Host filtering

Metagenomic reads (fastq)

Human reads were filtered using bbmap scrips vs GRCh37/hg19 with BBMap scripts

Humans host filtering process

Quality filltering

Quality filtering on each par of raw fastq files with Sickle

Quality filtered metagenomic reads (fw/rv + single reads[1])

Reads assembly into contigs with MEGAHIT

Reads taxonomy annotation with Kraken2/Bracken

Assembly

Metagenome assembly

Taxonomy annotation

Taxonomy annotation

Contigs > 200 bp

Kraken2 files were converted to BIOM tables

Functional annotation

Contigs aligned *vs* nr NCBI's database

Biom tables: kraken_biom tool

Contigs were aligned with DIAMOND tool

Relative abundances were used for downstream analyses

Downstream analyses

BLAST files loaded into MEGAN CE

Hill numbers, heatmap, PCA

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

Functional annotation: counts retrieve from MEGAN files

[1] Reads that passed quality filtering settings but lost their paired sequence, either forward or reverse.