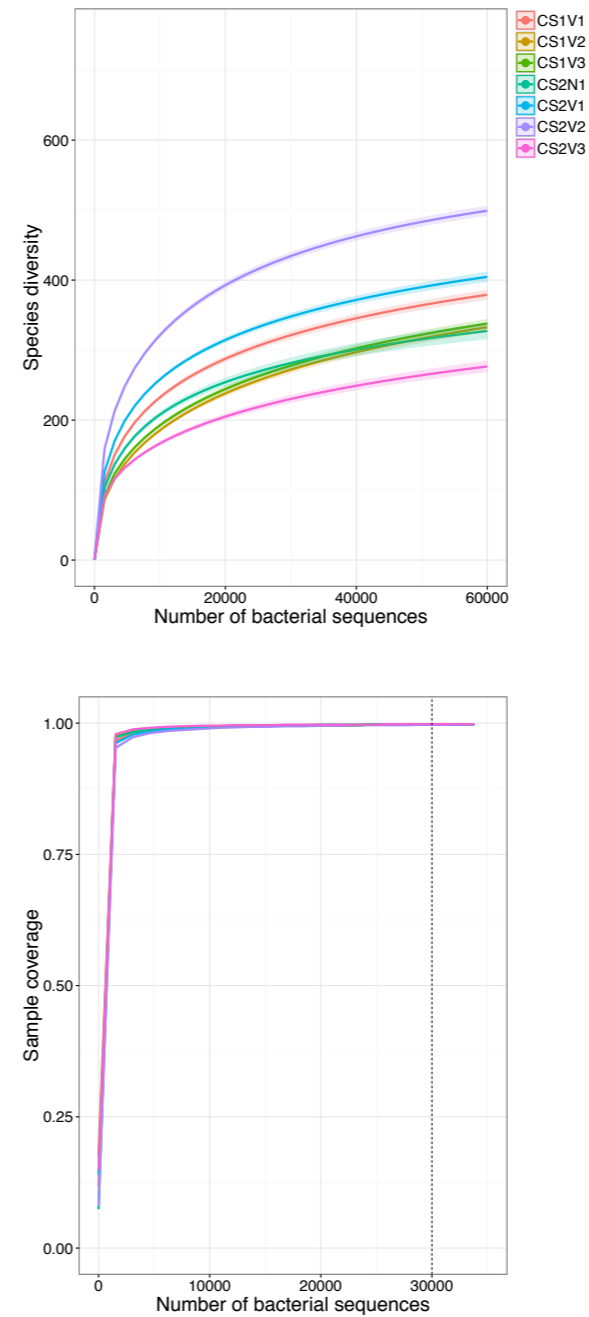
Saguaro flies



Cardón flies



Saguaro tissues



Cardón tissues

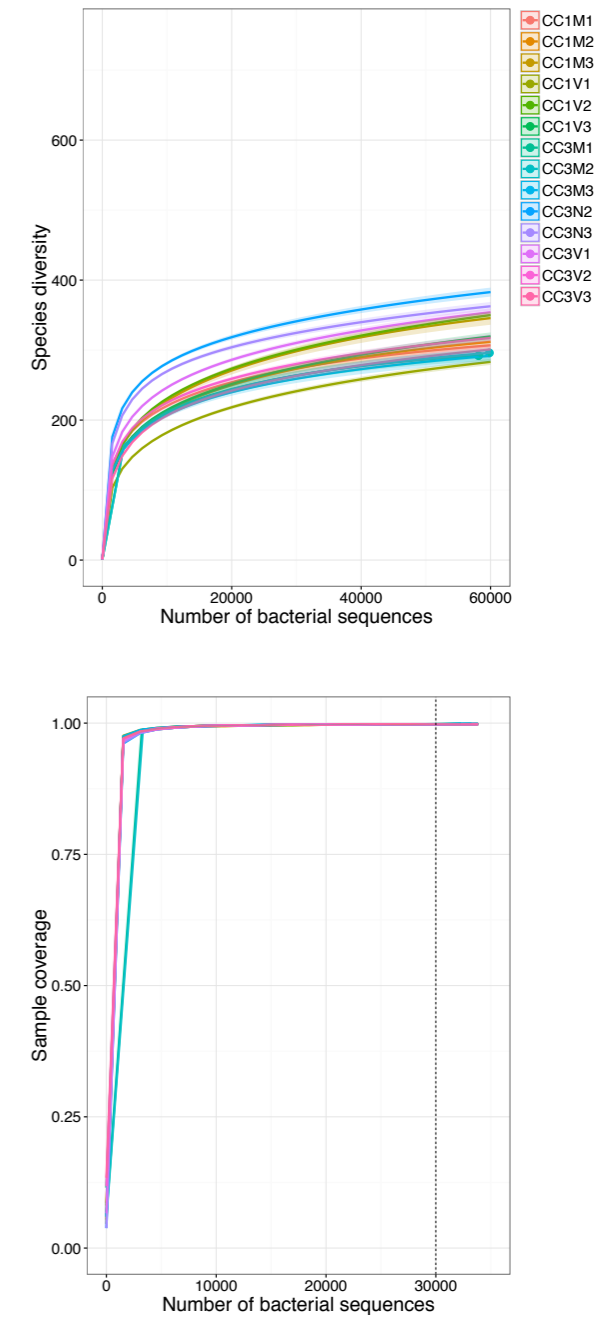


Figure S02. Rarefaction & sample completeness curves for each sample. Analysis performed with iNEXT in R. Vertical dashed line is the rarefaction level used to subsample (30,000 sequences/sample).

