

Supporting Information

S1 File. SF1_File_Supplemental_Materials.pdf Contains supplemental figures (1-13), supplemental methods, and tables (1-4).

S2 File. SF2_File_Pristine_Mangrove_Tidal_Zone_Literature_Review.odt - Here we present a short literature review of prokaryotic community studies that have focused on Impacted and Pristine Mangroves or which have studied differences between the tidal zone microhabitats.

S3 File. SF3_Files_Supplemental_QIIME2_visualization.zip - Visualization files capable of being viewed interactively using <https://view.qiime2.org/>:

ReadMe.txt - Internal nomenclature.

Feature_table.qzv - a visualization of Feature ID (aka ASV) within samples.

Taxa-bar-plots.qzv - a visualization of taxa proportion per taxonomic level per site.

Zhou_taxa-bar-plots.qzv - a visualization of taxa proportion per taxonomic level per site including data from Zhou et al. 2017.

S4 File. SF4_Files_Supplemental_QIIME2_taxonomy_files.zip - Visualization files capable of being viewed interactively using <https://view.qiime2.org/>:

ReadMe.txt - Internal nomenclature.

Taxonomy.qzv - visualization of the assigned taxa for each Feature ID.

S5 File. SF5_Files_Supplemental_Metadata.zip - This zipped folder contains metadata necessary to run QIIME2 and Vegan.

Environmental_Variables.csv - tab-separated table containing the environmental variable data (Supplemental Table 3) used by Vegan metaMDS, envfit.

MappingFile_Mangrove.csv - tab-separated table containing the replicate and site metadata for QIIME2.

Zhou_MappingFile_Mangrove.csv - tab-separated table containing the replicate and site metadata for this study and Zhou et al. 2017.

S6 File. SF6_Files_Supplemental_Scripts.zip - This zipped folder contains all Shell, Python, and R scripts used in this paper.

Aldex_run.r - R script for running ALDEx2 to calculate significant differences in KO abundance between sites.

juntar.py - python script for combining vsearch and paired-end reads. Used in 'Read_preprocessing.sh'

novembro.py - python script for performing taxa abundance analysis. Used in 'Novembro_run.sh'

Novembro_run.sh - shell script for running novembro.py

PICRUST2_run.sh - shell script for running PICRUST2

QIIME2_run.sh - shell script for running QIIME2

Read_preprocessing.sh - shell script for running QIIME2 vsearch and juntar.py

sigilo.py - python script for generating visualizations and analysis of PICRUST2 data.

Sigilo_run.sh - shell script for running sigilo.py

Vegan.r - R script for running, metaMDS, envfit, and capscale.

Zhou_QIIME2_run_v2.sh - shell script for running QIIME2 analysis on Zhou et al 2017.

S7 File. SF7_Files_Supplemental_Intermediary_Files.zip - Several files containing intermediate data used in the analysis of the data.

Normalized_taxa_abundance_family.tab - Tab-separated value table containing the normalized abundances for each family taxa. Columns are Taxa, Normalized abundances for Sublittoral, Intertidal, and Supralittoral, followed by Bonferroni corrected p-value calculations for binomial exact test between sites.

KO_taxa_specific_enrichment.tab - Tab-separated value table representing the output of sigilo script using labelled metabolic_KOs (from Supplemental File SF1). Columns are KO, Log10 transformed predicted functional abundance in Sublittoral, Intertidal, and Supralittoral.

KEGG Mapper_Reconstruction.tab - Tab-separated value table representing the output of KEGG Mapper Reconstruction performed on the significantly enriched KOs per zone identified using sigilo. Columns are Taxa, Zone, and Tab_delimited_modules.