**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 | replicateRID | 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 | manualEnds  metaEnds  metaStrand  metaSpike  metaSpecies |
| getRef | aws-cli 1.16.293  OR  deriva 1.0.0 | bicf/awscli  OR  bicf/gudmaprbkfilexfer |  | \*.ht2  genome.fna  genome.gtf  genome.bed |
| trimData | TrimGalore 0.6.4 | bicf/trimgalore | manualEnds  \*.fastq.gz | \*trimmed.fastq.gz  \*downsampled.fq.gz  \*.trimming\_report.txt |
| alignData | hisat 2.1.0  samtools 1.9 | bicf/gudmaprbkaligner | inferEnds  inferSpike  inferSpecies  \*trimmed.fq.gz  ht2 | \*.bam  \*.bam.bai  \*.alignSummary.txt |
| dedupData | Picard 2.21.7  samtools 1.9 | bicf/gudmaprbkdedup | \*.bam  \*.bam.bai | \*.dedup.bam  \*.dedup.bam.bai  \*.deduped.Metrics.txt |
| makeBigWig | Deeptools 3.3 | bicf/deeptools3.3 | \*.dedup.bam | \*.bw |
| countData | Subread 2.0.0  R 3.6.1  optparse 1.6.4 | bicf/subread2:2.0.0 | inferEnds  \*.dedup.bam  \*.dedup.bam.bai  \*.gtf | \*.countTable.csv |
| alignSampleData | hisat 2.1.0  samtools 1.9 | bicf/gudmaprbkaligner | \*downsampled.fq.gz  \*.ht2 | \*downsampled.bam  \*downsampled.bai |
| inferMetadata | RSeQC 3.0 | bicf/rseqc3.0 | \*.downsampled.bam  \*.downsampled.bai  genome.bed | inferEnds  inferStrand  inferSpike  inferSpecies |
| fastqc | Fastqc 0.11.8 | bicf/fastqc:2.0.0 | \*.fastq.gz | \*.fastqc.zip |
| tin | RSeQC 3.0 | bicf/rseqc3.0 | \*.dedup.bam  \*.dedup.bam.bai  genome.bed | \*.tin.xls |
| qc | python or R |  | infer/meta metadata  \*.fastqc.zip  \*.trimming\_report.txt  \*.alignSummary.txt  \*.deduped.Metrics.txt | \*.qc.json  multiqc\_report.html |
| uploadData | deriva 1.0.0 | bicf/gudmaprbkfilexfer | \*.countTable.csv  \*.qc.json |  |