



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
2. McMurdie PJ, Holmes S. 2013. phyloseq: an R package for reproducible interactive analysis and graphics of microbiome census data. *PLoS One* 8:e61217