Sep 29, 2025 Version 1

bettercallsal - *Salmonella* serotyping tool based on NCBI Pathogen Detection Project for *Salmonella*. V.1

DOI
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External link: http:// https://github.com/CFSAN-Biostatistics/bettercallsal

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Manuscript citation:
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Protocol status: In development
We are still developing and optimizing this protocol

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Keywords: Salmonella serotyping, whole genome sequences, shotgun metagenomic sequences, ncbi pathogen detection project for salmonella, salmonella serotyping tool, salmonella from whole genome isolate sequence, multiple salmonella serovar, compatibility with historical salmonella nomenclature scheme, historical salmonella nomenclature scheme, identified salmonella, ncbi pathogen detection project, genome indexing approach, metagenomic sequences since this tool, salmonella, whole genome isolate sequence, sequencing data, profiling integration with ncbi snp, metagenomic sequence, serotyping tool, several confidence metrics sequence quality control assessments sequence, detailed multiqc report, results antimicrobial resistance, profiling integration, more information about this tool, antimicrobial resistance

Disclaimer

This protocol describes a scientific tool developed for research and surveillance purposes. Use of bettercallsal does not constitute FDA endorsement and confers no regulatory benefits or preferential treatment in FDA oversight activities.

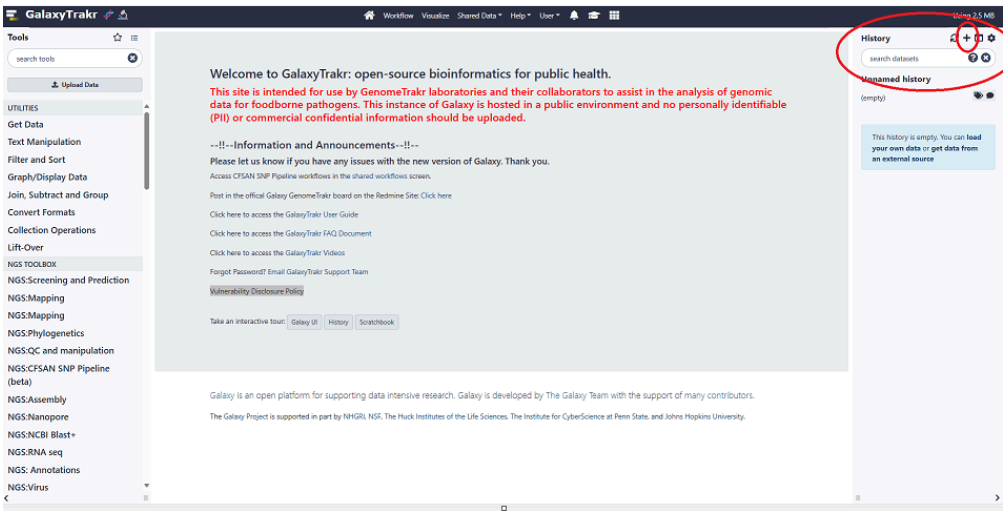
Abstract

This document outlines the steps necessary to run the tool - bettercallsal. bettercallsal tool is a *Salmonella* serotyping tool, that accepts both short-read and long-read sequencing data. This tool can serotype *Salmonella* from whole genome isolate sequences or from metagenomic sequences since this tool can identify multiple Salmonella serovars. The tool's ability to detect multiple *Salmonella* serovars simultaneously makes it particularly valuable for analyzing complex samples where traditional methods may fail. The tool employs a genome indexing approach while maintaining compatibility with historical *Salmonella* nomenclature schemes, ensuring continuity with existing surveillance systems and databases. More information about this tool can be found at this link : https://github.com/CFSAN-Biostatistics/bettercallsal and https://www.frontiersin.org/journals/microbiology/articles/10.3389/fmicb.2023.1200983/full and https://www.fda.gov/media/171312/download. bettercallsal generates a detailed MultiQC report that includes:

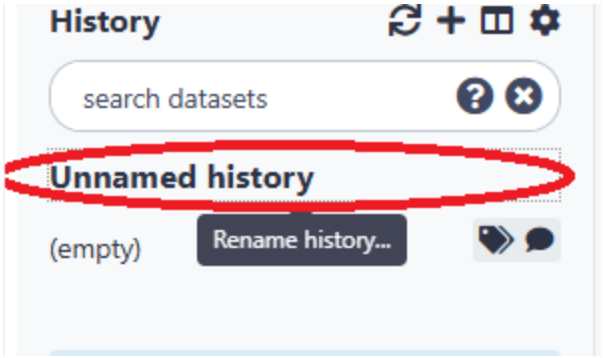
- Identified *Salmonella* serovars with several confidence metrics
- Sequence quality control assessments
- Sequence typing results
- Antimicrobial resistance (AMR) profiling
- Integration with NCBI SNP clustering analysis.

