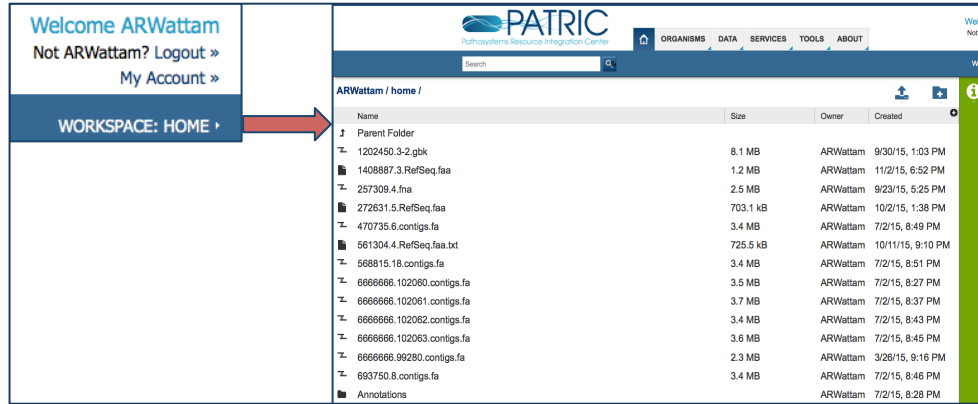
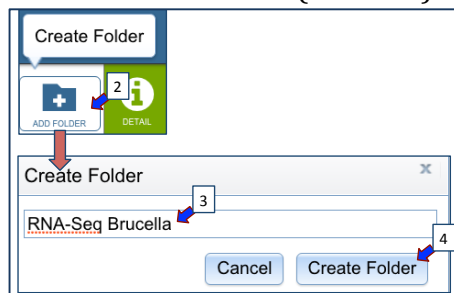


Transcriptomics Analysis: Submitting RNA-Seq data to PATRIC

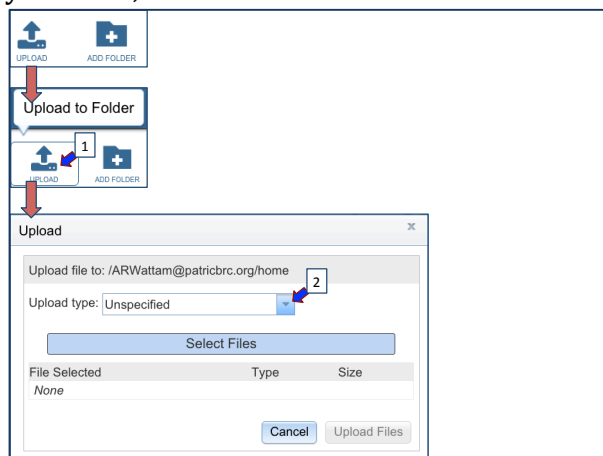
1. You must be logged in to use the PATRIC services. Once you are logged in, click on the Workspace that can be found at the top of any page in PATRIC. This will take you to your private workspace.



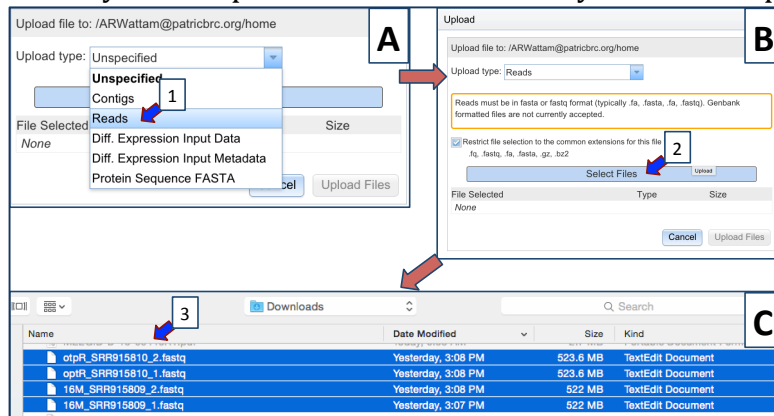
2. **Creating a folder for your experiment.** Click on the folder icon (Blue arrow 2) and this will open up a window where you can name a folder. Type the name for the folder in the text box (Arrow 3) and then click on Create Folder (Arrow 4).



