

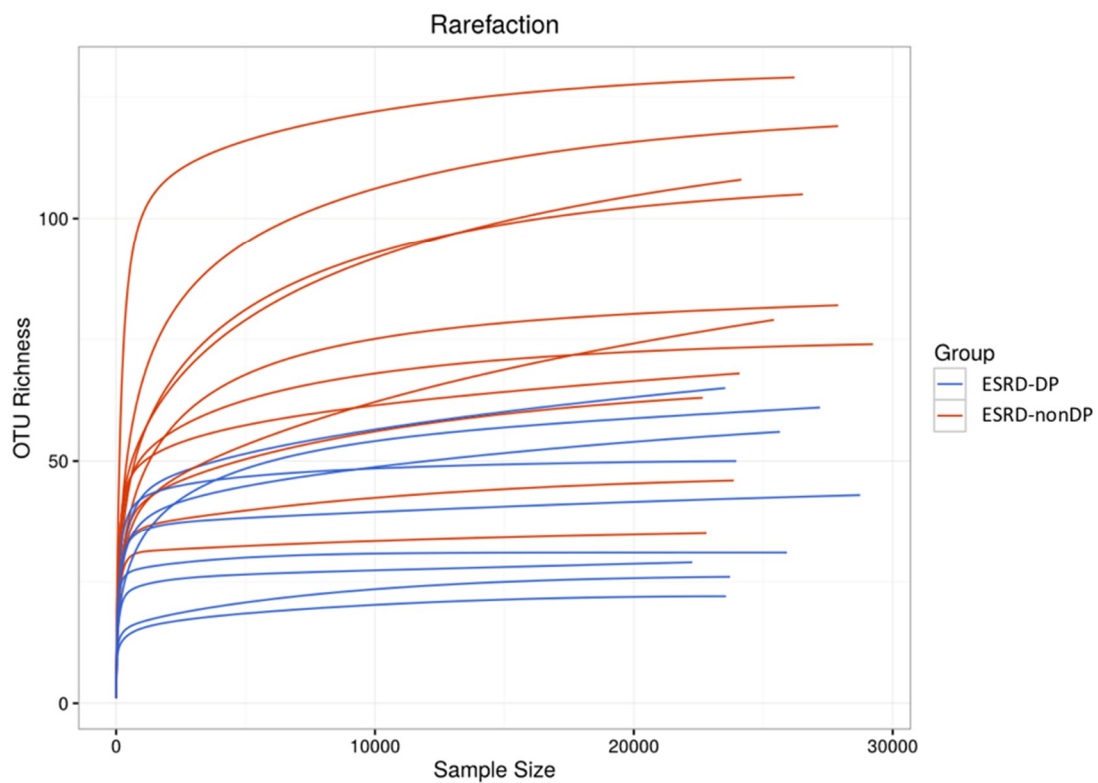
## Supplementary material

# Peritoneal Microbiome in End-Stage Renal Disease Patients and the Impact of Peritoneal Dialysis Therapy

Liliana Simões-Silva, Ricardo Araujo, Manuel Pestana, Isabel Soares-Silva,  
Benedita Sampaio-Maia

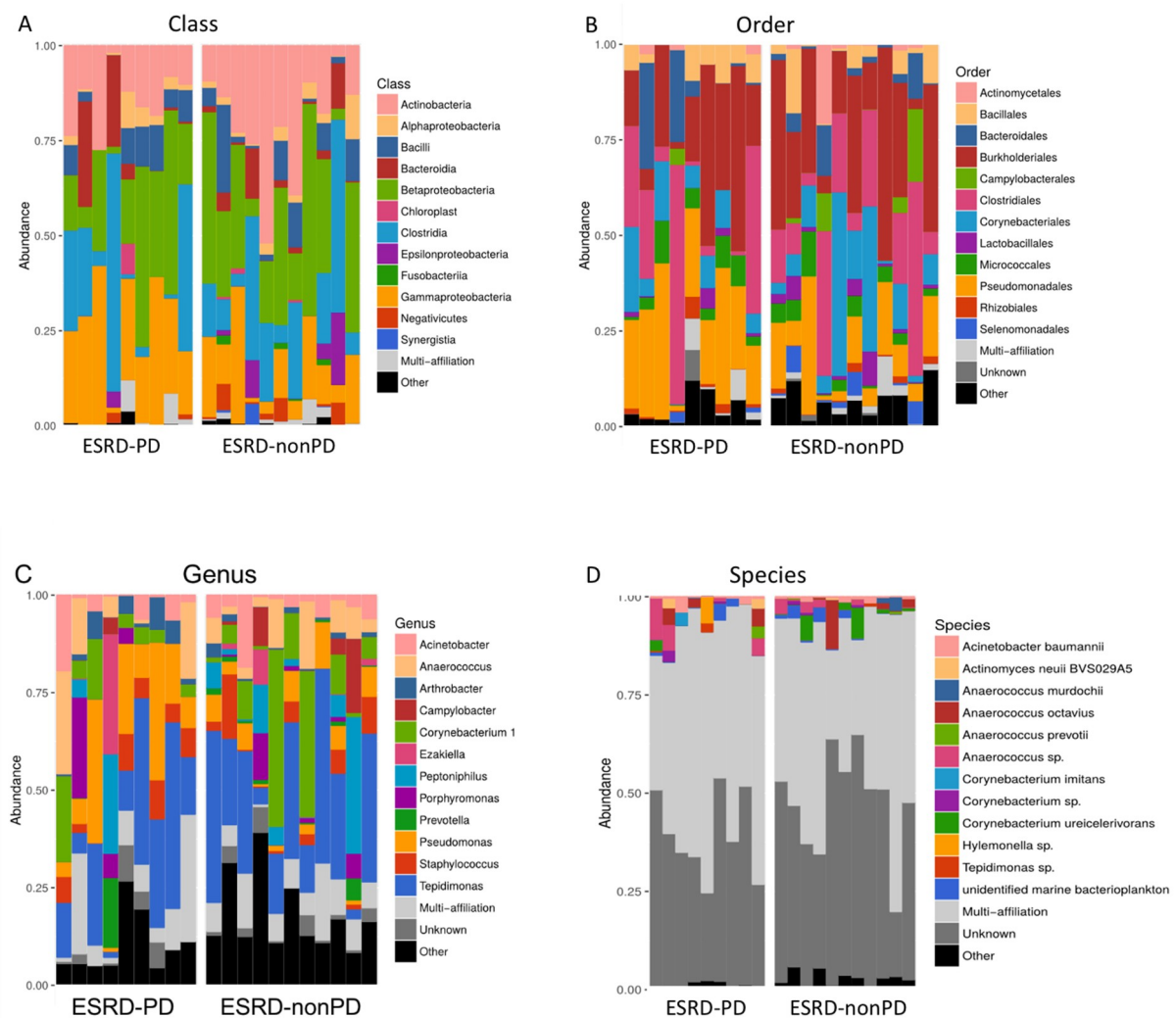
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**Figure S1**



**Figure S1:** The rarefaction curves plotted with all groups cumulatively. The rarefaction analysis curves suggest the sample diversity was captured as expected given the average sequence pairs classified into operational taxonomic units (OTU).

