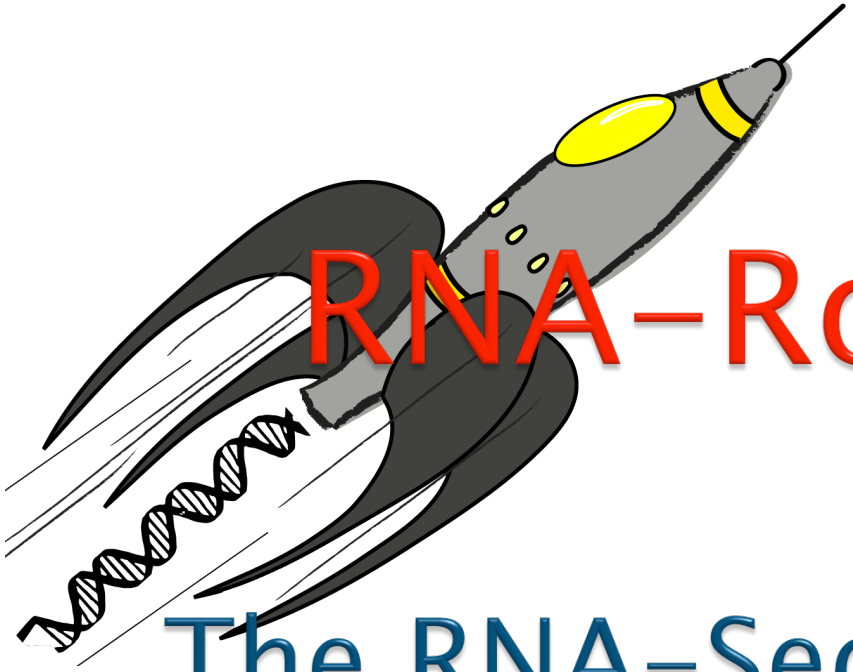

RNA-Rocket

The RNA-Seq Pipeline at

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Thank you.

Pathogen Portal

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Home | Data | Analyze | About | News and Announcements

Featuring...

RNA Rocket

Align your Illumina fastQ reads against supported genomes, view supported genomes, and estimate gene expression values using an **RNA-Seq Pipeline** running on Galaxy.

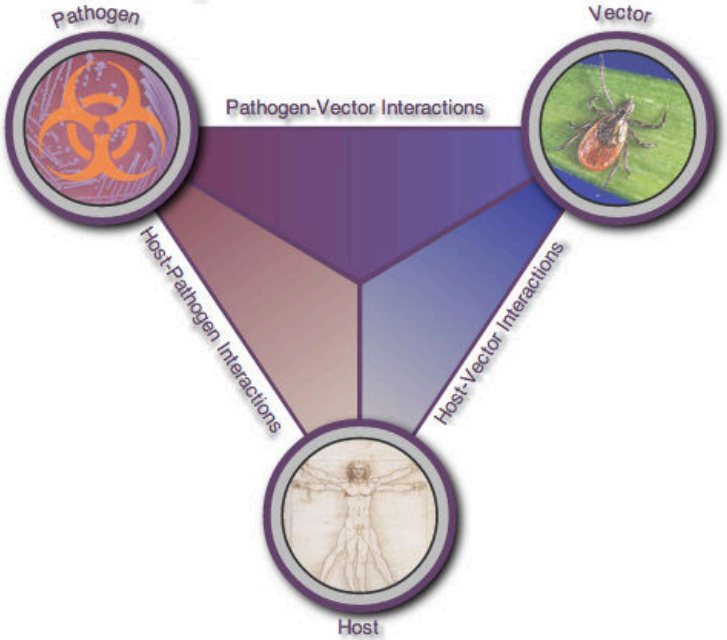
Improvements include:

