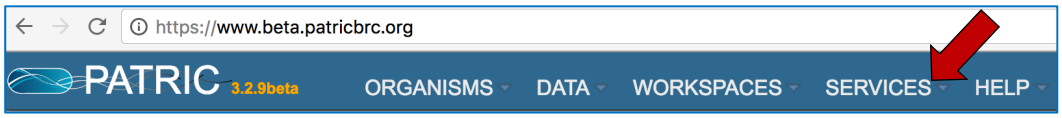
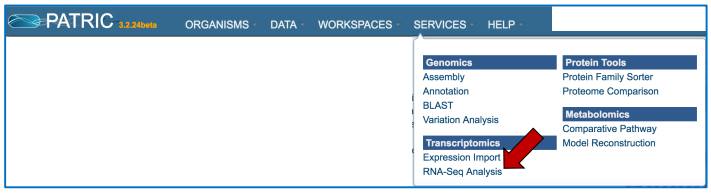
Submitting an RNA-Seq job at PATRIC

I. Locating the RNA-Seq Service App.

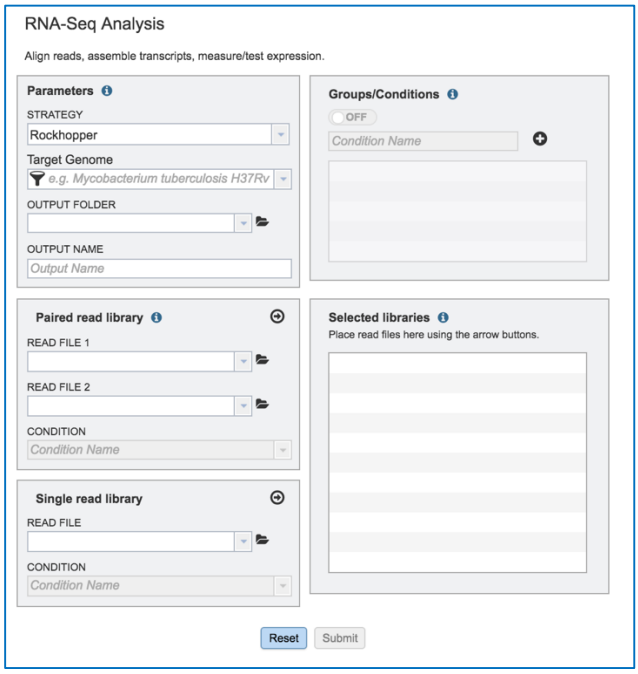
1. At the top of any PATRIC page, find the Services tab.



2. Click on RNA-Seq Analysis.

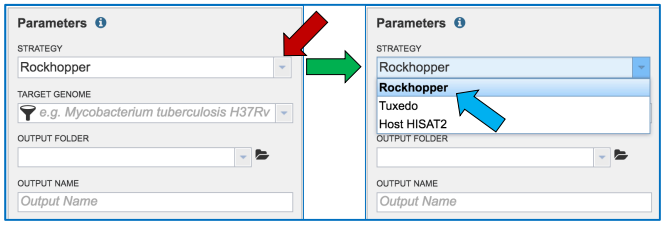


3. This will open up the RNA-Seq landing page where researchers can submit long reads, single or paired read files.



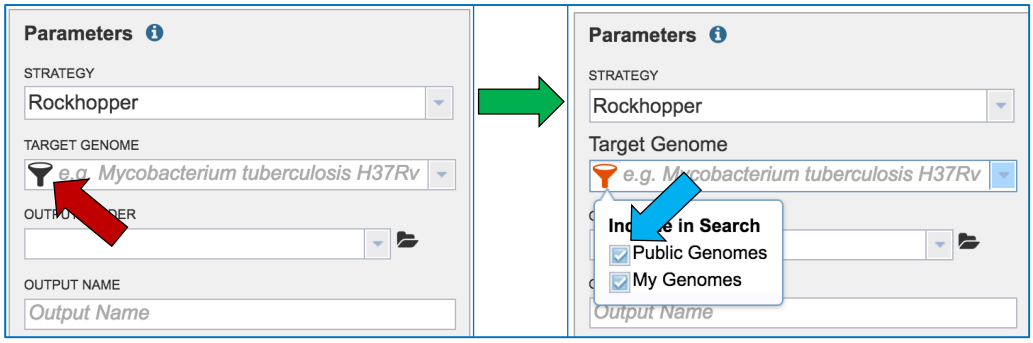
II. Filling in parameters - Strategy

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).

