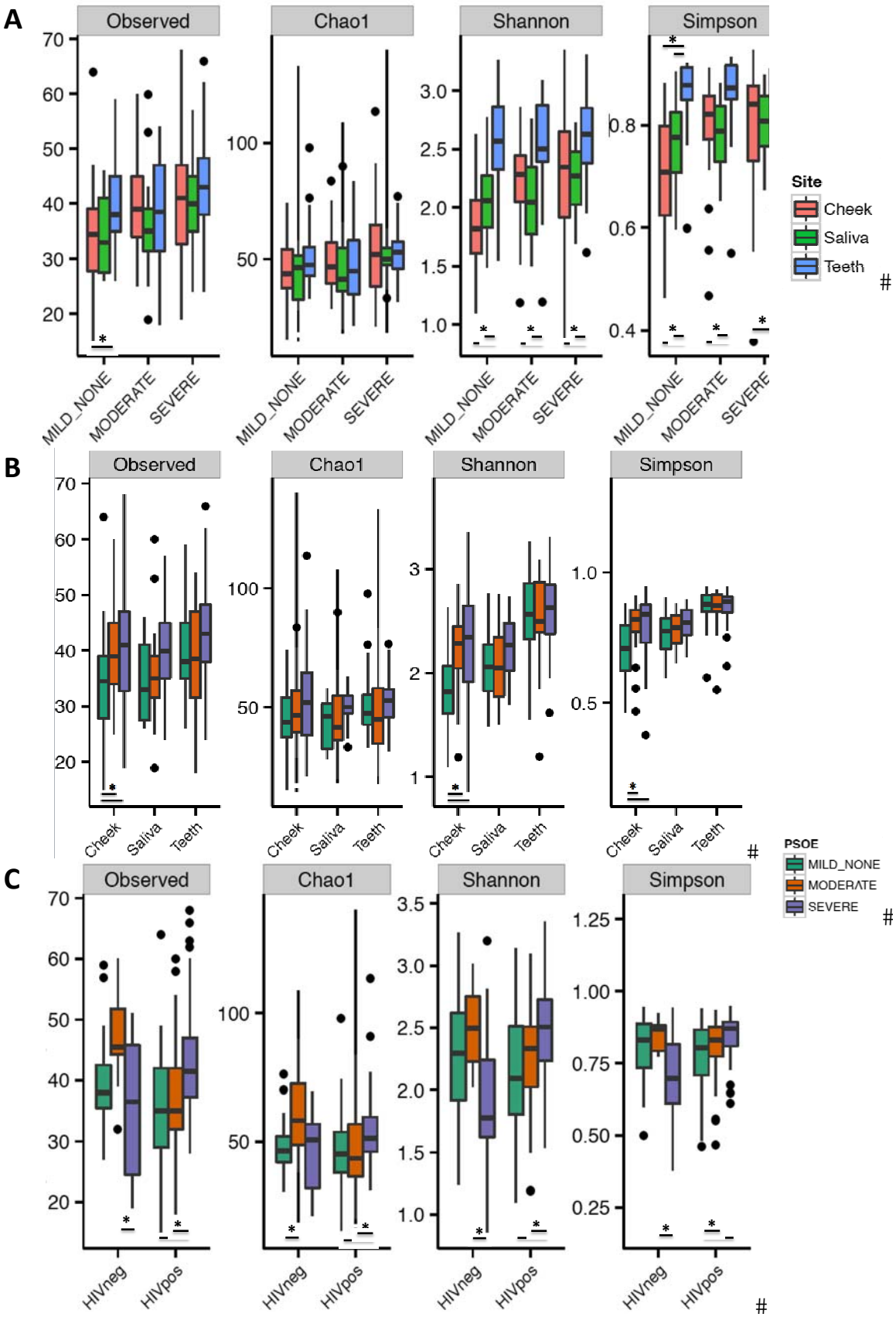


Figure S1. Richness (**Observed** species, **Chao1** indices) and Diversity (**Shannon** and **Simpson** indices) for different sampling sites by PD severity (**A**), PD severity by sampling site (**B**) and by PD and HIV infection status (**C**).

