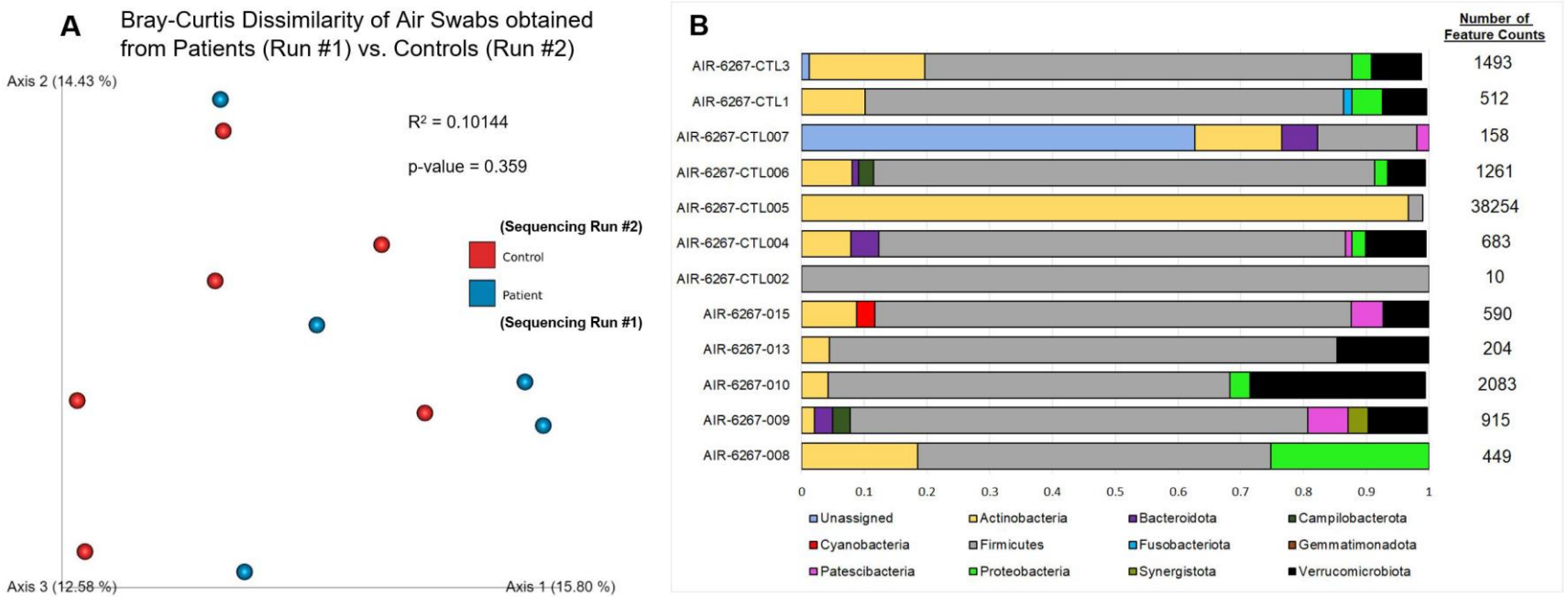

Supplemental Figure 1. Characterizing and comparing the microbial composition of negative control samples (air swabs) obtained from separate sequencing runs. A total of 12 air swabs were collected as negative control samples from patient and control subjects and sequenced separately during an initial (Run #1) and subsequent run (Run #2), respectively. Excluding CTL005 from the analysis as an outlier, there were no differences in beta-diversity between air swab samples obtained from separate sequencing runs based on **(A)** Bray Curtis distances ($p = 0.359$, $R^2 = 0.10144$, PERMANOVA). The axis values in the beta-diversity plot are the percentage of variance in phylogenetic beta diversity. **B)** The taxonomy barplot is represented by the relative abundance of amplicon sequence variants (ASVs) that are classified to a specific phylum. The number of feature counts are listed for the corresponding sample, with majority of samples containing <2000 features, consistent with the expected low burden of airborne contaminants. “CTL” in the sample name is defined as an air swab that was obtained during the time an ocular specimen was performed on a control subject. In samples without “CTL”, the air swabs were obtained during the time an ocular specimen was collected from a patient with unilateral glaucoma. The air swab collected with control subject #5 (CTL005) was significantly different in the number of feature counts and microbial composition compared to all other air swabs while matching closely in these characteristics with healthy control ocular swabs. Thus, it was highly likely that the air swab obtained from CTL005 did not represent

a true contaminant and likely contained ASVs of experimental relevance. ASVs identified in all other air swabs were treated as true contaminants and removed utilizing QIIME2. The relative abundance of genus classifications for the air swab samples can be found in **Supplemental Data 1**.