FIG S2 Phylogenetic tree of all ASVs of full-length 16S rRNA gene sequenced on Pacific Biosciences Sequel II platform. Package raxml (v8.0.0) (1) was used to construct the phylogeny, Phyloseq R package (2) was used to display the phylogeny.

1. Stamatakis A. 2014. RAxML version 8: a tool for phylogenetic analysis and post-analysis of large phylogenies. *Bioinformatics* 30:1312-3
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