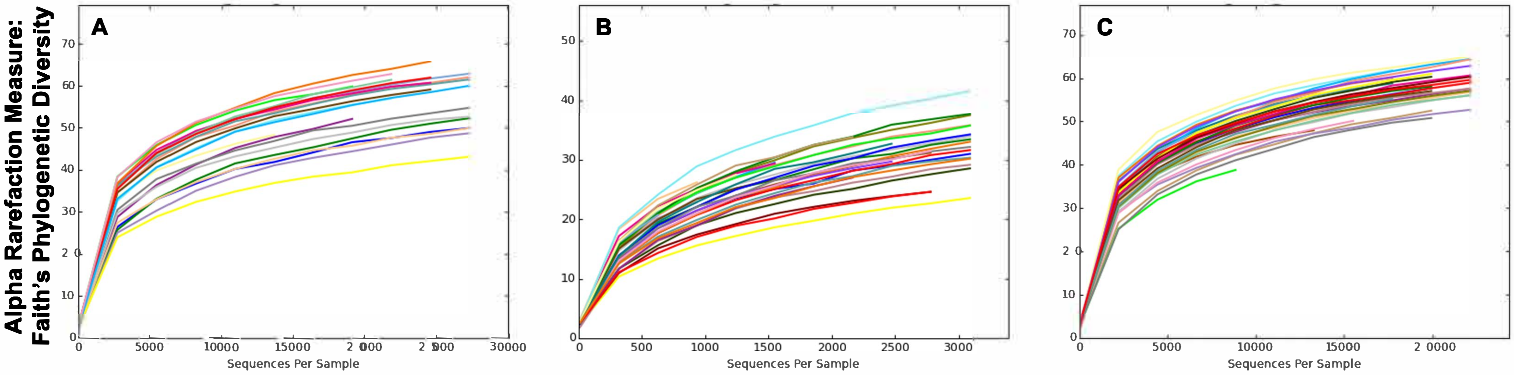

Figure S1. Alpha rarefaction curves for all three datasets, longitudinal (Illumina MiSeq; A), 454-Pyrosequencing (B) and Illumina MiSeq (C), comparing relative sampling rates across all samples utilized in the analyses**.**

