



RNA-Seq Pipeline Overview

Analysis for Walker lab

- **Prepared for:**
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 - **Process Executed on :** Jan-10-2024
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Data Access

- **Dropbox Folder:** /staging/01.RawData
- **Dropbox URL:** <https://www.dropbox.com/scl/fo/gwtyop1kmngqgxvic67ur/h?rlkey=x8mvw2srw65mbr2vhmy4uq353&dl=0>

FASTQ files

```
1.993Gi 2024-01-10 07:41:11 FB_2/FB_2_1.fq.gz
2.087Gi 2024-01-05 16:42:00 FB_2/FB_2_2.fq.gz
1.778Gi 2024-01-09 17:38:59 EV_3/EV_3_1.fq.gz
1.838Gi 2024-01-09 17:44:20 EV_3/EV_3_2.fq.gz
1.673Gi 2024-01-05 16:42:00 FB_3/FB_3_1.fq.gz
1.731Gi 2024-01-05 16:42:00 FB_3/FB_3_2.fq.gz
1.777Gi 2024-01-05 16:43:00 L6_3/L6_3_1.fq.gz
1.843Gi 2024-01-05 16:43:00 L6_3/L6_3_2.fq.gz
1.705Gi 2024-01-09 17:38:23 EV_4/EV_4_1.fq.gz
1.770Gi 2024-01-09 17:43:34 EV_4/EV_4_2.fq.gz
1.440Gi 2024-01-05 16:43:00 FB_4/FB_4_1.fq.gz
1.483Gi 2024-01-05 16:43:00 FB_4/FB_4_2.fq.gz
1.613Gi 2024-01-09 17:33:24 EV_2/EV_2_1.fq.gz
1.692Gi 2024-01-09 17:36:42 EV_2/EV_2_2.fq.gz
1.640Gi 2024-01-05 16:42:00 MT_2/MT_2_1.fq.gz
1.690Gi 2024-01-05 16:42:00 MT_2/MT_2_2.fq.gz
```

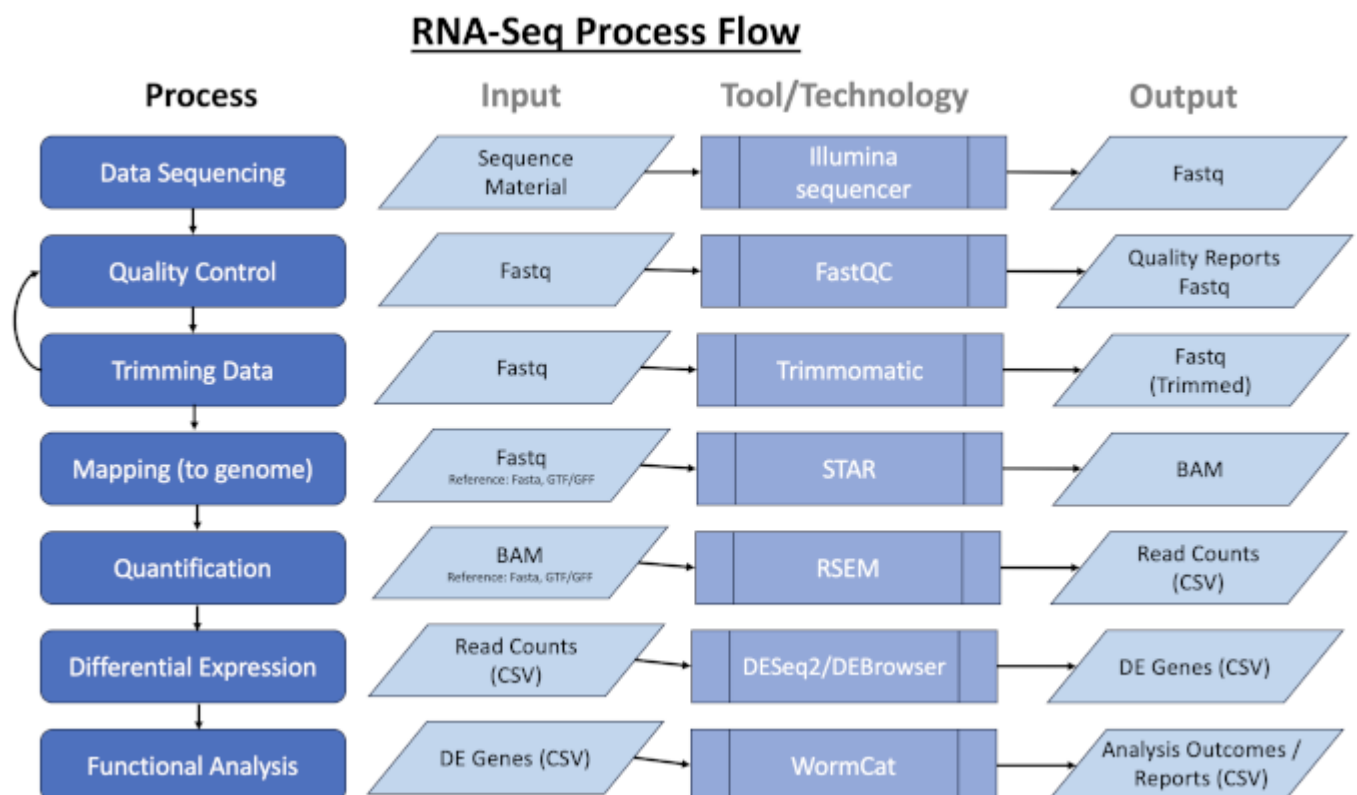


1.741Gi 2024-01-05 16:44:00 L6_4/L6_4_1.fq.gz
1.796Gi 2024-01-05 16:42:00 L6_4/L6_4_2.fq.gz
1.839Gi 2024-01-05 16:42:00 MT_4/MT_4_1.fq.gz
1.937Gi 2024-01-05 16:43:00 MT_4/MT_4_2.fq.gz
1.521Gi 2024-01-05 16:43:00 L6_2/L6_2_1.fq.gz
1.594Gi 2024-01-05 16:43:00 L6_2/L6_2_2.fq.gz
1.738Gi 2024-01-05 16:42:00 MT_3/MT_3_1.fq.gz
1.787Gi 2024-01-05 16:42:00 MT_3/MT_3_2.fq.gz

Gene Index files

Gene Index based on Wormbase Version: *WS289*

RNA Seq Process





Pipeline Outputs

- MD5 Checksum Report
- FAST QC Report
- Multi QC Report
- Isoform Quantification
- Gene Quantification
- DESeq2 Gene Normalizations (Up, Down, All Expressed) & Visualizations
- WormCat Annotations and Visualizations of gene set enrichment data

Source Code

The provided tagged repository is available to create reproducible outputs from the RNA-Seq Pipeline.

Config https://github.com/DanH-UMassMed/Walker_Lab

Pipeline <https://github.com/DanH-UMassMed/RNA-Seq-Nextflow> -r v1.0.*