

↩ input

<input function>
<input function>

output →

results/reads/{mgen}/preprocess/r1.fq.gz
results/reads/{mgen}/preprocess/r2.fq.gz

↩ input

../ref/GRCh38.bt2.d/GRCh38.1.bt2
../ref/GRCh38.bt2.d/GRCh38.2.bt2
../ref/GRCh38.bt2.d/GRCh38.3.bt2
../ref/GRCh38.bt2.d/GRCh38.4.bt2
../ref/GRCh38.bt2.d/GRCh38.rev.1.bt2
../ref/GRCh38.bt2.d/GRCh38.rev.2.bt2
results/reads/{mgen}/preprocess/r1{stem}fq.gz
results/reads/{mgen}/preprocess/r2{stem}fq.gz
workflow/scripts/filter_out_mapping_reads.sh

output →

results/reads/{mgen}/preprocess/r1{stem}hfilt.fq.gz
results/reads/{mgen}/preprocess/r2{stem}hfilt.fq.gz

↩ input

results/reads/{mgen}/preprocess/r1{stem}fq.gz
results/reads/{mgen}/preprocess/r2{stem}fq.gz
workflow/scripts/fastuniq_wrapper.sh

output →

results/reads/{mgen}/preprocess/r1{stem}dedup.fq.gz
results/reads/{mgen}/preprocess/r2{stem}dedup.fq.gz

↩ input

../ref/illumina_adapters.fa
results/reads/{mgen}/preprocess/{stem}.fq.gz

output →

results/reads/{mgen}/preprocess/{stem}.deadapt.fq.gz

↩ input

results/reads/{mgen}/preprocess/r1{stem}fq.gz
results/reads/{mgen}/preprocess/r2{stem}fq.gz

output →

results/reads/{mgen}/preprocess/r1{stem}qtrim.fq.gz
results/reads/{mgen}/preprocess/r2{stem}qtrim.fq.gz
results/reads/{mgen}/preprocess/r3{stem}qtrim.fq.gz

↩ input

results/reads/{mgen}/preprocess/{stem}.hfilt.dedup.deadapt.qtrim.fq.gz

output →

results/reads/{mgen}/preprocess/{stem}.proc.fq.gz

↩ input

../ref/gtpro
results/reads/{mgen}/preprocess/{r}.proc.fq.gz

output →

results/reads/{mgen}/gtpro/{r}.snv_counts_raw.bz2

↩ input

results/reads/{mgen}/gtpro/{r}.snv_counts_raw.bz2

output →

results/reads/{mgen}/gtpro/{r}.snv_counts.tsv.bz2

↩ input

results/reads/HSM67VDP/gtpro/r1.snv_counts.tsv.bz2
results/reads/HSM67VDP/gtpro/r2.snv_counts.tsv.bz2
results/reads/HSM6XRSI/gtpro/r1.snv_counts.tsv.bz2
results/reads/HSM6XRSI/gtpro/r2.snv_counts.tsv.bz2
results/reads/MSH79HCG/gtpro/r1.snv_counts.tsv.bz2
results/reads/MSH79HCG/gtpro/r2.snv_counts.tsv.bz2
results/reads/MSM79HCI/gtpro/r1.snv_counts.tsv.bz2
results/reads/MSM79HCI/gtpro/r2.snv_counts.tsv.bz2
results/reads/PSM6XWB3/gtpro/r1.snv_counts.tsv.bz2
results/reads/PSM6XWB3/gtpro/r2.snv_counts.tsv.bz2
results/reads/PSM7J1A2/gtpro/r1.snv_counts.tsv.bz2
results/reads/PSM7J1A2/gtpro/r2.snv_counts.tsv.bz2
workflow/scripts/merge_gtpro_counts.py

output →

results/species/{species}/gtpro/snv_counts.tsv.bz2

↩ input

results/species/{species}/gtpro/snv_counts.tsv.bz2

output →

results/species/{species}/sfacts/snv_counts.mgtp.nc

↩ input

results/species/{species}/sfacts/{stem}.mgtp.nc

output →

results/species/{species}/sfacts/{stem}.filt-poly{poly,[0-9]+}-cvrg{cvrg,[0-9]+}.mgtp.nc

