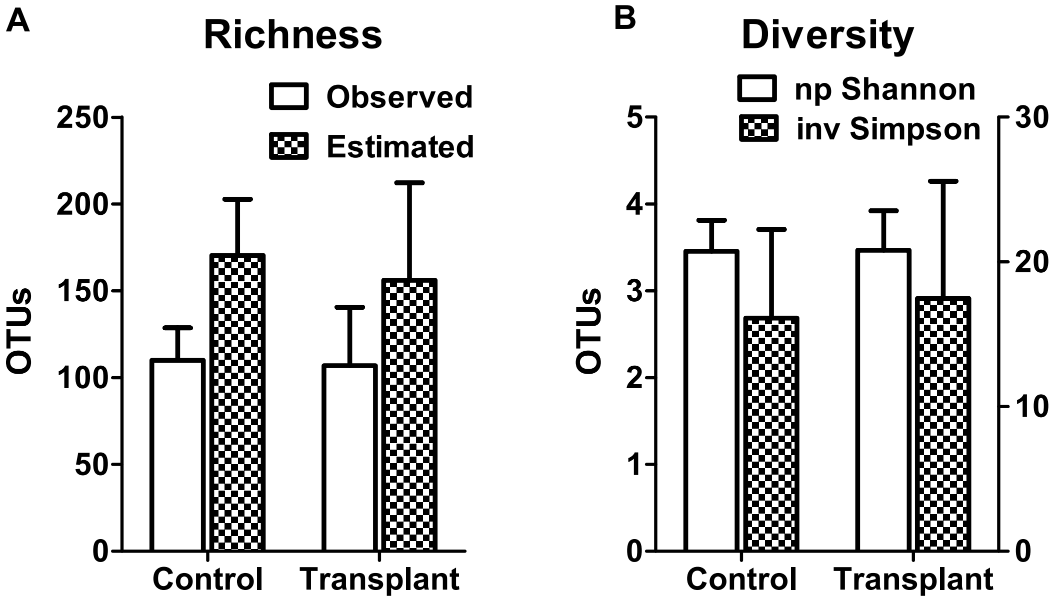


Figure S1. α-diversity in control and transplant subjects. Panel A depicts the average OTUs observed per subject and the average OTUs estimated by CatchAll to exist in each subject, for transplant and control groups. Panel B shows the average diversity found in each group as measured by the non-parametric Shannon index (np Shannon) and the inverse Simpson index (inv Simpson). There were no statistically significant differences between groups.