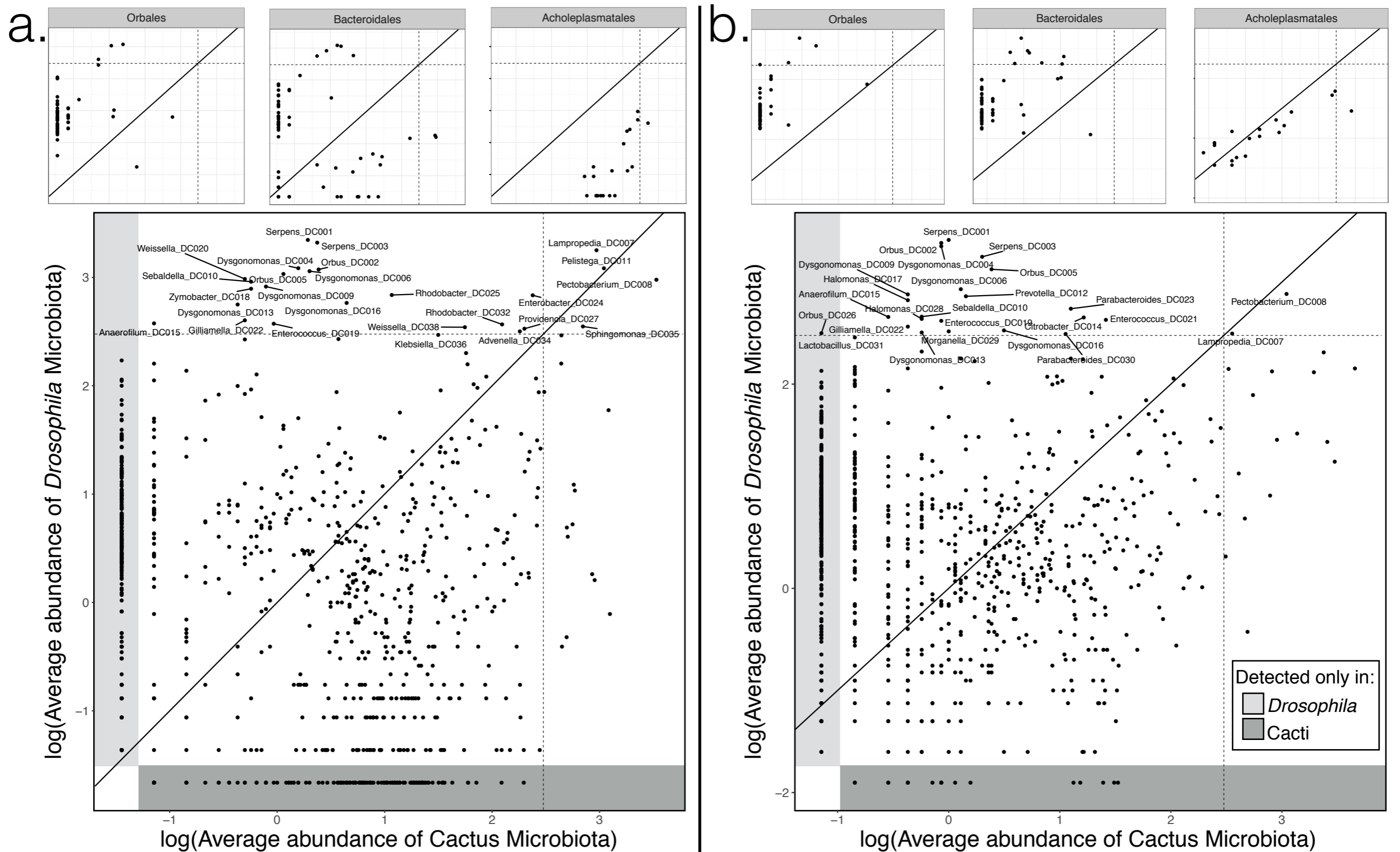


Figure S03. Paired comparisons of the average abundance for individual OTUs. **a)** *Drosophila*-cardón and **b)** *Drosophila*-saguaro. Bacterial OTUs that had an average abundance over 1% (dashed line) in *D. nigrospiracula* are labeled with their genus name and OTU ID. All OTUs belonging to Orbales, Bacteroidales or Acholeplasmatales are shown in smaller plots to show how taxonomic groups can be biased toward *Drosophila* or cactus.