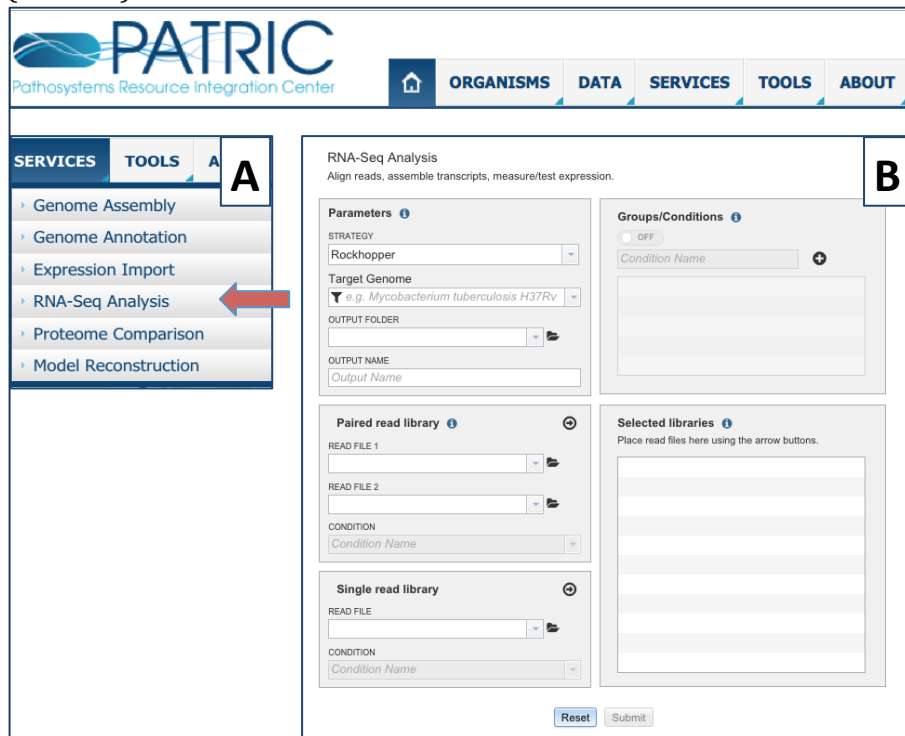
3. **Uploading the reads to your workspace.** Now you need to load the reads. Click on the upload icon (Blue arrow 1). This will open up a pop-up window. To find your files, click on the download arrow that follows Update type (Arrow 2).



4. Click on Reads (Blue arrow 1 in panel A). Then you will need to click on the blue Select File tab (Arrow 2 in Panel B). This will open up a file that allows you to select files in your computer. Select all the ones you want to upload (Arrow 3 in Panel C).

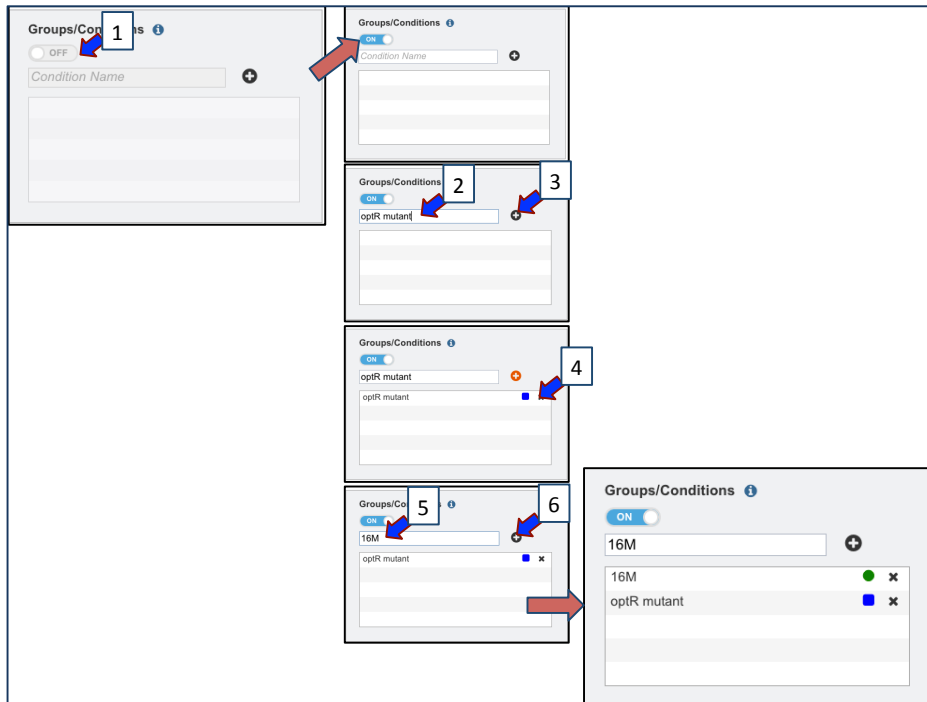


5. Starting the RNA-Seq analysis job. Now you're ready to start your RNA -Seq job. At the top of any PATRIC page, find the Services tab and select RNA-Seq Analysis (Panel A). This will open up the landing page where you will start the RNA-Seq job (Panel B).