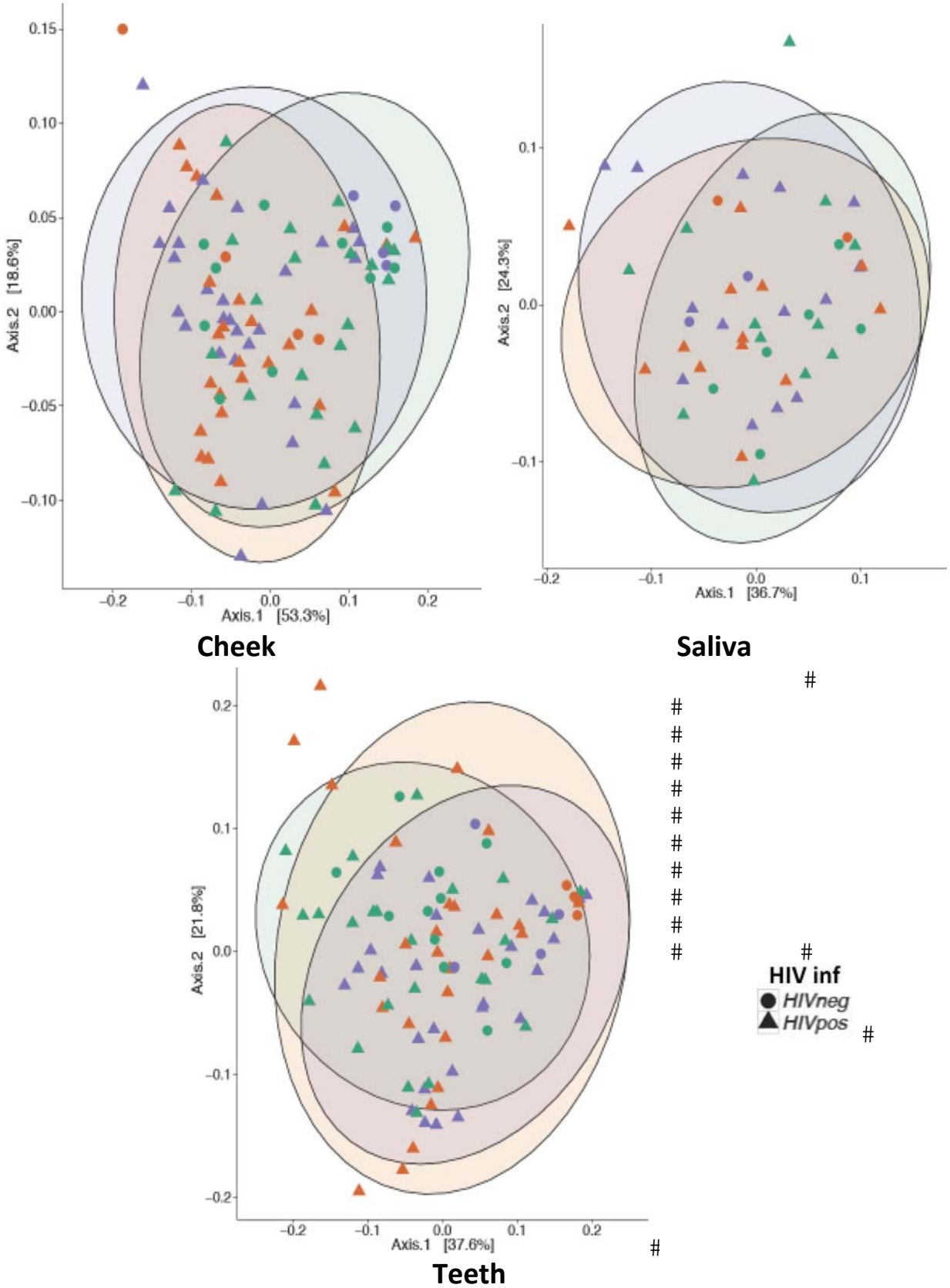
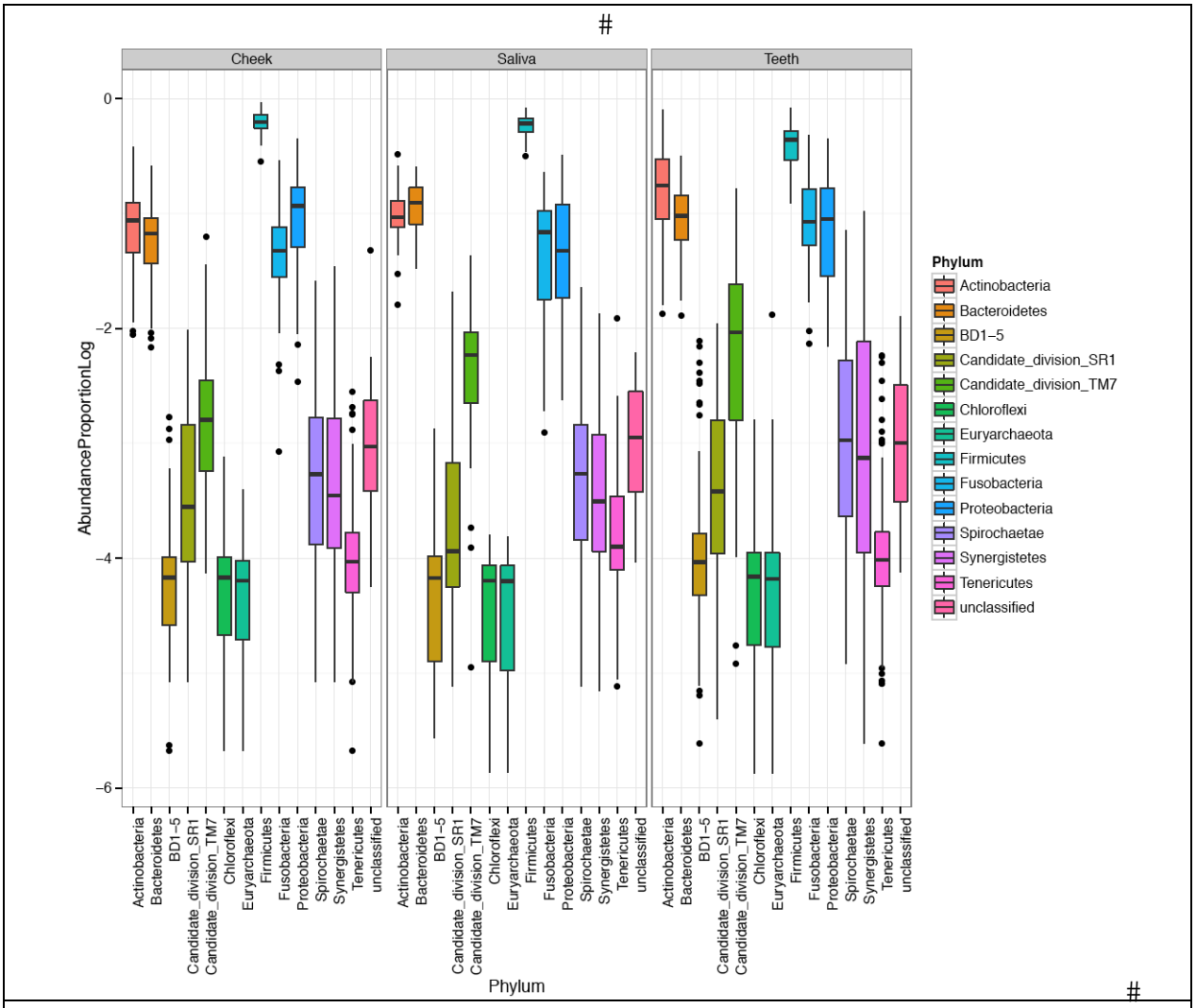