- New user interface
- New reference genomes
- New tools

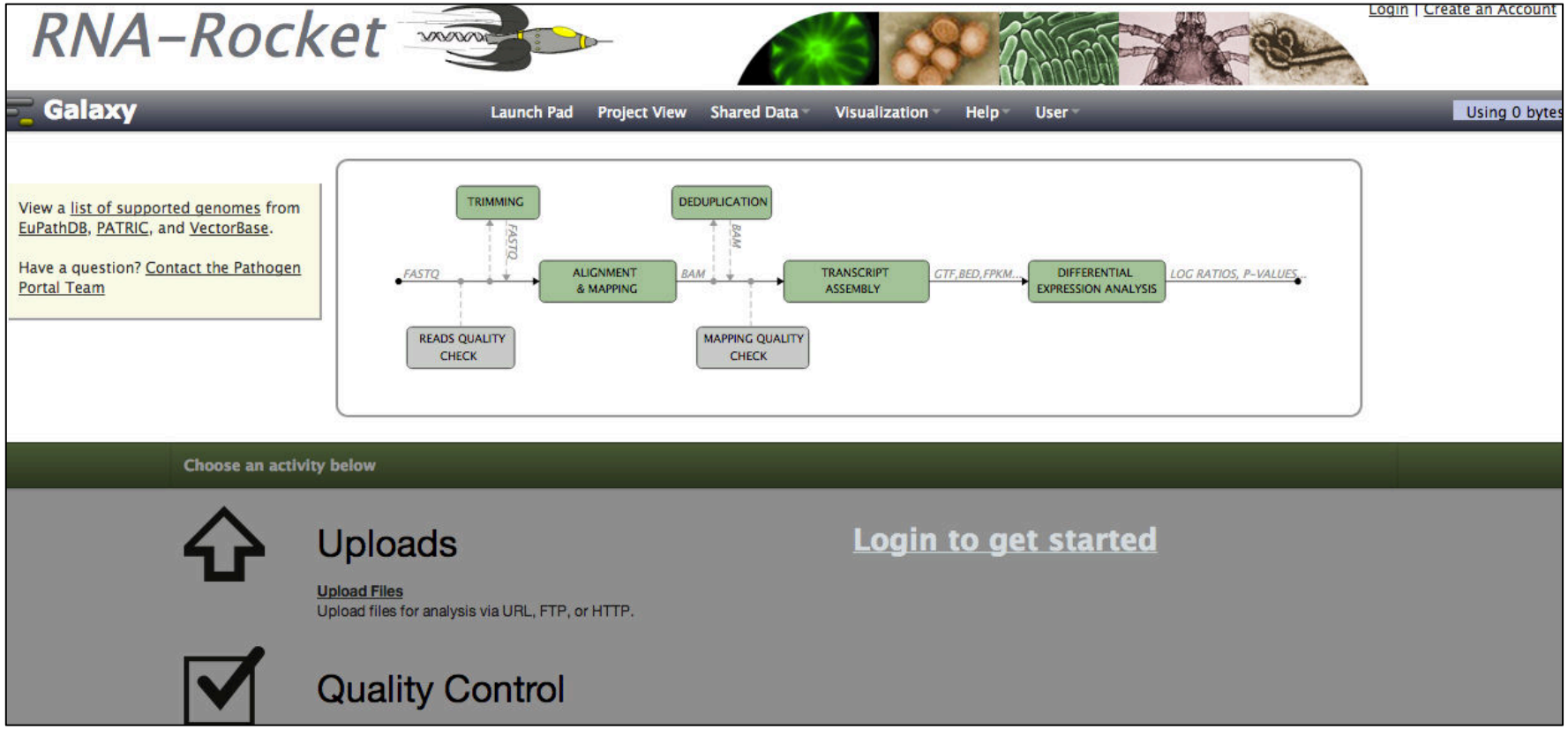
Pathogen Interaction Gateway

Generate a network graph of **Protein-Protein Interactions**, including **Host-Pathogen Interactions**, from your custom selection of hosts/vectors, bacteria, viruses, and eukaryotic pathogens.

Explore Infectious Disease



RNA-Rocket



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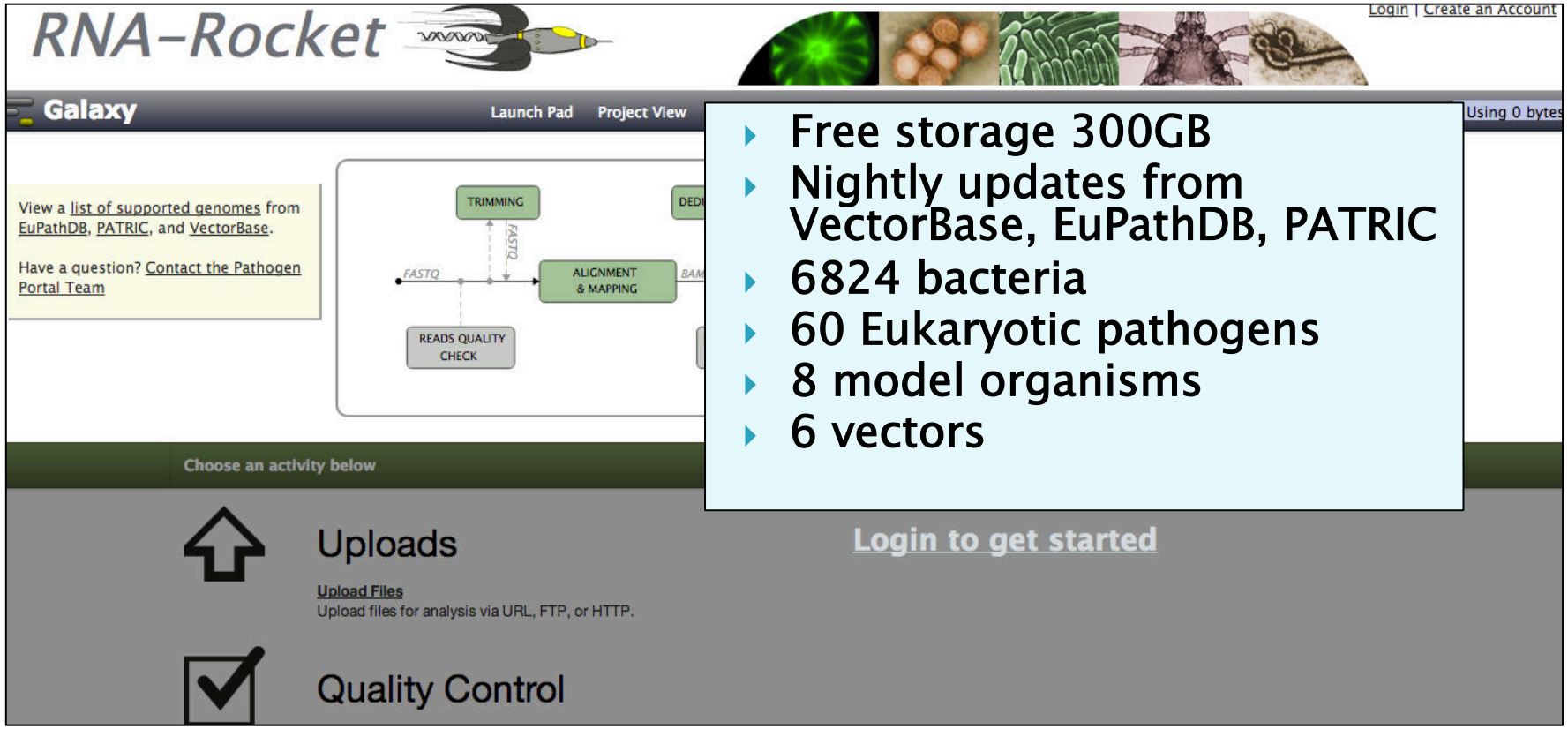
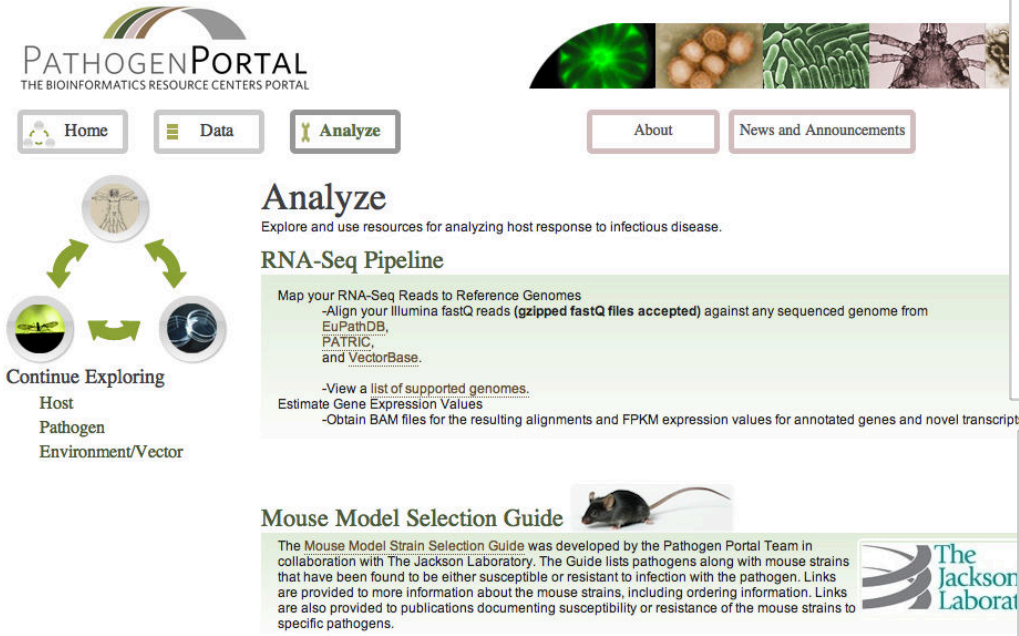
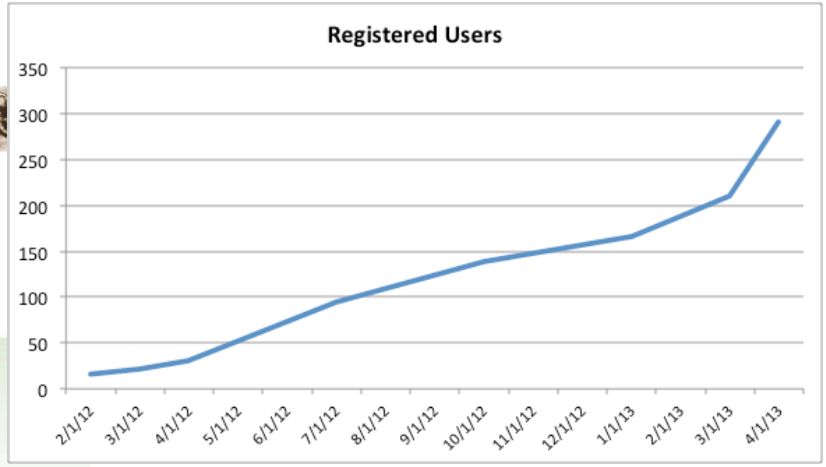
RNA-Rocket

