# Preprocessing

* adapter trimming
* quality trimming
* (contamination removal)
* FastUniq (Duplication removal)

Useful for visualization:

* FastQC
* MultiQC

# Assembly

* Megahit
* Settings:
  + meta-sensitive

Useful to assess assembly quality:

* assemstats

# Mapping

* Place the reads onto the contigs exactly:
  + Bowtie2
  + BBmap
* Assign each read to a contig (anywhere):
  + Kallisto (fast)
* Map all samples against all assemblies

# Binning

* Run once per assembly
* CONCOCT

Evaluate which bins are complete:

* CheckM

# Gene Prediction

* Prodigal ran on each assembly

# Annotation

Functional Annotation:

* EggNOG
* Pfam
* TigrFam
* COG

Taxonomic Annotation:

* Diamond (blast) + LCA
* Phylogenetic markers (better for bins) e.g. Phylophlan

Pathway annotation

* MinPath