## Metagenomic reads (fastq) Human reads were filtered using bbmap scrips vs GRCh37/hg19 with BBMap scripts Humans host filtering process Quality filtering on each par of raw fastq files with Sickle Quality filtered metagenomic reads (fw/rv + single reads1) Reads taxonomy annotation Reads assembly into contigs with Kraken2/Bracken with MEGAHIT Metagenome Taxonomy assembly annotation Kraken2 files were Contigs > 200 bp converted to BIOM Contigs aligned vs nr Biom tables: NCBI's database kraken\_biom tool Contigs were Relative abundances aligned with were used for downstream analyses

DIAMOND tool

## **BLAST files loaded** into MEGAN CE

**BLAST files and** contigs (fna) files were loaded into MEGAN for analyses

> **Functional** annotation: counts retrieve from **MEGAN files**

tables

Hill numbers,

heatmap, PCA

<sup>&</sup>lt;sup>1</sup> Reads that passed quality filtering settings but lost their paired sequence, either forward or reverse.