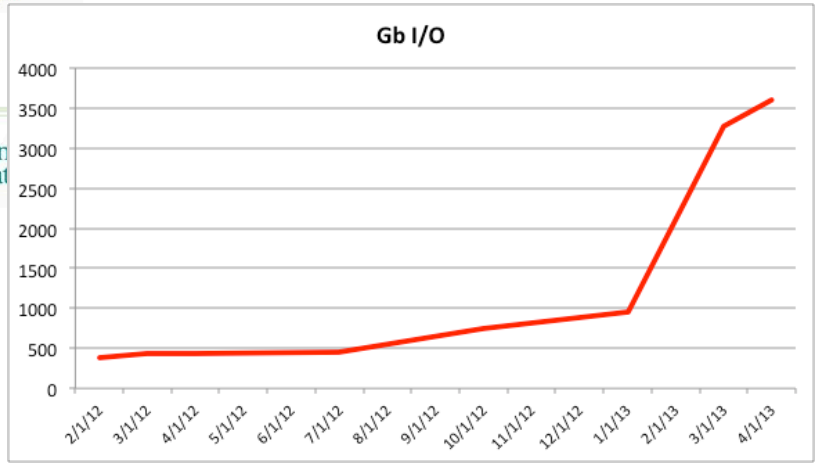


- Free storage 300GB
- Nightly updates from VectorBase, EuPathDB, PATRIC
- 6824 bacteria
- 60 Eukaryotic pathogens
- 8 model organisms
- 6 vectors

RNA-Seq Pipeline: Initial Release January 2012



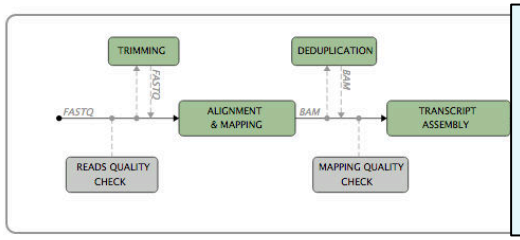




RNA-Seq Pipeline Features

View a list of supported genomes from EuPathDB, PATRIC, and VectorBase.

Have a question? Contact the Pathogen Portal Team



- Guided tour for naïve users

Choose an activity below

Uploads

Upload Files
Upload files for analysis via URL, FTP, or HTTP.

Quality Control

Check read quality
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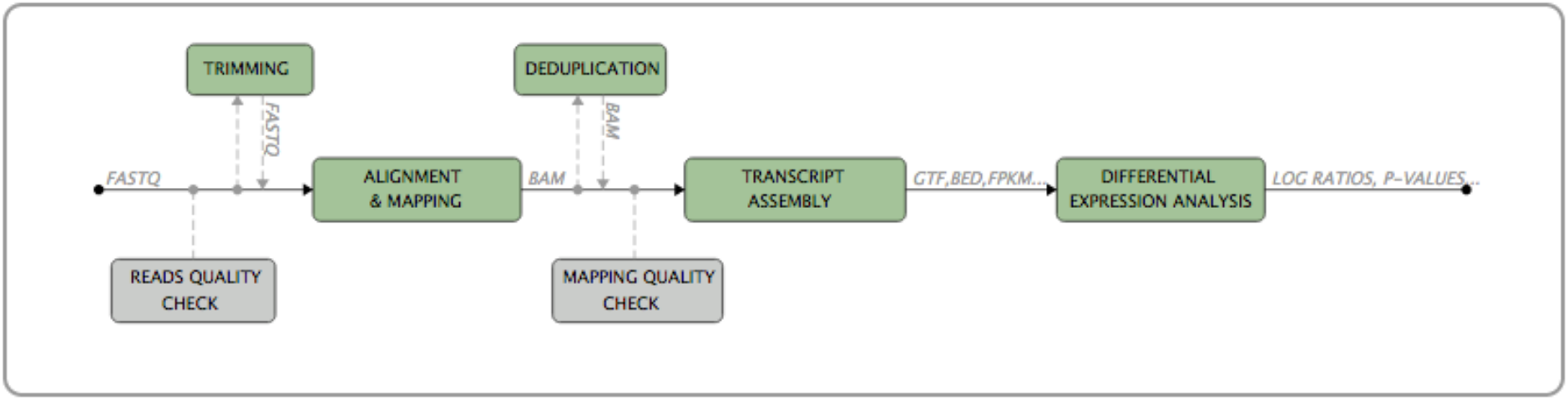
Features

- Guided tour for naïve users



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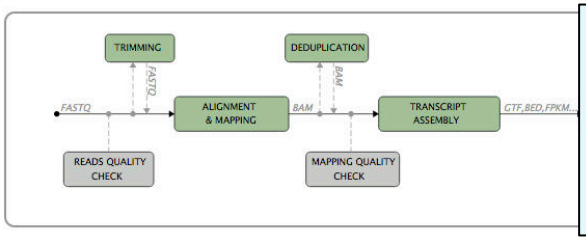