Figure S2. PCoA separate plots stratified by sampling site. No clustering is observed along different PD stages or HIV infection status when sampling sites are analyzed separately-. #



FigureS3. 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.#

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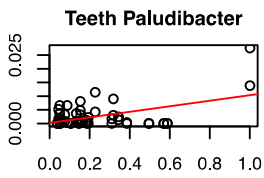
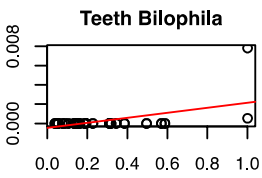
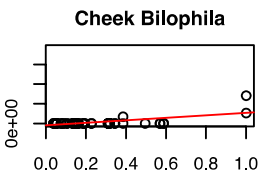


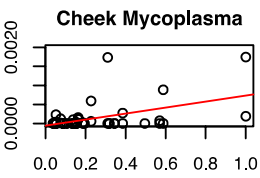
CD4/DR+Ki67+(CD38−ve)
R2: 0.23 p−adj(FDR) 0.03069



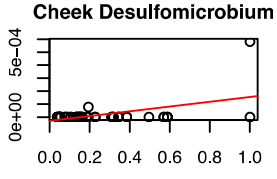
CD4/DR+Ki67+(CD38−ve)
R2: 0.27 p−adj(FDR) 0.01219