1 Go to and log into your GalaxyTrackr account at **Galaxy | GalaxyTrakr** 🧬🔬 .

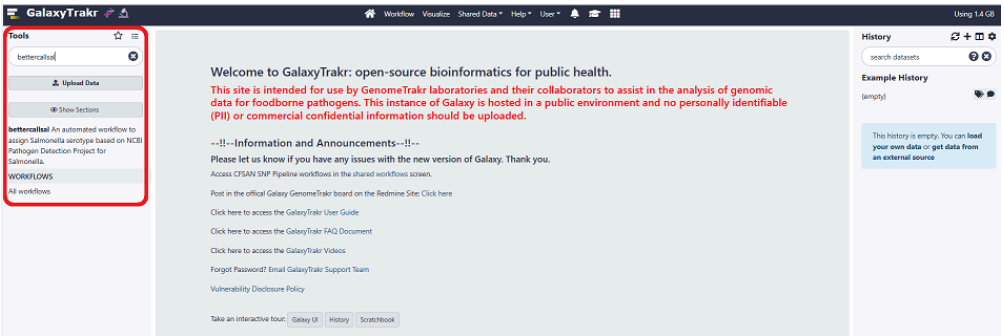
2 On the right-hand side of the screen, click the plus next to the History tab to create a new history.



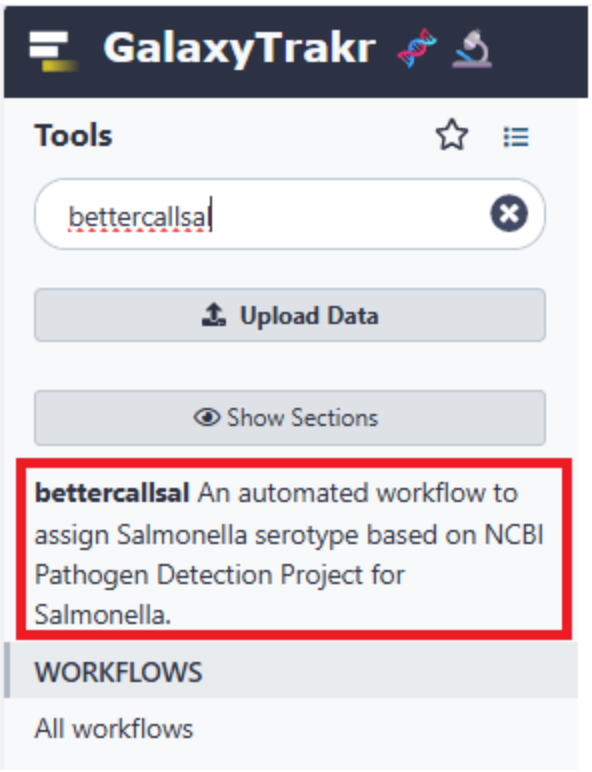
Click on **"Unnamed History"** and rename it according to your system.



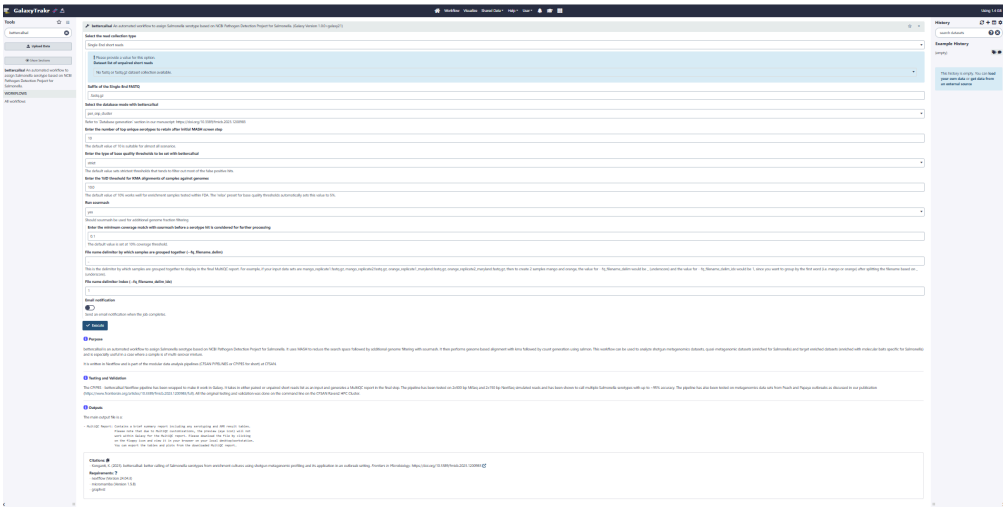
3 On the left-hand side of the screen, click the search bar in the "tools" section and search for "**bettercallsal**".



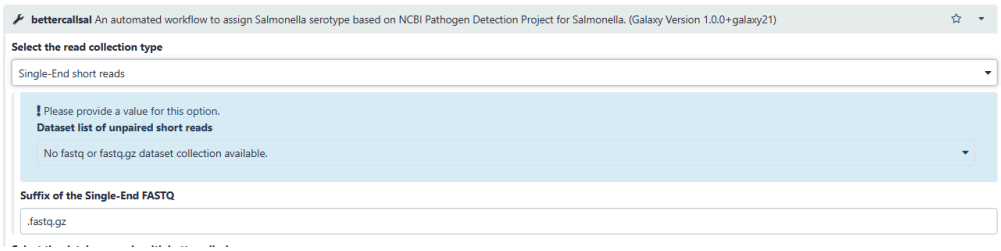
Click on the search result "**bettercallsal** An automated workflow to.....".