**Figure S2**



**Figure S2:** Relative proportion taxa for class (A), order (B), genus (C), and species (D).

Taxa are identified by name in the plot for abundance >1%. Taxa are merged into the

“Other” category only if it exists in any sample with abundance greater than 0.01%.

Taxa are merged into the “Multi-affiliation” category when they can correspond to

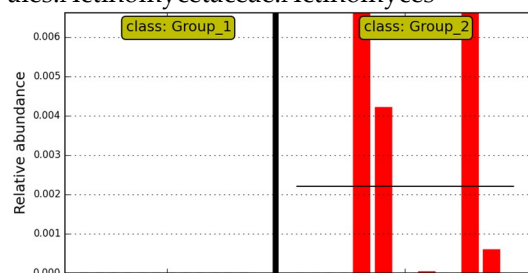
two or more different taxa. ESRD-PD – End-stage renal disease patients undergoing

peritoneal dialysis; ESRD-nonPD – End-stage renal disease patients with intact

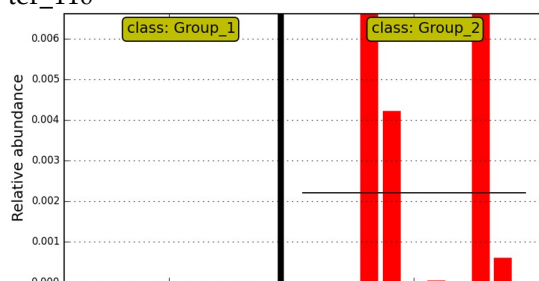
peritoneal cavity.

Figure S3

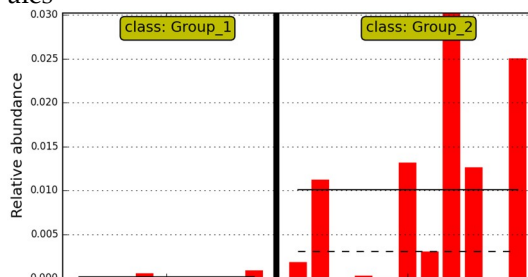
A Bacteria.Actinobacteria.Actinobacteria.Actinomycetales.Actinomycetaceae.Actinomyces



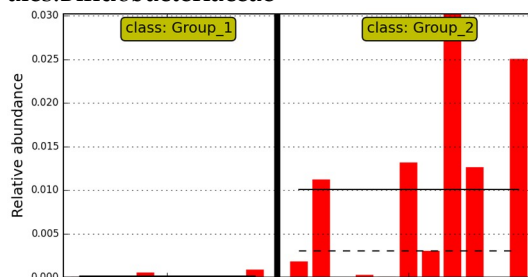
B Bacteria.Actinobacteria.Actinobacteria.Actinomycetales.Actinomycetaceae.Actinomyces.Unknown.Cluster\_110



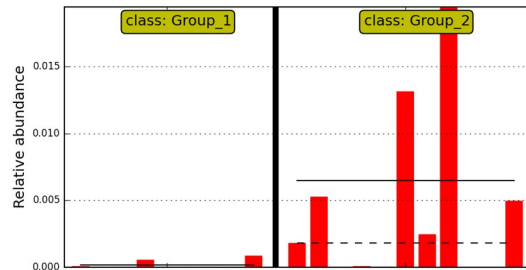
C Bacteria.Actinobacteria.Actinobacteria.Bifidobacteriales



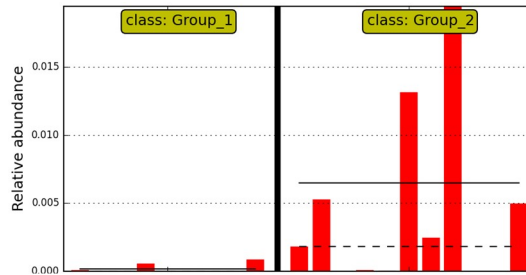
D Bacteria.Actinobacteria.Actinobacteria.Bifidobacteriales.Bifidobacteriaceae



E Bacteria.Actinobacteria.Actinobacteria.Bifidobacteriales.Bifidobacteriaceae.Bifidobacterium



F Bacteria.Actinobacteria.Actinobacteria.Bifidobacteriales.Bifidobacteriaceae.Bifidobacterium.Multi\_affiliation



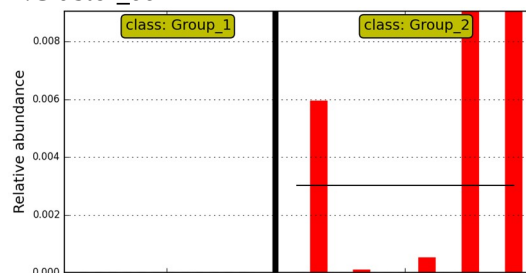
G Bacteria.Actinobacteria.Actinobacteria.Bifidobacteriales.Bifidobacteriaceae.Gardnerella



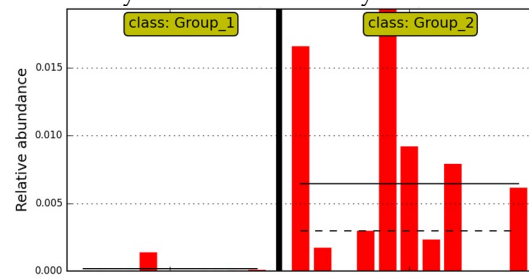
H Bacteria.Actinobacteria.Actinobacteria.Bifidobacteriales.Bifidobacteriaceae.Gardnerella.Multi\_affiliation



