

## Targeted resistome sequencing

INPUT paired fastq reads

QC and Host Filtering

AMR++ Resistome Analysis

BWA - Alignment to MEGARes

Resistome  
Analyzer

Rarefaction  
Analyzer

\*Count  
de-duplication

OUTPUT  
Resistome  
counts

OUTPUT  
Rarefaction

\*extract genes  
requiring  
"SNPConfirmation"

Resistance  
Gene  
Identifier

"SNP confirmed"  
OUTPUT  
Resistome counts

## 16S rRNA amplicon sequencing

INPUT paired fastq reads

Qiime2 Microbiome  
Analysis

DADA2 – Amplicon  
variant picking &  
QC filtering

Taxonomic classification  
with GreenGenes db

\*Export data

OUTPUT  
Microbiome counts