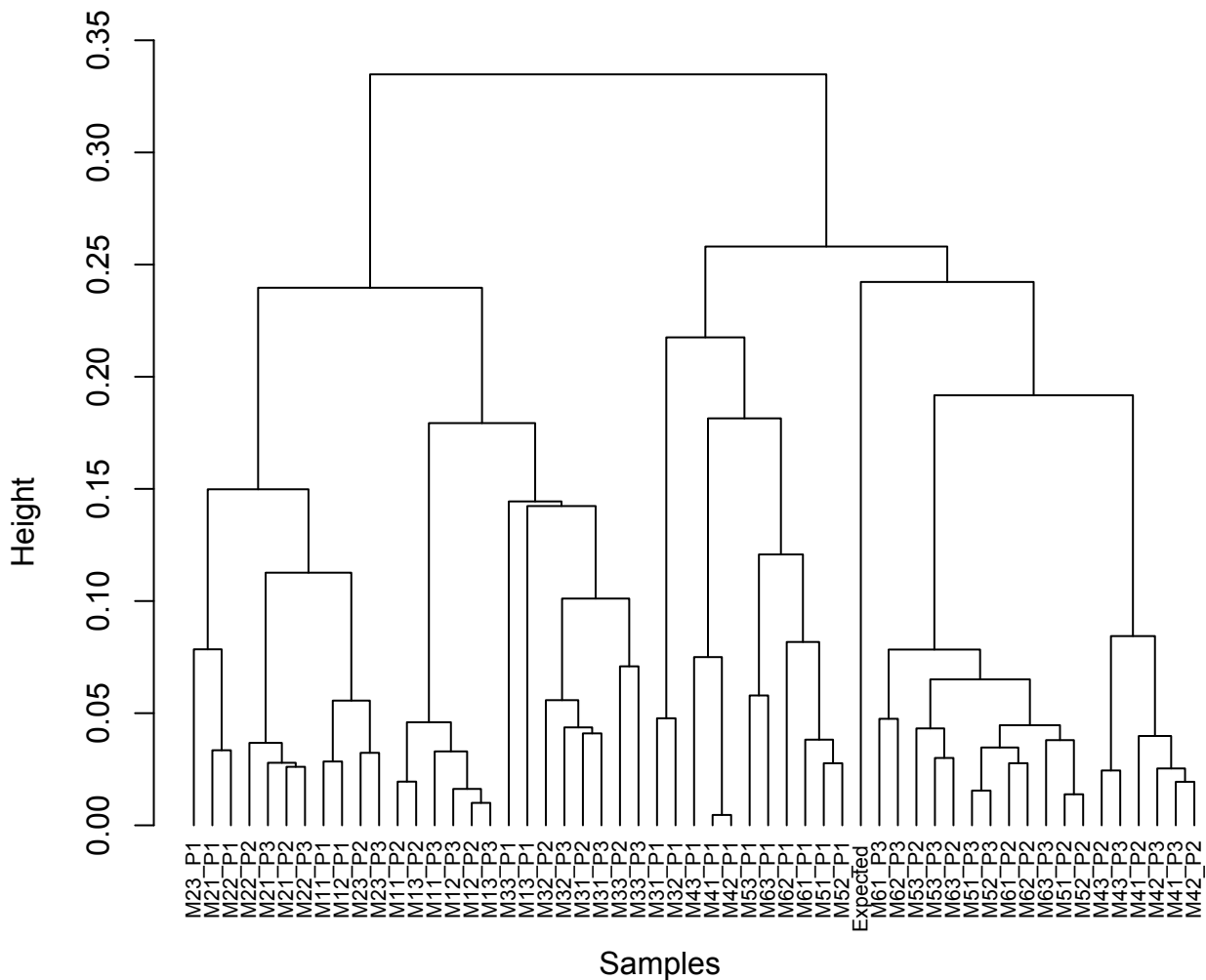


Impact of DNA extraction method and targeted 16S-rRNA hypervariable region on oral microbiota profiling

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Cluster Dendrogram



1 **Figure S1. Hierarchical clustering of the microbial profiles obtained using different**
2 **experimental protocols.** Bray–Curtis dissimilarity was calculated using the relative
3 abundance taxa at the species level. Based on the dissimilarity, the hierarchical clustering
4 analysis was performed using the complete linkage algorithm. Protocols that included
5 enzymatic-mechanical-lysis steps in DNA extraction procedure (e.g., M5 and M6) were
6 clustered with the expected microbiome structure, thus they produced better microbial diversity
7 representation than those without the extra steps in the procedure (e.g., M1, M2, and M3).
8 Moreover, samples from P2 (V3_V4) and P3 (V4_V5) tended to cluster closely to the expected
9 microbial structure.