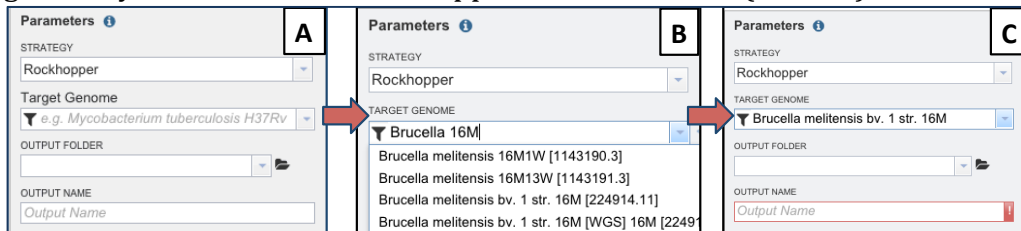


6. Creating the conditions. You can input the experimental conditions or treatments that your RNA-Seq job had. This will allow you to distinguish between the reads later when you are looking at the data. To do this, enable this ability by turning it on (Arrow 1 below). Now you can add the conditions that were used in the experiment. Type in the name of the condition in the text box (Arrow 2) and then click on the + sign (Arrow 3). Now you'll see that name in the text box below. Repeat with any

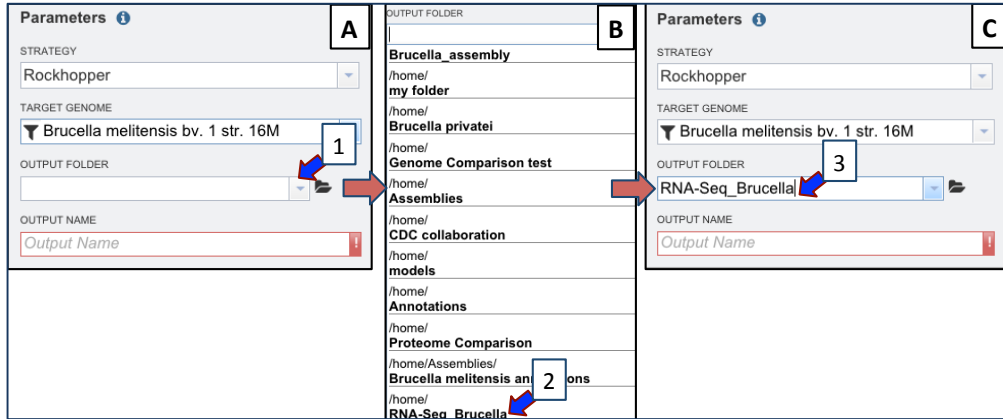
other conditions (Arrows 4 and 5) and then you'll find all the treatments used in the text box.



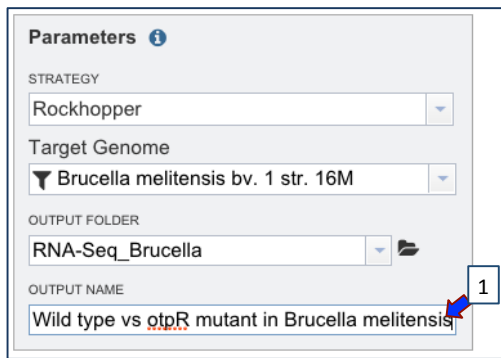
7. Assigning the Target Genome. You need to identify the target genome. You can do this by starting to type some distinctive text in the text box under Target Genome (Panel B) that will open a drop down box of possible choices. Double click on the genome you want, and that will appear in the text box (Panel C).



8. Identifying the Output Folder. Click on the down arrow next to Output folder (Blue Arrow 1 in A below). This will open up a drop down box Panel B). Double click on the folder where you want the job to be stored (Blue arrow 2) and you will see that name appear in the text box for the folder (Blue arrow 3 in C).



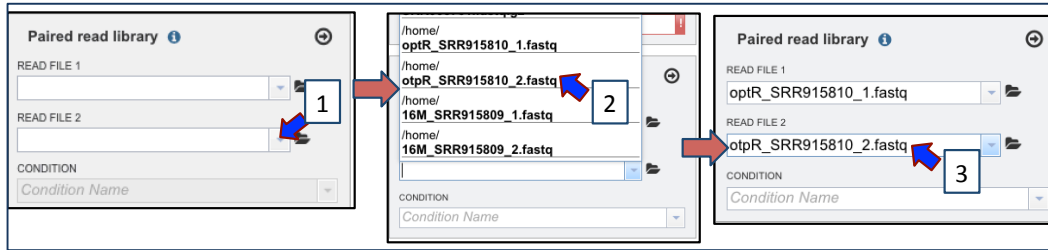
9. **The Output Name.** Give the experiment a distinctive name so you can recognize it later.



