fastp

→ input

- 2_Reads/1_Untrimmed/{sample}_1.fastq.gz
- 2_Reads/1_Untrimmed/{sample}_2.fastq.gz

output →

- 2_Reads/2_Trimmed/{sample}_trimmed_1.fastq.gz
- 2_Reads/2_Trimmed/{sample}_trimmed_2.fastq.gz
- 2_Reads/3_fastp_results/{sample}.html
- 2_Reads/3_fastp_results/{sample}.json

index_ref

→ input

1_References

output →

- 1_References/CattedRefs_renamed.fna.gz
- 1_References/CattedRefs_renamed.fna.gz.rev.2.bt2l

map_to_ref

→ input

- 1 References/CattedRefs renamed.fna.gz
- 1_References/CattedRefs_renamed.fna.gz.rev.2.bt2l
- 2_Reads/2_Trimmed/{sample}_trimmed_1.fastq.gz
- 2_Reads/2_Trimmed/{sample}_trimmed_2.fastq.gz

output →

- 2_Reads/4_Host_removed/{sample}_M_1.fastq
- 2_Reads/4_Host_removed/{sample}_M_2.fastq
- 3_Outputs/1_QC/1_BAMs/{sample}.bam
- 3_Outputs/1_QC/1_Host_BAMs/{sample}_host.bam

coverM

→ input

3_Outputs/1_QC/1_BAMs/{sample}.bam

output →

 ${\tt 3_Outputs/1_QC/2_CoverM/\{sample\}_coverM_mapped_host.tsv}$

nonpareil

→ input

- ${\tt 2_Reads/4_Host_removed/\{sample\}_M_1.fastq}$
- 2_Reads/4_Host_removed/{sample}_M_2.fastq

output →

3_Outputs/1_QC/3_nonpareil/{sample}.npo

report

→ input

- 2_Reads/3_fastp_results/ERR922785.json
- ${\tt 3_Outputs/1_QC/2_CoverM/ERR922785_coverM_mapped_host.tsv}$
- 3_Outputs/1_QC/3_nonpareil/ERR922785.npo

output →

- 3_Outputs/1_QC/_nonpareil_metadata.tsv
- 3_Outputs/1_QC/_report.tsv

all

→ input

- ${\tt 3_Outputs/1_QC/_nonpareil_metadata.tsv}$
- 3_Outputs/1_QC/_report.tsv