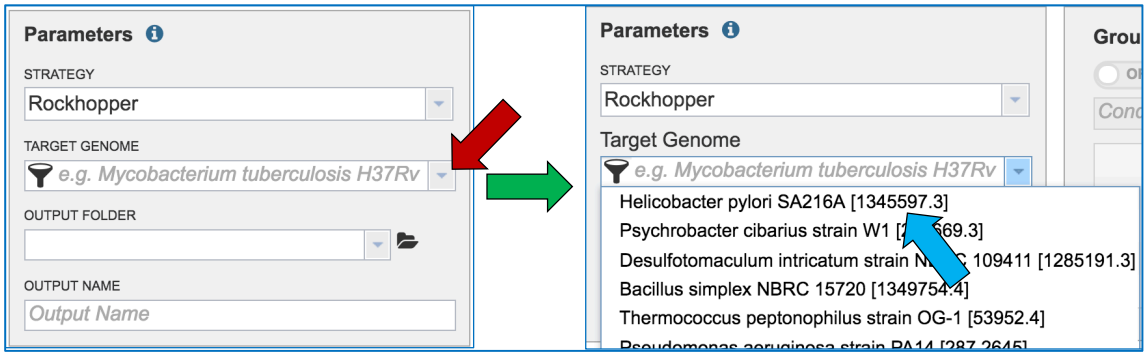


III. Filling in parameters - Target Genome

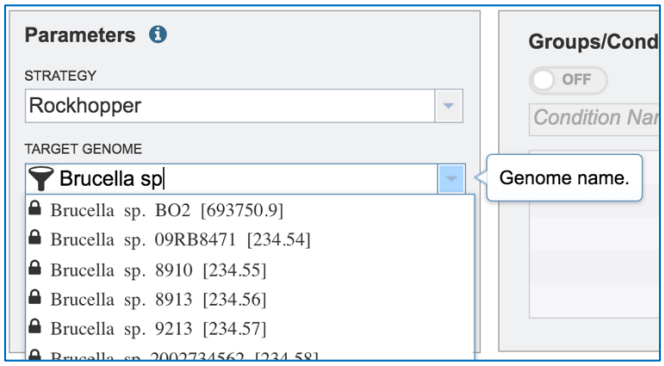
1. Researchers must select a Target Genome to align the reads against. If this genome is a private genome, the search can be narrowed by clicking on the filter icon under the words Target Genome (red arrow). This will open the filter where Public Genomes can be de-selected (blue arrow).



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).

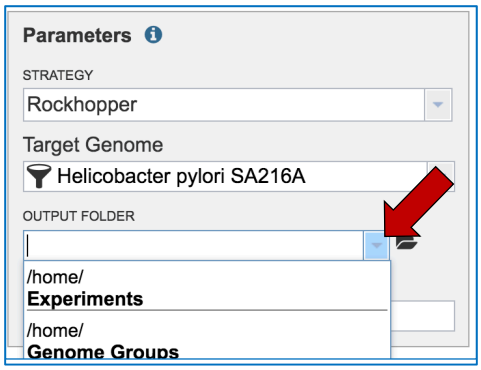


3. Researchers can also start typing the name of a genome. A box below Target Genome will show the closest matches that can be selected.

