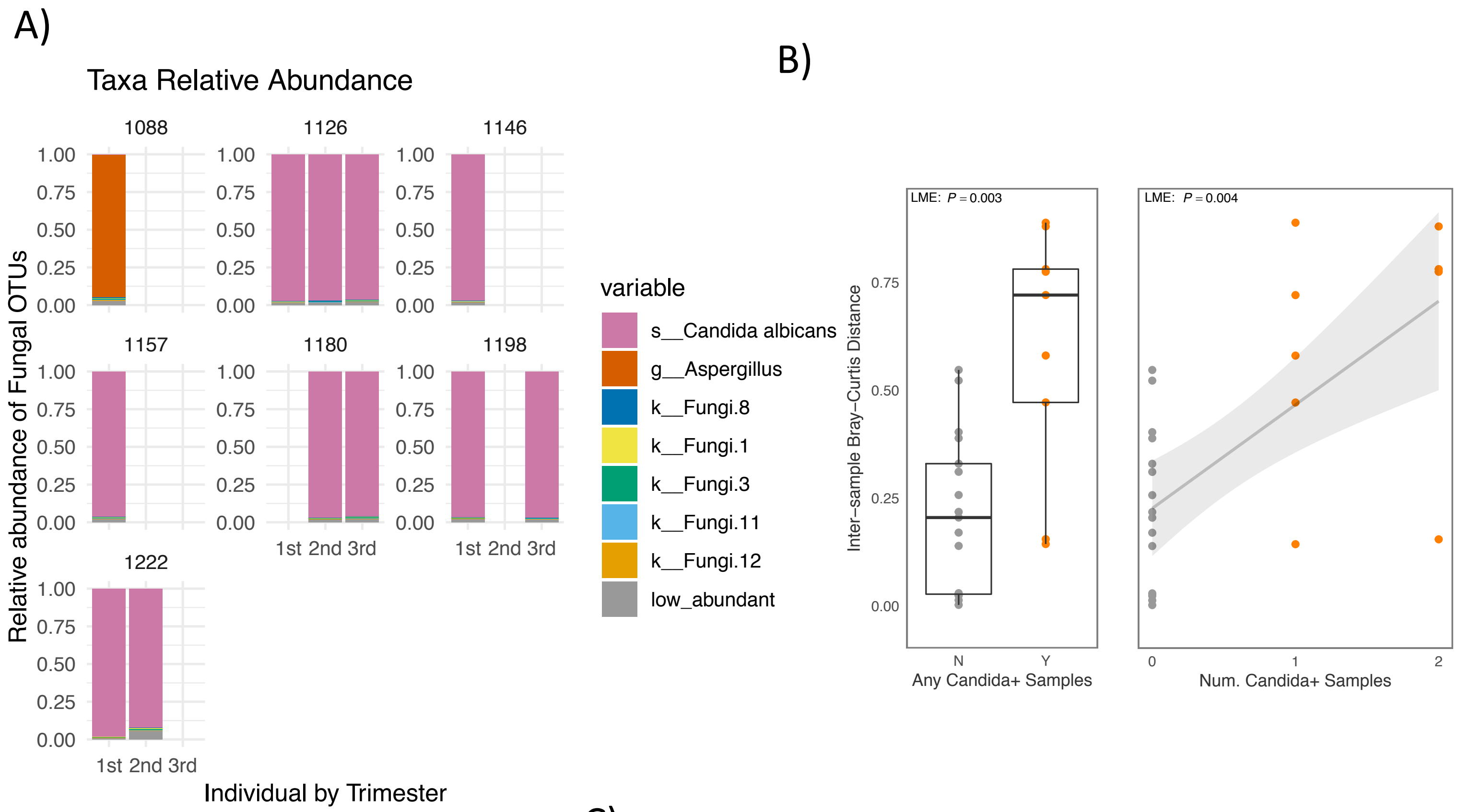

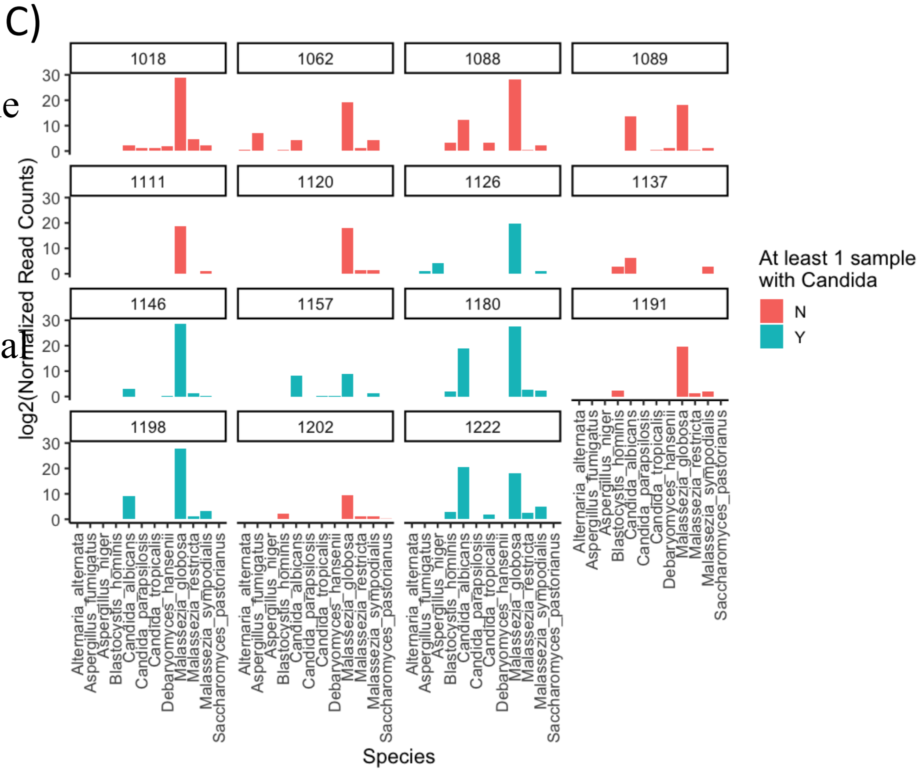

Supp. Fig. 2: A) Bar plot showing the relative abundance of fungal OTUs within subjects. The most abundant OTUs by far were all classified as *Candida albicans* (pink). All other OTUs made up very little of the fungal presence in these samples, save for subject 1088, who had a species of *Aspergillus* as its most abundant fungal taxon. B) Sample where *Candida* was detected had greater shifts in bacterial composition than samples without. C) Shotgun metagenomics was able to pick up reads aligning to database containing human-associated fungal species and confirmed ITS results and classified additional taxa.