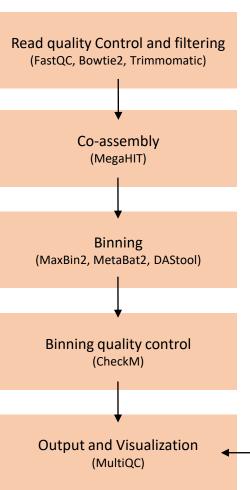


samplesheet input.csv

sample,group,short_reads_1,short_reads_2, SAMPLE1, UnO, /path/to/reads/SAMPLE1_1.fastq.gz, /path/to/reads/SAMPLE1_2.fastq.gz, SAMPLE2,UnO,/path/to/reads/SAMPLE2_1.fastq.gz,/path/to/reads/SAMPLE2_2.fastq.gz, SAMPLE3, UnO, /path/to/reads/SAMPLE3 1.fastq.gz, /path/to/reads/SAMPLE3 2.fastq.gz,





MIDAS2

- -combined_midas2_report.yaml
- -midas2_species_ID_mqc.tsv
- -midas2_output

FastQC

- -trimmed_(1,2)_fastqc.zip
- trimmed_(1,2)_fastqc.html
 - -paired _trim(1,2).fastq.gz -unpaired_trim(1,2).fastq.gz

Trimmomatic

-.summary

-.log

QC shortreads

- -remove host
- --host_removed.bowtie2.log

Assembly

--QC -MEGAHIT ----.bam --contigs.fa.gz ----.bam.bai --.log ----.bowtie2.log

GenomeBinning

DASTool MaxBin2 MetaBat2 depths -.summary.tsv -.eval -bins -.fa.gz -bins

-.seglength -unbinned -.log -unbinned --bin depth summary.tsv -bins

-contig2bin.tsv -discarded -discarded --.heatmap.png -unbinned -contigs

GenomeBinning

QC

-CheckM -checkm_report.mqc.yaml --_qa.txt -checkm_summary_mqc.tsv --_wf.tsv

multigc

-multiqc_report.html -multigc data -multigc plot

pipeline info

--params.json --execution_report.html --pipeline_dag.html --execution timeline.html --software versions.yml --execution trace.txt