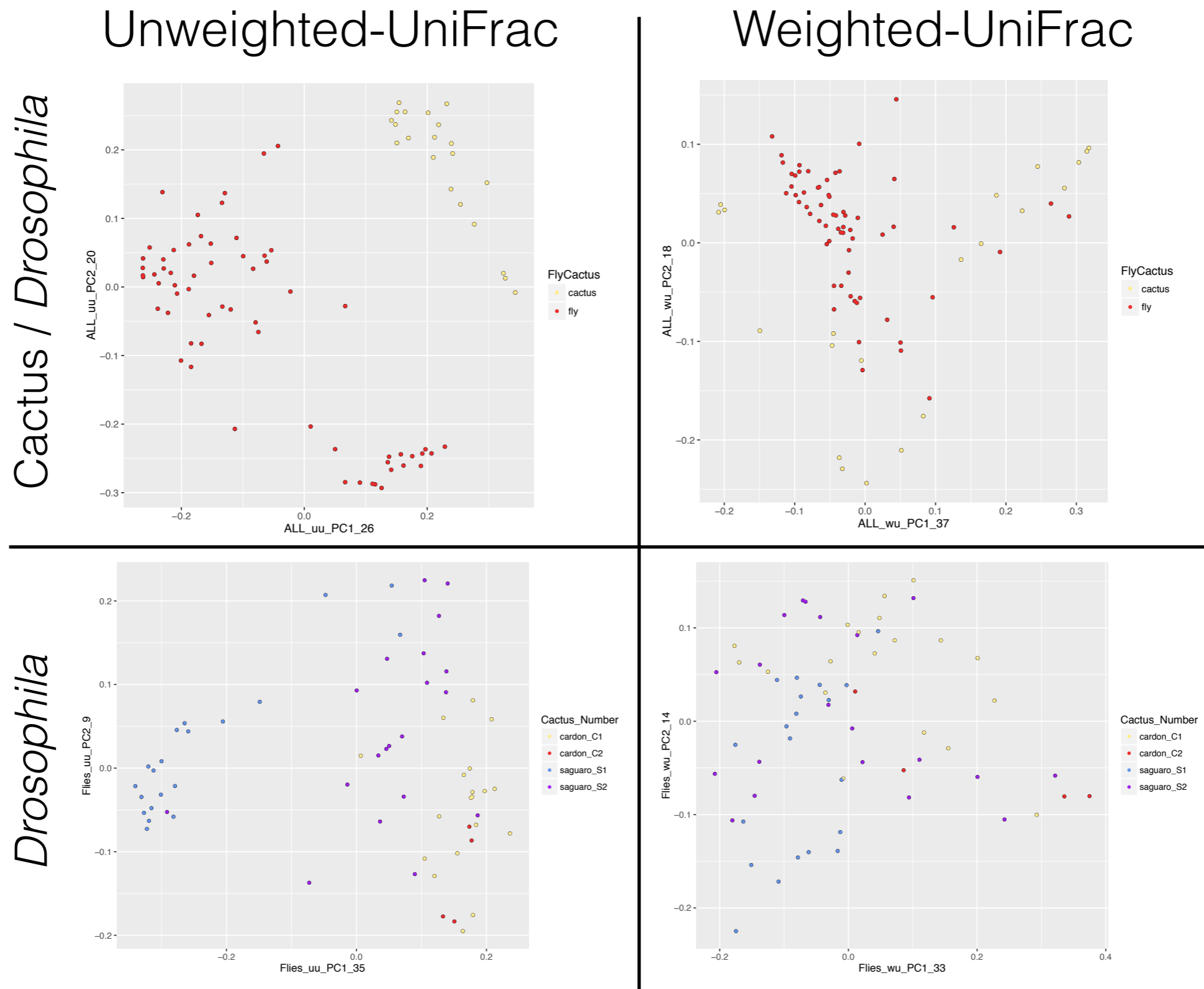


Figure S04. Principal coordinate analyses (PCoA) of the gut microbiota structure. **a)** between cactus tissue and *Drosophila* and **b)** among individual *D. nigrospiracula* collected at different cacti. Comparisons are based on Unweighted- and Weighted-UniFrac dissimilarity matrices using 97% similarity OTUs. Each point represents an individual sample. The percent of variation explained is listed on the axes.