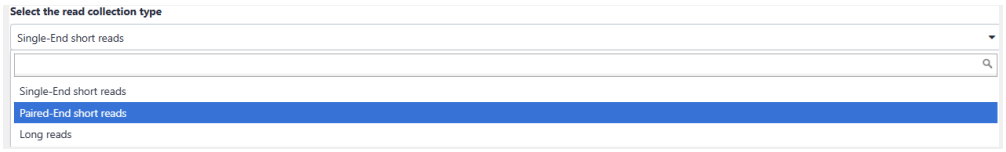


4 An interface will appear looking like this.



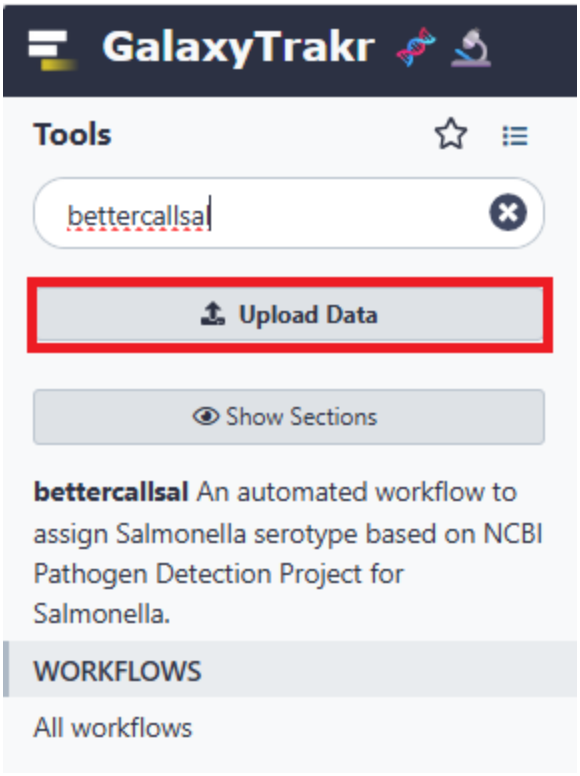
Change the "Select to read collection type" to "paired end short reads". It is the first option from the top.



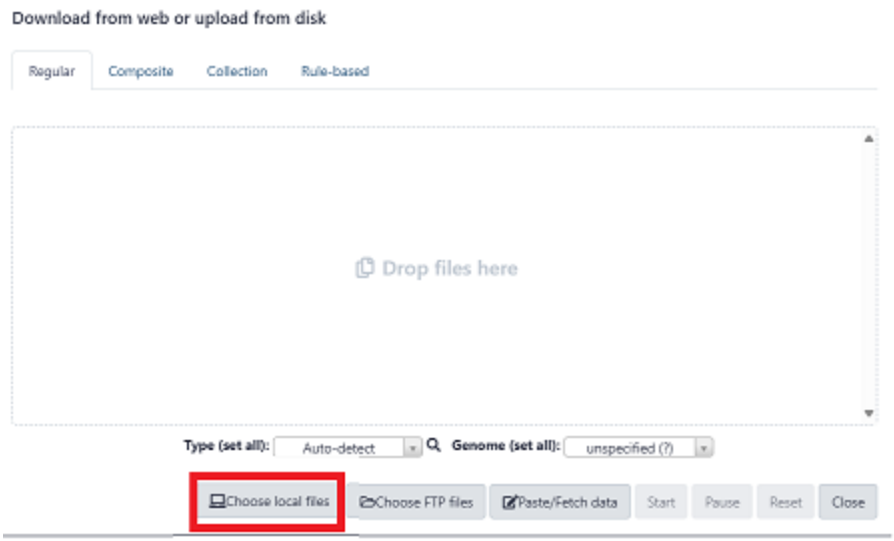


Once selected, the interface will change from "Single-End short pair reads" to the "Paired-End short reads. Everything else can be left alone.

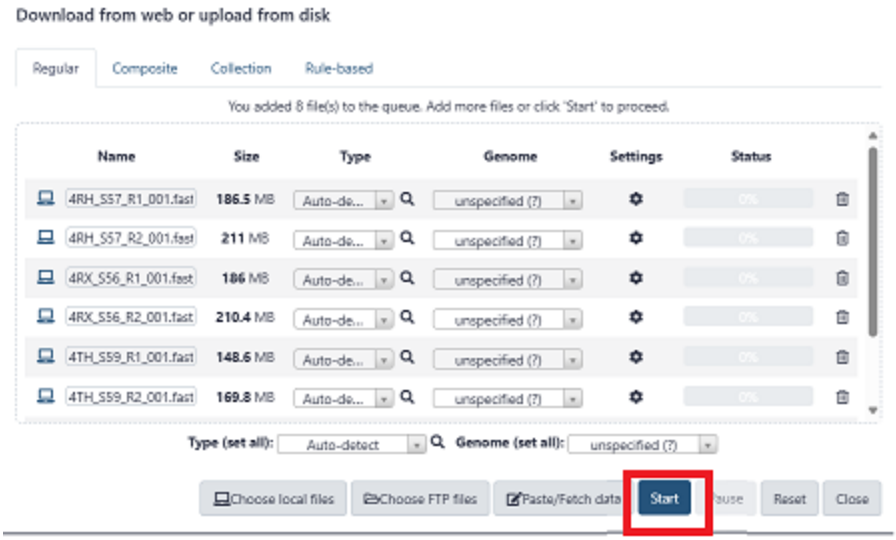
5 On the left side of the screen, where we searched for the "bettercallsal" tool, click the "Upload data" button.



