

↩ input

/lustre/BIF/nobackup/mulle088/data_rp/90-1196727703/00_fastq/{sample}_R1_001.fastq.gz
/lustre/BIF/nobackup/mulle088/data_rp/90-1196727703/00_fastq/{sample}_R2_001.fastq.gz

output →

results/01_trimmed/{sample}_R1_001.fastq.gz_trimming_report.txt
results/01_trimmed/{sample}_R1_val_1.fq.gz
results/01_trimmed/{sample}_R2_001.fastq.gz_trimming_report.txt
results/01_trimmed/{sample}_R2_val_2.fq.gz

↩ input

results/01_trimmed/{sample}_R1_val_1.fq.gz
results/01_trimmed/{sample}_R2_val_2.fq.gz

output →

results/02_assembly/{sample}/contigs.fasta
results/02_assembly/{sample}/scaffolds.fasta

↩ input

results/01_trimmed/{sample}_R1_val_1.fq.gz
results/01_trimmed/{sample}_R2_val_2.fq.gz
results/02_assembly/{sample}/contigs.fasta

output →

results/04_binning/{sample}/{sample}_mapped.sorted.bam
results/04_binning/{sample}/{sample}_mapped.sorted.bam.bai

↩ input

results/02_assembly/{sample}/contigs.fasta
results/04_binning/{sample}/{sample}_mapped.sorted.bam

output →

results/04_binning/{sample}/coverage_table.tsv

↩ input

results/02_assembly/{sample}/contigs.fasta
results/04_binning/{sample}/coverage_table.tsv

output →

results/04_binning/{sample}/bins
results/04_binning/{sample}/bins_completed.txt
results/04_binning/{sample}/concoct_clustering.csv

↩ input

results/04_binning/{sample}/bins
results/04_binning/{sample}/bins_completed.txt

output →

results/06_checkm/{sample}/checkm_results.txt
results/06_checkm/{sample}/good_bins.txt

↩ input

results/02_assembly/{sample}/contigs.fasta

output →

results/03_gc/assembly/{sample}/report.txt

↩ input

results/01_trimmed/163_R1_001.fastq.gz_trimming_report.txt
results/01_trimmed/1_R1_001.fastq.gz_trimming_report.txt
results/01_trimmed/291_R1_001.fastq.gz_trimming_report.txt
results/01_trimmed/2_R1_001.fastq.gz_trimming_report.txt
results/01_trimmed/336_R1_001.fastq.gz_trimming_report.txt
results/01_trimmed/3_R1_001.fastq.gz_trimming_report.txt
results/01_trimmed/459_R1_001.fastq.gz_trimming_report.txt
results/01_trimmed/468_R1_001.fastq.gz_trimming_report.txt
results/01_trimmed/482_R1_001.fastq.gz_trimming_report.txt
results/01_trimmed/4_R1_001.fastq.gz_trimming_report.txt
results/01_trimmed/536_R1_001.fastq.gz_trimming_report.txt
results/01_trimmed/5_R1_001.fastq.gz_trimming_report.txt
results/01_trimmed/6_R1_001.fastq.gz_trimming_report.txt
results/03_gc/assembly/1/report.txt
results/03_gc/assembly/163/report.txt
results/03_gc/assembly/2/report.txt
results/03_gc/assembly/291/report.txt
results/03_gc/assembly/3/report.txt
results/03_gc/assembly/336/report.txt
results/03_gc/assembly/4/report.txt
results/03_gc/assembly/459/report.txt
results/03_gc/assembly/468/report.txt
results/03_gc/assembly/482/report.txt
results/03_gc/assembly/5/report.txt
results/03_gc/assembly/536/report.txt
results/03_gc/assembly/6/report.txt
results/06_checkm/1/checkm_results.txt
results/06_checkm/163/checkm_results.txt
results/06_checkm/2/checkm_results.txt
results/06_checkm/291/checkm_results.txt
results/06_checkm/3/checkm_results.txt
results/06_checkm/336/checkm_results.txt
results/06_checkm/4/checkm_results.txt
results/06_checkm/459/checkm_results.txt
results/06_checkm/468/checkm_results.txt
results/06_checkm/482/checkm_results.txt
results/06_checkm/5/checkm_results.txt
results/06_checkm/536/checkm_results.txt
results/06_checkm/6/checkm_results.txt