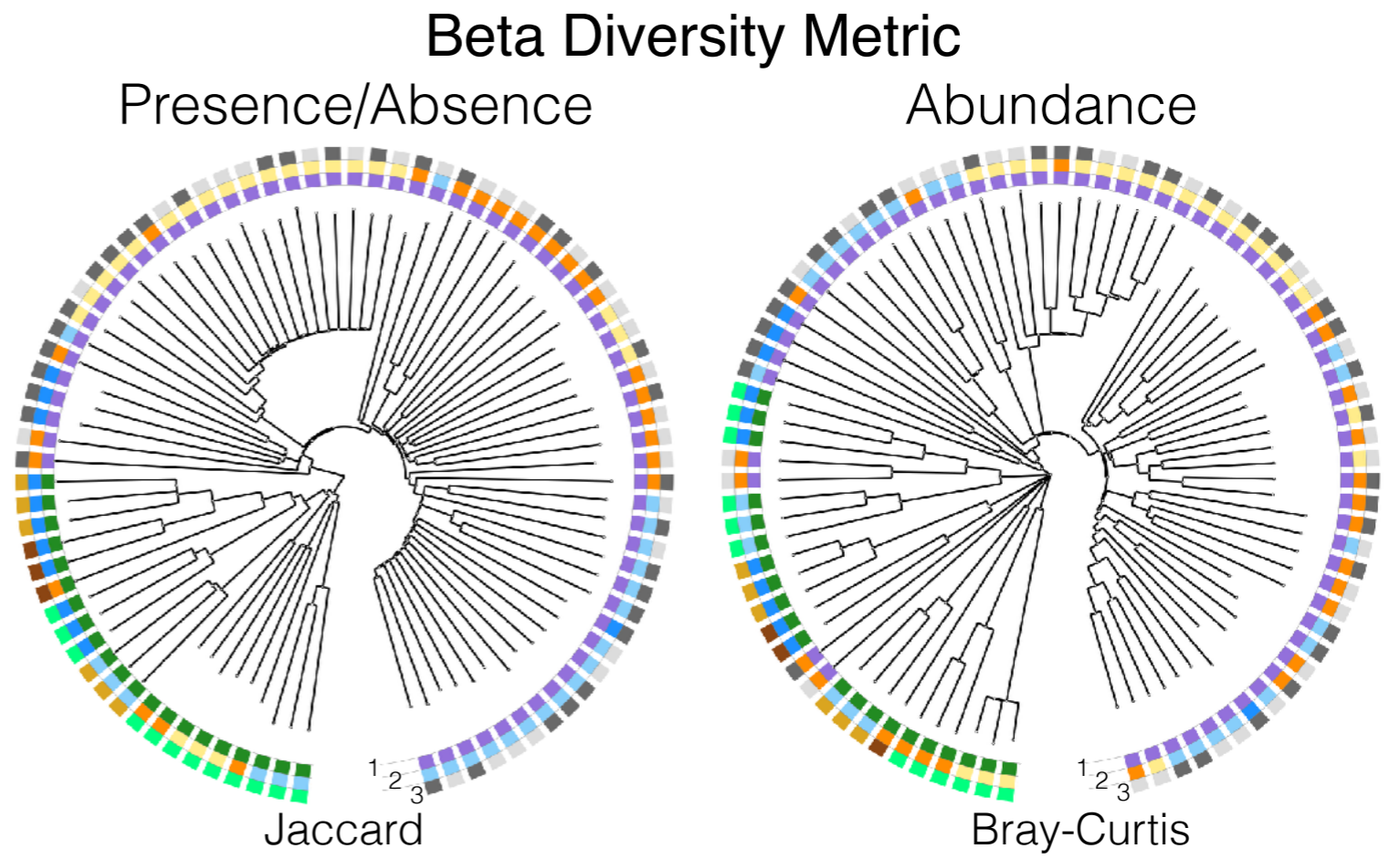
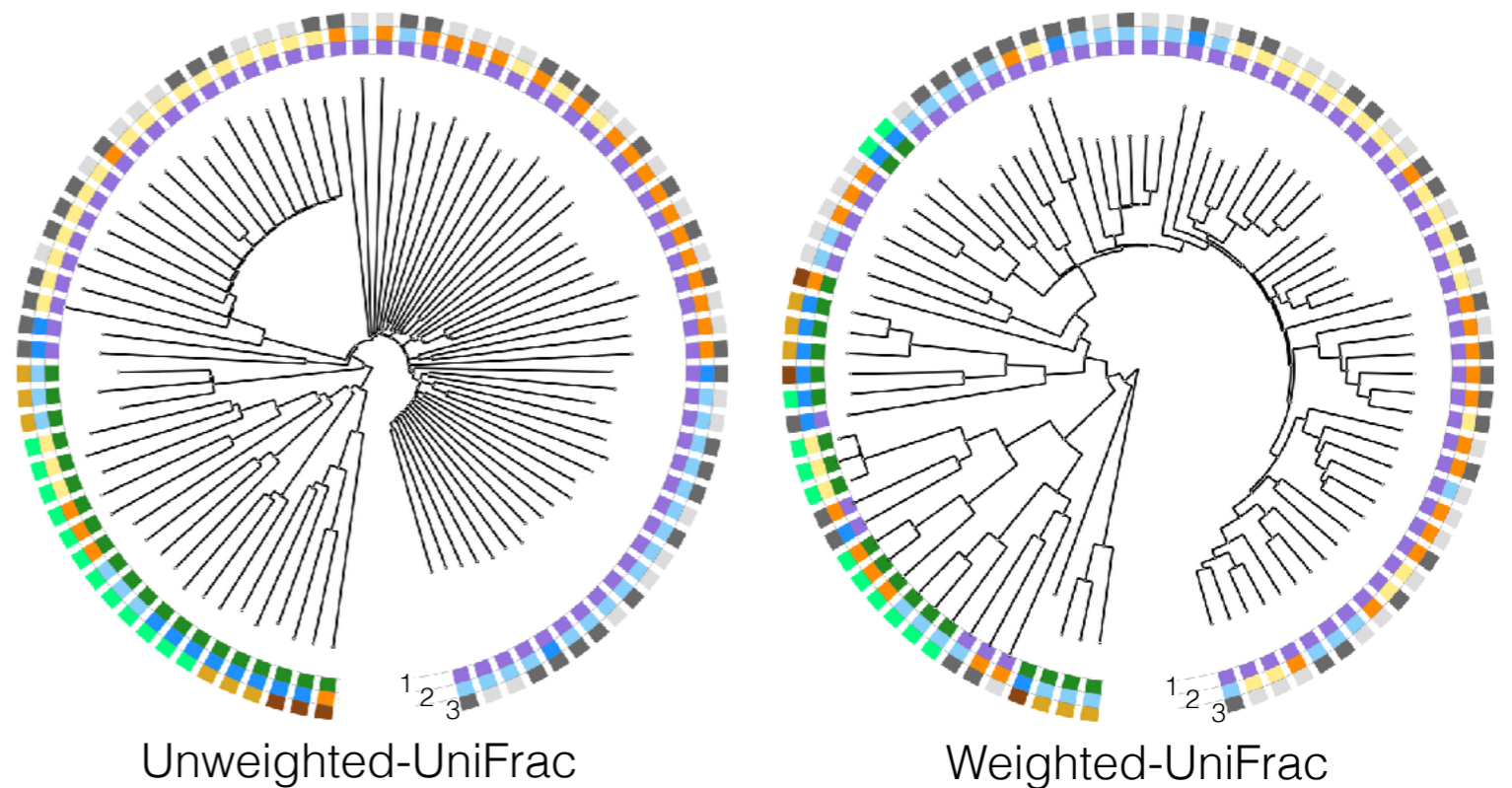
Ring 1	 <i>D. nigrospiracula</i>  Cactus tissue
Ring 2	 Saguaro, Locality 1  Saguaro, Locality 2  Cardón, Locality 1  Cardón, Locality 2
Ring 3	<i>D. nigrospiracula</i> Sex  Male  Female Cactus decay state  Green  Intermediate  Dark brown