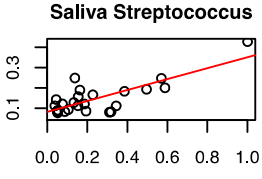
CD4/DR+Ki67+(CD38−ve)
R2: 0.43 p−adj(FDR) 4e−05



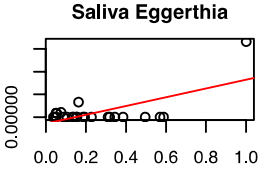
CD4/DR+Ki67+(CD38−ve)
R2: 0.22 p−adj(FDR) 0.02874



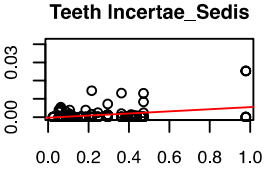
CD4/DR+Ki67+(CD38−ve)
R2: 0.24 p−adj(FDR) 0.02304



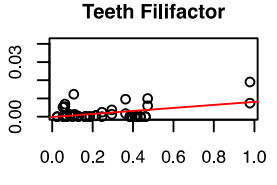
CD4/DR+Ki67+(CD38−ve)
R2: 0.61 p−adj(FDR) 7e−04



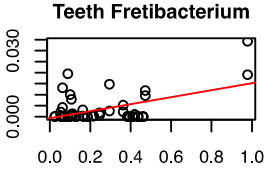
CD4/DR+Ki67+(CD38−ve)
R2: 0.42 p−adj(FDR) 0.02959



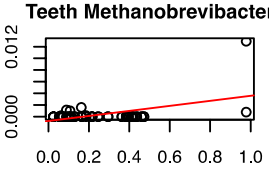
CD4/Ki67+(DR−ve, CD38−ve)
R2: 0.11 p−adj(FDR) 0.00171



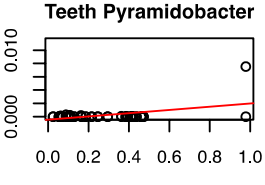
CD4/Ki67+(DR−ve, CD38−ve)
R2: 0.19 p−adj(FDR) 0.01425



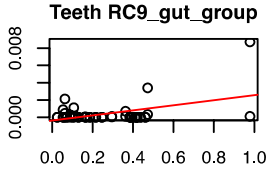
CD4/Ki67+(DR−ve, CD38−ve)
R2: 0.24 p−adj(FDR) 0.00427



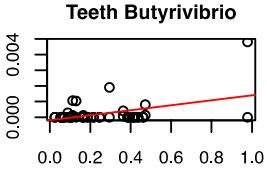
CD4/Ki67+(DR−ve, CD38−ve)
R2: 0.24 p−adj(FDR) 0.00427



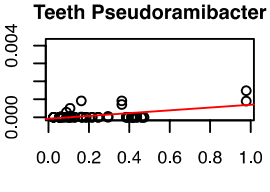
CD4/Ki67+(DR−ve, CD38−ve)
R2: 0.24 p−adj(FDR) 0.005



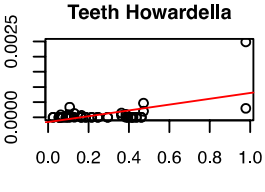
CD4/Ki67+(DR−ve, CD38−ve)
R2: 0.21 p−adj(FDR) 0.01024