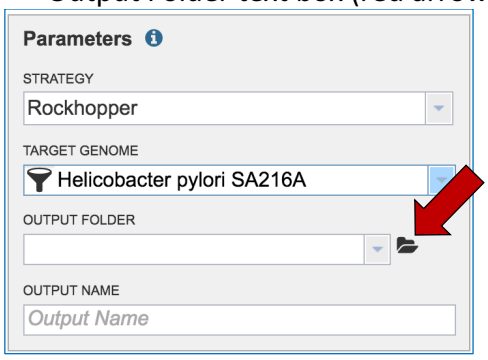


IV. Filling in parameters – Output folder

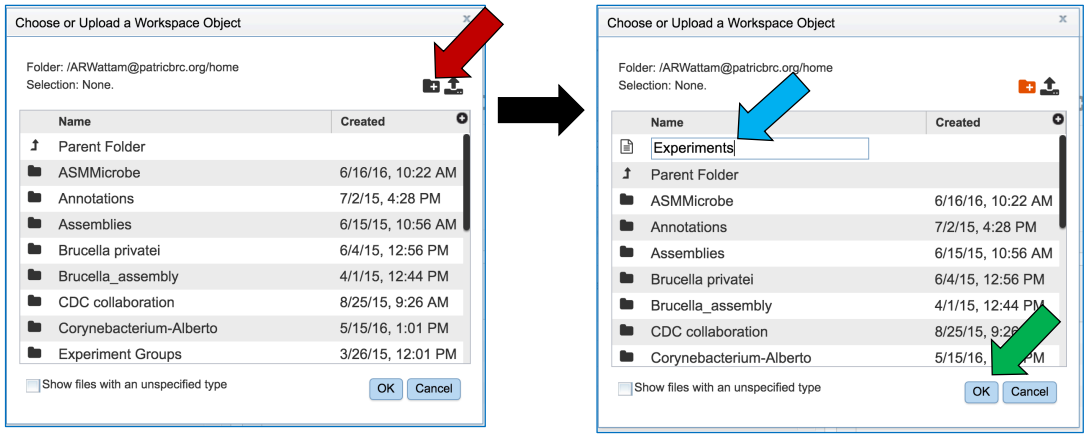
1. Researchers that have used PATRIC before can click on the down arrow at the end of the Output Folder text box. This will open a dropdown box that will show the folders that exist in the workspace (red arrow).



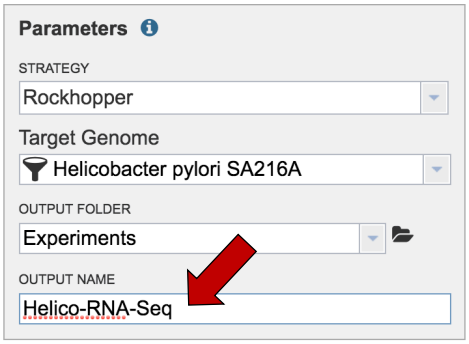
2. Researchers that have not previously submitted a RNA-Seq job and want to create a new folder to store the results will need to click on the folder icon at the end of the Output Folder text box (red arrow).



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).

