



Katie Lennard <katieviljoen@gmail.com>

[nfcore/RNAseq] Successful: mad_ptolemy

1 message

kviljoen@srvslshpc613.uct.ac.za <kviljoen@srvslshpc613.uct.ac.za>

Tue, Apr 24, 2018 at 6:12 PM

To: katie.viljoen@uct.ac.za

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nfcore/RNAseq: version 1.5dev

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Run Name: mad_ptolemy

nfcore/RNAseq execution completed successfully!

nfcore/RNAseq execution completed successfully!

The workflow was completed at Tue Apr 24 18:12:13 SAST 2018 (duration: 4h 47m 38s)

The command used to launch the workflow was as follows:

```
nextflow -log /researchdata/fhgfs/katie/NGI-RNAseq-test/nextflow.log run uct-cbio/RNAseq -r dev --reads
/researchdata/fhgfs/katie/NGI-RNAseq-test/*_R{1,2}.fastq.gz --genome GRCh37 -profile uct_hex -with-singularity
/scratch/DB/bio/singularity-containers/uct-cbio-rnaseq.img --outdir /researchdata/fhgfs/katie/NGI-RNAseq-test/nf-outdir
-w /researchdata/fhgfs/katie/NGI-RNAseq-test/nf-workdir --email katie.viljoen@uct.ac.za
```

Pipeline Configuration:

```
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- Run Name: mad_ptolemy
- Reads: /researchdata/fhgfs/katie/NGI-RNAseq-test/*_R{1,2}.fastq.gz
- Data Type: Paired-End
- Genome: GRCh37
- Strandedness: None
- Trim R1: 0
- Trim R2: 0
- Trim 3' R1: 0
- Trim 3' R2: 0
- Aligner: STAR
- STAR Index: /scratch/DB/bio/rna-seq/references/Homo_sapiens/Ensembl/GRCh37/Sequence/STARIndex/
- GTF Annotation: /scratch/DB/bio/rna-seq/references/Homo_sapiens/Ensembl/GRCh37/Annotation/Genes/genes.gtf
- BED Annotation: /scratch/DB/bio/rna-seq/references/Homo_sapiens/Ensembl/GRCh37/Annotation/
Genes/genes.bed
- Save Reference: No
- Save Trimmed: No
- Save Intermeds: No
- Max Memory: 256 GB
- Max CPUs: 64
- Max Time: 24d 20h 31m 24s
- Output dir: /researchdata/fhgfs/katie/NGI-RNAseq-test/nf-outdir
- Working dir: /researchdata/fhgfs/katie/NGI-RNAseq-test/nf-workdir
- Container: /scratch/DB/bio/singularity-containers/uct-cbio-rnaseq.img
- Pipeline Release: dev
- Current home: /home/kviljoen
- Current user: kviljoen
- Current path: /researchdata/fhgfs/katie/NGI-RNAseq-test
- R libraries: false
- Script dir: /home/kviljoen/.nextflow/assets/uct-cbio/RNAseq
- Config Profile: uct_hex
- E-mail Address: katie.viljoen@uct.ac.za
```

- Date Started: Tue Apr 24 13:24:36 SAST 2018
- Date Completed: Tue Apr 24 18:12:13 SAST 2018
- Pipeline script file path: /home/kviljoen/.nextflow/assets/uct-cbio/RNAseq/main.nf
- Pipeline script hash ID: 97bc7021d0bdefedff03ea45beec1f39
- Pipeline repository Git URL: <https://github.com/uct-cbio/RNAseq.git>
- Pipeline repository Git Commit: 718fb1aff1f374cb3c6e2af0fe976d353c544737
- Pipeline Git branch/tag: dev
- Docker image: /scratch/DB/bio/singularity-containers/uct-cbio-maseq.img

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nfcore/RNAseq is a bioinformatics best-practice analysis pipeline used for RNA sequencing data at the National Genomics Infrastructure at SciLifeLab Stockholm, Sweden.

The pipeline uses Nextflow, a bioinformatics workflow tool. It pre-processes raw data from FastQ inputs, aligns the reads and performs extensive quality-control on the results.

For more information, please see the pipeline homepage: <https://github.com/nf-core/RNAseq>

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