**SAMPLE**

**Host DNA Removal (Bowtie2)**

**Duplication removal (bbmap)**

**Merge overlapping (FLASH)**

**Metagenomics data pre-processing**

**Duplication removal (bbmap)**

**Merge overlapping (FLASH)**

**Restriction site detection (perl script)**

**Hi-C data pre-processing**

**De novo assembly (metaSPAdes)**

**Hi-C realignment (Bowtie2, perl script)**

**Louvain network resolution (C program, perl script)**

**Splitting and extending CCs (perl script)**

**AMR prediction, pairwise comparison, taxonomy (BLAST, mash, GTDBtk)**

**Assembly and post processing**

**Clade refinement**

**Comparison with assemblies from other samples, clade formation by UPGMA algorithm (mash, Julia script)**

**Finding the best exemplar in each clade (GTDBtk, perl script)**

**BLAST the exemplar to other samples full contig list with high identity threshold (98%). (BLAST, perl script)**

**Checking inter-contig Hi-C contacts in the new reference based assemblies, excluding non-connected contigs. (perl script)**

**Assembly extension with contigs containing AMR genes based on Hi-C contacts (high sensitivity & specificity) (perl script)**

**Assembly final extension by contigs without AMR genes based on Hi-C contacts (lower sensitivity and specificity) (perl script, BLAST)**

**Generating a temporary reference specific to the clade**

**Reference based assemblies for all samples**

**Hi-C refined reference based assemblies**

**AMR genes finally associated to assemblies with high precision**

**Final extended and refined assemblies**

**Within-clade pairwise comparison, AMR association tables, taxonomical identification (mash, GTDBtk, perl and Julia script)**