

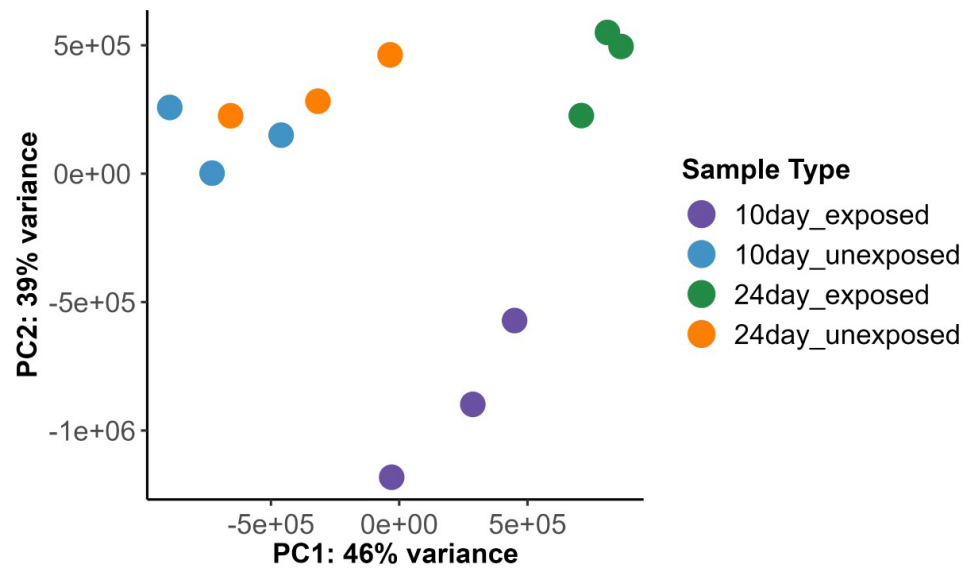
Supplemental Figure 4.1: Metatranscriptomic analysis of remaining unmapped reads. Number of reads assigned to the various Phyla across Kingdoms for each sample replicate.