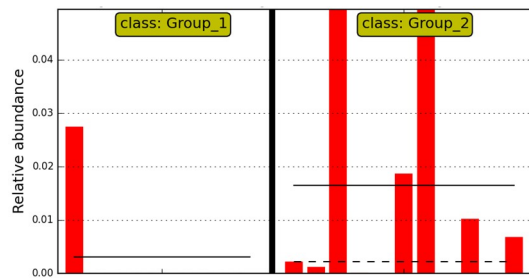
I Bacteria.Actinobacteria.Actinobacteria.Bifidobacteriales.Bifidobacteriaceae.Gardnerella.Multi\_affiliation.Cluster\_88



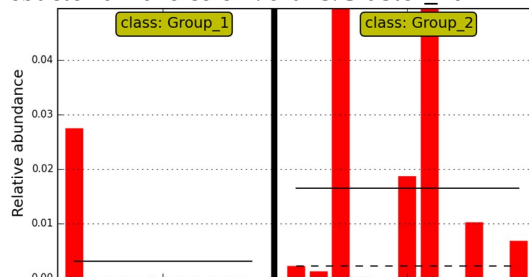
J Bacteria.Actinobacteria.Actinobacteria.Corynebacterales.Corynebacteriaceae.Corynebacterium



K Bacteria.Actinobacteria.Actinobacteria.Corynebacterales.Corynebacteriaceae.Corynebacterium1.Corynebacteriummureicelerivorans



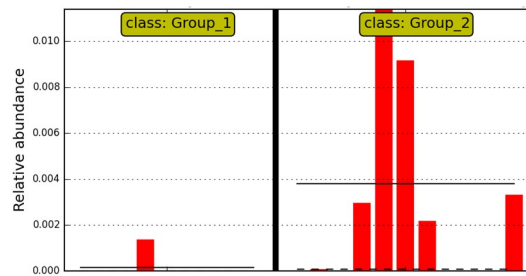
L Bacteria.Actinobacteria.Actinobacteria.Corynebacterales.Corynebacteriaceae.Corynebacterium1.Corynebacteriummureicelerivorans.Cluster\_26



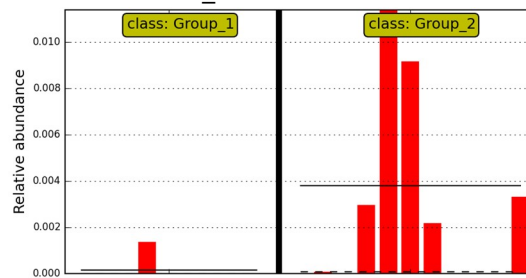
M Bacteria.Actinobacteria.Actinobacteria.Corynebacterales.Corynebacteriaceae.Corynebacterium1.Unknown.Cluster\_18



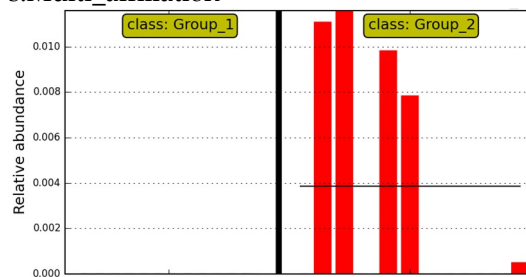
N Bacteria.Actinobacteria.Actinobacteria.Corynebacterales.Corynebacteriaceae.Corynebacterium.Multi-affiliation



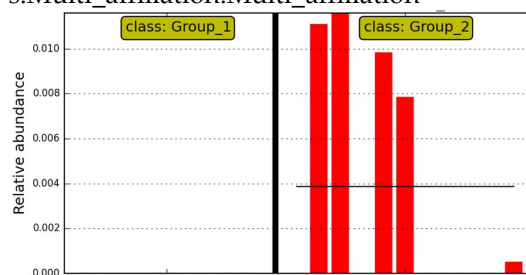
O Bacteria.Actinobacteria.Actinobacteria.Corynebacteriales.Corynebacteriaceae.Corynebacterium.Multi\_affiliation.Cluster\_82



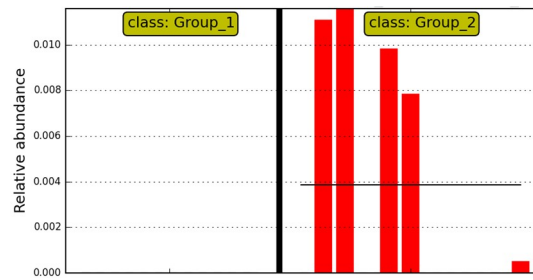
P Bacteria.Actinobacteria.Actinobacteria.Micrococcales.Multi\_affiliation



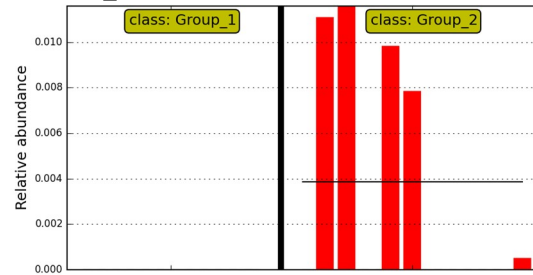
Q Bacteria.Actinobacteria.Actinobacteria.Micrococcales.Multi\_affiliation.Multi\_affiliation



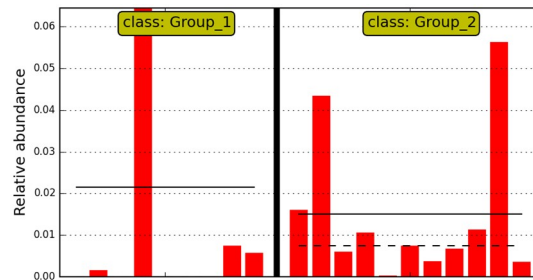
R Bacteria.Actinobacteria.Actinobacteria.Micrococcales.Multi\_affiliation.Multi\_affiliation.Multi\_affiliation