CD4/Ki67+(DR−ve, CD38−ve)
R2: 0.2 p−adj(FDR) 0.0139



CD4/Ki67+(DR−ve, CD38−ve)
R2: 0.26 p−adj(FDR) 0.00427



CD4/Ki67+(DR−ve, CD38−ve)
R2: 0.32 p−adj(FDR) 0.00171

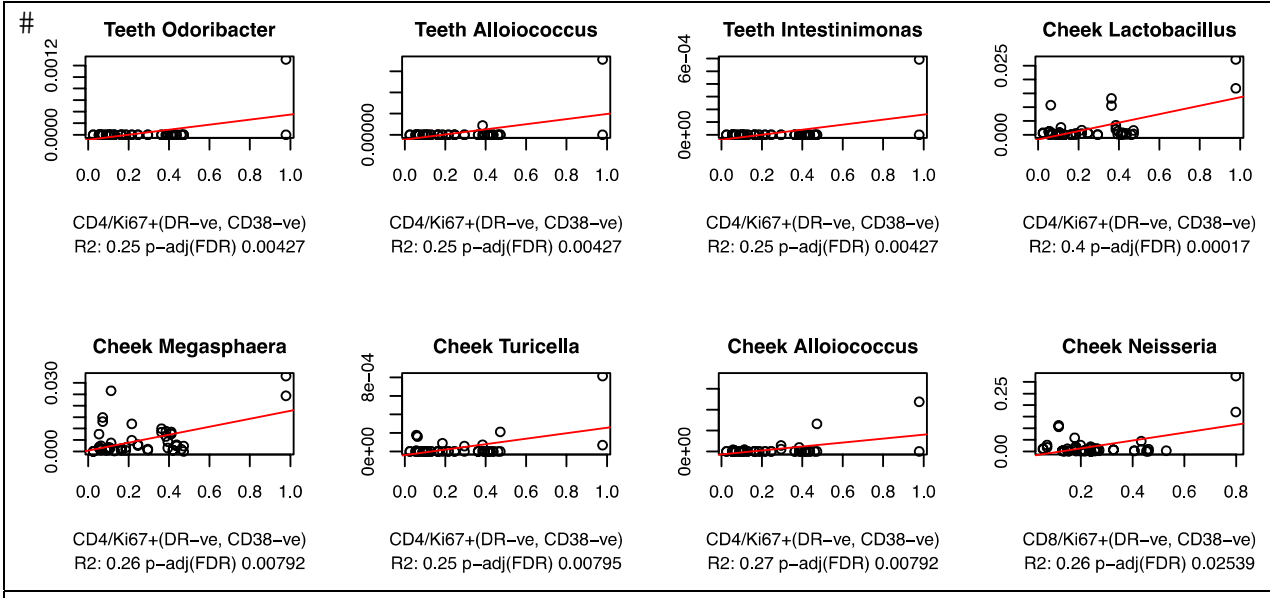


Figure S4. Scatter plots and for significant correlations between the different bacterial genera and immune markers. Note strong Streptococcus genus abundance and the DR+Ki67+(CD38-ve) immune markers.

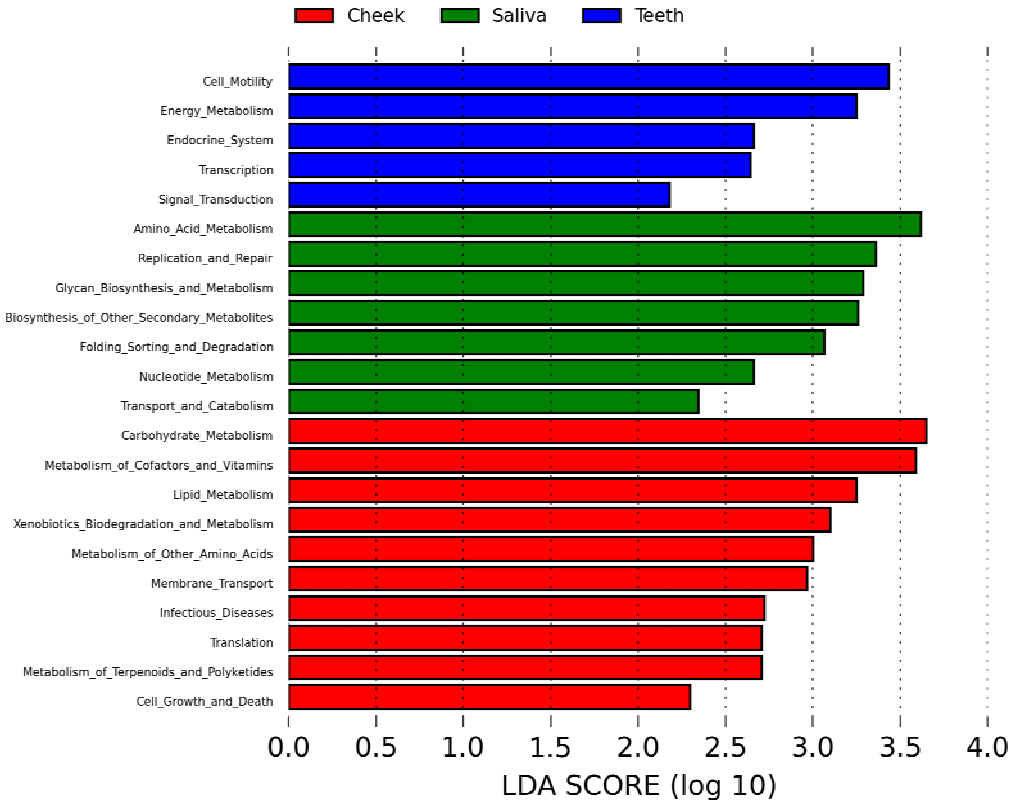


Figure S5. LDA scores for marker KEGG pathways enriched in each sampling site.