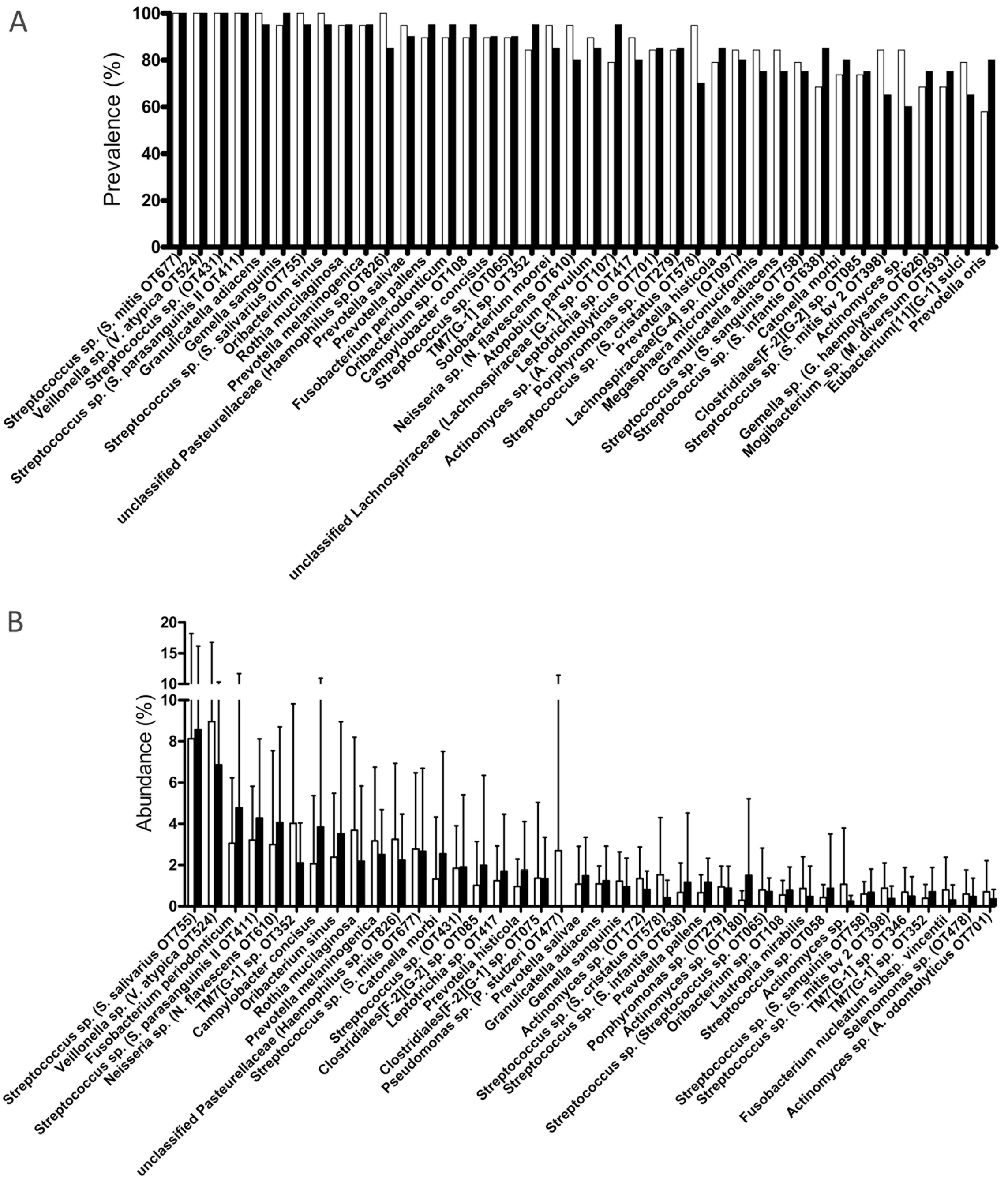


Figure S2. Most prevalent and most abundant OTUs in salivary communities. Panel A depicts the 40 most prevalent OTUs in control (white) and transplant (black) groups, while panel B depicts the 40 most abundant OTUs. No statistically significant differences in prevalence or abundance of these OTUs were found between groups.