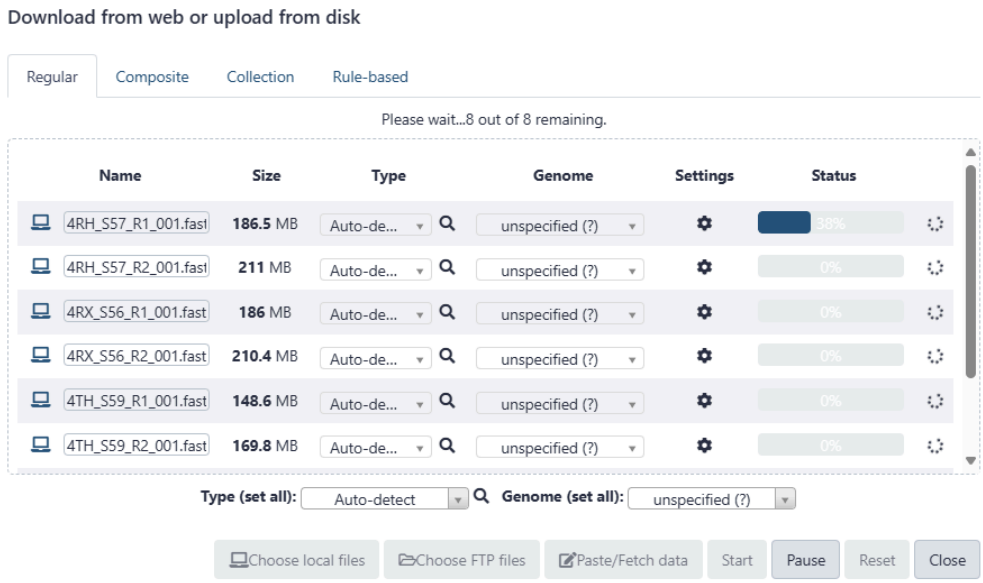
An interface where we can find and select files to upload will appear, for most users, the files will be on local files so choose that option unless otherwise noted.



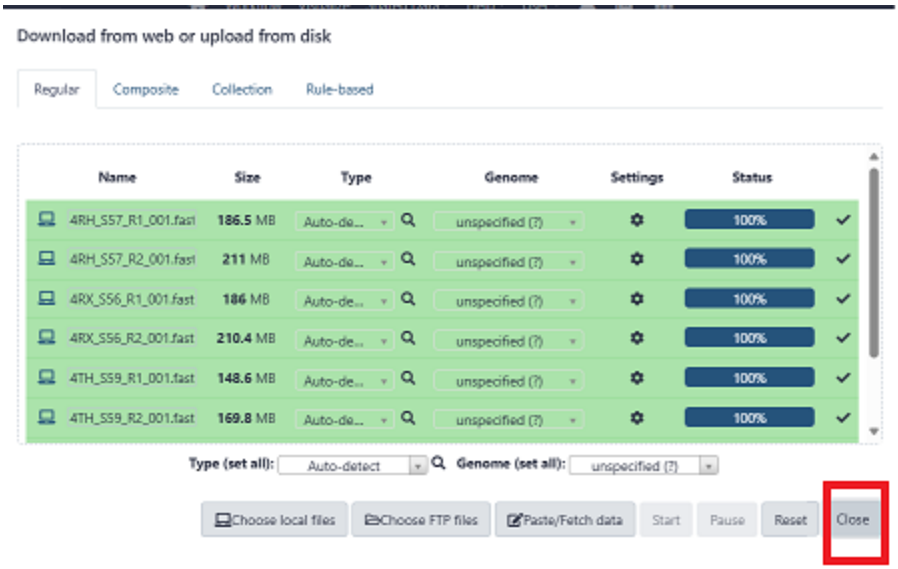
Select all files to be processed, It should resemble this:
Click "Start" to begin uploading.