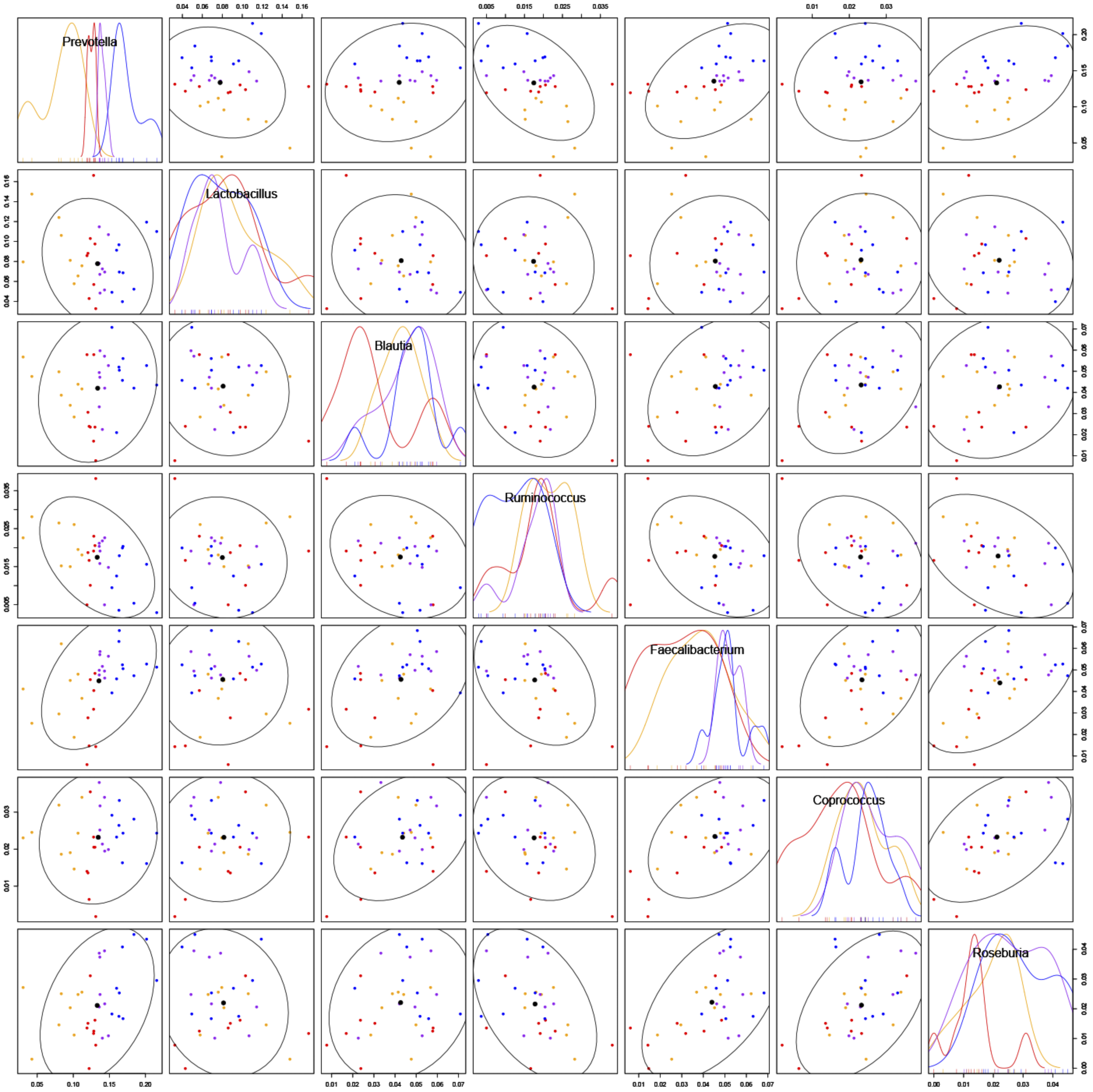

Figure S2. Pearson's correlations among abundant (>1%) genera in the 454-pyrosequencing data. Diagonals indicate the frequency distribution of each genus. Orange, red, purple and blue colors indicate samples categorized by quartiles of Prevotella abundance.

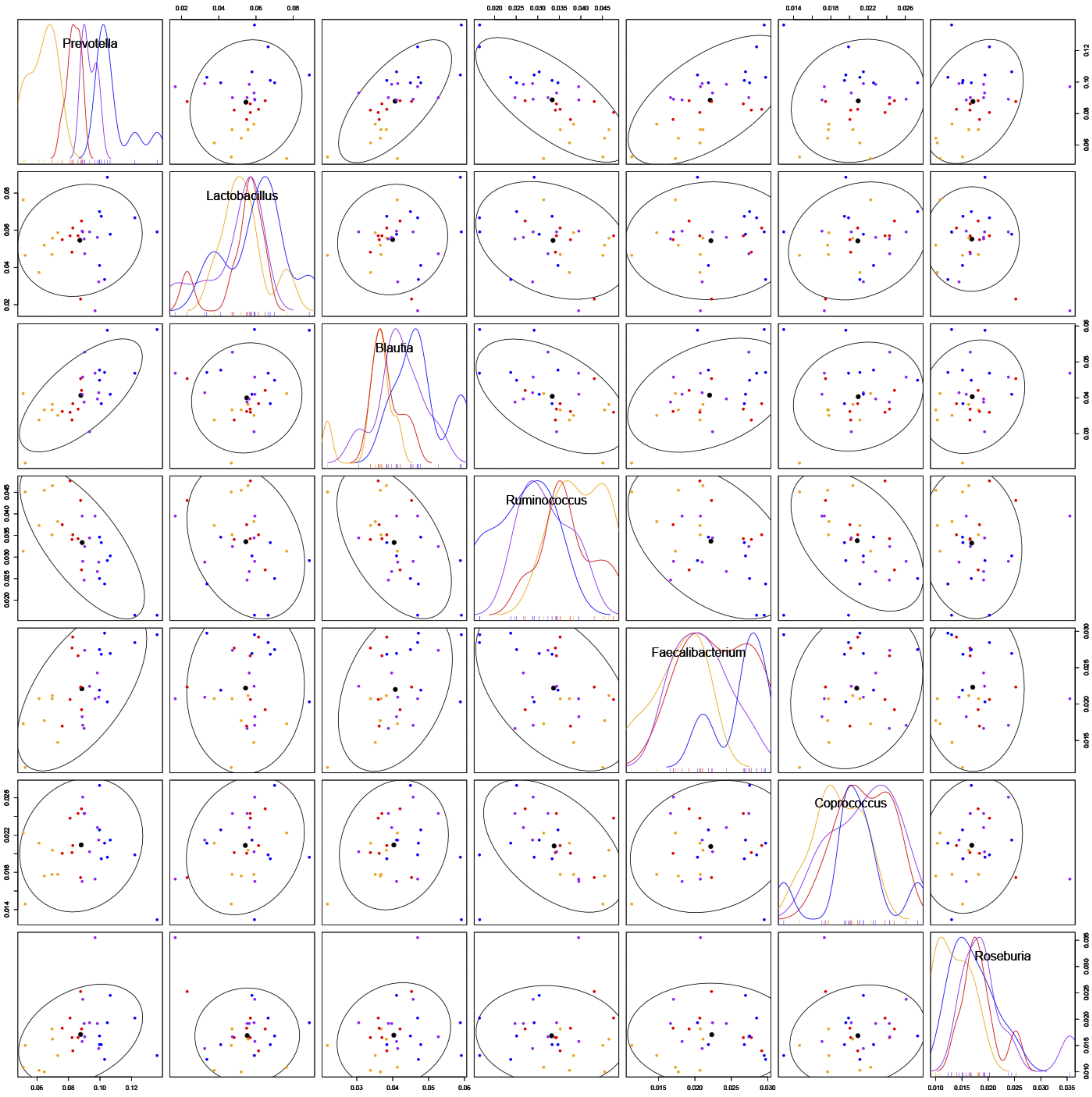

Figure S3. Pearson's correlations among abundant (>1%) genera in the Illumina MiSeq data. Diagonals indicate the frequency distribution of each genus. Orange, red, purple and blue colors indicate samples categorized by quartiles of Prevotella abundance.

