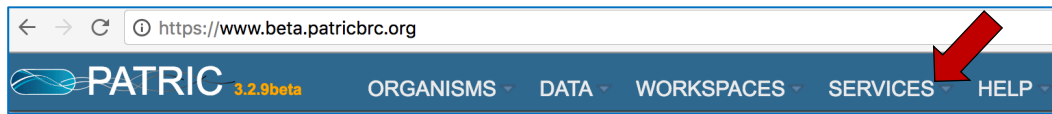


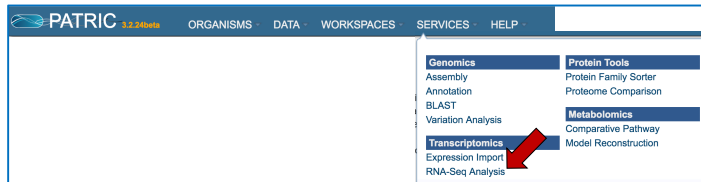
Submitting an RNA-Seq job at PATRIC

I. Locating the RNA-Seq Service App.

1. At the top of any PATRIC page, find the Services tab.



2. Click on RNA-Seq Analysis.



3. This will open up the RNA-Seq landing page where researchers can submit long reads, single or paired read files.

The screenshot shows the RNA-Seq Analysis landing page. The page contains several input fields for parameters, groups/conditions, paired read library, and single read library. A red arrow points to the STRATEGY dropdown menu.

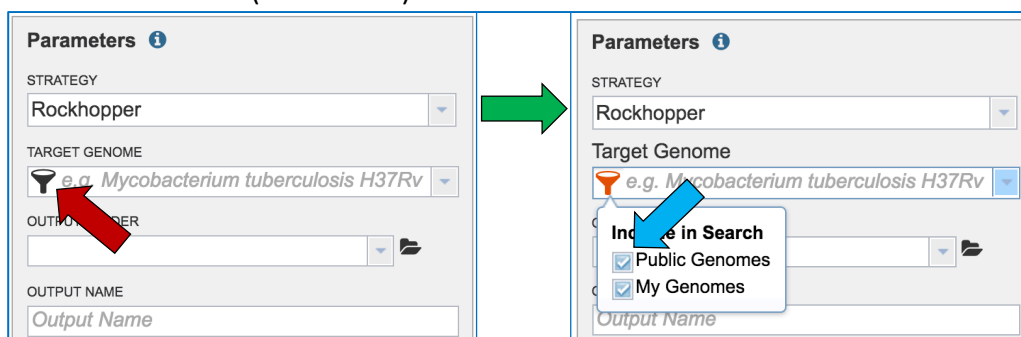
II. Filling in parameters - Strategy

1. PATRIC offers three different RNA-Seq strategies. Clicking on the down that follows the Strategy text box arrow (red arrow) will show the three options (Rockhopper, Tuxedo and HostHISAT2). Click on the desired strategy (blue arrow).

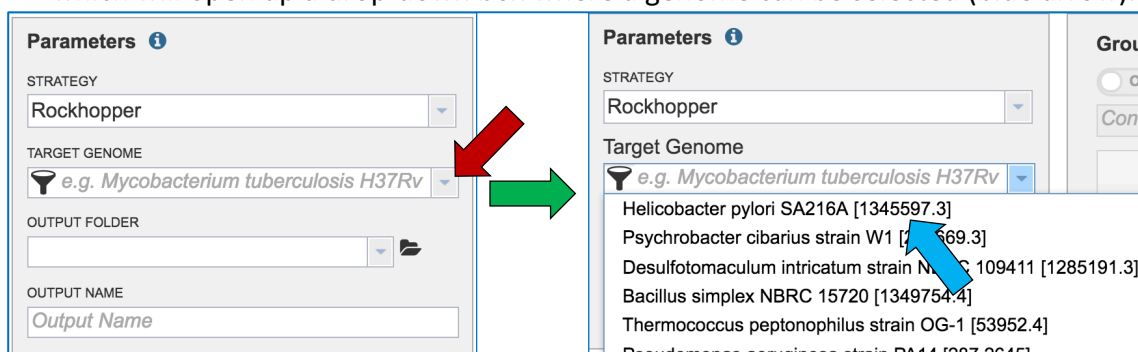
The screenshot shows the RNA-Seq Analysis landing page with the STRATEGY dropdown menu open. The dropdown menu displays three options: Rockhopper, Tuxedo, and HostHISAT2. A red arrow points to the dropdown arrow, and a blue arrow points to the Rockhopper option.