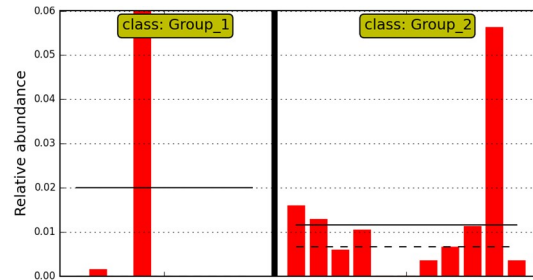
S Bacteria.Actinobacteria.Actinobacteria.Micrococcale  
s.Multi\_affiliation.Multi\_affiliation.Multi\_affiliation  
.Cluster\_77



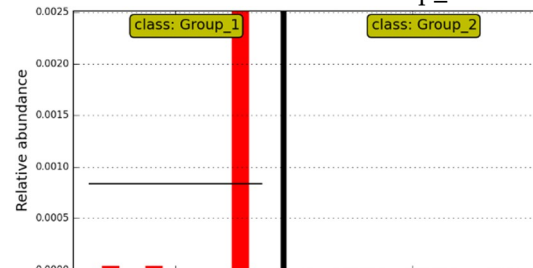
T Bacteria.Bacteroidetes.Bacteroidia.Bacteroidales.Pre  
votellaceae



U Bacteria.Bacteroidetes.Bacteroidia.Bacteroidales.Pre  
votellaceae.Prevotella

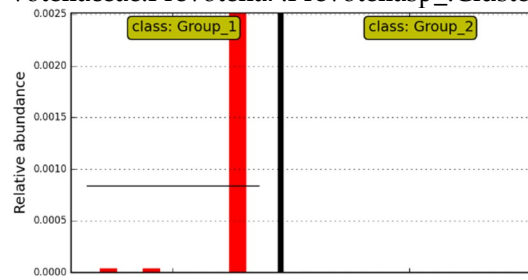


V Bacteria.Bacteroidetes.Bacteroidia.Bacteroidales.Pre  
votellaceae.Prevotella7.Prevotellasp\_

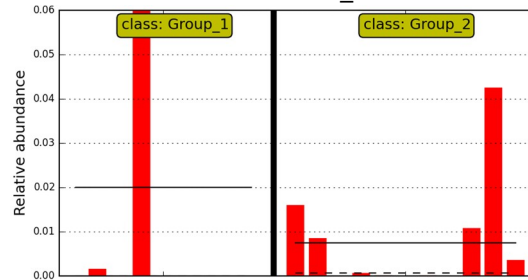




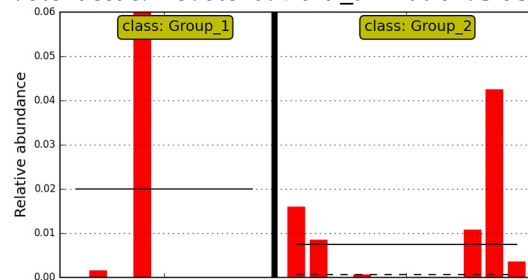
W Bacteria.Bacteroidetes.Bacteroidia.Bacteroidales.Pre  
votellaceae.Prevotella7.Prevotellasp\_.Cluster\_227



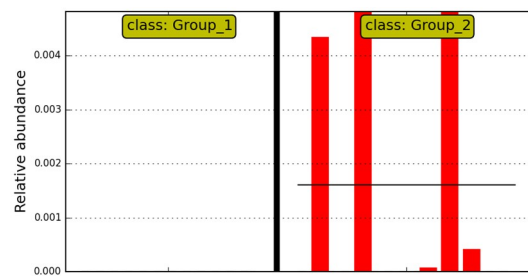
X Bacteria.Bacteroidetes.Bacteroidia.Bacteroidales.Pre  
votellaceae.Prevotella.Multi\_affiliation



Y Bacteria.Bacteroidetes.Bacteroidia.Bacteroidales.Pre  
votellaceae.Prevotella.Multi\_affiliation.Cluster\_17



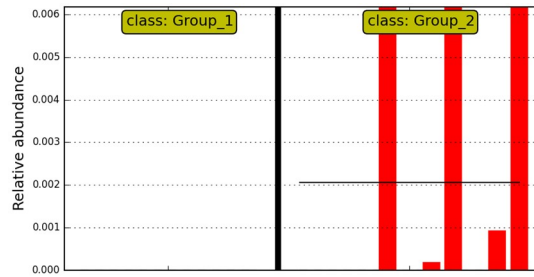
Z Bacteria.Bacteroidetes.Bacteroidia.Bacteroidales.Pre  
votellaceae.Prevotella.Unknown



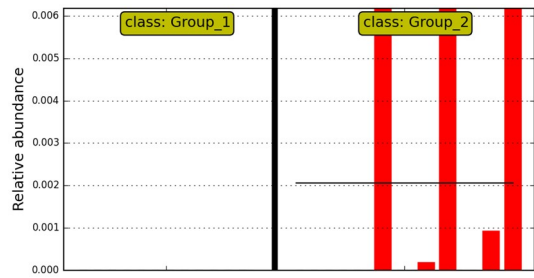
AA Bacteria.Firmicutes.Bacilli.Bacillales.Staphylococcaeae.Staphylococcus.Multi\_affiliation.Cluster\_78



AB Bacteria.Firmicutes.Bacilli.Lactobacillales.Lactobacil  
laceae



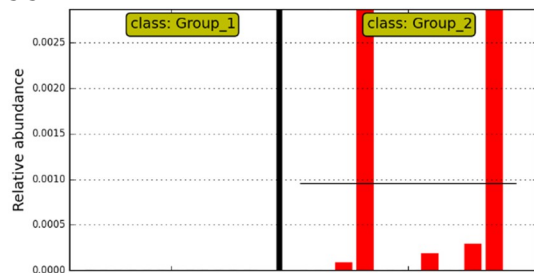
AC Bacteria.Firmicutes.Bacilli.Lactobacillales.Lactobacil  
laceae.Lactobacillus



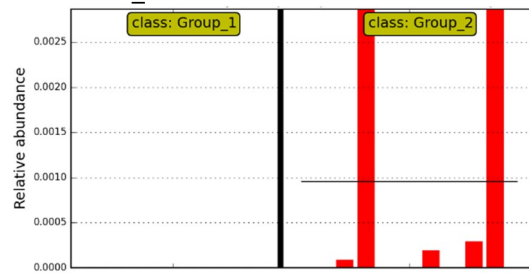
AD Bacteria.Firmicutes.Bacilli.Lactobacillales.Lactobacil  
laceae.Lactobacillus.Multi\_affiliation



