Supplement Figure 1. Rarefaction analysis of sequencing “depth” shows the relationship between the number of observed OTUs/phylotypes and the total number of sequences analyzed. Species representation in most conjunctival sample had entered the plateau phase, indicating that novel bacteria would unlikely be recovered with additional sequencing efforts.
Supplement Figure 2. The analysis of technical replicate pairs for each tested subject showed that the distributions of the nine most abundant genera in the subjects #1, 2 and 4 were nearly identical. The subject #3 displayed notable difference in microbial distribution in the two replicates (mainly due to the difference in the relative abundance of Acinetobacter, 38.4% vs. 18.8% in two technical replicates), but the overall microbial distributions displayed no statistically significant difference (p=0.675, Kolmogorov-Smirnov test).
Supplement Figure 3. The analysis of bacterial community recovery using deep vs. soft swabbing techniques. *Propionibacteria* and *Actinobacteria* dominate in all deep swab samples; *Firmicutes* and *Actinobacteria* show major “spike” in soft swab samples.