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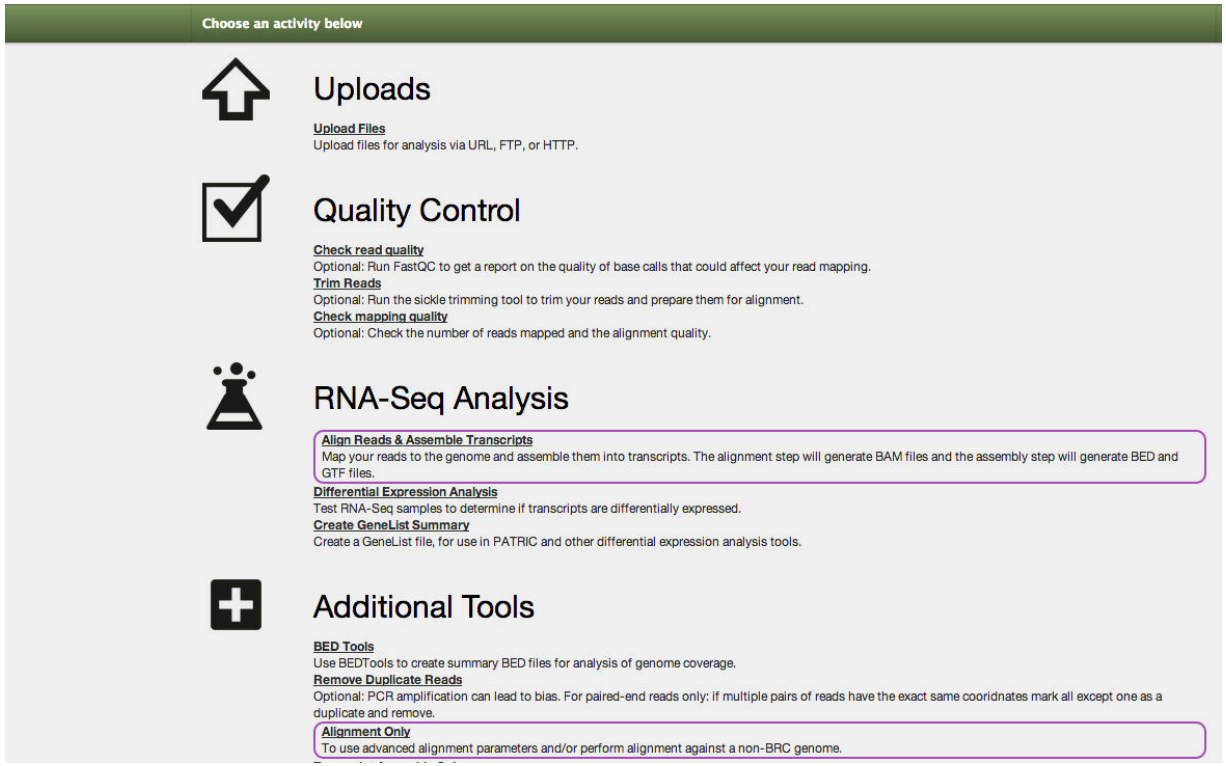
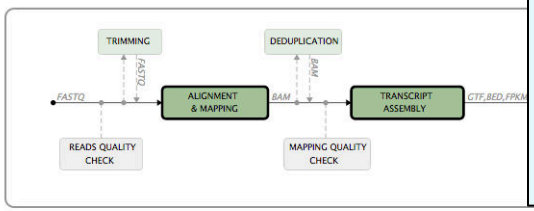


RNA-Seq Pipeline Features



- Guided tour for naïve users

Align Reads & Assemble Transcripts

Purpose:
This procedure will map RNA-Seq reads to one of the provided reference genomes and use this mapping to assemble transcripts, map transcripts to existing annotations, and determine the level of expression. Choose the appropriate option for your organism (Eukaryotic/Prokaryotic) and read type (Paired-end/ Single-end) below.
Required Input:
FastQ files
Output:
Read alignments (BAM Files), tab delimited assembly and expression files for known genes, isoforms, and novel transcripts.

Select Analysis Type
- Eukaryotic Single-End Analysis
- Prokaryotic Single-End Analysis
- Eukaryotic Paired-End Analysis
- Prokaryotic Paired-End Analysis

Select an existing Project or create a new Project to be used during this analysis and populate the Project with the necessary files. Output from this analysis will be saved in the selected Project.
Currently Selected Project: None Selected

Select and copy files from Uploads or existing project(s) to populate your current Project.

Target Project:
Select existing project — OR — Create project

← Copy

Source Project:
Select source
imported: CSU Demo

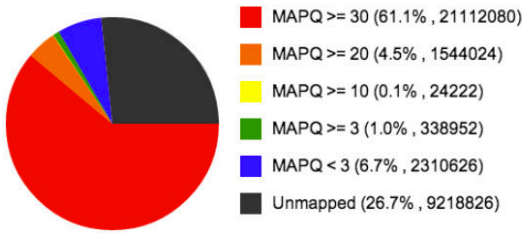
- Upstream_READ1.fastq
- Downstream_READ2.fastq
- Trimmed_Upstream_READ1.fastq
- Trimmed_Downstream_READ2.fastq
- BaseQuality_Upstream_READ1.fastq.html
- BaseQuality_Trimmed_Upstream_READ1.fastq.html
- Align with Bowtie2 Original
- Align with Bowtie2 Trimmed
- SamStat for Align with Bowtie2 on Original
- SamStat for Align with Bowtie2 Trimmed.html