Figure S05. UPGMA dendrograms showing the beta-diversity relationships among the microbiotas of individual *D. nigrospiracula* and cactus tissues. The rings surrounding dendrograms, from inside to outside, are colored by fly/cactus, cactus species/locality, sex/decay state. UPGMA analyses were performed with different diversity metrics in QIIME and visualized with GraPhlAn.

Non-Phylogenetic



Phylogenetic



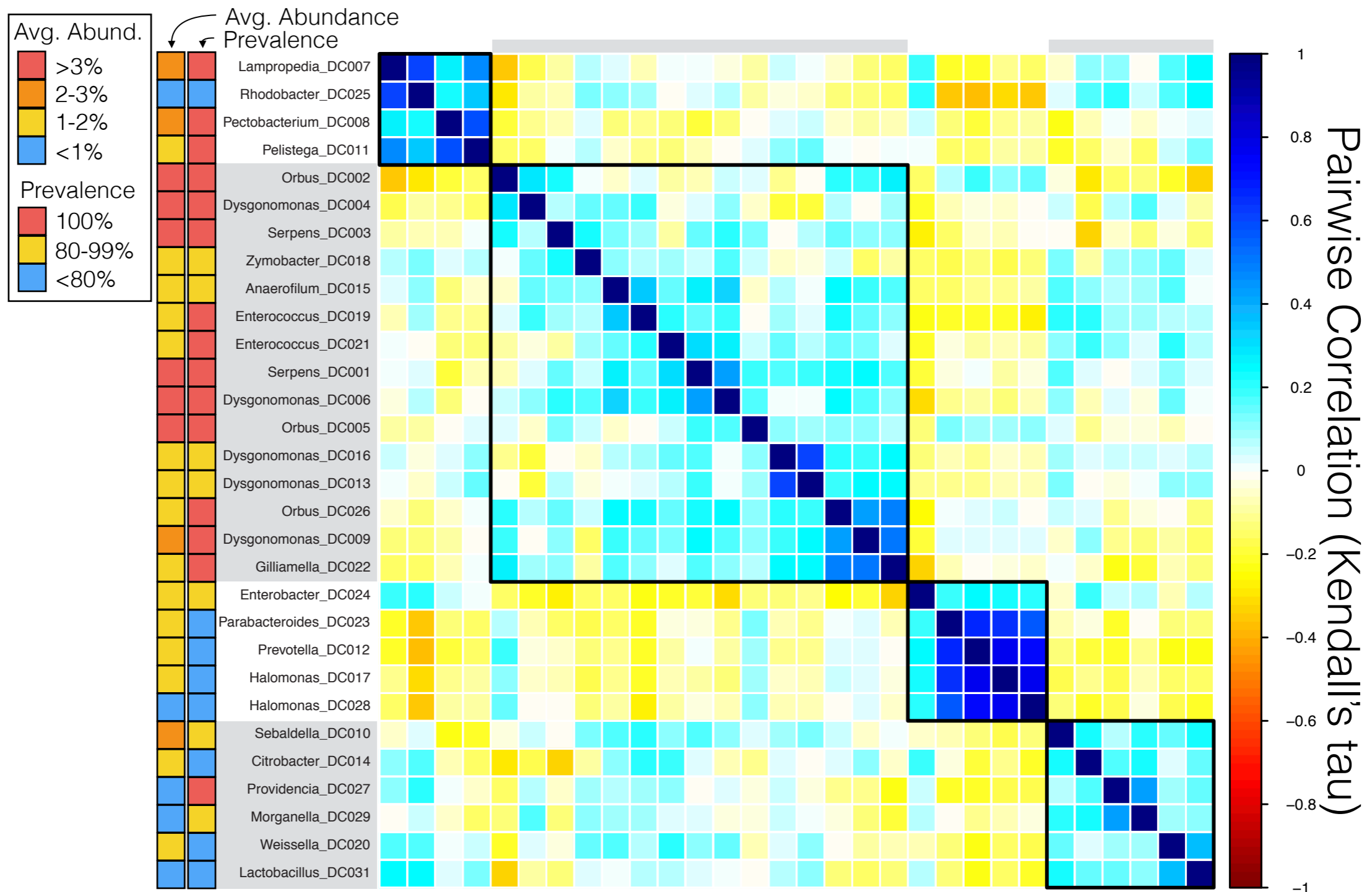


Figure S06. Pairwise correlations (Kendall's tau) between the top 30 most abundant OTUs present in *D. nigrospiracula* individuals. Positive correlations are darker blue and negative correlations are yellow to red. The average abundance and prevalence across *D. nigrospiracula* individuals are provided. Clusters were identified with the hclust using the "complete" method.