↩ input

results/species/{species}/sfacts/{stem}.mgtp.nc

output →

results/species/{species}/sfacts/{stem}.ss-g{num_positions}-block{block_number}-seed{seed}.mgtp.nc

↩ input

results/species/{species}/sfacts/{stem}.mgtp.nc
sfacts_strategy.args

output →

results/species/{species}/sfacts/{stem}.sfacts-s{strain_exponent}-seed{seed}.loss_history
results/species/{species}/sfacts/{stem}.sfacts-s{strain_exponent}-seed{seed}.sfacts-fit.nc

↩ input

{stem}.sfacts-fit.nc

output →

{stem}.strain_composition.tsv

↩ input

results/species/{species}/sfacts/snv_counts.filt-poly05-cvrg05.ss-g1000-block0-seed0.sfacts-s85-seed0.strain_composition.tsv

output →

results/species/{species}/spgc/strain_pure_samples.tsv

↩ input

results/species/{species}/sfacts/snv_counts.mgtp.nc
results/species/{species}/spgc/strain_pure_samples.tsv
workflow/scripts/aggregate_strain_metagenotypes_across_strain_samples.py

output →

results/species/{species}/snv_counts.strain_pure.mgtp.nc

↩ input

results/species/{species}/midas/pangenome_profile.depth.tsv.bz2
results/species/{species}/spgc/species_genes.list
results/species/{species}/spgc/strain_pure_samples.tsv

output →

results/species/{species}/spgc/spgc.results.nc

↩ input

results/species/{species}/snv_counts.strain_pure.mgtp.nc
results/species/{species}/spgc/spgc.results.nc
workflow/scripts/compile_spgc_results_metadata.py

output →

results/species/{species}/spgc.strain.tsv

↩ input

results/species/{species}/spgc/spgc.results.nc
workflow/scripts/extract_strain_gene_hits_from_spgc_netcdf.py

output →

results/species/{species}/spgc.gene.tsv

↩ input

results/species/102506/spgc.gene.tsv
results/species/102506/spgc.strain.tsv

↩ input

species.list

output →

results/midasdb_initialized.flag

↩ input

results/midasdb_initialized.flag
species.list

output →

results/pangenomes.bt2.d

↩ input

results/pangenomes.bt2.d
results/reads/{mgen}/preprocess/r1.proc.fq.gz
results/reads/{mgen}/preprocess/r2.proc.fq.gz
species.list

output →

results/reads/{mgen}/midas/pangenome_profile_raw.bam

↩ input

results/reads/{mgen}/midas/pangenome_profile_raw.bam

output →

results/reads/{mgen}/midas/pangenome_profile_raw.gene_mapping_tally.tsv.bz2

↩ input

results/midasdb_initialized.flag

output →

results/species/{species}/midas/genes_info.tsv

↩ input

results/reads/HSM67VDP/midas/pangenome_profile_raw.gene_mapping_tally.tsv.bz2
results/reads/HSM6XRSI/midas/pangenome_profile_raw.gene_mapping_tally.tsv.bz2
results/reads/MSH79HCG/midas/pangenome_profile_raw.gene_mapping_tally.tsv.bz2
results/reads/MSM79HCI/midas/pangenome_profile_raw.gene_mapping_tally.tsv.bz2
results/reads/PSM6XWB3/midas/pangenome_profile_raw.gene_mapping_tally.tsv.bz2
results/reads/PSM7J1A2/midas/pangenome_profile_raw.gene_mapping_tally.tsv.bz2
results/species/{species}/midas/genes_info.tsv
workflow/scripts/merge_and_aggregate_pangenome_profiles.py

output →

results/species/{species}/midas/pangenome_profile.depth.tsv.bz2

↩ input

species_gene.tsv

output →

results/species/{species}/spgc/species_genes.list