dpe = days post exposure

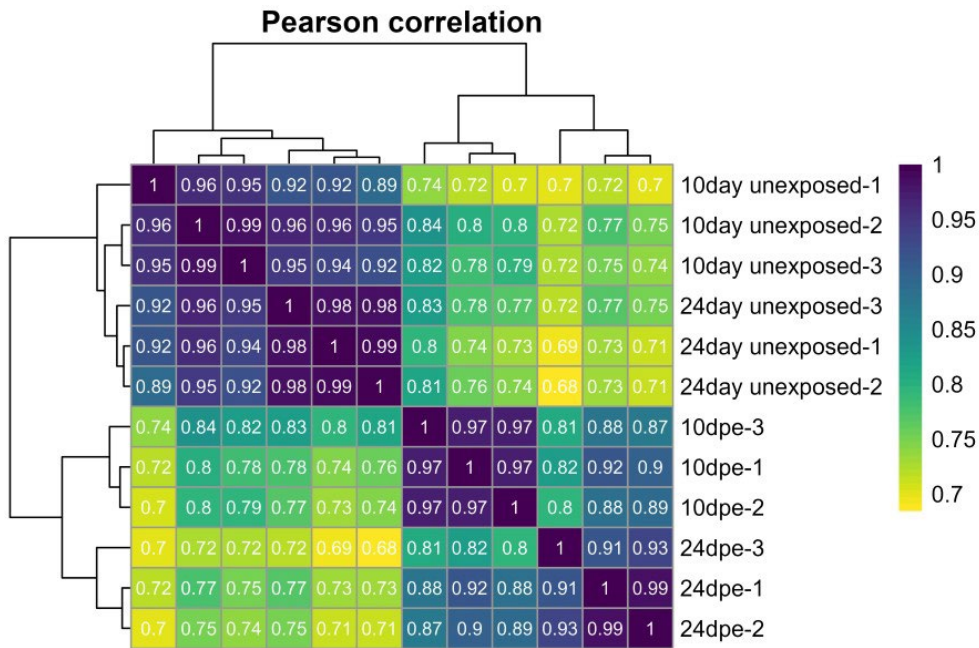
10d unexp = 10 day unexposed control

24d unexp = 24 day unexposed control

A

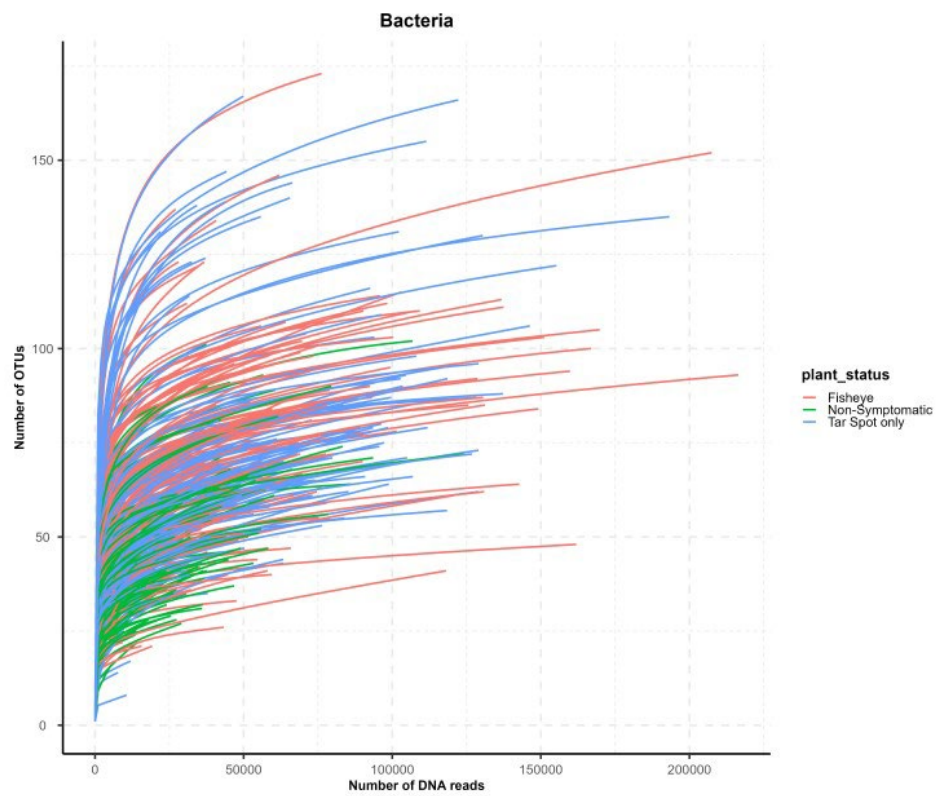
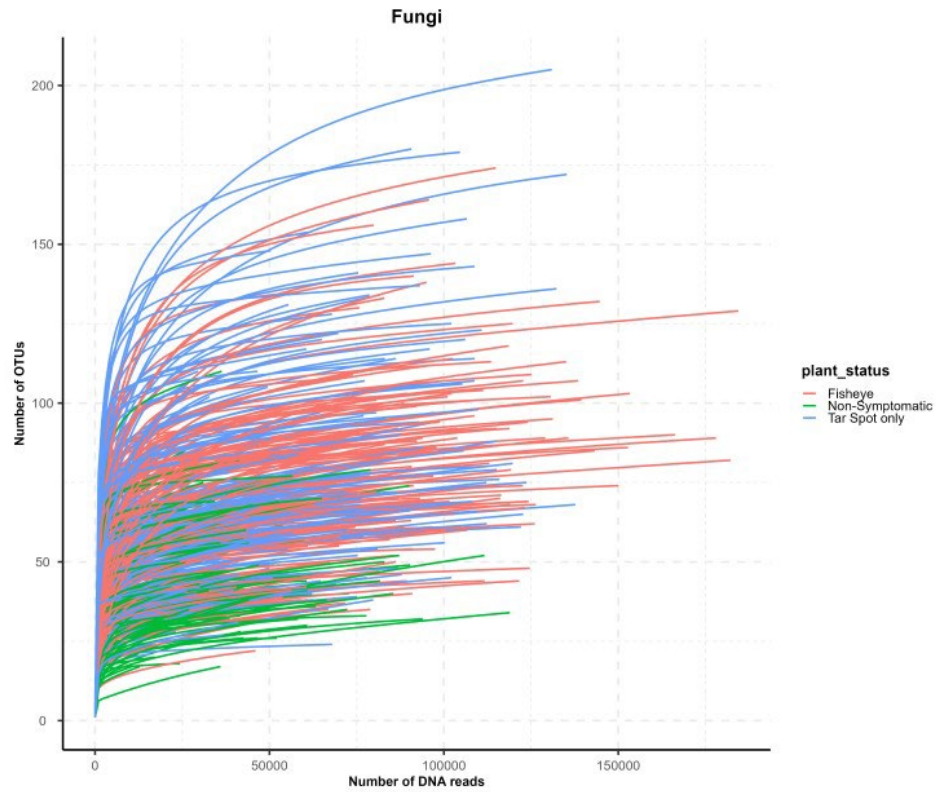