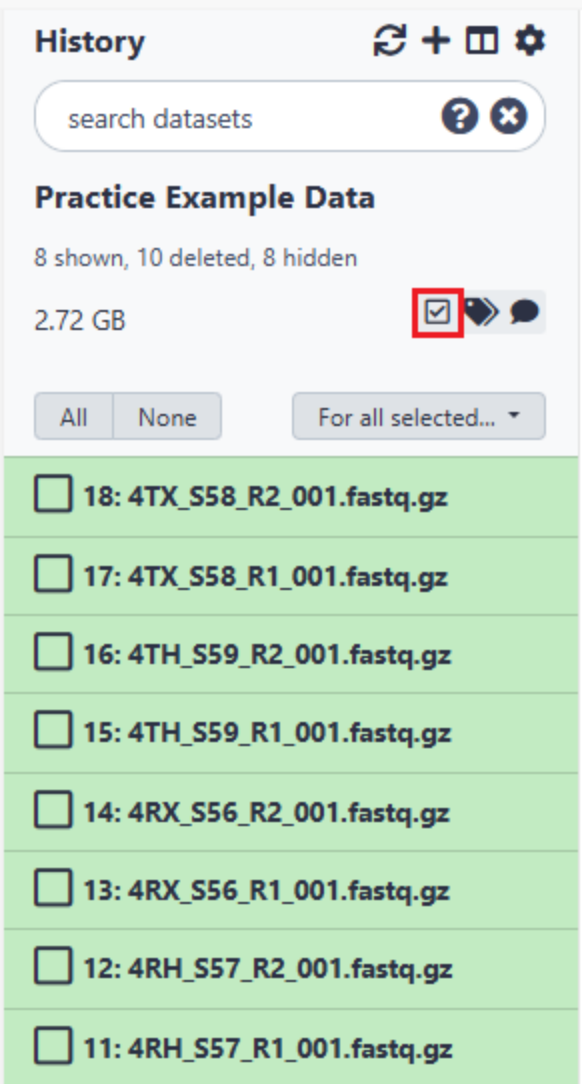
Note* Depending on the number of files, it can take a while to upload. This is what it looks like when uploading has started.



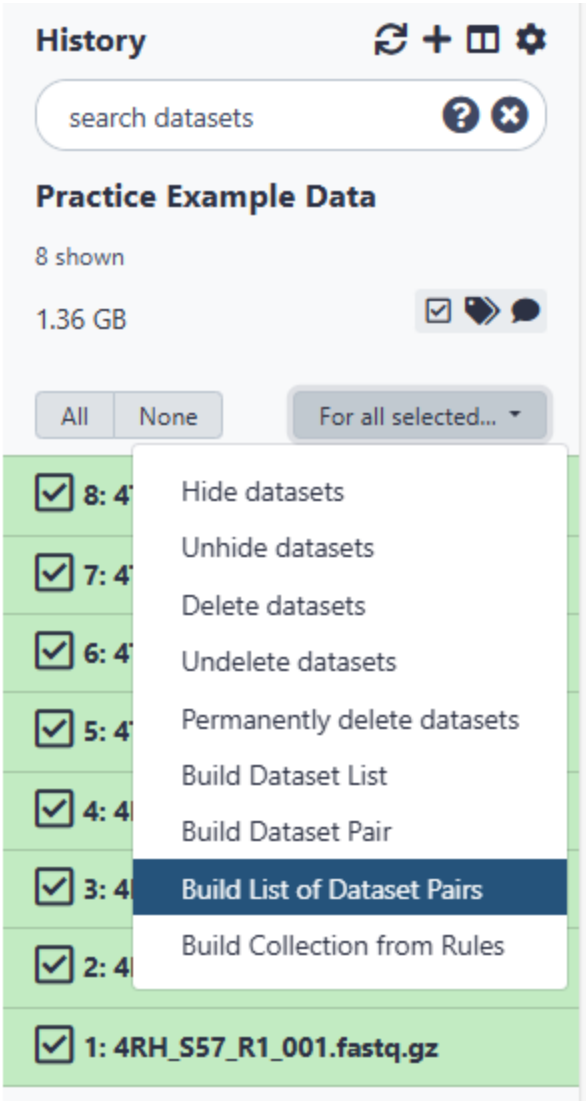
Once all files have been uploaded, click close.



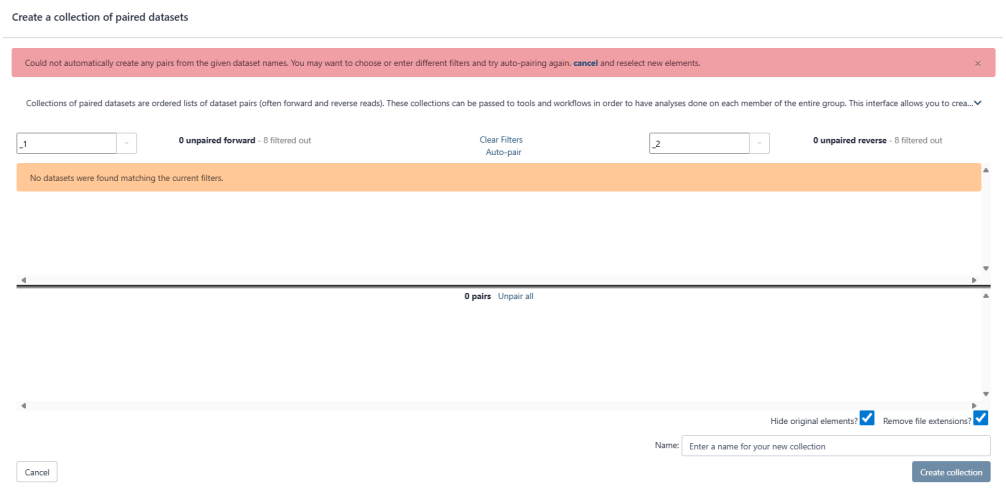
6 Before running "bettercallsal", the dataset needs to be paired.
Click on the square icon, or the "Operations on multiple datasets" on the right side of the tab. select boxes will appear on the green file list. This will allow you to select all files in your dataset.