III. Filling in parameters - Target Genome

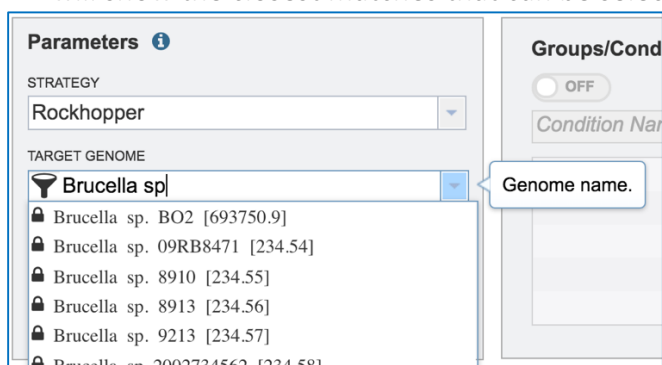
1. Researchers must select a Target Genome to align the reads against. If this genome is a private genome, the search can be narrowed by clicking on the filter icon under the words Target Genome (red arrow). This will open the filter where Public Genomes can be de-selected (blue arrow).



2. Researchers can also click on the down arrow at the end of the text box (red arrow) which will open up a drop-down box where a genome can be selected (blue arrow).



3. Researchers can also start typing the name of a genome. A box below Target Genome will show the closest matches that can be selected.



IV. Filling in parameters – Output folder


1. Researchers that have used PATRIC before can click on the down arrow at the end of the Output Folder text box. This will open a dropdown box that will show the folders that exist in the workspace (red arrow).

Parameters ⓘ

STRATEGY
Rockhopper

Target Genome
🔍 **Helicobacter pylori SA216A**

OUTPUT FOLDER
/home/
Experiments
/home/
Genome Groups



2. Researchers that have not previously submitted a RNA-Seq job and want to create a new folder to store the results will need to click on the folder icon at the end of the Output Folder text box (red arrow).


Parameters ⓘ

STRATEGY
Rockhopper

TARGET GENOME
🔍 **Helicobacter pylori SA216A**

OUTPUT FOLDER
/home/
Experiments
/home/
Genome Groups

OUTPUT NAME
Output Name



3. This will open a pop-up window. To create a new folder, click on the folder icon (red arrow) which will reload the window (black arrow) to show a text box where the new folder can be named (blue arrow). Once the folder has been named, click on OK to finalize it (green arrow).



Choose or Upload a Workspace Object

Folder: /ARWattam@patricbrc.org/home
Selection: None.

Name	Created
Parent Folder	
ASMMicrobe	6/16/16, 10:22 AM
Annotations	7/2/15, 4:28 PM
Assemblies	6/15/15, 10:56 AM
Brucella privatei	6/4/15, 12:56 PM
Brucella_assembly	4/1/15, 12:44 PM
CDC collaboration	8/25/15, 9:26 AM
Corynebacterium-Alberto	5/15/16, 1:01 PM
Experiment Groups	3/26/15, 12:01 PM

☐ Show files with an unspecified type

OK Cancel



Choose or Upload a Workspace Object

Folder: /ARWattam@patricbrc.org/home
Selection: None.

