Retain-resolve Algorithm: Exported QC Files: If export = TRUE $\overline{\Pi}$ mraprev_original.csv Original input Mean relative abundance and prevalence of each taxa in dir/retainresolve the original phyloseq object (dat) phyloseq object /plot_AbundSummary original_mra_prev.tiff Mean relative abundance and prevalence summary plots for taxa in the original phyloseg object (dat) Remove empty taxa 1. (prevalence = 0) dir/retainresolve /plot_AbundSummary rm-empty_mra_prev.tiff Empty taxa removed dat_empty Mean relative abundance and prevalence summary plots for taxa in dat_empty phyloseq object phyloseq object /TotalAbundance abund_diff_glomprefilter.csv **User Input:** 2. Glom ASVs below set thresholds 1) mra_prev.ASV Total abundance difference between original phyloseq and 2) prev.ASV retain-resolve phyloseq object pre-filter for each sample /mra_prevalence \blacksquare mraprev glomgenus.csv Mean relative abundance and prevalence of each taxa after ASV retention/genus glom and prior to genus filtering. All resolved genus-level taxa and retained ASVs /plot_AbundSummary dir/retainresolve glom-prefilter_mra_prev.tiff dat_retres_prefilter Mean relative abundance and prevalence summary plots after ASV retention/genus glom and prior to genus filtering. phyloseq object /taxa_lists passASV.csv and failASV.csv **User Input:** 3. Filter genus-level taxa below set thresholds ← List of ASVs that were retained (passed at least 1 minimum threshold) or were resolved (failed minimum thresholds). 1) mra_prev.genus 2) prev.genus /taxa_lists retainresolve_taxonomy_prefilter.csv Taxonomy of each retained ASV and resolved genus taxa. Filtered genus-level taxa and retained ASVs /TotalAbundance \blacksquare abund_diff_glom_postfilter dat_glom phyloseq object Total abundance difference between original phylosea and retain-resolve phyloseq object after filtering genus-level taxa. Total abundance difference is expected at this step. "Other" taxa counts are derived from this file. Add filtered counts to "Other" taxa 4. /mra prevalence Retain-resolved taxa with Other \blacksquare abund diff glom postfiler.csv taxa classification Total abundance difference between original phyloseq and dir/retainresolve retain-resolve phyloseq object after filtering genus-level Note: Total abundance is equivalent to dat. taxa. Difference will be 0 for all samples. dat_glom_aldex phyloseq object /plot_AbundSummary original_mra_prev.tiff Mean relative abundance and prevalence summary plots for taxa in the original phyloseq object (dat). Return taxonomic level Return retain-resolved (ASV or genus) for each phyloseq objects taxa **Exported Phyloseq (.RData):** If export = TRUE dir/Physeq_glommed_objects dat = original input phyloseq object glom.spID.levels dat_glom, dat_rel_glom, dat_glom_aldex dat empty = empty taxa removed dat_empty_rel = relative abundance calculated from dat_empty dat_retres_prefilter = retained ASVs and resolved genus taxa before genus filter dat_glom = retained ASV-level and filtered genus-level taxa

Phyloseq objects

Quality control files

Export graphs

Dataframe

dat_glom_aldex = ASV-retained and postfilter genus-level phyloseq with Other taxa dat_rel_glom = relative abundance

calculated from dat_glom_aldex. Other

taxa removed.