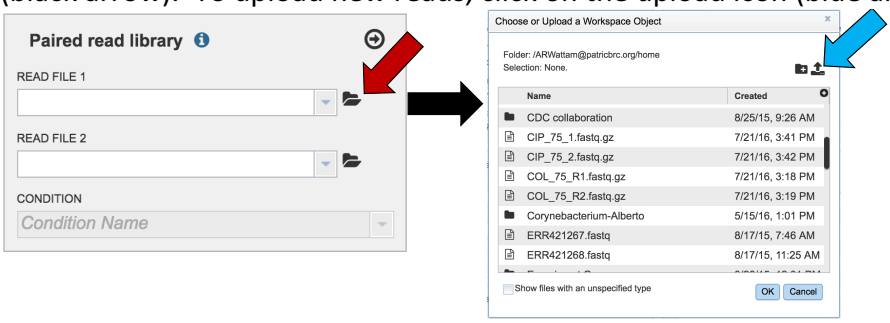


4. Finally, researchers must name the RNA-seq job (red arrow).

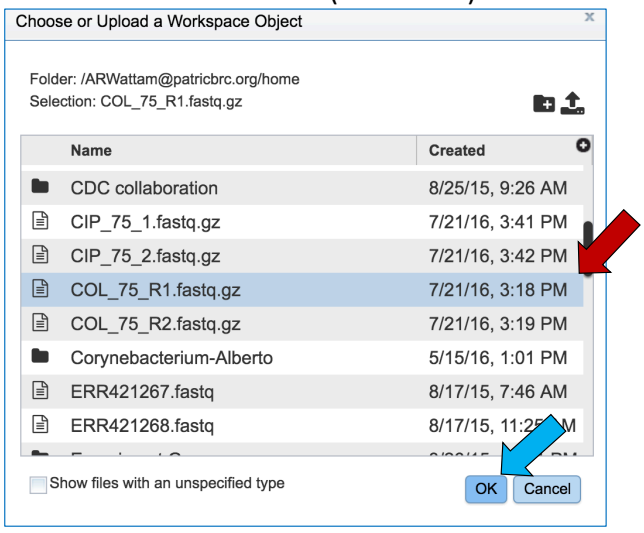


V. Uploading reads from your computer that are not in the workspace

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).

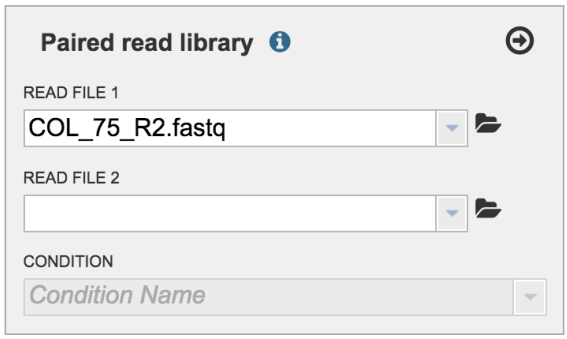


2. Select the file of interest (red arrow) and then click OK (blue arrow).



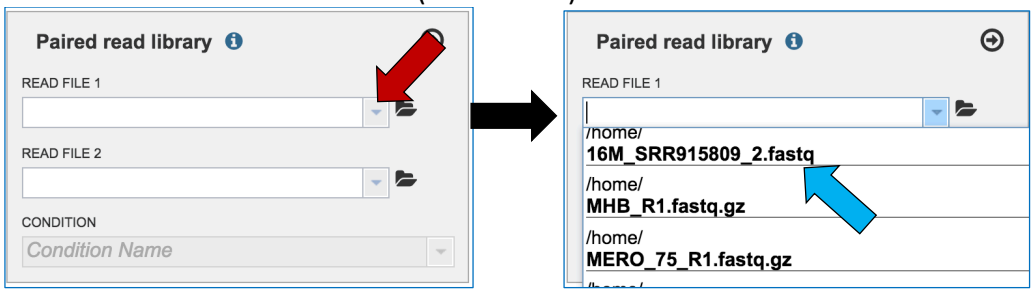
3. Once a file is selected, researchers must play particular attention to the Uploads monitor at the bottom of the page, which will show the progress in upload.

