



Supplemental Figure 2. Diversity analysis and taxonomic classification based on sampled eye (Left vs. Right). Alpha- and beta-diversity comparisons were restricted to control subjects to avoid confounding effects of treatment and/or ocular disease. Analysis was further divided into conjunctiva and margin to control for sampling location. Sampled eye was represented by right (“OD”) (n = 6) compared to left (“OS”) eyes (n = 6). **(A)** No differences were found in alpha-diversity metrics between right and left eyes for Shannon diversity ($p = 0.109$, Kruskal-Wallis) for conjunctival eye samples. There were no differences in beta-diversity between right and left eyes for conjunctival eye samples based on **(B)** Bray Curtis distances ($p = 0.942$, $R^2 = 0.10161$, PERMANOVA) as visualized on principal coordinates analysis plots. **(C)** No differences were noted in alpha-diversity metrics between right and left eyes in margin samples for Shannon diversity ($p = 0.565$, Kruskal-Wallis). In addition, there were no

differences in microbiome composition based on beta-diversity between the right and left eyes of margin samples based on **(D)** Bray Curtis distances ($p = 0.501$, $R^2 = 0.13225$, PERMANOVA). The average relative abundance of taxonomic classifications to amplicon sequence variants (ASVs) for right and left margin/conjunctival eye samples are displayed at the phylum **(E)** and genus **(F)** level, with no significant differentially abundant taxa. Only taxonomic classifications with $>1\%$ (0.01) average relative abundance are shown. The axis values in beta-diversity plots **(C, D)** are the percentage of variance of phylogenetic beta diversity.