Cactophilic *Drosophila* OTUs

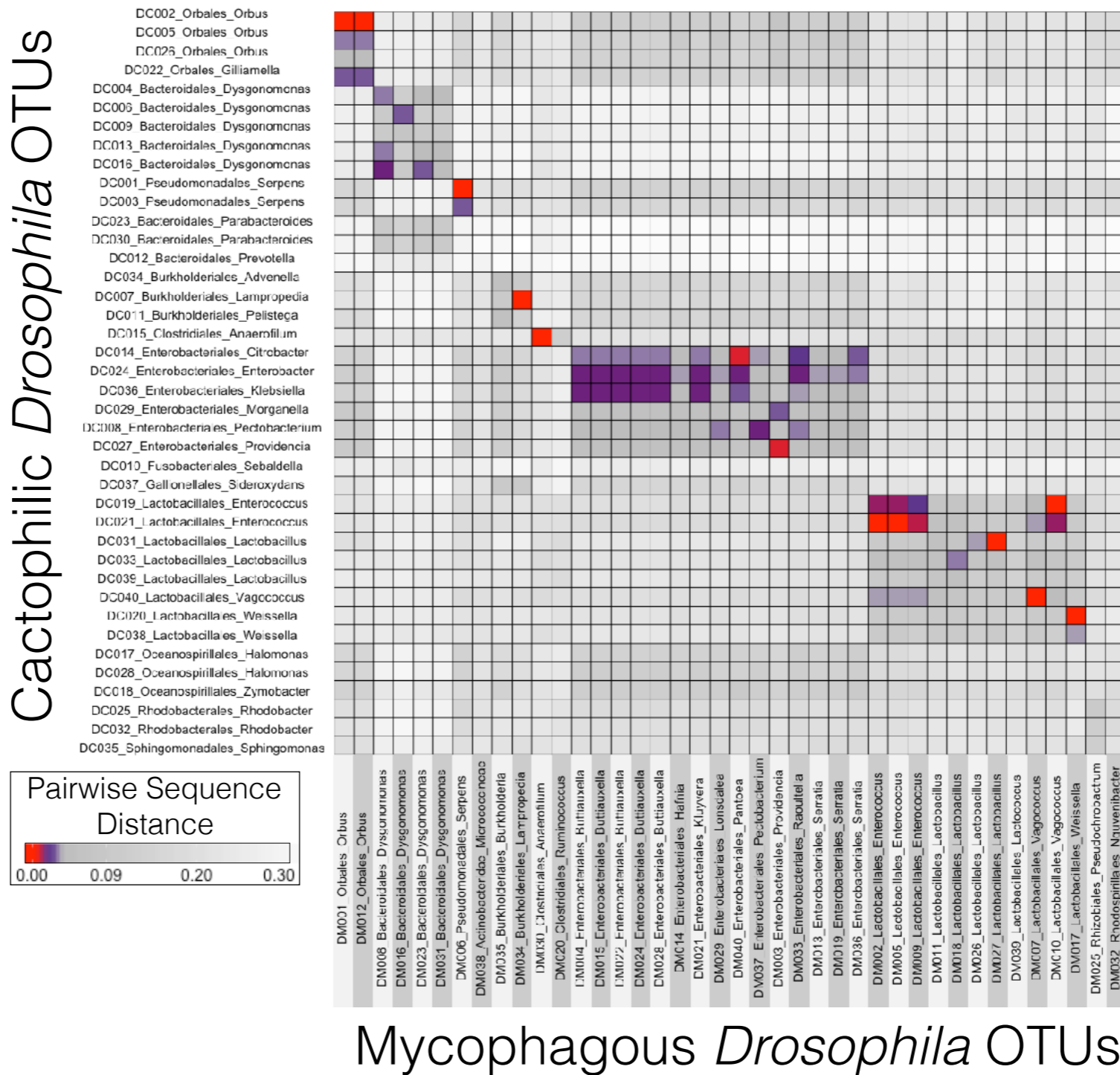


Figure S07. Pairwise sequence distance between the top 40 most abundant OTUs present in cactophilic *D. nigrospiracula* and mycophagous *Drosophila* species (*D. falleni*, *D. recens*, *D. neotestacea*, *D. putrida*) (Martinson et al. 2017). Pairs that have no sequence differences along the 263 bp region of the 16S rRNA gene are shown in red, and pairs that are less than 5% different are in purple.

Supplementary Material References:

- Martinson VG, Douglas AE, Jaenike J. 2017. Community structure of the gut microbiota in sympatric species of wild *Drosophila*. *Ecol Lett* 20:629-639.
- Pfeiler E, Markow TA. 2011. Phylogeography of the cactophilic *Drosophila* and other arthropods associated with cactus necroses in the Sonoran desert. *Insects* 2:218-31.
- Turner RM, Bowers JE, Burgess TL. 1995. *Sonoran Desert Plants: An Ecological Atlas*. University of Arizona Press, Tucson, AZ.