Figure S1. Richness (Observed species, Chao1 indices) and Diversity (Shannon and Simpson indices) for different sampling sites by PD severity (A), PD severity by sampling site (B) and by PD and HIV infection status (C).
Figure S2. PCoA separate plots stratified by sampling site. No clustering is observed along different PD stages or HIV infection status when sampling sites are analyzed separately.`
Figure S3. Boxplots showing bacterial phylum log$_{10}$ transformed abundance proportions for Cheek, Saliva and Teeth samples. *Firmicutes, Actinobacteria, Bacteroidetes, Fusobacteria* and *Proteobacteria* are the most abundant phylums in all sampling sites.
Figure S4. Scatter plots and for significant correlations between the different bacterial genera and immune markers. Note strong Streptococcus genus abundance and the DR+Ki67+(CD38-ve) immune markers.
Figure S5. LDA scores for marker KEGG pathways enriched in each sampling site.
Figure S6. Bray-Curtis dissimilarity measures for inter and intra participant cheek (upper) and teeth (lower) samples. In both sampling sites, intra-participant samples show significantly greater similarity than inter-participant samples, while teeth samples show higher variability.