Nextflow run

nextflow run nf-core/rnaseq -r 3.14.0 -profile pdc\_kth -c resource.config -work-dir /cfs/klemming/projects/snic/naiss2024-23-363/nf-rnaseq/work -resume -params-file nf-params\_240712.json --project=naiss2024-22-778

Nextflow parameters (nf-params\_240712.json)

{

"input": "\/cfs\/klemming\/projects\/snic\/naiss2024-23-363\/nf-rnaseq\/samplesheet.csv",

"outdir": "\/cfs\/klemming\/projects\/snic\/naiss2024-23-363\/nf-rnaseq\/output",

"email": "sidhant.chaudhary@slu.se",

"fasta": "\/cfs\/klemming\/projects\/supr\/naiss2024-23-363\/genomes\/three\_org\_combined\_240712.fna",

"gtf": "\/cfs\/klemming\/projects\/supr\/naiss2024-23-363\/genomes\/three\_org\_combined\_240712.gtf",

"remove\_ribo\_rna": true,

"pseudo\_aligner": "salmon",

"extra\_salmon\_quant\_args": "--dumpEq --gcBias --seqBias --posBias",

"skip\_alignment": true

}

Software versions

CUSTOM\_DUMPSOFTWAREVERSIONS:

python: 3.11.7

yaml: 5.4.1

CUSTOM\_GETCHROMSIZES:

getchromsizes: 1.16.1

DESEQ2\_QC\_PSEUDO:

bioconductor-deseq2: 1.28.0

r-base: 4.0.3

FASTQC:

fastqc: 0.12.1

FQ\_SUBSAMPLE:

fq: 0.9.1 (2022-02-22)

GTF2BED:

perl: 5.26.2

GTF\_FILTER:

python: 3.9.5

MAKE\_TRANSCRIPTS\_FASTA:

rsem: 1.3.1

star: 2.7.10a

SALMON\_INDEX:

salmon: 1.10.1

SALMON\_QUANT:

salmon: 1.10.1

SE\_GENE:

bioconductor-summarizedexperiment: 1.24.0

r-base: 4.1.1

SORTMERNA:

sortmerna: 4.3.4

TRIMGALORE:

cutadapt: '3.4'

trimgalore: 0.6.7

TX2GENE:

python: 3.9.5

TXIMPORT:

bioconductor-tximeta: 1.12.0

r-base: 4.1.1

Workflow:

Nextflow: 23.10.1

nf-core/rnaseq: 3.14.0