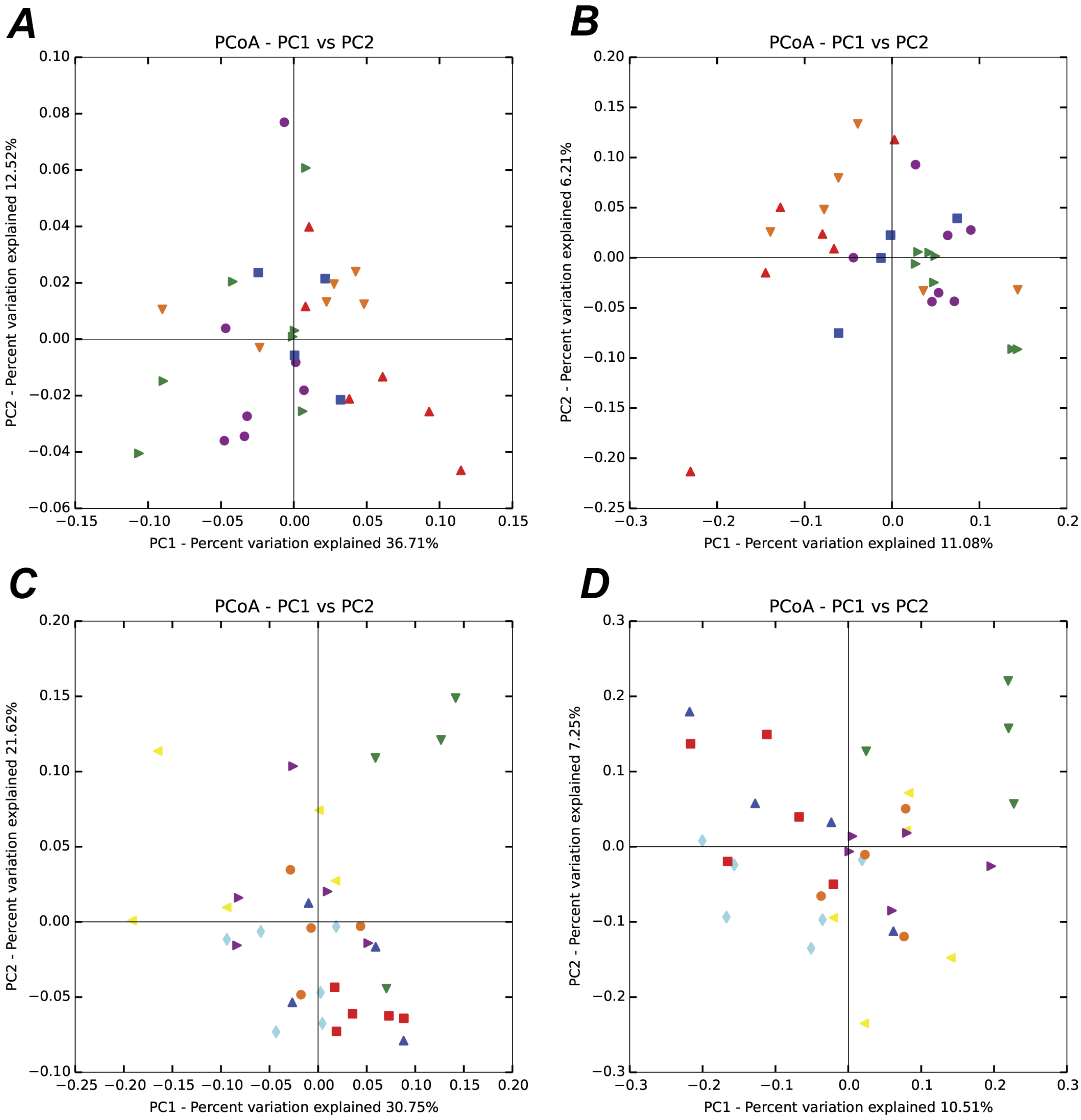

Figure S4. PCoA of beta diversity showing the microbial clustering among members in a social group. Microbial profiles of monkeys within a group were more similar in spite of individual differences in Prevotella abundance and associated taxa and overlap between some groups. Analyses of dissimilarity indicated significant differences in microbiota profiles across the 7 groups sequenced by Illumina MiSeq, using both weighted and unweighted UNIFRAC (A and B), and across the 5 groups sequenced with 454-pyrosequencing (C and D). See Results section for more details.