RNA-Seq Pipeline Features

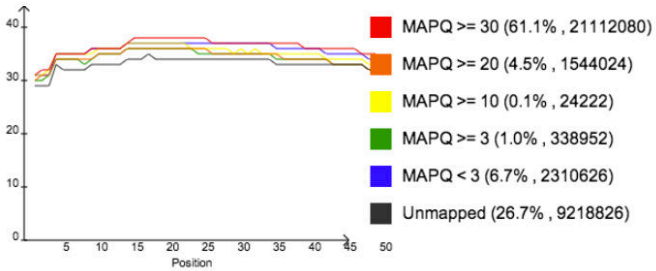
- Quality control tools for read data

Statistics for Align with Bowtie2 on data 1 and data 2: n reads

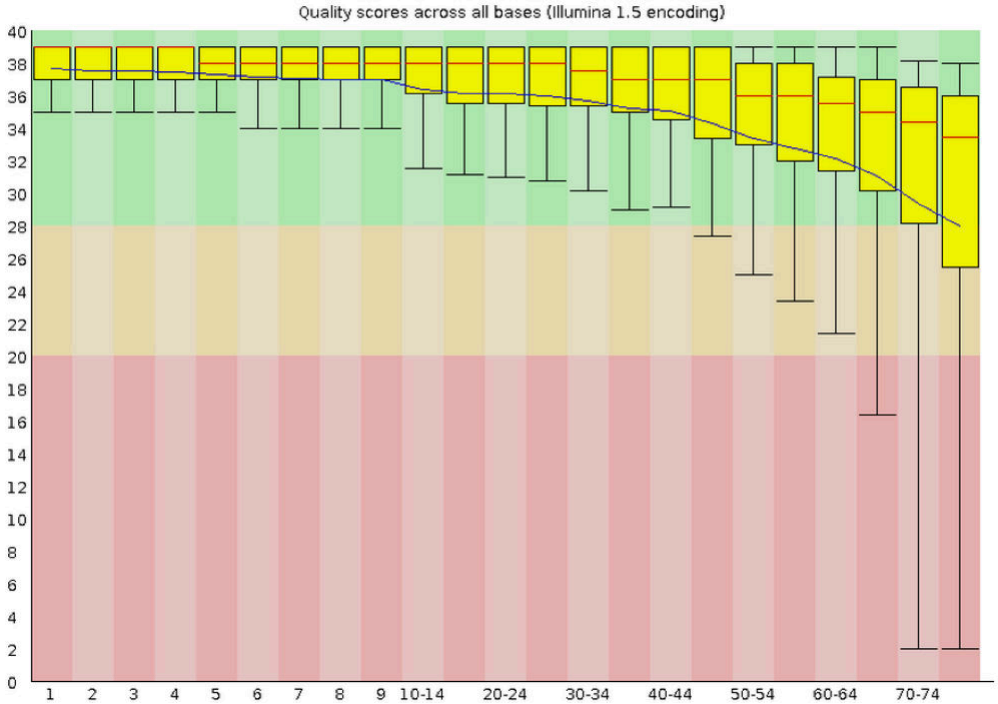
Mapping stats: 73% aligned (25.3M aligned out of 34.5M total)



Mean Base Quality



Per base sequence quality



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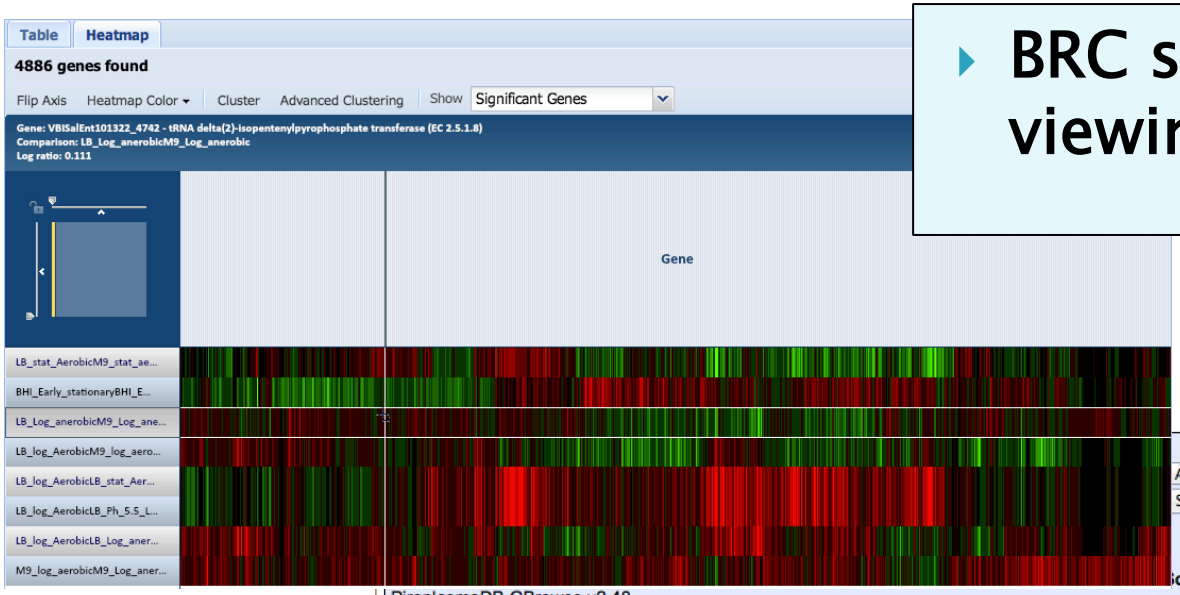
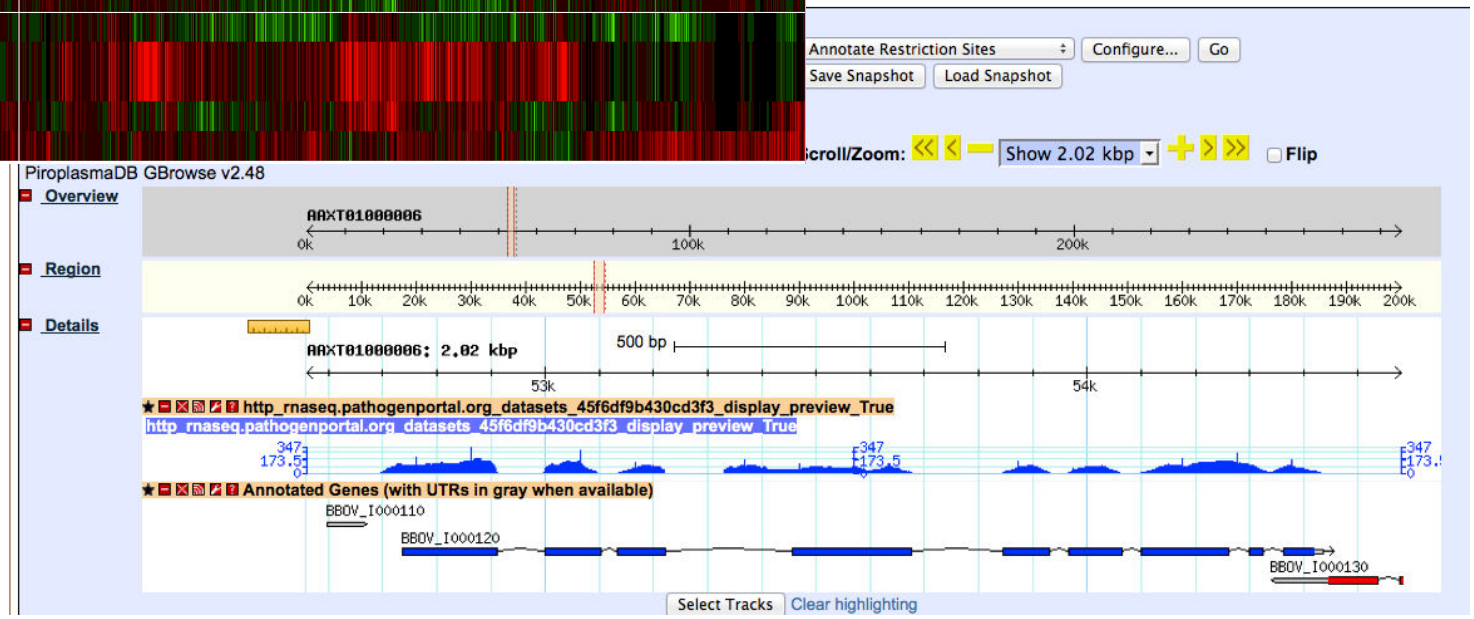
RNA-Seq Pipeline Features