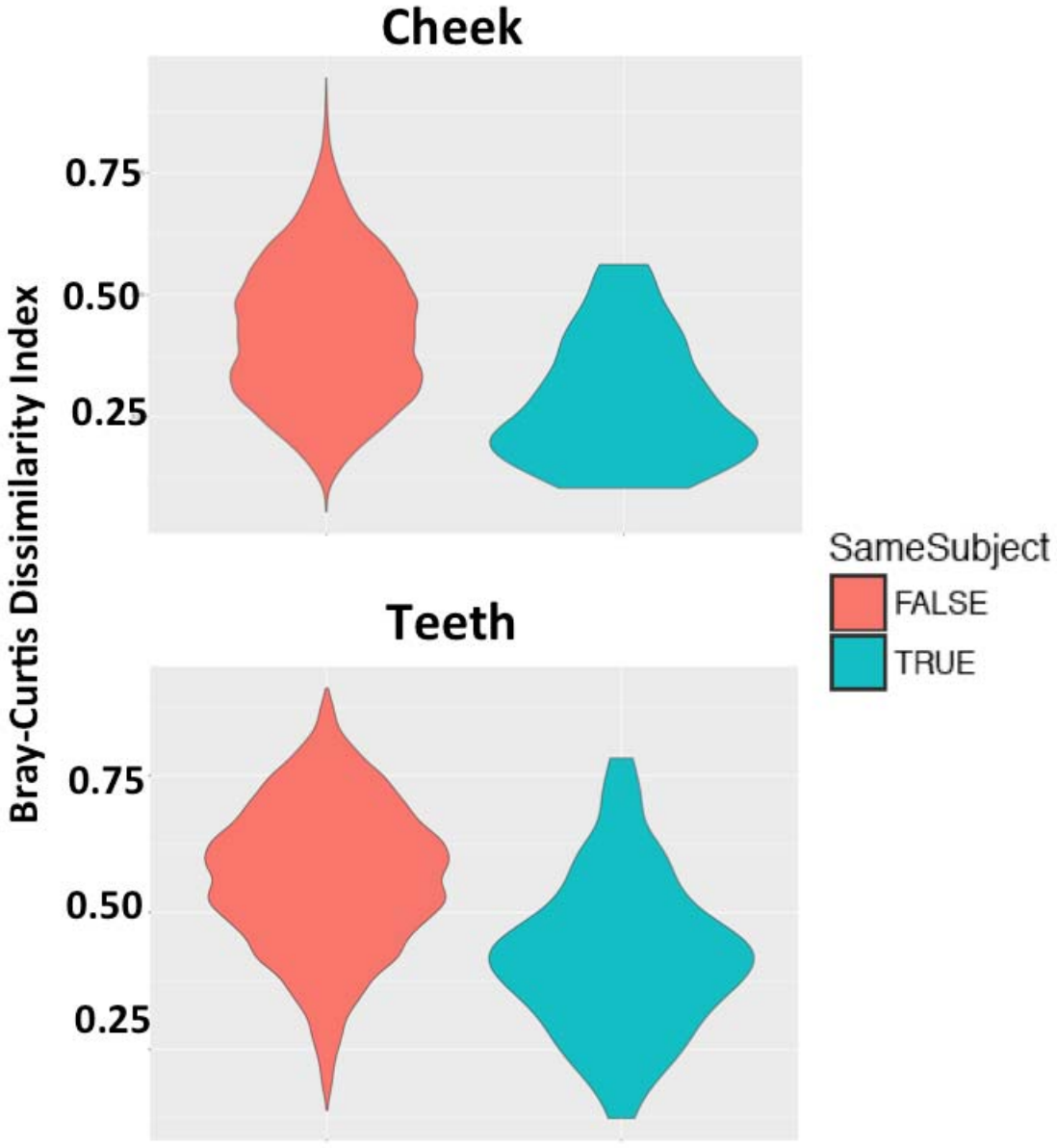


Figure S6. Bray-Curtis dissimilarity measures for inter and intra participant cheek (upper) and teeth (lower) samples. In both sampling sites, intra-participant samples show significantly greater similarity than inter-participant samples, while teeth samples show higher variability.

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