



RNA-Seq Pipeline Overview

Analysis for Francis lab

- Prepared for:
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 - Process Executed on : Dec-13-2023
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Data Access

- **Dropbox Folder:** Francis lab_KB_wholeworm RNAseq data_March 2023_Share AW lab/PQ_treatment_and_control_November_experiment_2023
- **Dropbox URL:** <https://www.dropbox.com/scl/fo/e8eldk0yrvs56g0d5sr54/h?rlkey=681znxai9mpm834n4a2v2hqlu&dl=0>

FASTQ files

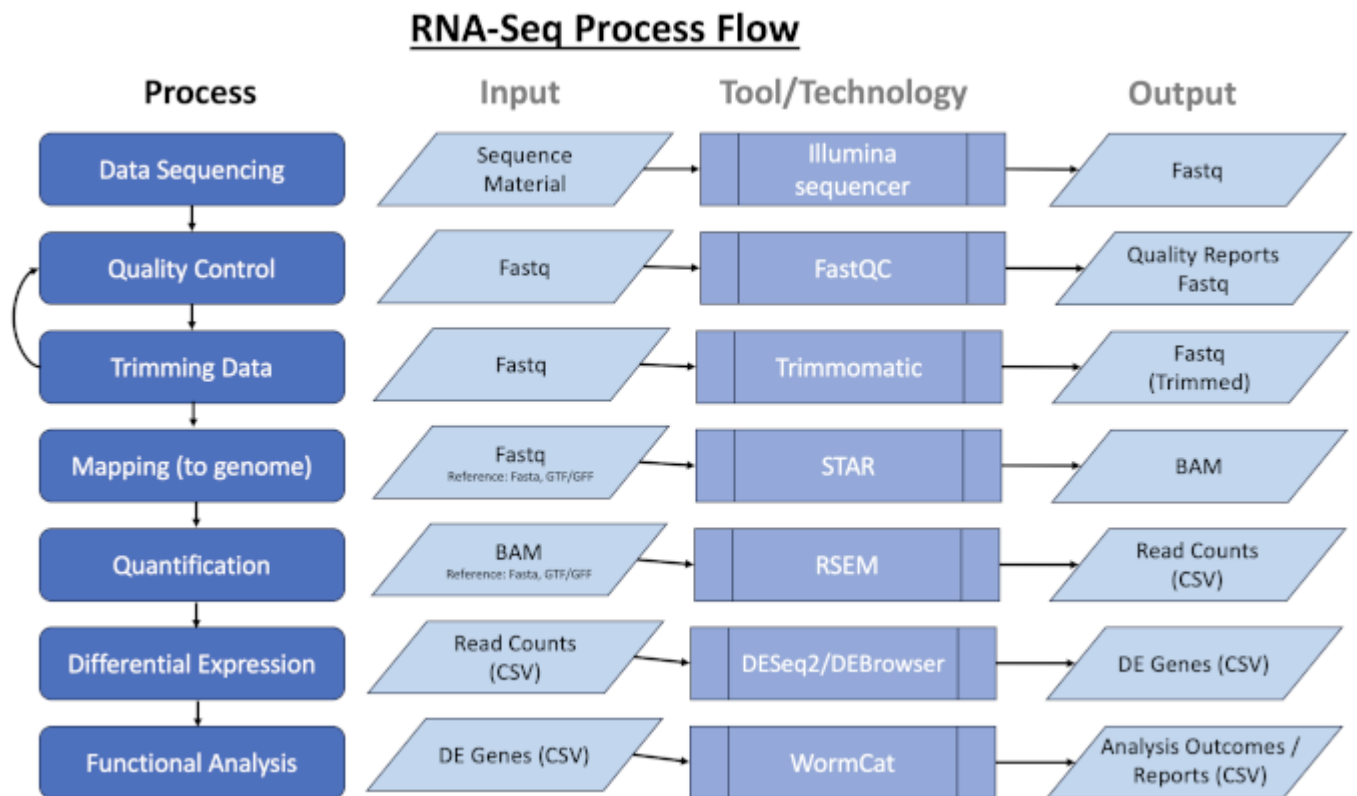
```
1.687Gi 2023-11-30 07:51:00 PQ_2_day_N2/PQ_N2_set1_102223_harvest/PQ_N2_set1_1.fq.gz
1.716Gi 2023-11-30 07:51:00 PQ_2_day_N2/PQ_N2_set1_102223_harvest/PQ_N2_set1_2.fq.gz
2.202Gi 2023-11-30 07:52:00 control_N2/Control_N2_set1_102223_harvest/Con_N2_set1_1.fq.gz
2.261Gi 2023-11-30 07:52:00 control_N2/Control_N2_set1_102223_harvest/Con_N2_set1_2.fq.gz
2.814Gi 2023-11-30 07:51:00 PQ_2_day_N2/PQ_N2_set2_110623_harvest/PQ_N2_set2_1.fq.gz
2.967Gi 2023-11-30 07:51:00 PQ_2_day_N2/PQ_N2_set2_110623_harvest/PQ_N2_set2_2.fq.gz
2.411Gi 2023-11-30 07:52:00 control_N2/Control_N2_set2_110623_harvest/Con_N2_set2_1.fq.gz
2.517Gi 2023-11-30 07:52:00 control_N2/Control_N2_set2_110623_harvest/Con_N2_set2_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/Francis_Lab

Pipeline <https://github.com/DanH-UMassMed/RNA-Seq-Nextflow> -r v1.0.7