Name	Created
Experiments	
Parent Folder	
ASMMicrobe	6/16/16, 10:22 AM
Annotations	7/2/15, 4:28 PM
Assemblies	6/15/15, 10:56 AM
Brucella privatei	6/4/15, 12:56 PM
Brucella_assembly	4/1/15, 12:44 PM
CDC collaboration	8/25/15, 9:26 AM
Corynebacterium-Alberto	5/15/16, 1:01 PM

☐ Show files with an unspecified type

OK Cancel

4. Finally, researchers must name the RNA-seq job (red arrow).

Parameters ⓘ

STRATEGY
Rockhopper

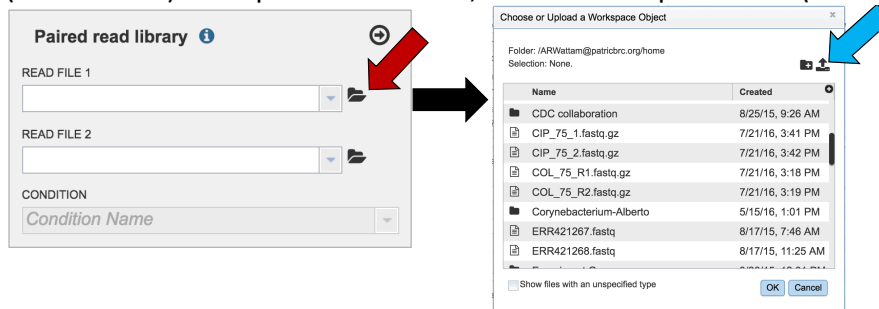
Target Genome
Helicobacter pylori SA216A

OUTPUT FOLDER
Experiments

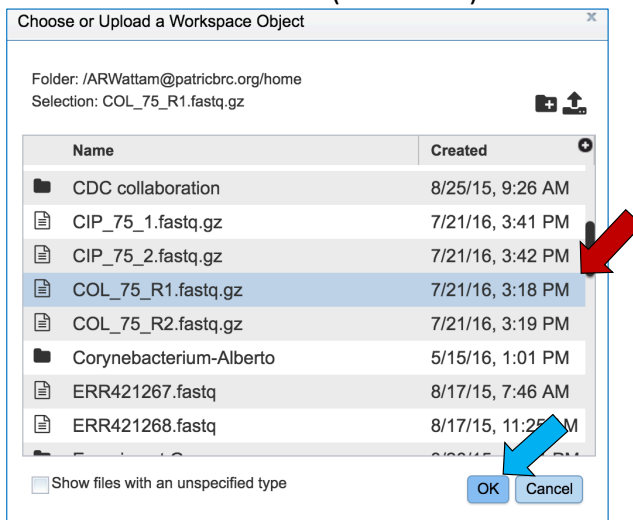
OUTPUT NAME
Helico-RNA-Seq

V. Uploading reads from your computer that are not in the workspace

1. To upload reads that have not previously been uploaded into PATRIC, click on the folder icon that follows the Read File text box (red arrows). This will open a pop-up window (black arrow). To upload new reads, click on the upload icon (blue arrow).



2. Select the file of interest (red arrow) and then click OK (blue arrow).



3. Once a file is selected, researchers must play particular attention to the Uploads monitor at the bottom of the page, which will show the progress in upload.



4. The name of the uploaded file will appear in the text box.

Paired read library ⓘ

READ FILE 1
COL_75_R2.fastq

READ FILE 2

CONDITION
Condition Name

V. Uploading reads from your computer that are in the workspace

1. Clicking on the down arrow that follows the text box (red arrow) will open a drop down box where files can be selected (blue arrow).

Paired read library ⓘ

READ FILE 1
/home/16M_SRR915809_2.fastq

READ FILE 2

CONDITION
Condition Name

2. Another way to upload reads that are already in the workspace is to click on the folder icon that follows the text box (red arrow) which will open a pop-up box where reads can be selected (blue arrow). The upload is completed by clicking OK (blue arrow).