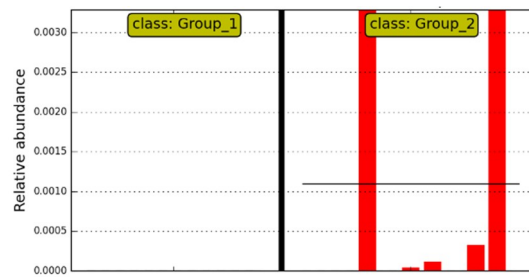
AE Bacteria.Firmicutes.Clostridia.Clostridiales.FamilyX  
I.Peptoniphilus.CandidatusPeptoniphilusmassilien  
sis



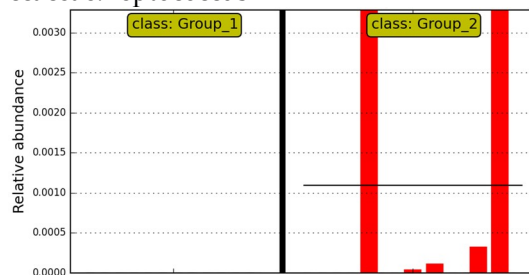
AF Bacteria.Firmicutes.Clostridia.Clostridiales.FamilyX  
I.Peptoniphilus.CandidatusPeptoniphilusmassilien  
sis.Cluster\_211



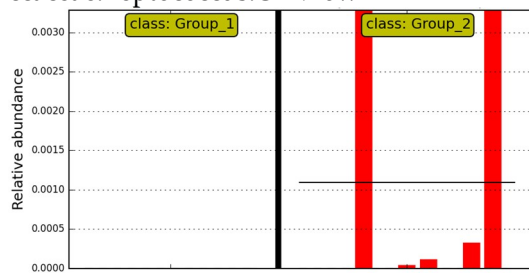
AG Bacteria.Firmicutes.Clostridia.Clostridiales.Peptoco  
ccaceae



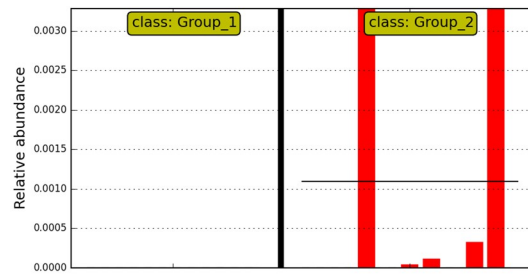
AH Bacteria.Firmicutes.Clostridia.Clostridiales.Peptoco  
ccaceae.Peptococcus



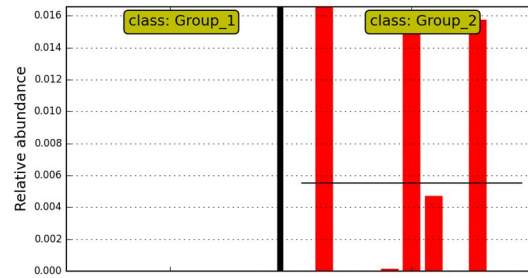
AI Bacteria.Firmicutes.Clostridia.Clostridiales.Peptoco  
ccaceae.Peptococcus.Unknown



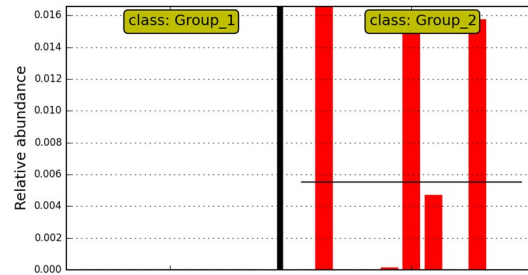
AJ Bacteria.Firmicutes.Clostridia.Clostridiales.Peptoco  
ccaceae.Peptococcus.Unknown.Cluster\_158



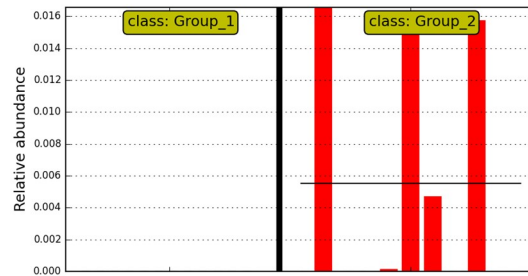
AK Bacteria.Fusobacteria



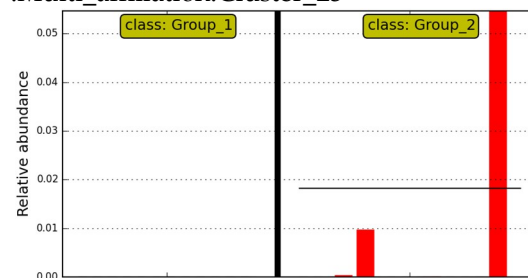
AL Bacteria.Fusobacteria.Fusobacteriia



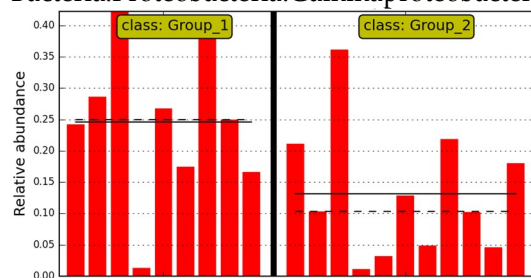
AM Bacteria.Fusobacteria.Fusobacteriia.Fusobacteriales



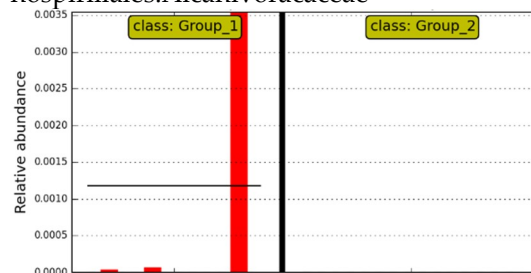
AN Bacteria.Proteobacteria.Epsilonproteobacteria.Campylobacteriales.Campylobacteraceae.Campylobacter .Multi\_affiliation.Cluster\_23



