Participants (n=106)
- Questionnaire
- Fecal samples

CE-TOFMS
- Control (n=54)
- Gastrectomy participants (n=44)

Whole shotgun metagenomic sequencing
- Control (n=56)
- Gastrectomy participants (n=50)

Metabolite profile

Reads quality filtering
- Elimination of reads which include N
- Elimination of Phix sequences
- Trimming of adapter sequences
- Length filtering ( > 50 bp)
- Quality filtering ( average > 25)
- Elimination of human genome sequence
- Elimination of unpaired reads

High-quality reads

mOTU catalog
- RefMG catalog

Calculate and summarize gene abundances

mOTU pipeline

mOTU pipeline

RefMG catalog

Scaffolds
- Assembly
- Mapping

Gene prediction
- Coverage of scaffolds

Predicted genes
- Calculation of gene abundance

Alignment with KEGG gene
- Coverage of genes

KO profile
- Annotation with KEGG Orthology (KO)

KO module
- KEGG gene profile

HUMAnN2 pipeline
- Map to MetaPhlAn2 reference

HUMAnN2 pipeline (based on UniRef90)

UniRef90 gene profile

MetaPhlAn2 pipeline

Taxonomic profile

Taxonomic profile

Taxonomic profile