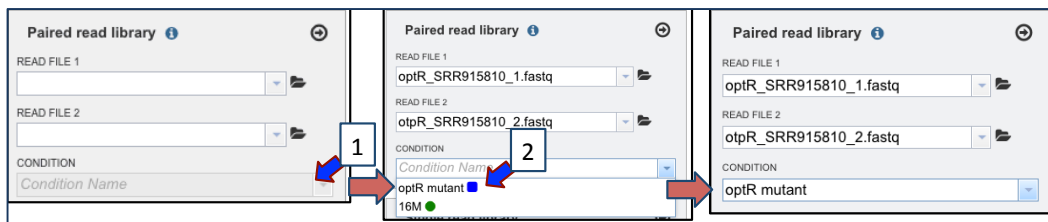
10. **Loading the reads.** In this example, we will use paired end reads. Click on the down arrow next to Read File 1 (Blue arrow 1). This will open a drop down box that will show you the reads that you have already uploaded in Step 4. Click on the first of the pair or reads (Arrow 2). This will fill the box to show that reads you selected (Arrow 3).



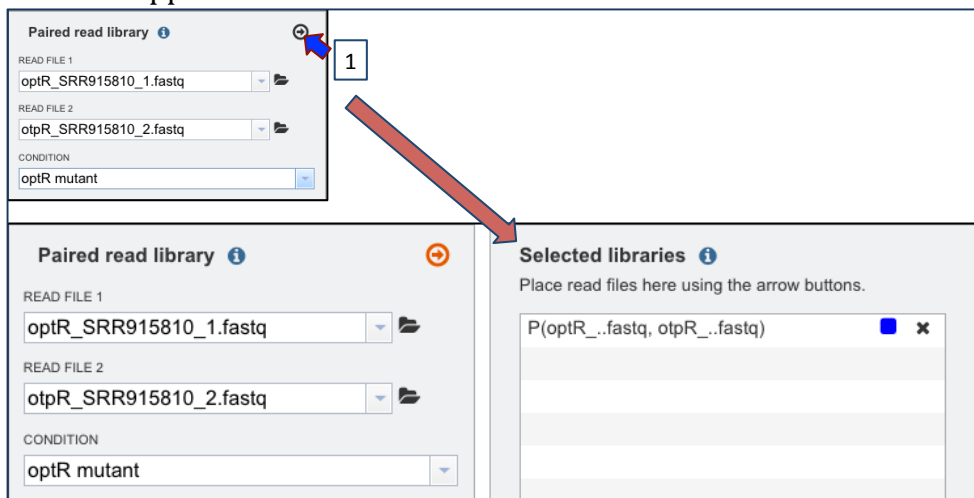
11. Now you need to choose the second of the pairs. Click on the down arrow next to Read File 2 (Blue arrow 1). This will open a drop down box that will show you the variable reads. Click on the first of the pair or reads (Arrow 2). This will fill the box to show that reads you selected (Arrow 3).



12. Now you need to map the read to the condition or treatment that was used in the experiment. Click on down arrow next to Condition Name (Blue arrow 1). This will open up a drop down box that shows all the condition. Select the appropriate one by clicking on it (Arrow 2), which will fill the box to show the condition you selected.



13. The last step is to click on the + sign (Blue arrow 1). Once you do this, the paired ends will appear in the Selected libraries box.



14. Repeat steps 10-13 to add the second part of the paired reads. Be sure to assign the second condition.

Paired read library +

READ FILE 1

READ FILE 2

CONDITION

Selected libraries i

Place read files here using the arrow buttons.

P(16M_S..fastq, 16M_S..fastq)	●	✕
P(optR_..fastq, otpR_..fastq)	■	✕

15. Once you've filled everything in, you're ready to start the annotation job. You can do this by clicking on the Submit button (Blue arrow 1).

RNA-Seq Analysis
Align reads, assemble transcripts, measure/test expression.

Parameters i

STRATEGY

Target Genome

OUTPUT FOLDER

OUTPUT NAME

Groups/Conditions i

ON

16M	●	✕
optR	■	✕

Paired read library +

READ FILE 1

READ FILE 2

CONDITION

Selected libraries i

Place read files here using the arrow buttons.

P(16M_S..fastq, 16M_S..fastq)	●	✕
P(optR_..fastq, otpR_..fastq)	■	✕

Single read library +

READ FILE

CONDITION

1

16. A message will appear below the box that indicated that your job is now in the queue.

RNA-Seq job has been queued.

17. You can check the status of your annotation job by clicking on the Jobs indicator at the bottom of the PATRIC page.

Uploads
4·0

Jobs
43·0·0·7