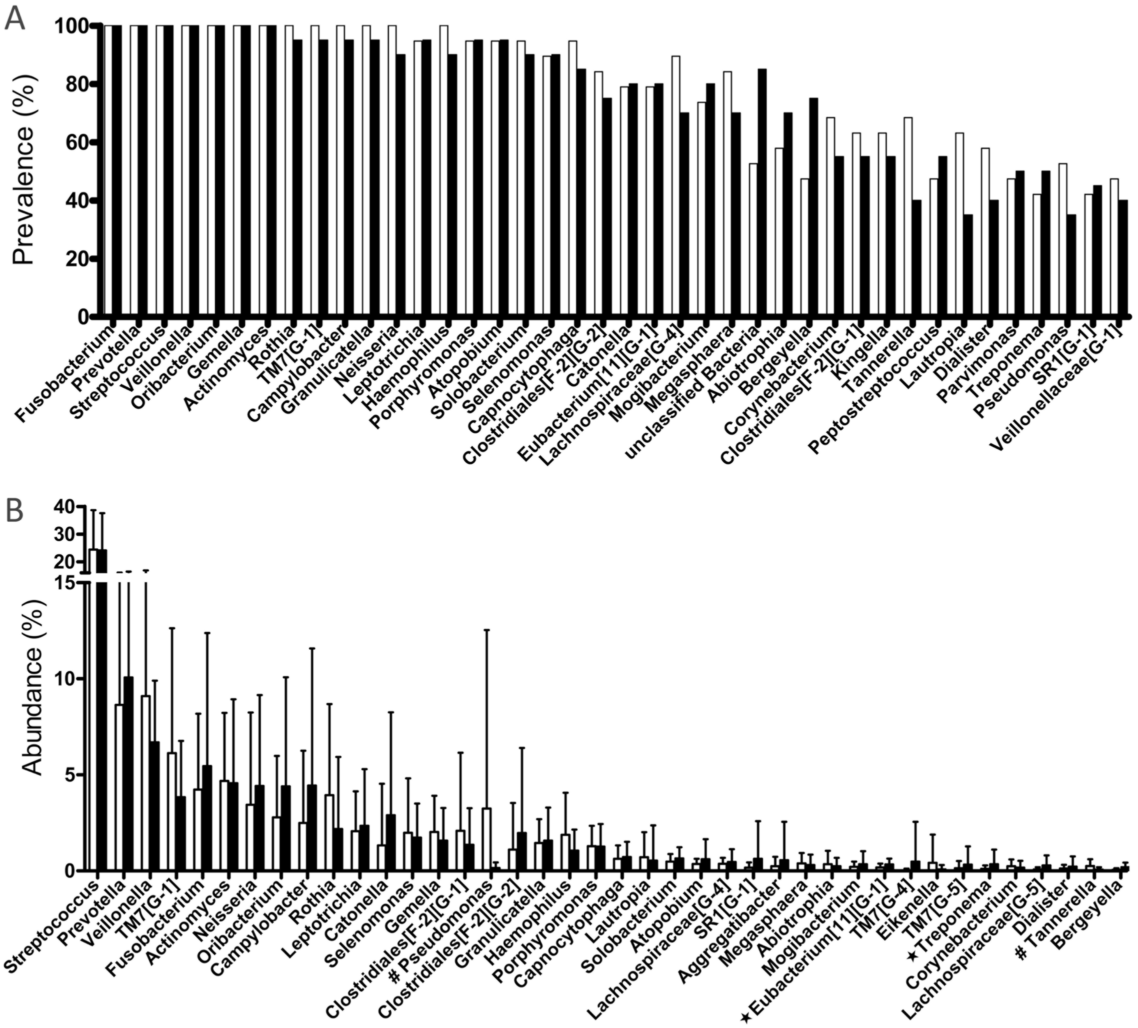