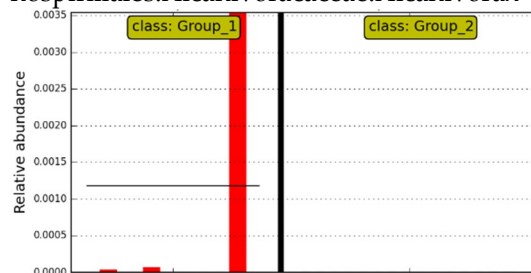
AO Bacteria.Proteobacteria.Gammaproteobacteria



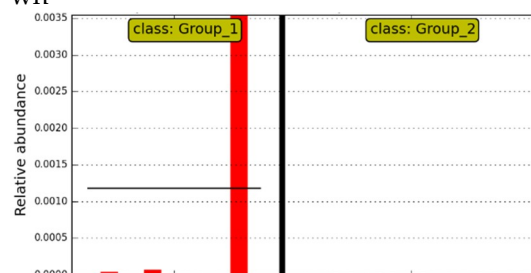
AP Bacteria.Proteobacteria.Gammaproteobacteria.Oceanospirillales.Alcanivoracaceae



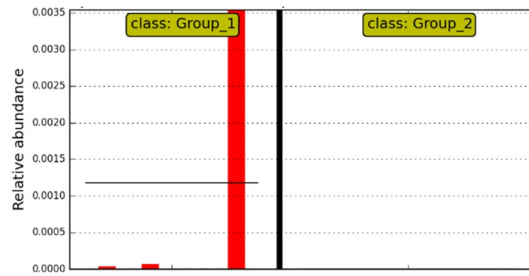
AQ Bacteria.Proteobacteria.Gammaproteobacteria.Oceanospirillales.Alcanivoracaceae.Alcanivorax



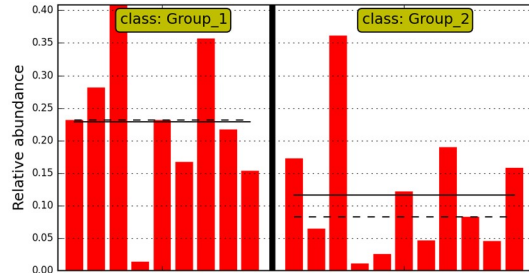
AR Bacteria.Proteobacteria.Gammaproteobacteria.Oceanospirillales.Alcanivoracaceae.Alcanivorax.Unknown



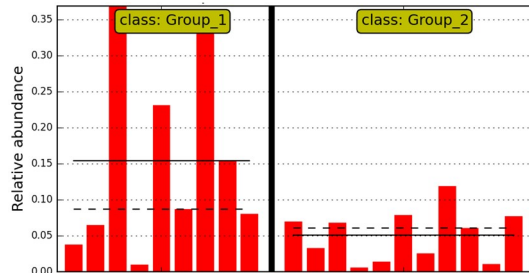
AS Bacteria.Proteobacteria.Gammaproteobacteria.Oceanospirillales.Alcanivoracaceae.Alcanivorax.Unknown.Cluster\_198



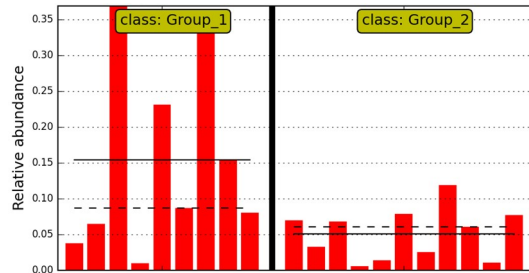
AT Bacteria.Proteobacteria.Gammaproteobacteria.Pseudomonadales



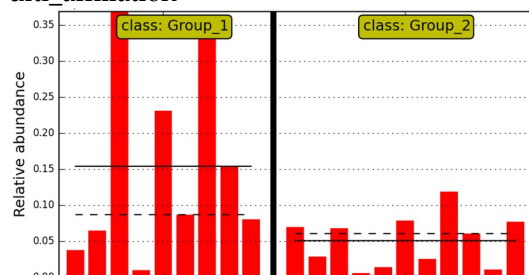
AU Bacteria.Proteobacteria.Gammaproteobacteria.Pseudomonadales.Pseudomonadaceae



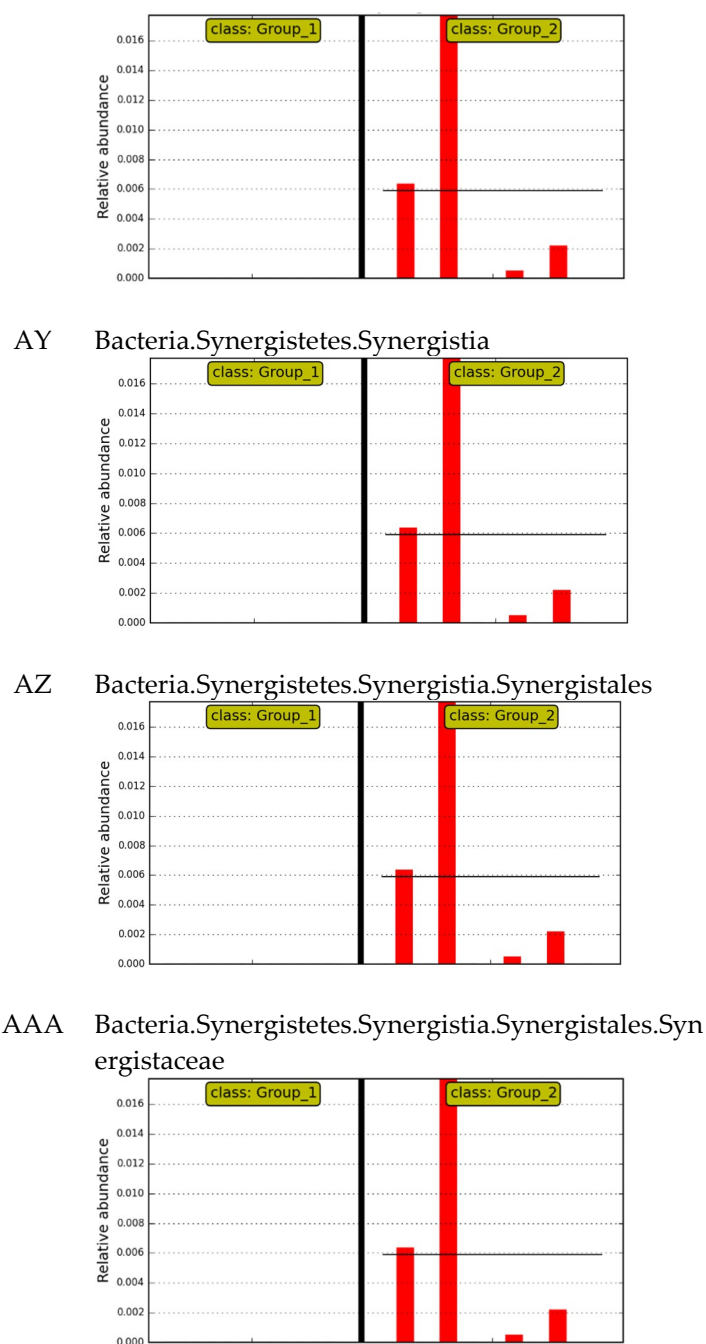
AV Bacteria.Proteobacteria.Gammaproteobacteria.Pseudomonadales.Pseudomonadaceae.Pseudomonas