- BRC streaming and viewing of results





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Galaxy Modifications

View a list of supported genomes from EuPathDB, PATRIC, and VectorBase.

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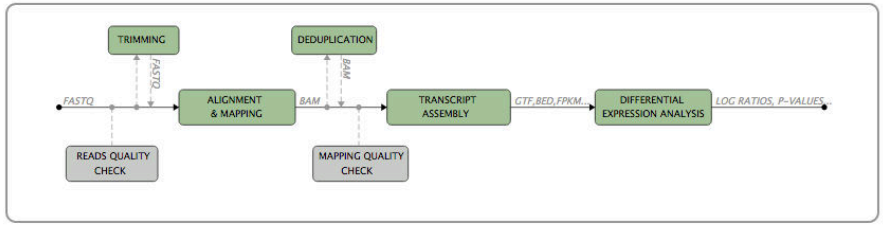

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- Launch Pad
  - D3 library concept diagram

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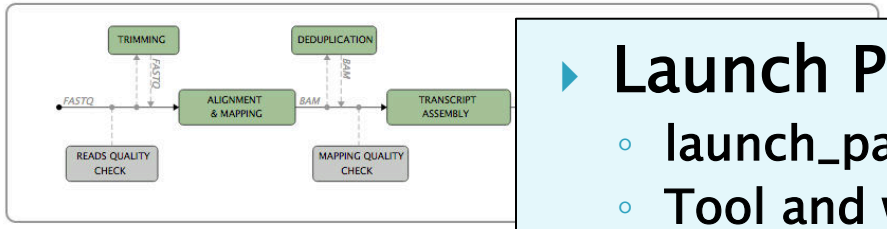

- **Launch Pad**
  - launch_pad.py controller
  - Tool and workflow lists

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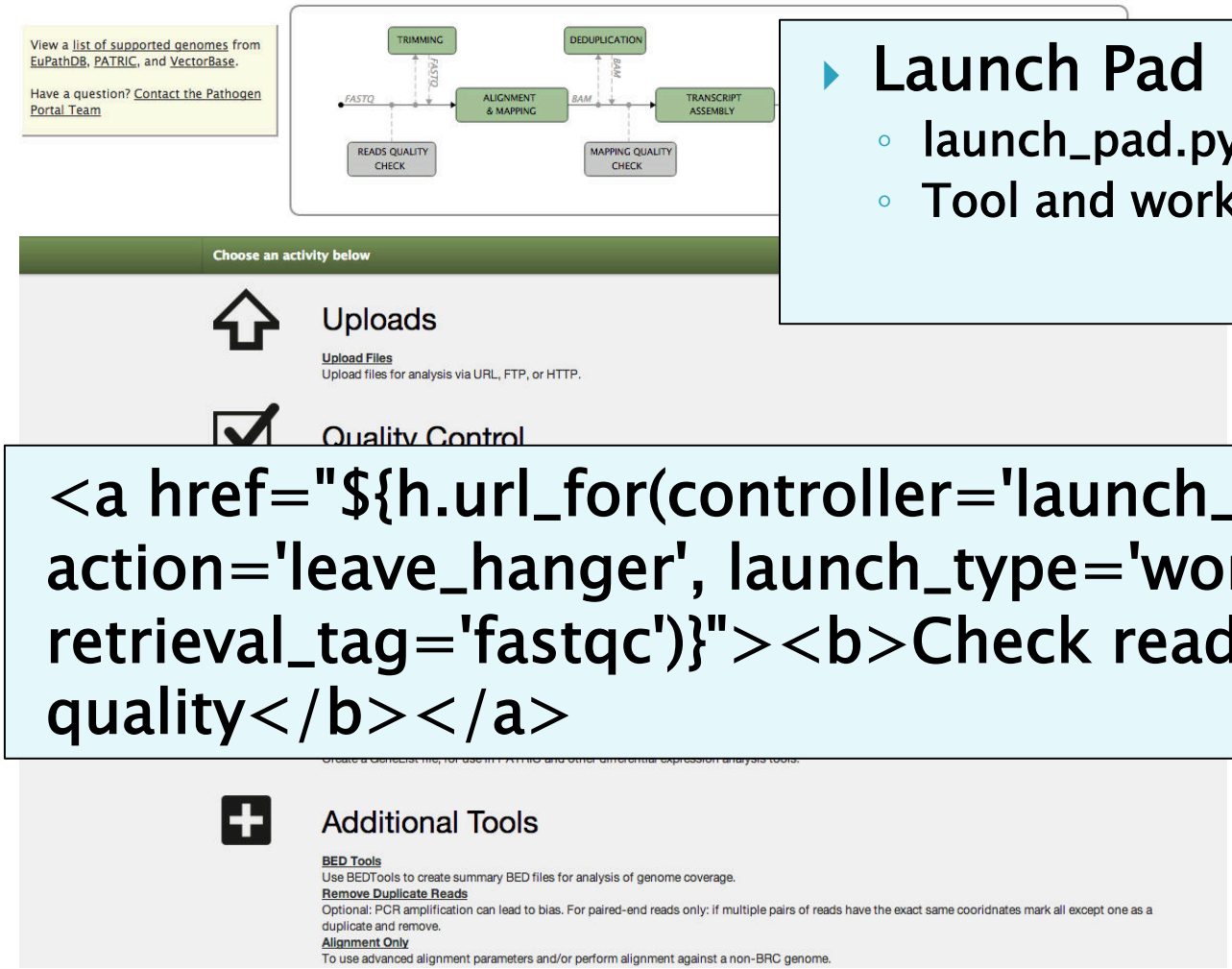
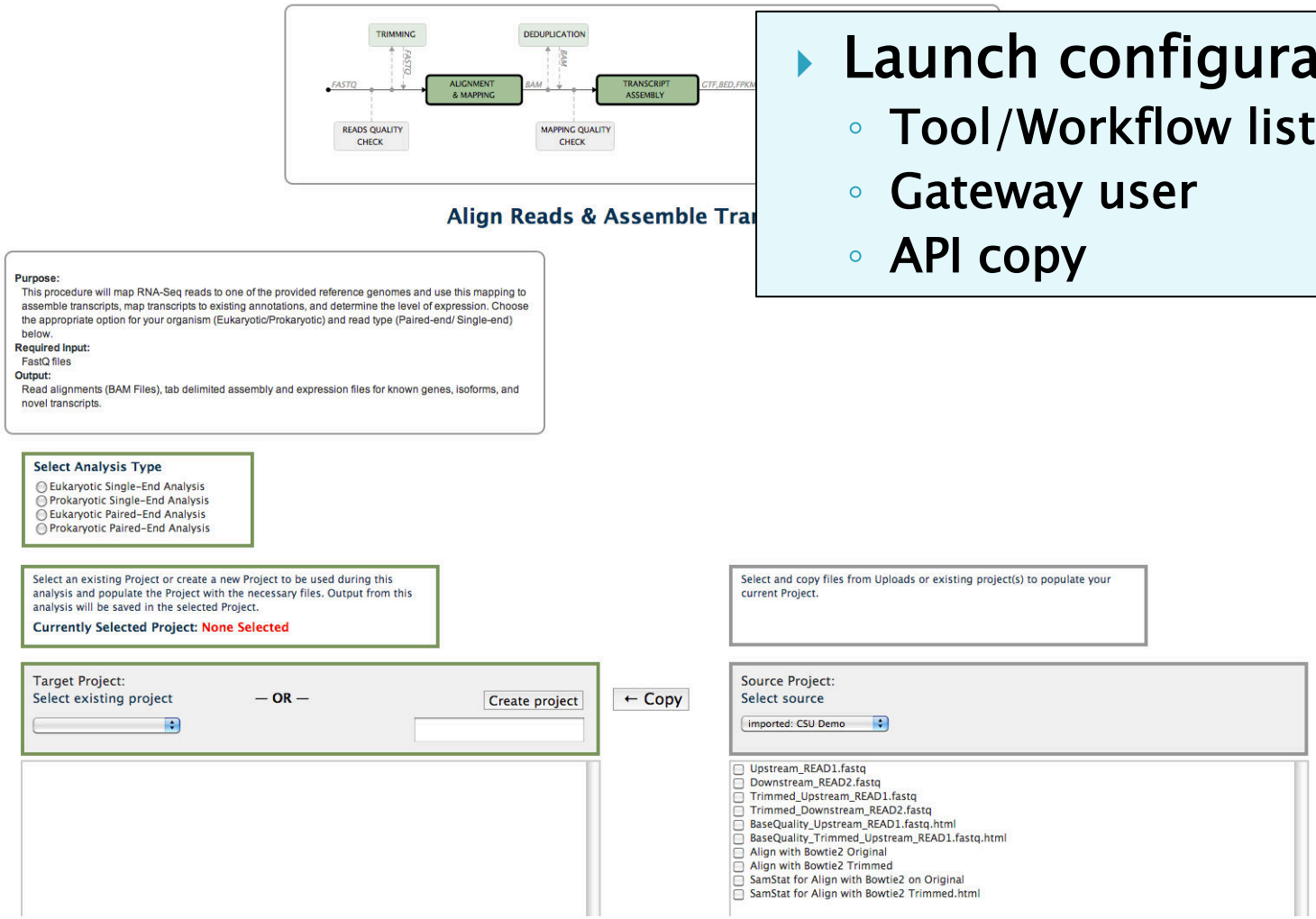