Paired read library ⓘ

READ FILE 1

READ FILE 2

CONDITION
Condition Name

Choose or Upload a Workspace Object

Folder: /ARWattam@patricbrc.org/home
Selection: MERO_75_R2.fastq.gz

Name	Created
holger-	3/12/16, 12:04 PM
Holger-vulpis	3/15/16, 12:05 PM
MERO_75_R1.fastq.gz	7/21/16, 3:27 PM
MERO_75_R2.fastq.gz	7/21/16, 3:31 PM
MHB_R1.fastq.gz	7/21/16, 3:16 PM
MHB_R2.fastq.gz	7/21/16, 3:15 PM
Proteome Comparison	8/22/15, 10:18 AM
R2.txt	7/13/15, 9:27 AM
RNA-Seq_Brucella	12/1/15, 12:04 PM

Show files with an unspecified type

OK Cancel

3. Single or paired end reads should be selected and then will appear in the text box(es).

Paired read library ⓘ

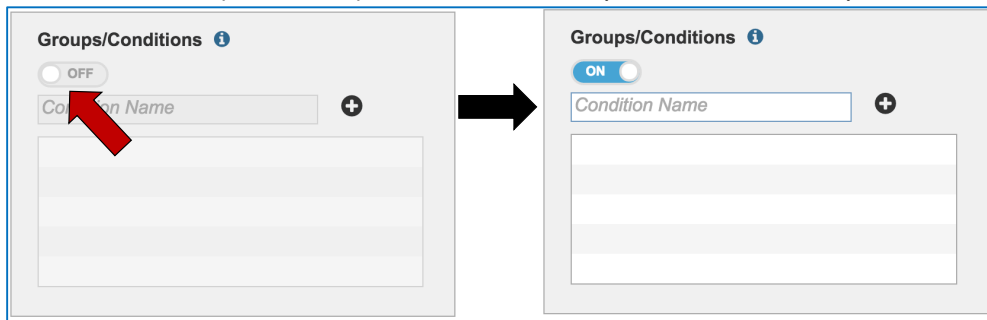
READ FILE 1
MERO_75_R1.fastq.gz

READ FILE 2
MERO_75_R2.fastq.gz

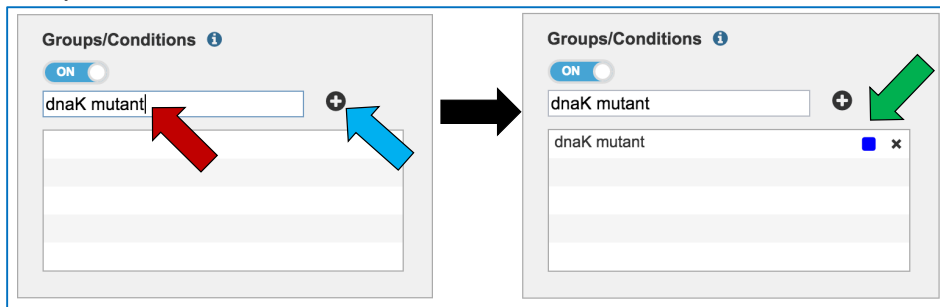
CONDITION
Condition Name

VI. Selecting a condition or group that will be linked to a read (Optional)

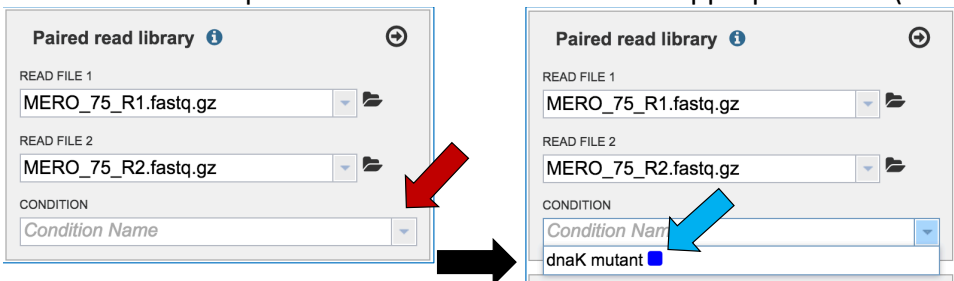
1. Metadata can be assigned to selected reads. This will make identification easier in some of the downstream tools available on PATRIC. To do this, locate the Condition box and click the On box (red arrow). This will make it possible to name specific conditions.



