

Table S1. Analysis workflow and QIIME2 parameter settings used in this study\*

QIIME2 command (A)	Options
qiime tools import	--type 'SampleData[PairedEndSequencesWithQuality]' --input-path manifest_XX.csv --output-path demux_XX.qza --input-format PairedEndFastqManifestPhred33
qiime demux summarize	--i-data demux_XX.qza --o-visualization demux.qzv
qiime dada2 denoise-paired	--i-demultiplexed-seqs demux_XX.qza --o-table table_XX.qza --o-representative-sequences rep-seqs_XX.qza --p-trim-left-f 0 --p-trim-left-r 0 --p-trunc-len-f 250 --p-trunc-len-r 250 --o-denoising-stats stats_XX.qza --p-n-threads 0
qiime metadata tabulate	--m-input-file stats_XX.qza --o-visualization stats_XX.qzv
qiime feature-table summarize	--i-table table_XX.qza --o-visualization table_XX.qzv --m-sample-metadata-file XX.txt
qiime feature-table tabulate-seqs	--i-data rep-seqs_XX.qza --o-visualization rep-seqs_XX.qzv
qiime feature-classifier classify-sklearn	--i-classifier (B).qza --i-reads rep-seqs_XX.qza --o-classification taxonomy.rep-seqs_XX.qza --p-n-jobs 18
qiime metadata tabulate	--m-input-file taxonomy.rep-seqs_XX.qza --o-visualization taxonomy.rep-seqs_XX.qzv
qiime taxa barplot	--i-table table_XX.qza --i-taxonomy taxonomy.rep-seqs_XX.qza --m-metadata-file XX.txt --o-visualization taxa-bar-plots_XX.qzv
qiime phylogeny align-to-tree-mafft-fasttree	--i-sequences rep-seqs_XX.qza

	--o-alignment aligned-rep-seqs_XX.qza --o-masked-alignment masked-aligned-rep-seqs_XX.qza --o-tree unrooted-tree_XX.qza --o-rooted-tree rooted-tree_XX.qza --p-n-threads 0
qiime diversity alpha-rarefaction	--i-table table_XX.qza --i-phylogeny rooted-tree_XX.qza --p-max-depth XXXXX --m-metadata-file XX.txt --o-visualization alpha-rarefaction_XX.qzv
qiime diversity core-metrics-phylogenetic	--i-phylogeny rooted-tree_XX.qza --i-table table_XX.qza --p-sampling-depth XXXX --m-metadata-file XX.txt --output-dir core-metrics-results-XX
qiime diversity beta-group-significance (for bray curtis distance)	--i-distance-matrix bray_curtis_distance_matrix.qza --m-metadata-file XX.txt --m-metadata-column XX --o-visualization bray_curtis_distance_Group.qzv --p-pairwise
qiime diversity beta-group-significance (for weighted unifrac distance)	--i-distance-matrix weighted_unifrac_distance_matrix.qza --m-metadata-file XX.txt --m-metadata-column XX --o-visualization weighted_unifrac_distance_Group.qzv --p-pairwise

A : QIIME2 version 2019.4 (<https://docs.qiime2.org/2019.4/>) was used in this study.

B : silva-132-99-nb-classifier

\*The default setting of QIIME2 software, where the confidence of the taxon classification was 0.7, was used in this study.