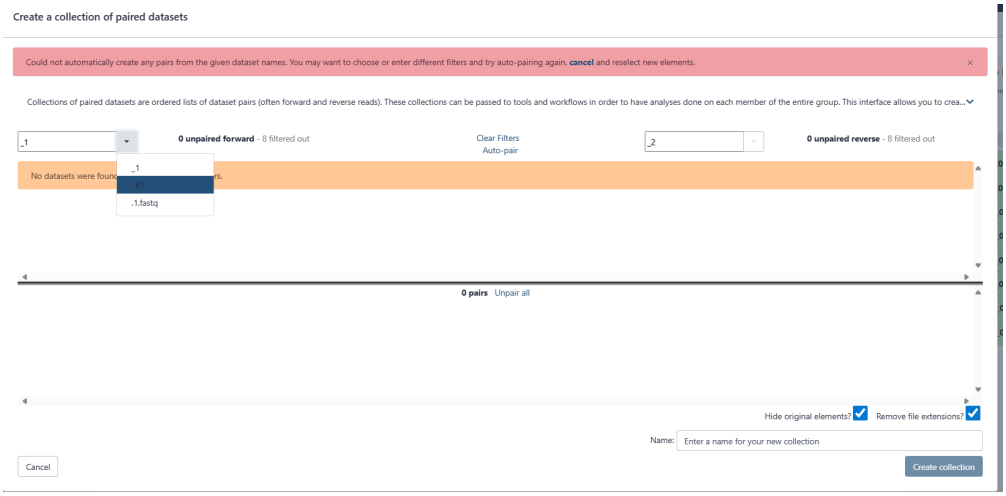
Select all files in the workspace, then click the dropdown that says for all selected. A menu will appear, select "Build List of Dataset Pairs".

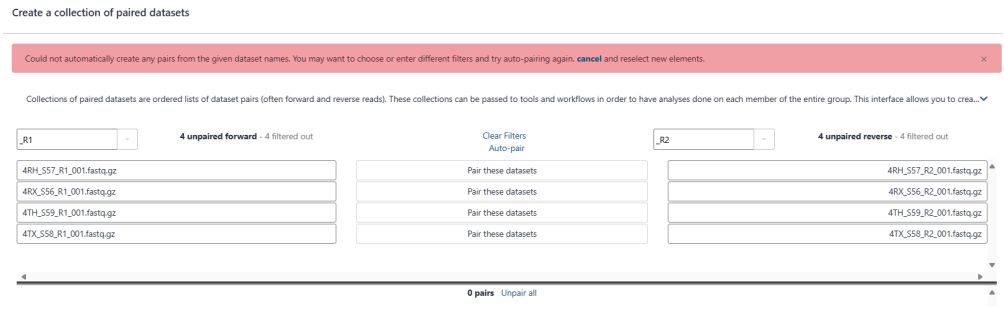


7 A new interface will appear.



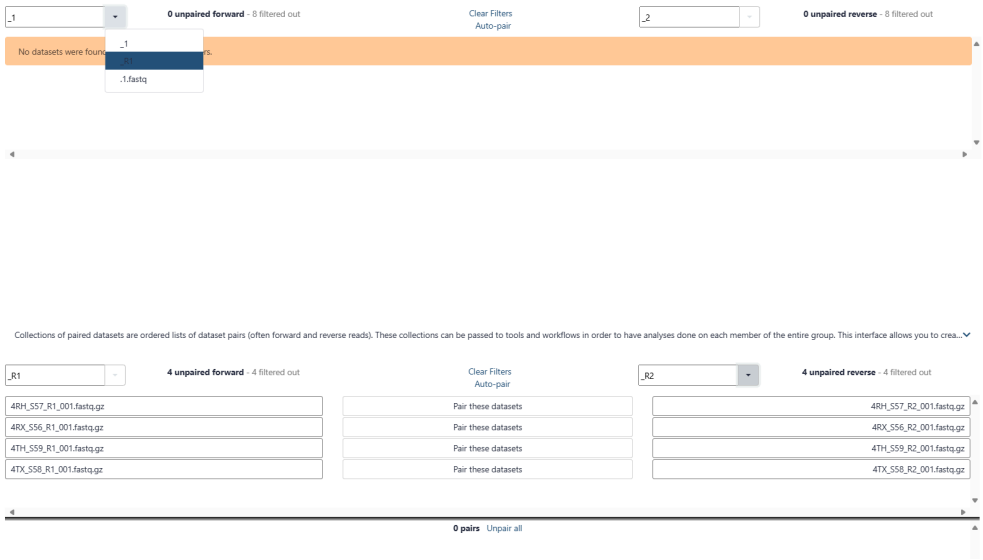
In the dropdown on the left, select _R1. This will auto select _R2 for the other dropdown.



