



FIG. S3. Unweighted Pair Group Method with Arithmetic Mean (UPGMA) cluster analysis of those samples from the three main sampling regions with four or more clones represented by full-length sequences, generated by calculating pairwise abundance-weighted non-normalized UniFrac metrics. Red, green, and blue branch colorings indicate sample origin (Loihi Seamount, Southern Mariana Trough, and the south Pacific Ocean group, respectively). Only jackknife values above 20 are shown at nodes. The scale bar represents the distance between samples in UniFrac units. The UniFrac distance metric between identical samples is 0, whereas samples with no lineage overlap have a value of 0.5 UniFrac units.