AW Bacteria.Proteobacteria.Gammaproteobacteria.Pseudomonadales.Pseudomonadaceae.Pseudomonas.Multi-affiliation

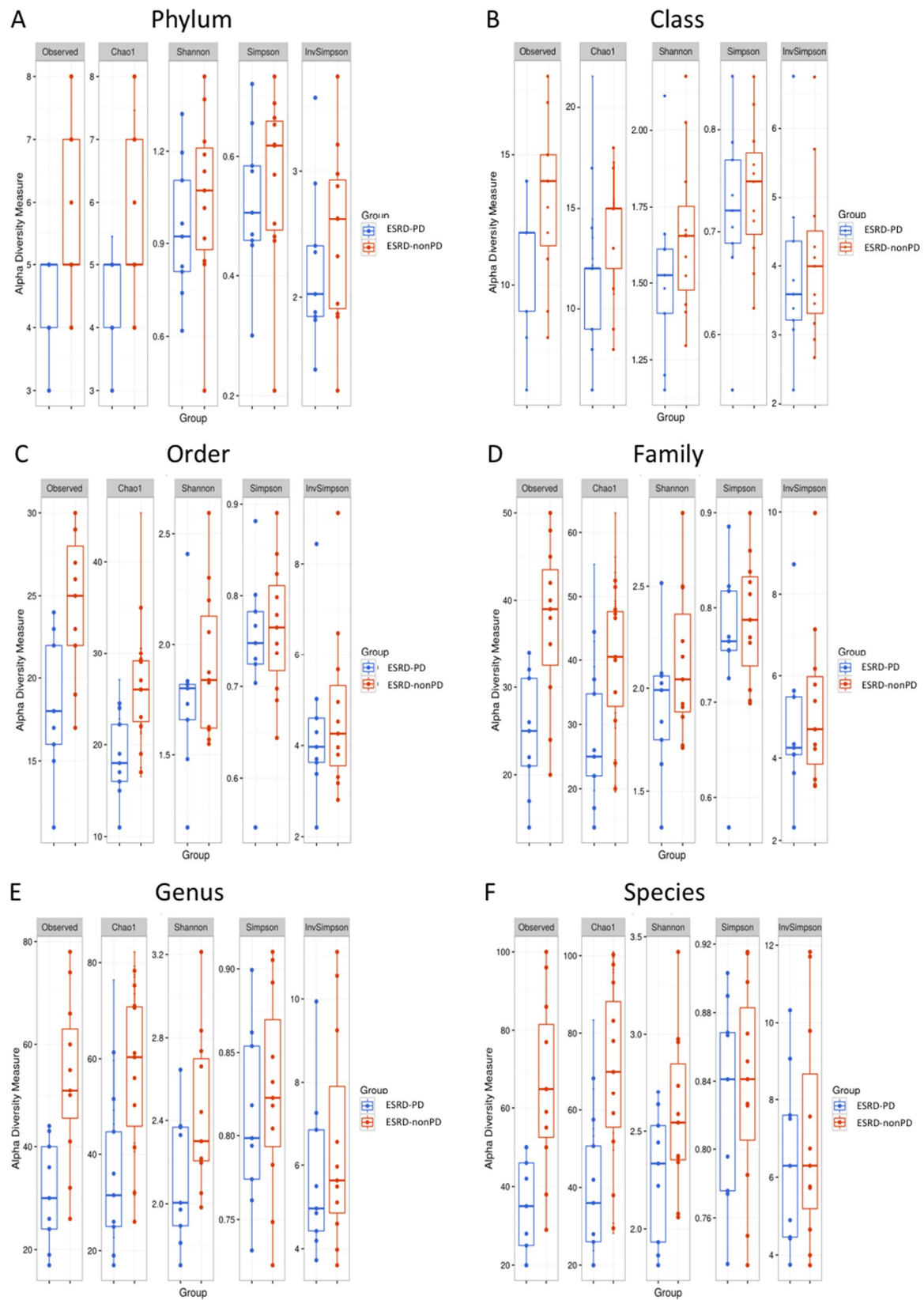


AX Bacteria.Synergistetes

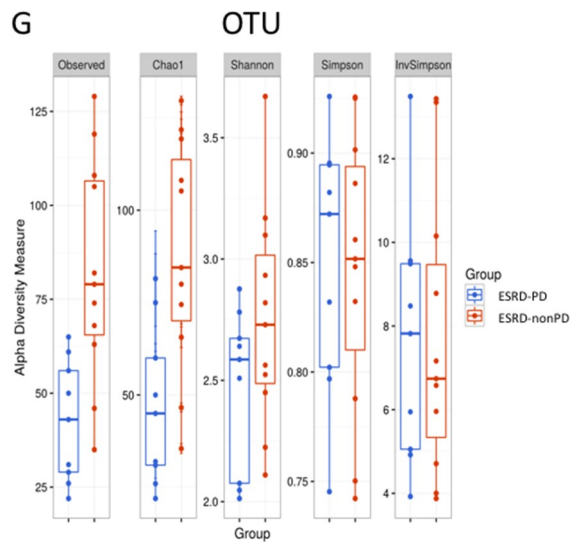


**Figure S3:** A–AAA Barplots show the abundances of the genera and families between the ESRD-PD and ESRD-nonPD. Each bar represents a sample. Group 1 – End-stage renal disease patients undergoing peritoneal dialysis (ESRD-PD); Group 2 – End-stage renal disease patients with intact peritoneal cavity (ESRD-nonPD).