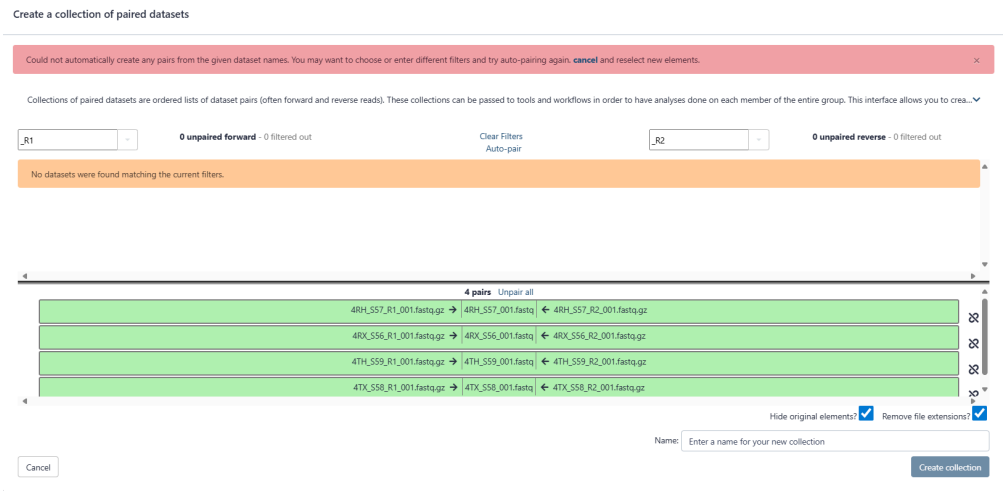


You will see both columns populate with filenames. Double check that the files have the same name other than "R1" or "R2". Once you know the program has properly paired the files, Click the "Pair these datasets" for all entries. There two columns will be empty if you do it correctly and they appear in green below the black bar.

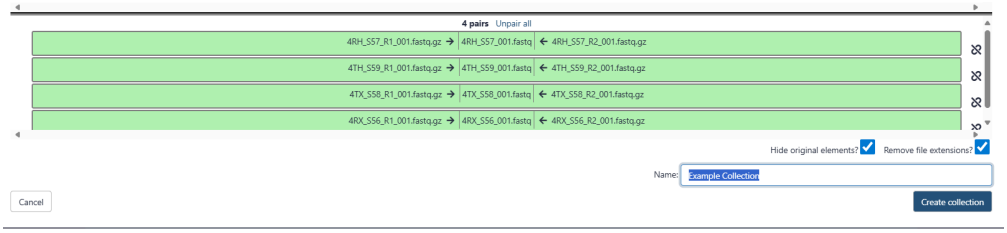
8



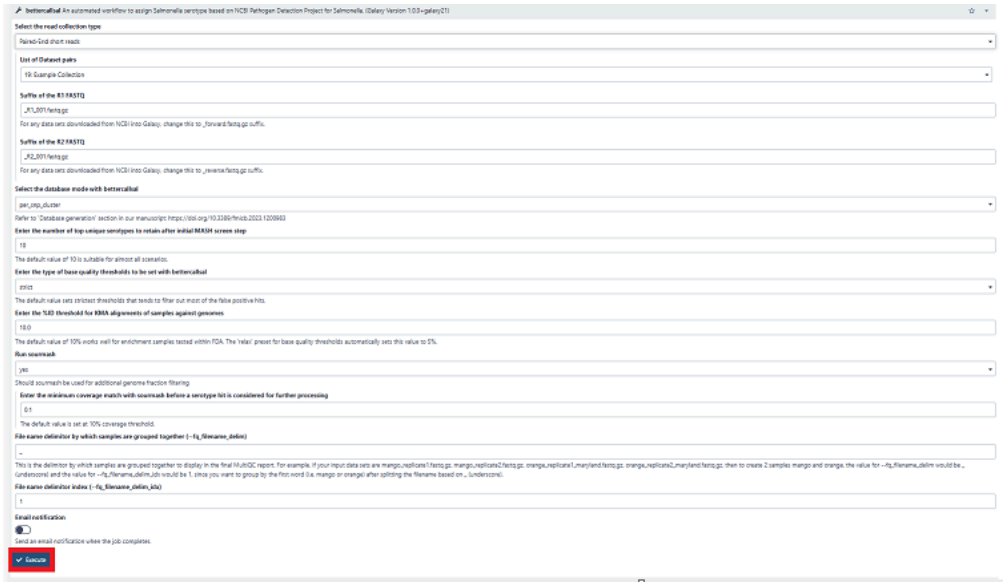
9



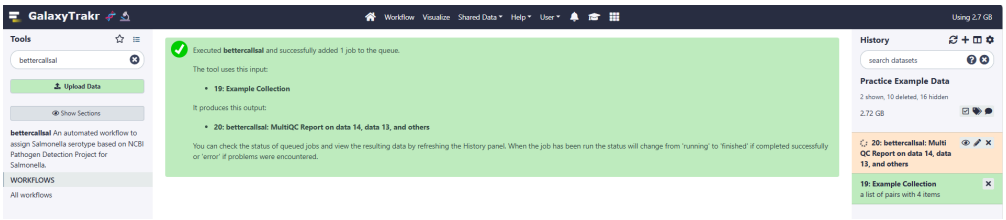
Create a name for your collection and click the"Create collection" button.