- **Launch Pad**
  - launch_pad.py controller
  - Tool and workflow lists

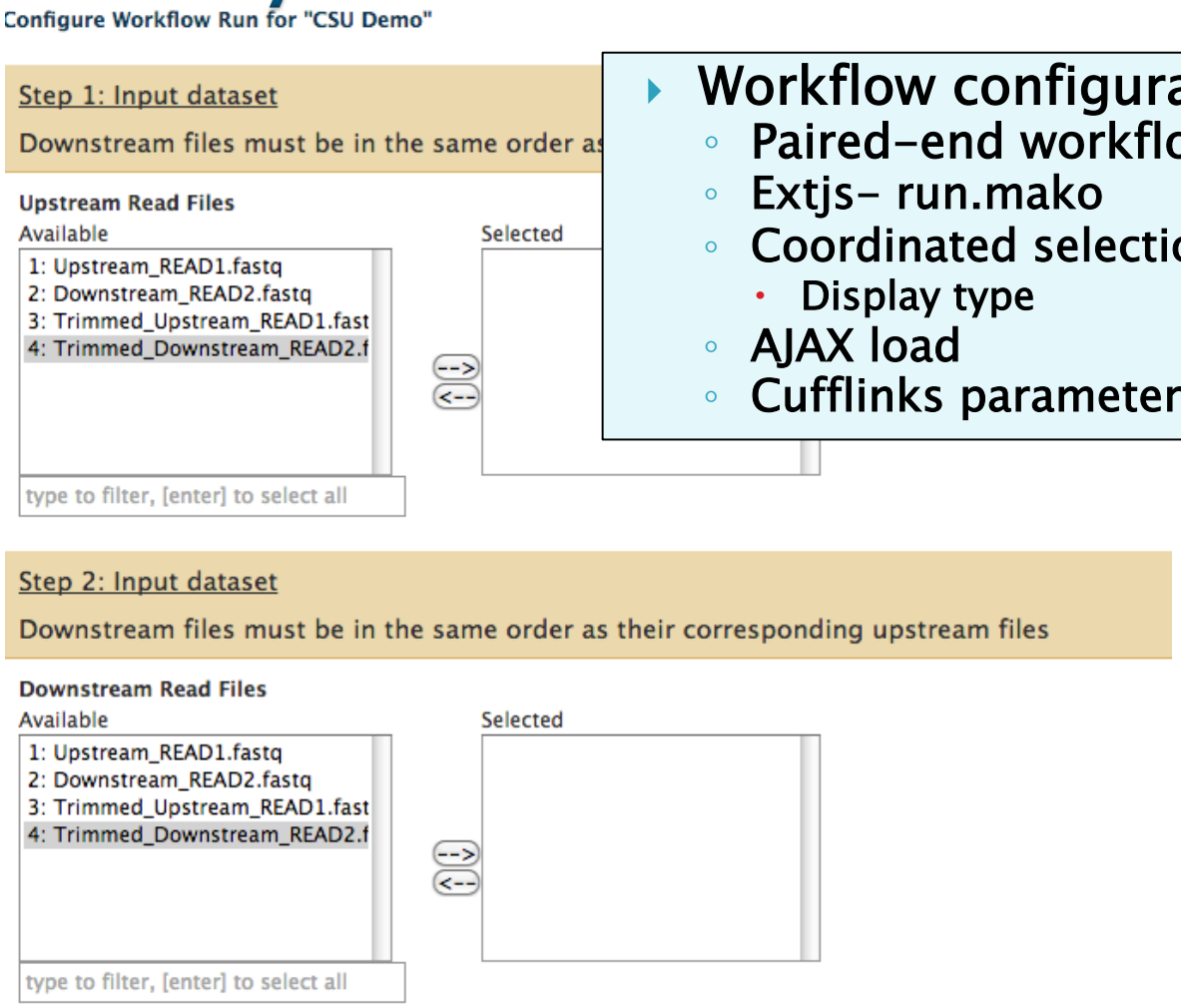
```
<a href="${h.url_for(controller='launch_pad', action='leave_hanger', launch_type='workflow', retrieval_tag='fastqc')}"><b>Check read quality</b></a>
```