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

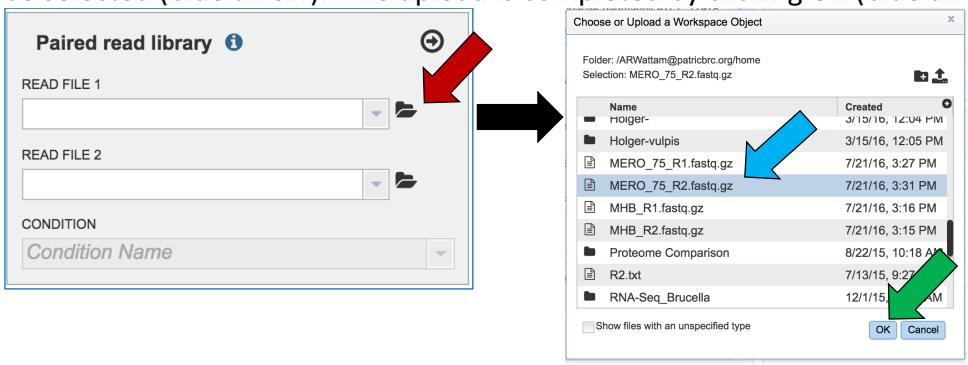


V. Uploading reads from your computer that are in the workspace

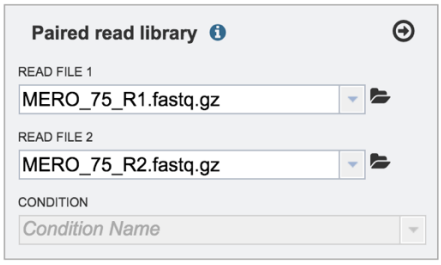
1. Clicking on the down arrow that follows the text box (red arrow) will open a drop down box where files can be selected (blue arrow).



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).

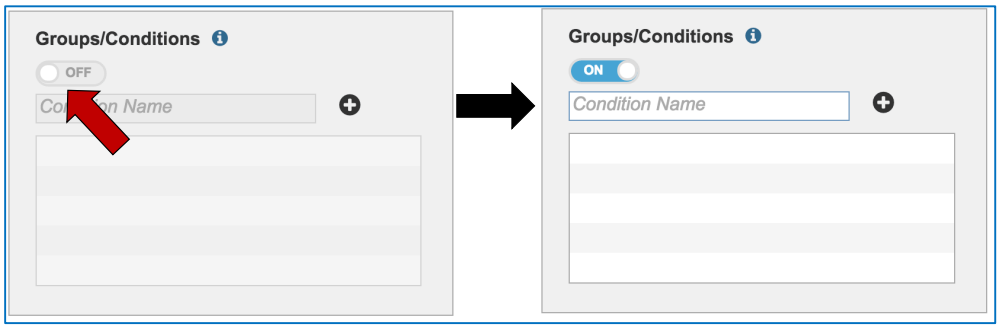


3. Single or paired end reads should be selected and then will appear in the text box(es).

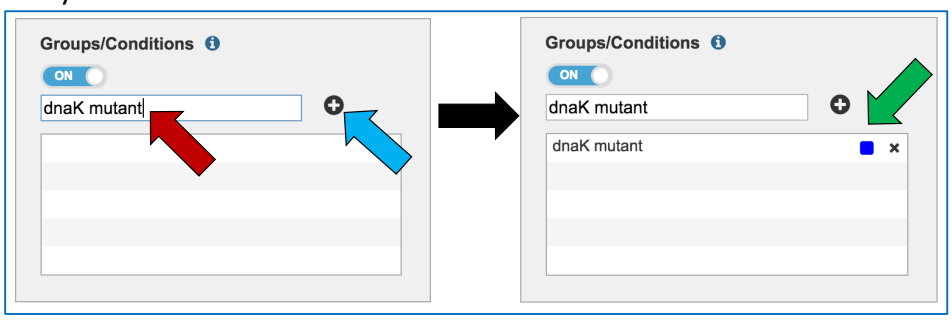


VI. Selecting a condition or group that will be linked to a read (Optional)

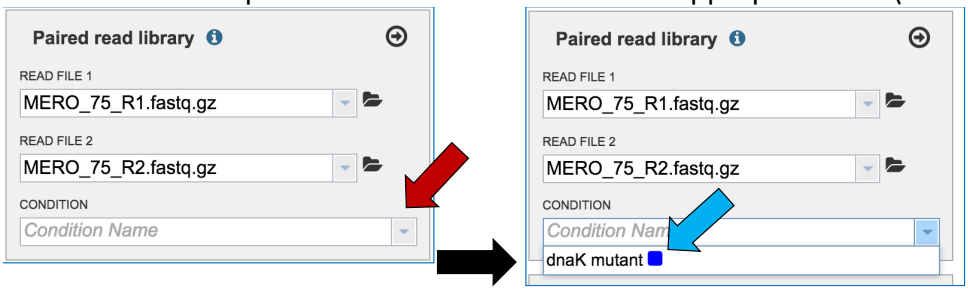
1. Metadata can be assigned to selected reads. This will make identification easier in some of the downstream tools available on PATRIC. To do this, locate the Condition box and click the On box (red arrow). This will make it possible to name specific conditions.