**Figure S4**

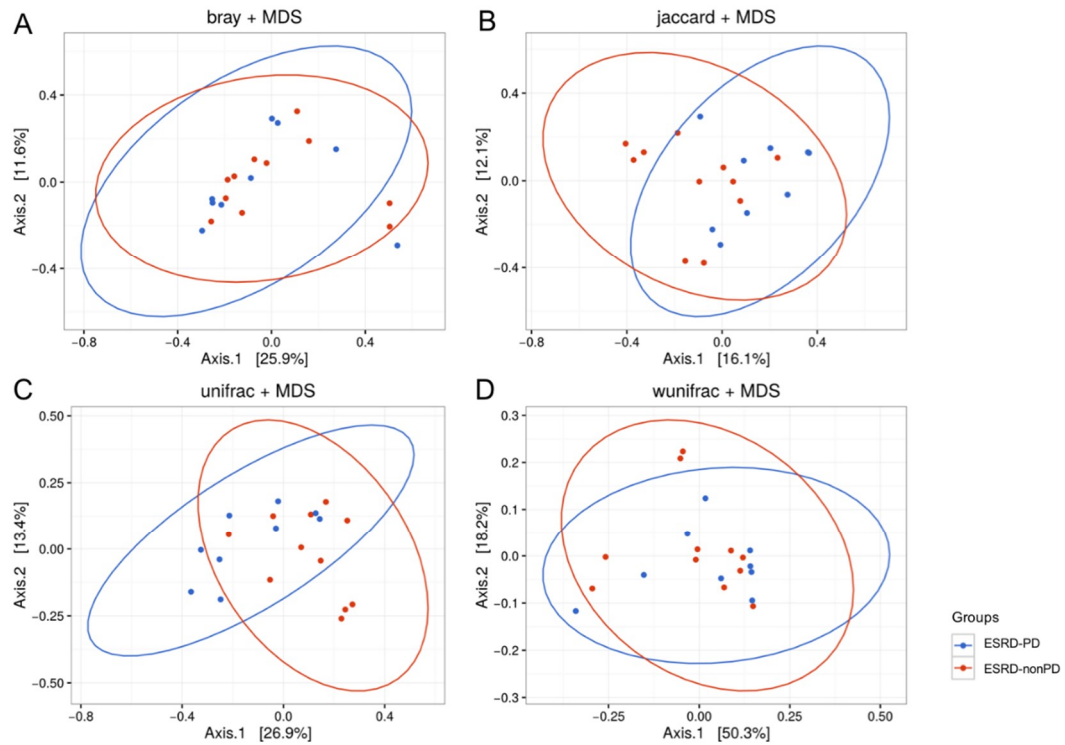






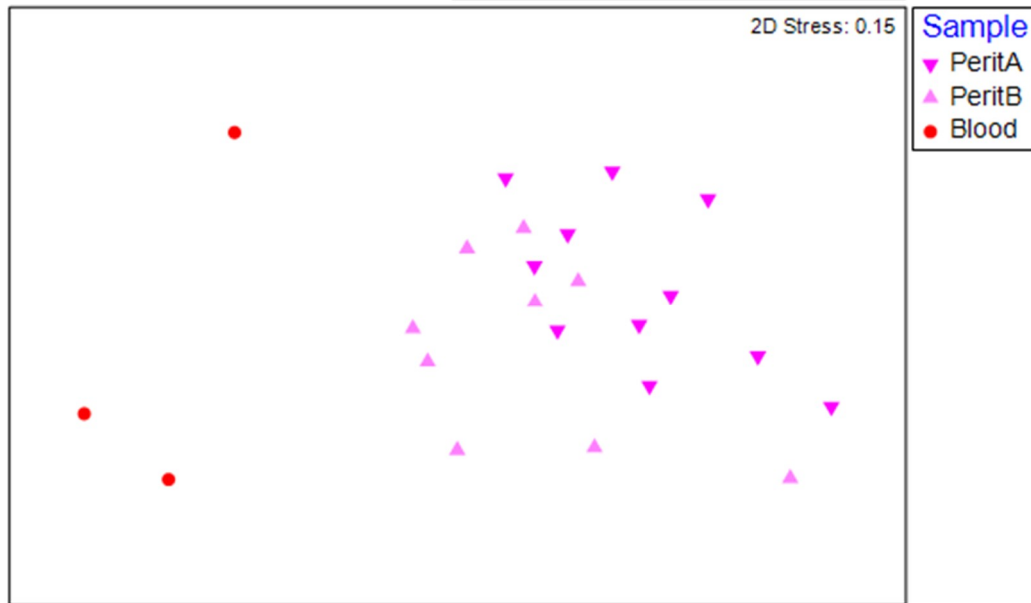
**Figure S4:** Alpha diversity of the peritoneum microbiome community at phylum (A), class (B), order (C), family (D), genus (E), species (F) and OUT (G) taxonomic levels calculated with Observed, Chao1, Shannon, Simpson, and Inverse Simpson indexes. ESRD-PD – End-stage renal disease patients undergoing peritoneal dialysis; ESRD-nonPD – End-stage renal disease patients with intact peritoneal cavity.

**Figure S5**



**Figure S5:** Beta-diversity of the peritoneum microbiome community at OTU level with Bray-Curtis (A), Jaccard (B), unweighted Unifrac (C), and Weighted Unifrac (D) distance derived from 16S rRNA gene -based sequencing data. ESRD-PD – End-stage renal disease patients undergoing peritoneal dialysis; ESRD-nonPD – End-stage renal disease patients with intact peritoneal cavity.

**Figure S6**



**Figure S6:** Non-metric multidimensional scaling (NMDS) of blood (red sphere) and peritoneum microbiomes of non-PD (pink triangles) and PD (light pink triangles) patients described in this study. The graph was produced in Primer 7 software using the microbiome information for the genera (total reads per taxa were converted to percentage for each sample), squared-root transformed data and using resemblance matrices (similarity data types using Bray-Curtis similarities and adding dummy value).