B

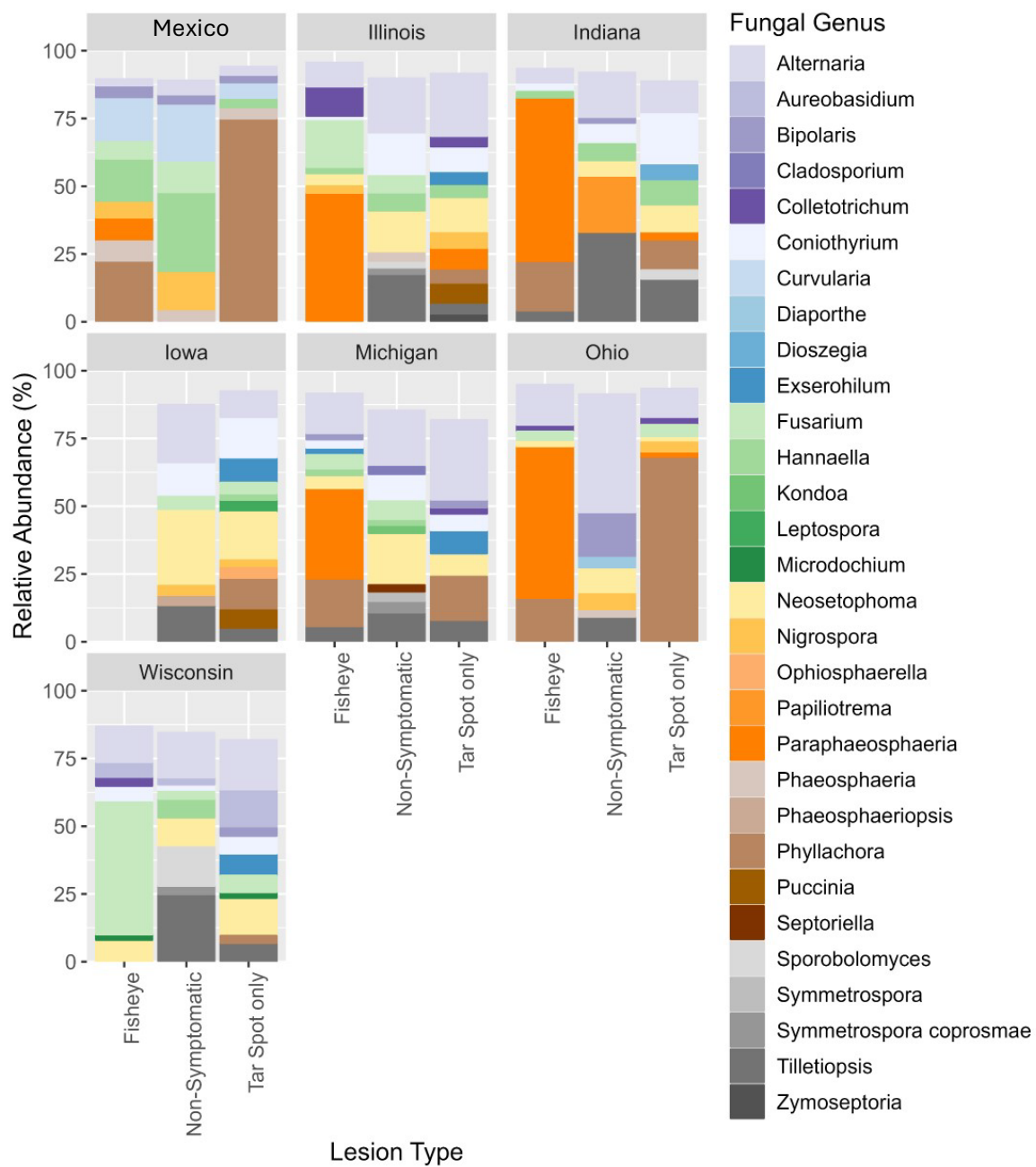


Supplemental Figure 4.2

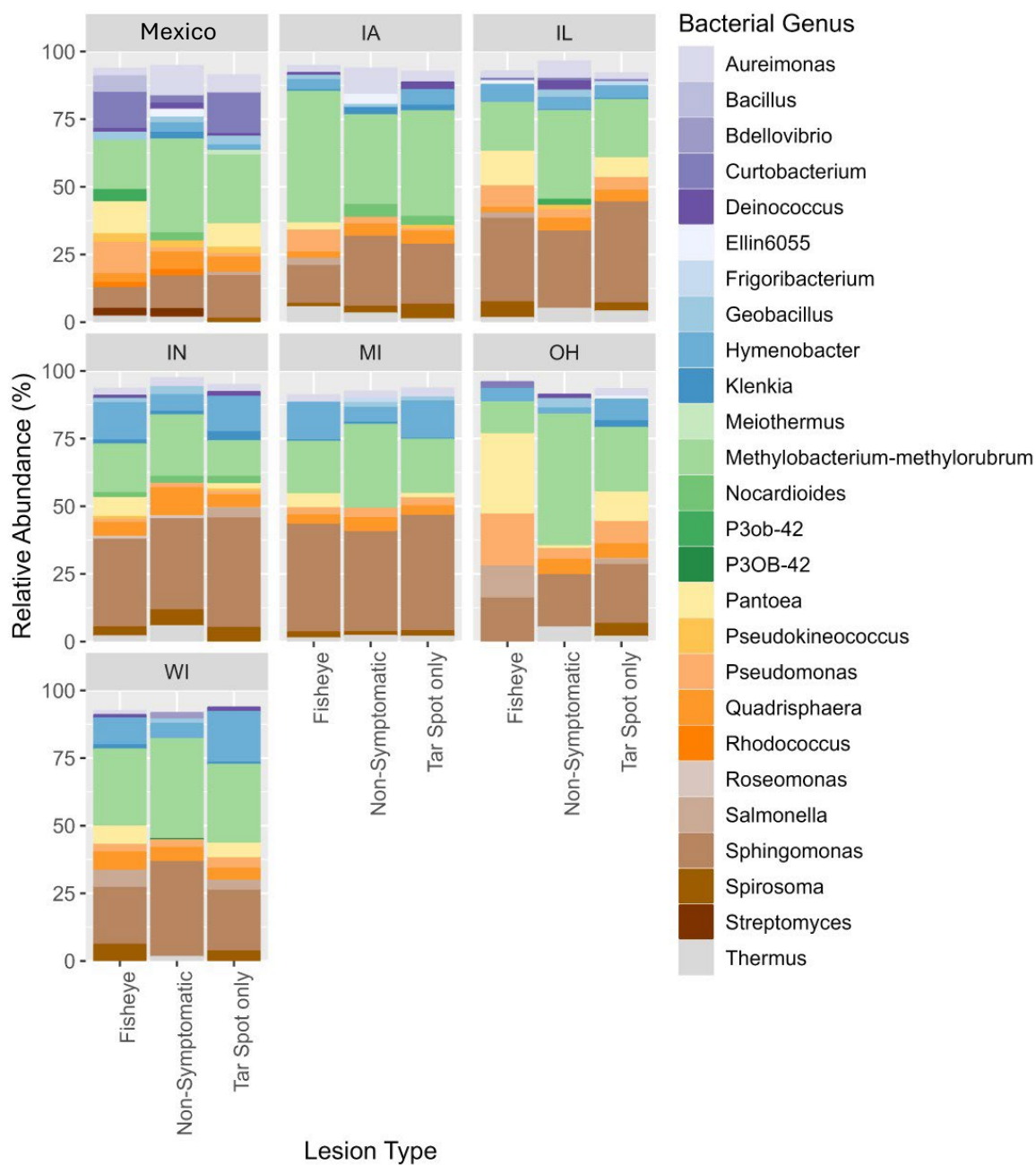
- A. Principle coordinate analysis of sample replicates based on gene expression patterns.
- B. Pearson's correlation of sample replicates based on gene expression patterns