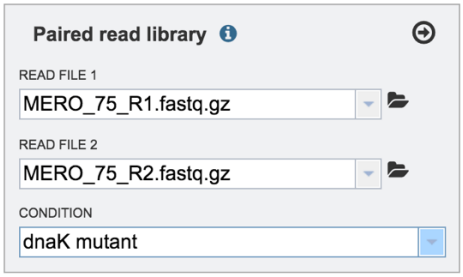
2. Name the condition (red arrow) and click the plus icon (blue arrow). This will show the name of the condition and a color code assigned to it in the text box (green arrow). As many conditions as desired can be entered.



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).

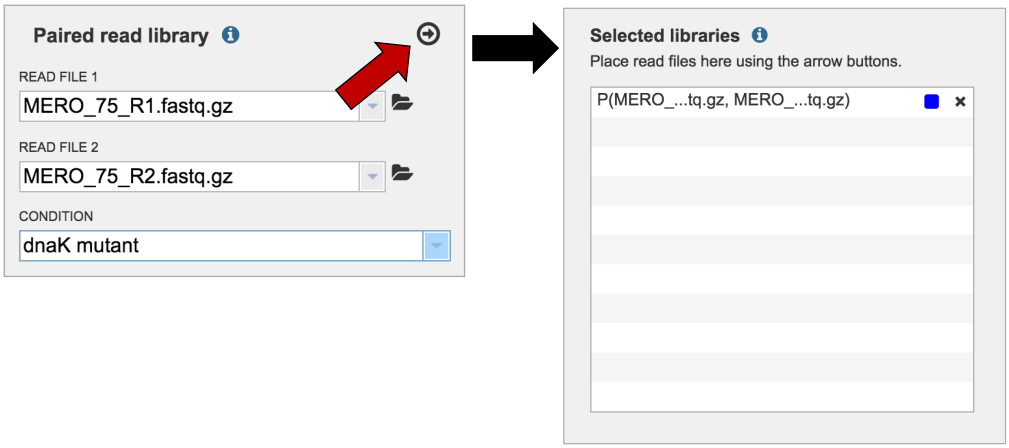


4. This will autofill the Condition text box with the name of the condition.

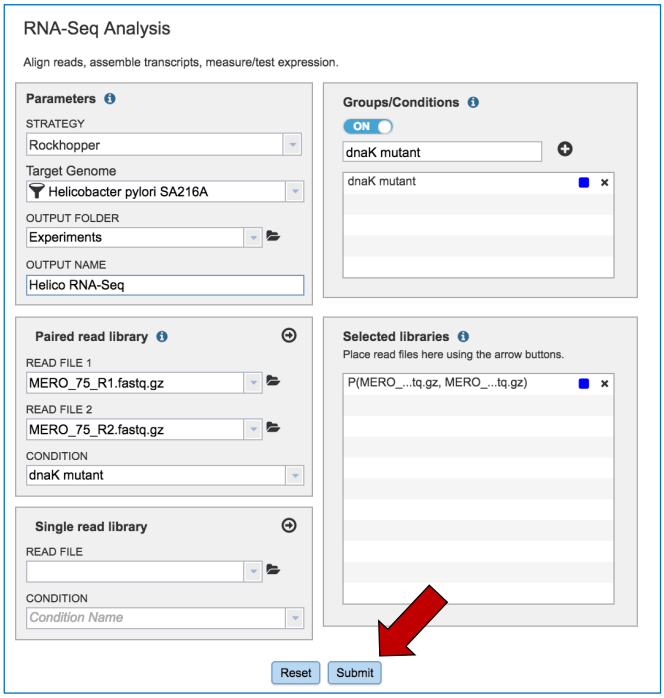


VI1. Selecting a condition or group that will be linked to a read

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.



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



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

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.