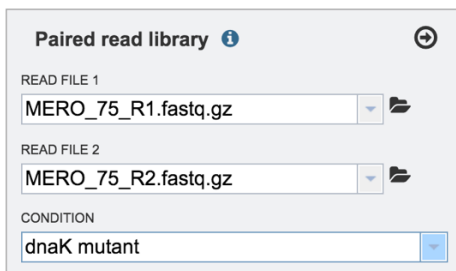
2. Name the condition (red arrow) and click the plus icon (blue arrow). This will show the name of the condition and a color code assigned to it in the text box (green arrow). As many conditions as desired can be entered.



3. To link the name of the condition or group to the selected reads, click on the down arrow that follows the text box under Condition (red arrow). This will open a drop down box that shows all possible conditions. Click on the appropriate one (blue arrow).



4. This will autofill the Condition text box with the name of the condition.



VI1. Selecting a condition or group that will be linked to a read

1. Clicking on the arrow icon in any read library box (red arrow) will load the reads (shown together in the same line for paired reads) with their assigned condition into the selected library.

The diagram illustrates the process of moving a read library. On the left, the 'Paired read library' section contains two read file inputs (READ FILE 1 and READ FILE 2) both set to 'MERO_75_R1.fastq.gz' and 'MERO_75_R2.fastq.gz' respectively, and a 'CONDITION' dropdown set to 'dnaK mutant'. A red arrow points to the right-pointing arrow icon in the top right corner of this section. A black arrow points from this icon to the 'Selected libraries' section on the right. The 'Selected libraries' section has a header 'Place read files here using the arrow buttons.' and a list containing one entry: 'P(MERO_...tq.gz, MERO_...tq.gz)' with a blue square icon and a close button (x).

2. To submit the completed job, click the Submit button (red arrow).

This screenshot shows the 'RNA-Seq Analysis' form. It includes sections for 'Parameters' (Strategy: Rockhopper, Target Genome: Helicobacter pylori SA216A, Output Folder: Experiments, Output Name: Helico RNA-Seq), 'Groups/Conditions' (ON toggle, list with 'dnaK mutant'), 'Paired read library' (same as the previous diagram), and 'Single read library' (empty). The 'Selected libraries' section is also present with the same entry as before. At the bottom, there are 'Reset' and 'Submit' buttons. A red arrow points to the 'Submit' button.

3. If the job was submitted successfully, a message will appear that indicates that the job has entered the assembly queue.

A message box with a green border and background. It contains the text 'RNA-Seq job has been queued.' in green. Below the message are 'Reset' and 'Submit' buttons.

4. To check the status of the assembly job, click on the Jobs indicator at the bottom of the PATRIC page.



5. Clicking on Jobs opens the Jobs Status page, where researchers can see the progression of the assembly job as well as the status of all the previous service jobs that have been submitted.

PATRIC 3.2.24beta						
ORGANISMS · DATA · WORKSPACES · SERVICES · HELP ·						
All Data Types						
Status	Submit	App	Output Name	Start	Completed	
● completed	10/14/16, 2:51 PM	RNASeq	Ab-COL_75	10/14/16, 2:52 PM	10/14/16, 2:52 PM	
● completed	10/10/16, 7:53 PM	Proteome Comparison	8913 as ref 10-09-2016	10/10/16, 7:53 PM	10/10/16, 8:07 PM	