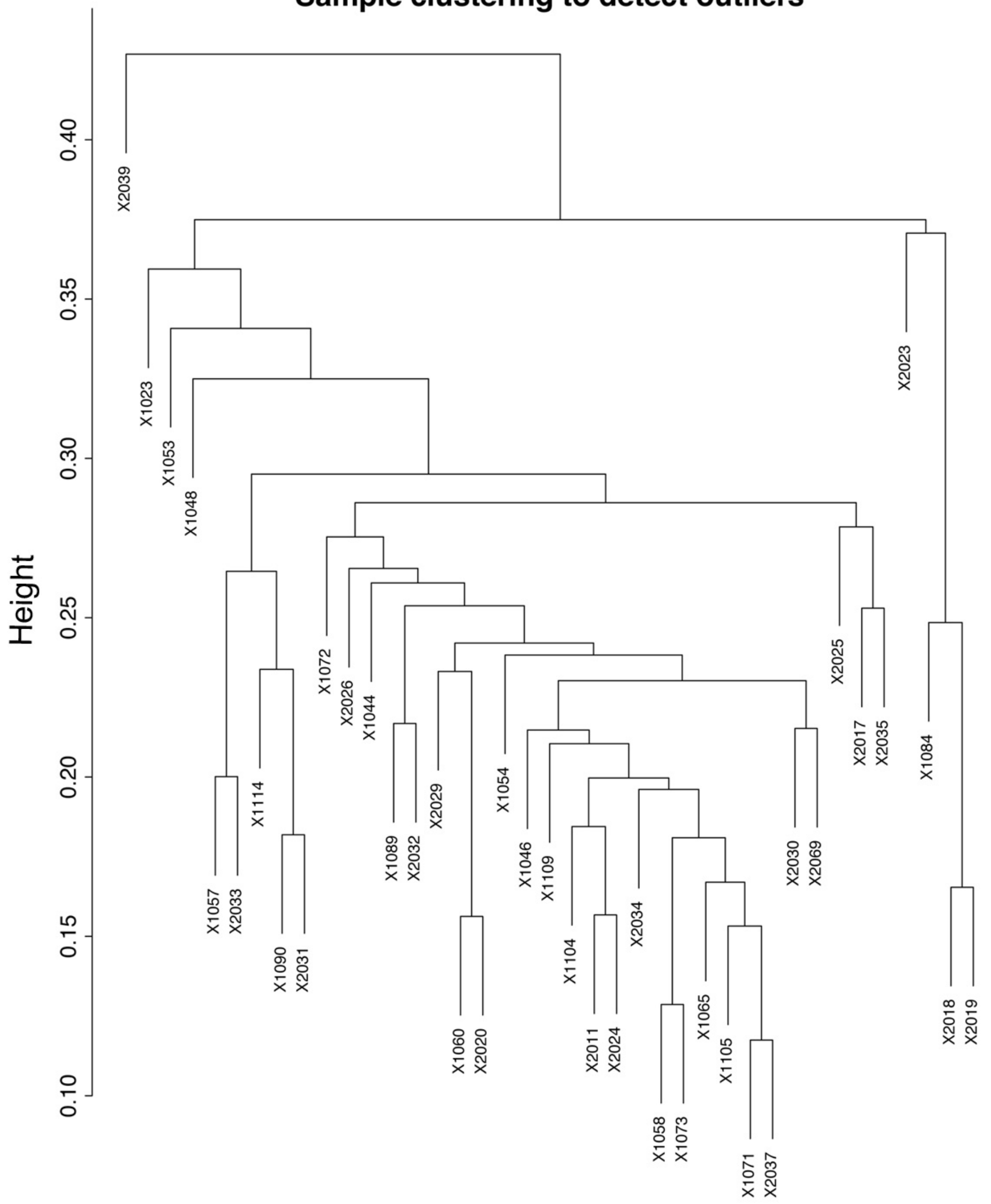