Galaxy Modifications

- Launch configuration
  - Tool/Workflow lists
  - Gateway user
  - API copy

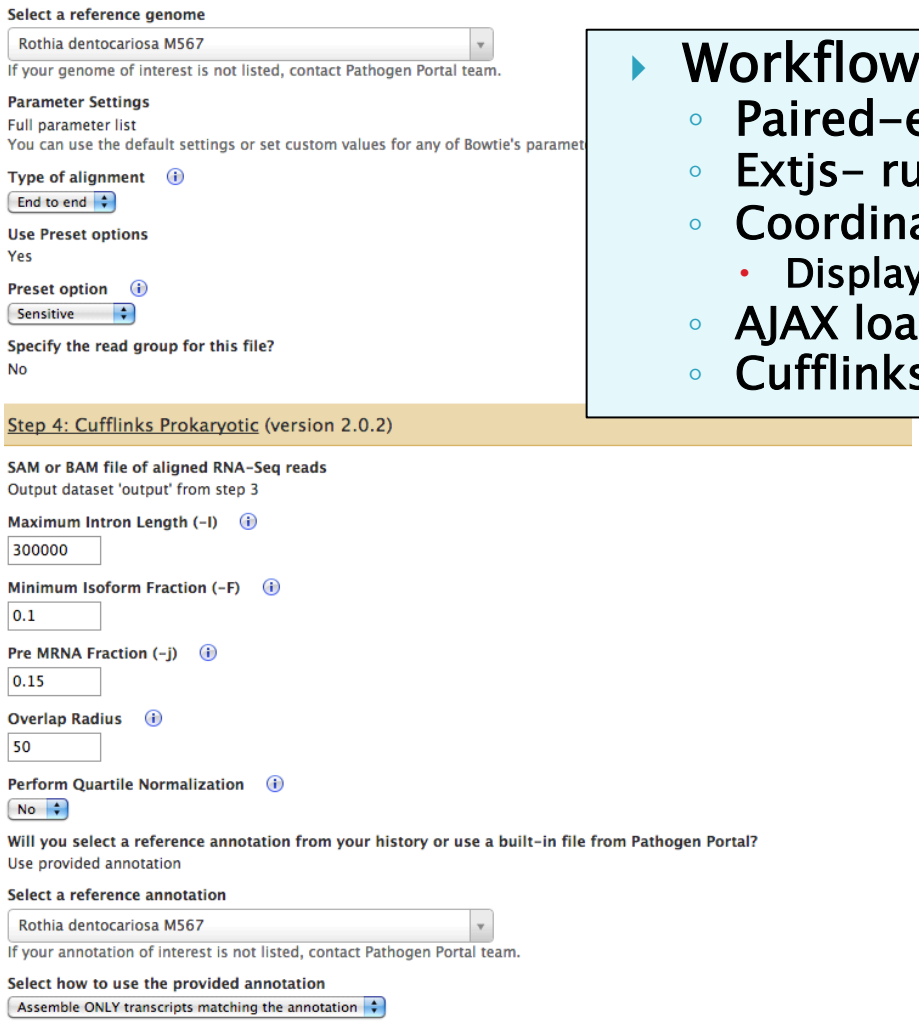


Galaxy Modifications



- Workflow configuration
  - Paired-end workflows
  - Extjs- run.mako
  - Coordinated selection
    - Display type
  - AJAX load
  - Cufflinks parameters e.g.

Galaxy Modifications



- Workflow configuration
  - Paired-end workflows
  - Extjs- run.mako
  - Coordinated selection
    - Display type
  - AJAX load
  - Cufflinks parameters e.g.

Other Modifications

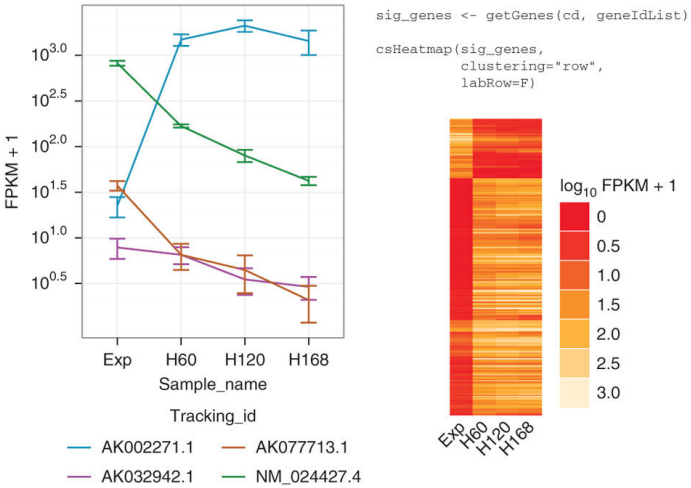
- Cuffdiff/cuffmerge integration
- SAM Stat
- Select2 wait time
- Power users

Challenges

- Controller system
- Workflow vs tool runners
  - Fixed parameters
  - Inputs
- Advanced parameters

Future Plans

- Visualization of results
  - CummeRbund
- Organism specific tools
- Link outs to BRCs
  - Annotation differences
  - Differential Expression Visualization
  - Alignment results streaming



Acknowledgements

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- Eric Nordberg
- Dustin Machi
- Chunhong Mao
- This project has been funded in whole or in part with Federal funds from the National Institute of Allergy and Infectious Diseases, National Institutes of Health, Department of Health and Human Services, under Contract No. HHSN272200900040C, awarded to BWS Sobral.

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