10 Double check that you have paired end short reads selected from step 4 and your paired collection is selected under "**List of Dataset pairs**" and match with the example below. If everything matches, click the "Execute" button.

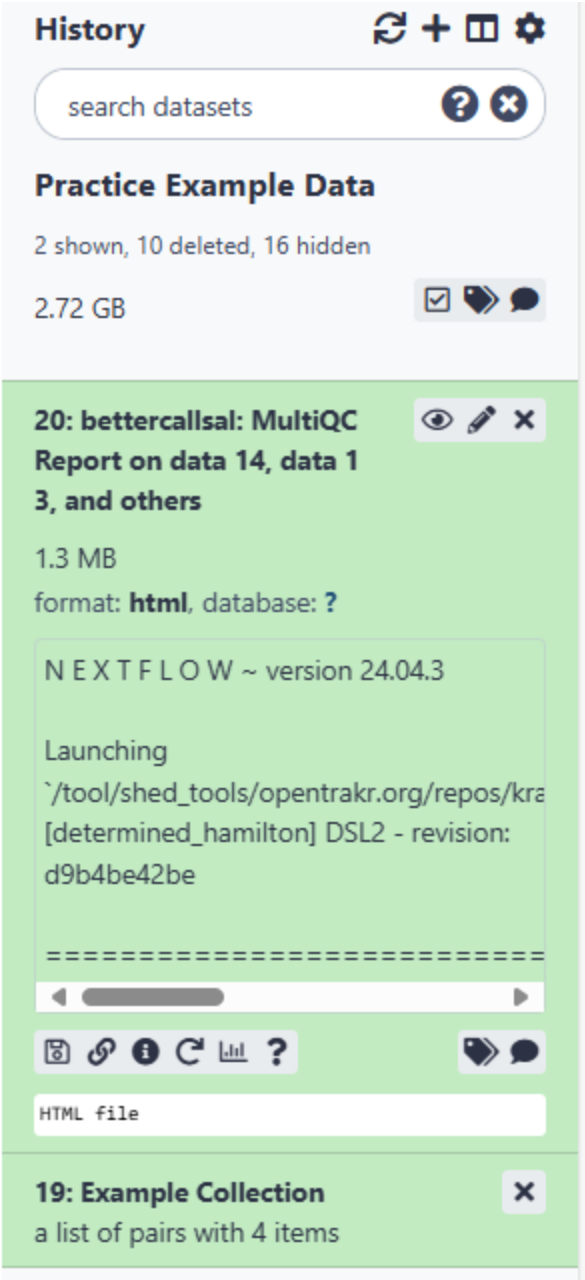


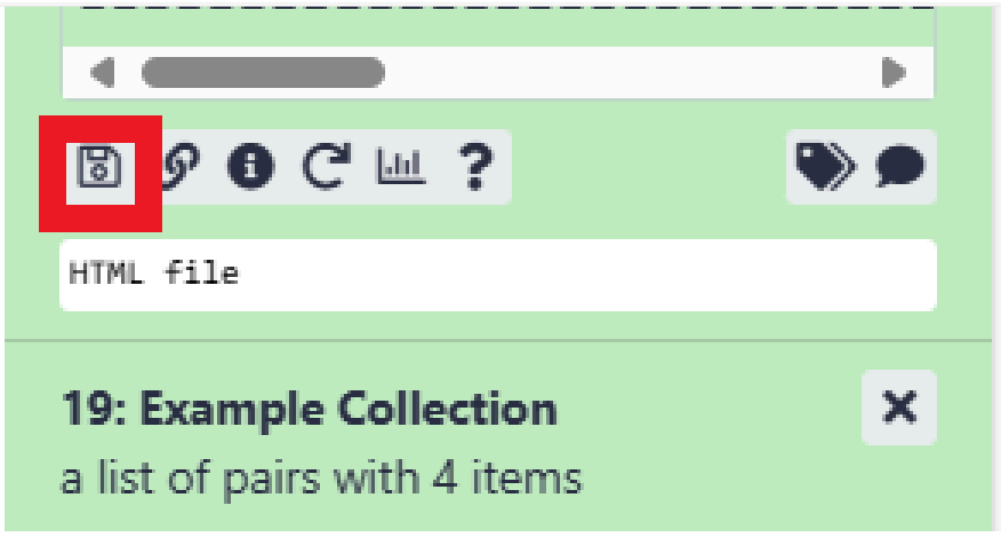
11 The program will begin; you can tell it is started by an orange tab appearing above your green paired collection beginning with "bettercallsal: MultiQC Report.....".



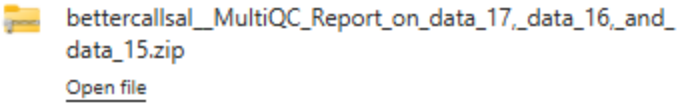
Wait until the job completes. You can tell when the processing is finished by the orange tab turning green. **This process can take upwards of 45 minutes to an hour**, depending on queue times and number of files uploaded.

12 Once the dataset is done and turns green, click on it. A dropdown will appear.





In the bottom left, there will be a button to download the file. This is a zipped HTML file that needs to be downloaded and extracted before it can be opened. It will open in google.



The report will look like this. If you see this, then the program was run successfully!