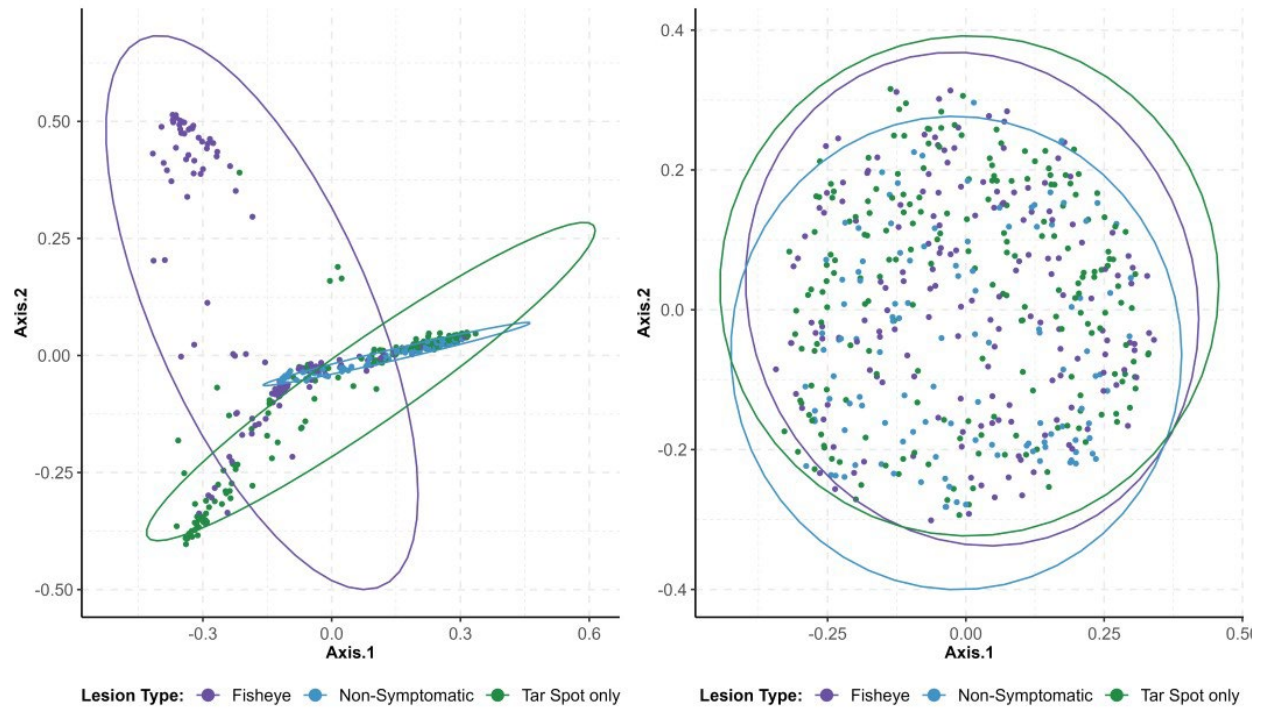
Supplemental Figure 5.1: Rarefaction curves



Supplemental Figure 5.2: Average relative abundant fungal genera by state in US and Mexico