Figure S3. Most prevalent and most abundant genera in salivary communities. Panel A depicts the 40 most prevalent genera in transplant and control groups, while panel B depicts the most abundant genera. Genera with increased relative abundance in control subjects are marked with #, while genera with increased relative abundance in transplant subjects are marked with a star.



Sample clustering to detect outliers

Figure S4. Dendogram depicting absolute hierarchical clustering of all samples (transplant and control groups combined) prior to correlation network analysis.

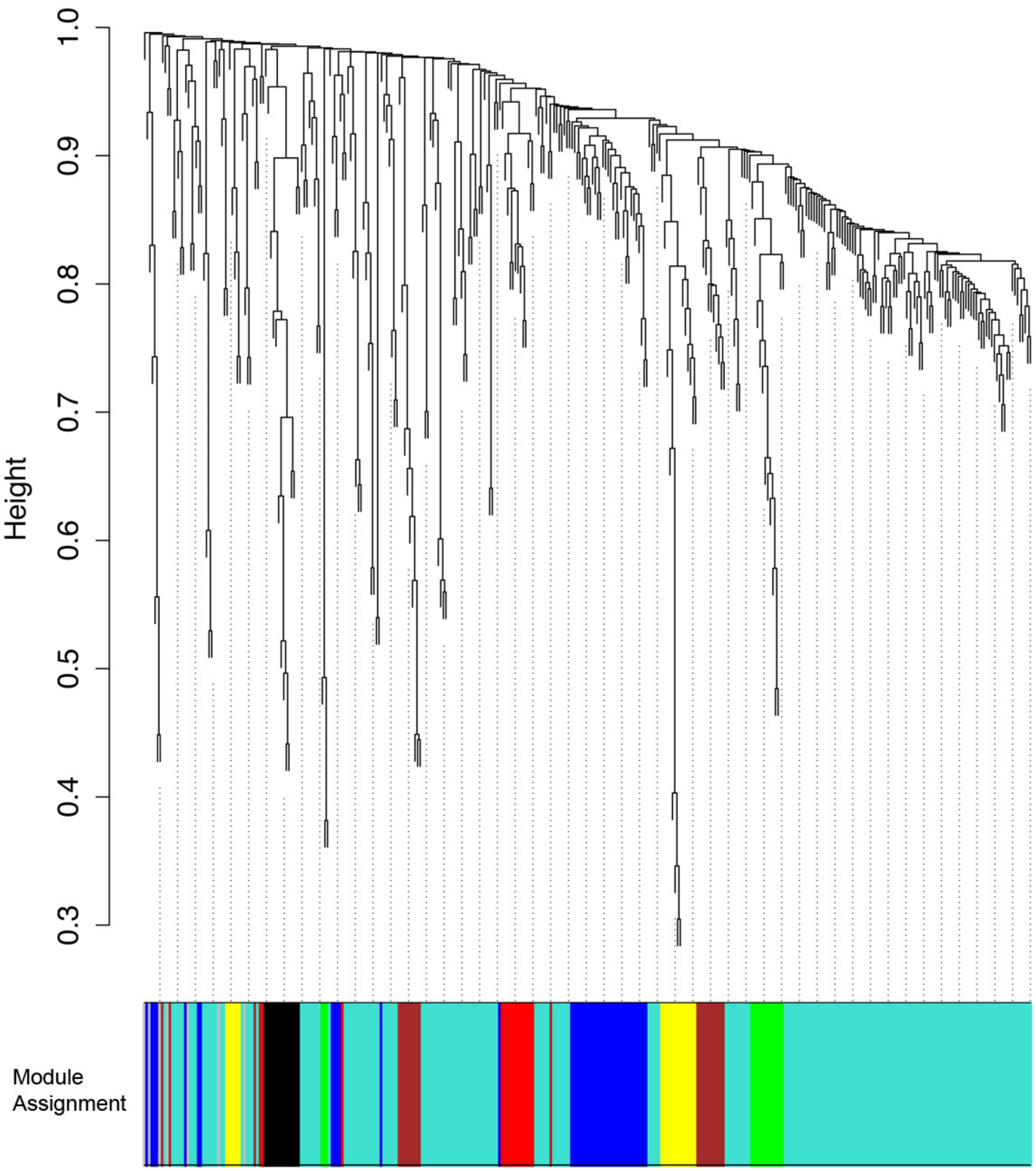


Figure S5. WGCNA correlation network results for OTUs in all samples. Figure depicts clustering dendogram for OTUs based on relative abundance data and the modules to which they were assigned. Eight different modules were identified, each represented by a different color.

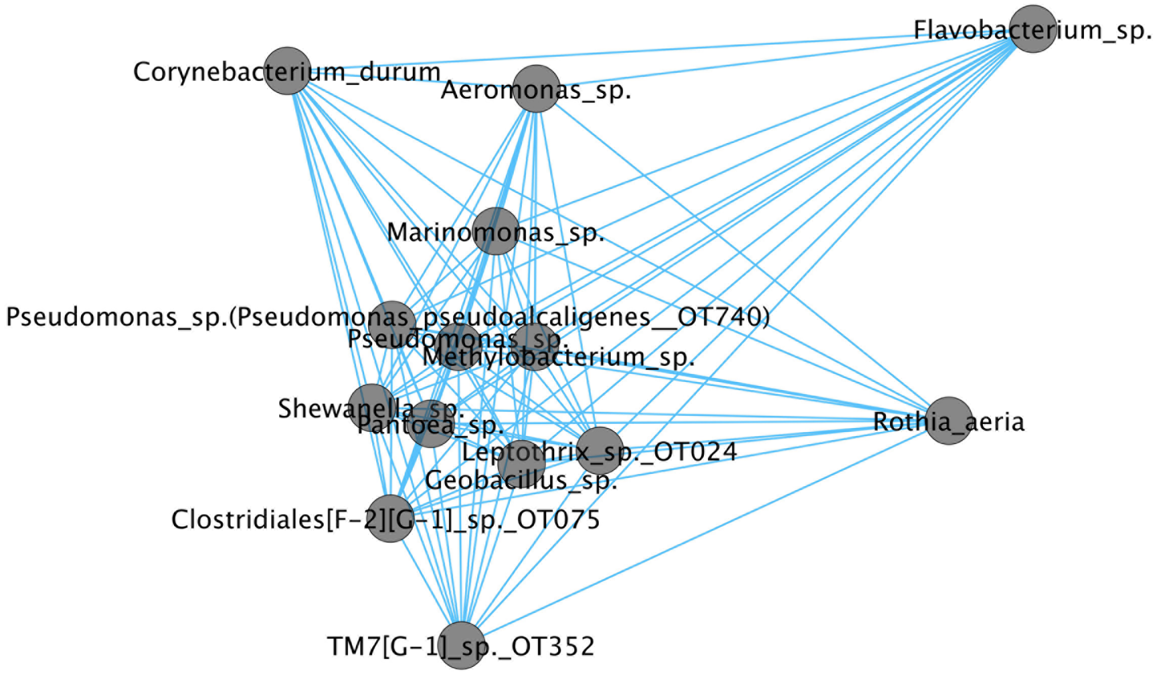


Figure S6. OTUs that comprise the black cluster, which was negatively associated with transplant status, and their connections. Each node in the network represents an OTU. Edge length represents adjacency between pairs of nodes.