**RNA-Seq Analytic Pipeline for GUDMAP/RBK**

**Process Design Table**

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| --- | --- | --- | --- | --- |
| **Process** | **Tool (version)** | **Docker Container (version)** | **Inputs** | **Outputs** |
| getBag | deriva 1.0.0 | bicf/gudmaprbkfilexfer | Replicate RID | bagit.zip |
| getData | deriva 1.0.0 | bicf/gudmaprbkfilexfer | bagit.zip | \*.fastq.gz  File.csv  Experiment Settings.csv  Experiment.csv |
| parseMetadata | python 3.7.4  argparse 1.4.0  pandas 0.25.3 | bicf/python3 | File.csv  Experiment Settings.csv Experiment.csv | Replicate RID  Strandedness  Spike  Species |
| getRef | aws-cli 1.16.293  OR  deriva 1.0.0 | bicf/awscli  OR  bicf/gudmaprbkfilexfer | Spike  Species | HiSat2 Reference  Reference .bed |
| trimData | TrimGalore 0.6.4 | bicf/trimgalore | Strandedness  \*.fastq.gz | \*trimmed.fq.gz |
| alignData | hisat 2.1.0  samtools 1.9 | bicf/gudmaprbkaligner | Strandedness  Spike  Species \*trimmed.fq.gz  HiSat2 Reference | \*.bam  \*bam.bai |
| dedupData | Picard 2.21.7  samtools 1.9 | bicf/gudmaprbkdedup | \*.bam  \*.bai | \*dedup.bam  \*dedup.bam.bai |
| makeBigWig | Deeptools 3.3 | bicf/deeptools3.3 | \*dedup.bam | \*.bw |
| countData | Subread OR RSEM  python OR R |  | \*dedup.bam | \*.count.csv  \*.tpm.csv  \*.fpkm.csv |
| fastqc | Fastqc 0.11.8 |  | \*.fastq.gz | \*.fastqc.zip |
| inferMetadata | RSeQC 3.0 | bicf/rseqc3.0 | \*.dedup.bam  \*dedup.bam.bai  Reference .bed |  |
| qc | python or R 3.0 |  | Replicate RID  Strandedness  Spike  Species  \*.fastqc.zip  additional qc files | \*.qc.json  multiqc\_report.html |
| uploadData | deriva 1.0.0 | bicf/gudmaprbkfilexfer | \*dedup.bam  \*.count.csv  \*.tpm.csv  \*.fpkm.csv  \*.fastqc.zip  \*.qc.json |  |