output →

results/10_final_gc/final_report.html

↩ input

results/04_binning/{sample}/bins
results/06_checkm/{sample}/good_bins.txt

output →

results/05_bins/{sample}/bins_to_process.txt

↩ input

/lustre/BIF/nobackup/mulle088/snakeake/input/Marinacidobacteraceae_fa
results/05_bins/1/bins_to_process.txt
results/05_bins/163/bins_to_process.txt
results/05_bins/2/bins_to_process.txt
results/05_bins/291/bins_to_process.txt
results/05_bins/3/bins_to_process.txt
results/05_bins/336/bins_to_process.txt
results/05_bins/4/bins_to_process.txt
results/05_bins/459/bins_to_process.txt
results/05_bins/468/bins_to_process.txt
results/05_bins/482/bins_to_process.txt
results/05_bins/5/bins_to_process.txt
results/05_bins/536/bins_to_process.txt
results/05_bins/6/bins_to_process.txt

output →

results/07_gtdbtk/batch_genomes
results/07_gtdbtk/batch_genomes_list.txt

↩ input

results/07_gtdbtk/batch_genomes
results/07_gtdbtk/batch_genomes_list.txt

output →

results/07_gtdbtk/batch_results/gtdbtk.bac120.summary.tsv
results/07_gtdbtk/batch_results/gtdbtk_complete.txt

↩ input

results/07_gtdbtk/batch_results/gtdbtk.bac120.summary.tsv
results/07_gtdbtk/batch_results/gtdbtk_complete.txt

output →

results/07_gtdbtk/batch_results_parsed.txt

↩ input

<input function>
results/07_gtdbtk/batch_results_parsed.txt

output →

results/05_bins/{sample}/all_bins_processed.txt

↩ input

results/03_gc/assembly/1/report.txt
results/03_gc/assembly/163/report.txt
results/03_gc/assembly/2/report.txt
results/03_gc/assembly/291/report.txt
results/03_gc/assembly/3/report.txt
results/03_gc/assembly/336/report.txt
results/03_gc/assembly/4/report.txt
results/03_gc/assembly/459/report.txt
results/03_gc/assembly/468/report.txt
results/03_gc/assembly/482/report.txt
results/03_gc/assembly/5/report.txt
results/03_gc/assembly/536/report.txt
results/03_gc/assembly/6/report.txt
results/04_binning/1/bins_completed.txt
results/04_binning/163/bins_completed.txt
results/04_binning/2/bins_completed.txt
results/04_binning/291/bins_completed.txt
results/04_binning/3/bins_completed.txt
results/04_binning/336/bins_completed.txt
results/04_binning/4/bins_completed.txt
results/04_binning/459/bins_completed.txt
results/04_binning/468/bins_completed.txt
results/04_binning/482/bins_completed.txt
results/04_binning/5/bins_completed.txt
results/04_binning/536/bins_completed.txt
results/04_binning/6/bins_completed.txt
results/05_bins/1/all_bins_processed.txt
results/05_bins/163/all_bins_processed.txt
results/05_bins/2/all_bins_processed.txt
results/05_bins/291/all_bins_processed.txt
results/05_bins/3/all_bins_processed.txt
results/05_bins/336/all_bins_processed.txt
results/05_bins/4/all_bins_processed.txt
results/05_bins/459/all_bins_processed.txt
results/05_bins/468/all_bins_processed.txt
results/05_bins/482/all_bins_processed.txt
results/05_bins/5/all_bins_processed.txt
results/05_bins/536/all_bins_processed.txt
results/05_bins/6/all_bins_processed.txt
results/06_checkm/1/checkm_results.txt
results/06_checkm/163/checkm_results.txt
results/06_checkm/2/checkm_results.txt
results/06_checkm/291/checkm_results.txt
results/06_checkm/3/checkm_results.txt
results/06_checkm/336/checkm_results.txt
results/06_checkm/4/checkm_results.txt
results/06_checkm/459/checkm_results.txt
results/06_checkm/468/checkm_results.txt
results/06_checkm/482/checkm_results.txt
results/06_checkm/5/checkm_results.txt
results/06_checkm/536/checkm_results.txt
results/06_checkm/6/checkm_results.txt
results/07_gtdbtk/batch_results_parsed.txt
results/09_gapseq/fasta/Marinacidobacteraceae_fa/Marinacidobacteraceae_fa_model.RDS
results/10_final_gc/final_report.html

↩ input

<input function>

output →

results/09_gapseq/fasta/{sample}/{sample}-Pathways.tbl

↩ input

<input function>

output →

results/09_gapseq/fasta/{sample}/{sample}-Transporter.tbl

↩ input

<input function>
results/09_gapseq/fasta/{sample}/{sample}-Pathways.tbl
results/09_gapseq/fasta/{sample}/{sample}-Transporter.tbl

output →

results/09_gapseq/fasta/{sample}/{sample}_draft.RDS

↩ input

<input function>
results/09_gapseq/fasta/{sample}/{sample}_draft.RDS

output →

results/09_gapseq/fasta/{sample}/{sample}_model.RDS