Supplemental Figure 5.3: Average relative abundant bacterial genera by state in US and Mexico

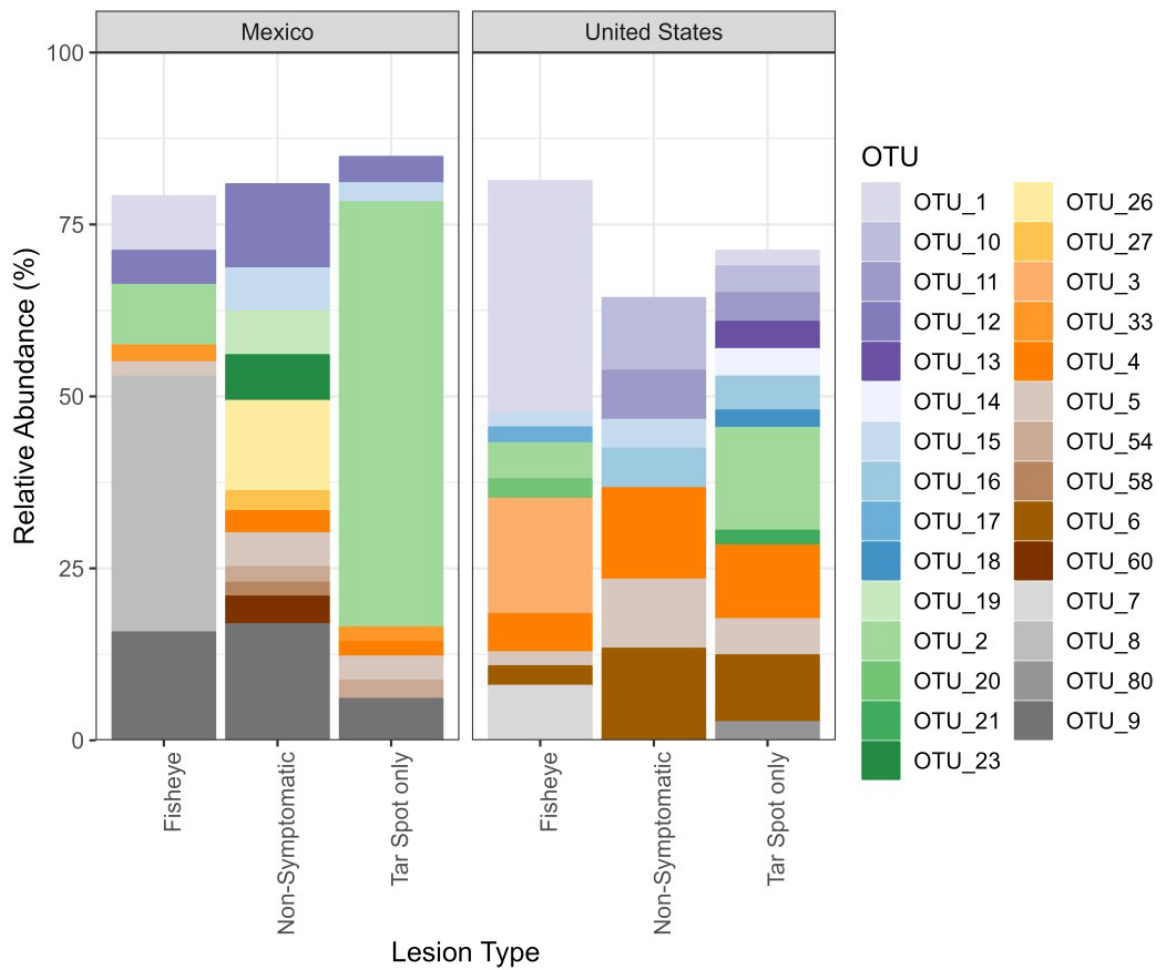


Supplemental Figure 5.4: Beta-diversity by Jaccard distances

A. Fungi

B. Bacteria

Colored by lesion type and ellipses show 95% confidence interval based on lesion type



Supplemental Figure 5.5: OTU average relative abundance by country.
 Taxonomy found in Supplemental Table 5.8



Supplemental Figure 5.6