

Feb 27, 2024

Version 6

## Quality control assessment for microbial genomes: GalaxyTrakr MicroRunQC workflow V.6

 In 1 collection

DOI

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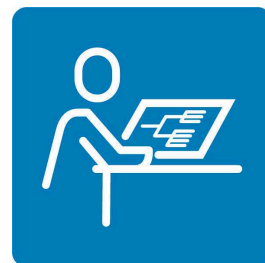
GenomeTrakr

Tech. support email: [genomeTrakr@fda.hhs.gov](mailto:genomeTrakr@fda.hhs.gov)



**Ruth Timme**

US Food and Drug Administration



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**Protocol status:** Working

**We use this protocol and it's working**

**Created:** January 05, 2024

**Last Modified:** February 27, 2024

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## Abstract

**PURPOSE:** Step-by-step instructions for checking WGS sequence quality for bacterial pathogens. The MicroRunQC workflow, implemented in a custom Galaxy instance, will produce quality assessments for raw reads (Illumina paired-end fastq files) and draft de novo assemblies, along with reporting the sequence type for each isolate. This workflow will work on most microbial pathogens, so we advise laboratories to upload their entire MiSeq/NextSeq run through this workflow.

**SCOPE:** This protocol covers the following tasks:

1. Quick access to GenomeTrakr sequence quality thresholds by organism
2. Create a GalaxyTrakr account
3. Set up an account in GalaxyTrakr
4. Create a new history/workspace
5. Upload data
6. Execute the MicroRunQC workflow
7. Interpret the results - check against GenomeTrakr QC thresholds

### Version updates:

V6: Minor edits, including section reorganization and addition of clarifying notes

V5: New column in the output table to capture additional mlst data fields when available in Sequence Type definition files (not available for all species)

V4: MicroRunQC updated to V1.1 Includes updates to skeza and mlst methods, as well as adjusted assembly QC thresholds for E.coli. Added *Enterobacter* QC thresholds to threshold table.

V3: updated with *Cronobacter* thresholds

## Troubleshooting

## Quick Access to QC Benchmarks

- 1 This protocol will walk the user through various aspects of the quality assessment of bacterial genome sequences, from setting up a GalaxyTrakr account to the quality control (QC) benchmarks GenomeTrakr uses for its sequencing efforts. For quick access, GenomeTrakr QC benchmarks are included in the table below.

These are also relevant for NARMS and VetLIRN contributors.

\*MicroRunQC users should follow QC threshold guidelines established by their respective surveillance coordinating body(s).

|  | A  | B                                  | C                           | D                         | E                                | F                                     | G                                   | H                                   | I   | J   |
|--|--|------------------------------------|-----------------------------|---------------------------|----------------------------------|---------------------------------------|-------------------------------------|-------------------------------------|---|---|
|  | Quality metric                             | <i><b>Salm<br/>onell<br/>a</b></i> | <i><b>List<br/>eria</b></i> | <i><b>E.<br/>coli</b></i> | <i><b>Shi<br/>gell<br/>a</b></i> | <i><b>Camp<br/>yloba<br/>cter</b></i> | <i><b>Vibri<br/>o<br/>para.</b></i> | <i><b>Cron<br/>obac<br/>ter</b></i> | <i><b>Enter<br/>ococc<br/>us<br/>faeci<br/>um</b></i> | <i><b>Enterococ<br/>cus<br/>faecali<br/>s</b></i> |
|  | Average read quality Q score for R1 and R2 | >=30                               | >=30                        | >=30                      | >=30                             | >=30                                  | >=30                                | >=30                                | >=30  | >=30  |
|  | Average coverage                           | >=30X                              | >=20X                       | >=40X                     | >=40X                            | >=20X                                 | >=40X                               | >=20X                               | >=50X   | >=40X   |
|  | <i>De novo</i> assembly: Seq. length (Mbp) | ~4.3-5.2                           | ~2.7-3.2                    | ~4.5-5.9                  | ~4.0-5.0                         | ~1.5-1.9                              | ~4.8-5.5                            | ~4-5                                | ~2.5-3.5  | ~2.5-3.25   |
|  | <i>De novo</i> assembly: no. contigs       | <=300                              | <=300                       | <=400                     | <=550                            | <=300                                 | <=300                               | <=500                               | <=350   | <=200   |

## Account set up

- 2 1. Create a GalaxyTrakr account here: <https://account.galaxytrakr.org/Account/Register>



## Note

This is a more detailed form than what is available by clicking "Register here" on the [genometrakr.org](https://genometrakr.org) main page. Please use the form linked here when creating a new account.

## User Registration Form

Location

California Department of Public Health - Food and Drug Laboratory Branch

[Add New Location](#)

First Name

Enter First Name, Do not use characters: \[ ] ; : | ' = + - \* ? < > @ .

Last Name

Enter First Name, Do not use characters: \[ ] ; : | ' = + - \* ? < > @ .

Email

Email will be used for automated messages to include registration information!

Primary Phone

Please enter number with country code, without dashes, for example +17035456789

If possible please use a mobile number than can accept text messages, only used for support

Title

Requirements

Please annotate intended use of Galaxy and Analysis tools. List specific tools you would like to see deployed in Galaxy.

Register

## 2.1 Log into your GalaxyTrakr account: <https://galaxytrakr.org>

GalaxyTrakr

Workflow Visualize Shared Data Help Login or Register

Using 0 bytes

Welcome to Galaxy, please log in

Public Name or Email Address

Password

Forgot password? Click here to reset your password.

Login

Don't have an account? Register here.

Welcome to GalaxyTrakr: open-source bioinformatics for public health.

This site is intended for use by GenomeTrakr laboratories and their collaborators to assist in the analysis of genomic data for foodborne pathogens. This instance of Galaxy is hosted in a public environment and no personally identifiable (PII) or commercial confidential information should be uploaded.

--!!--Information and Announcements--!!--

Please let us know if you have any issues with the new version of Galaxy. Thank you.

Access CFSAN SNP Pipeline workflows in the shared workflows screen.

Post in the official Galaxy GenomeTrakr board on the Redmine Site: Click here

Click here to access the GalaxyTrakr User Guide

Click here to access the GalaxyTrakr FAQ Document

## Create a new history

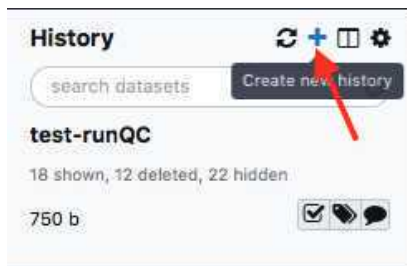
### 3 Create a new history.

We recommend creating a new history for each new MiSeq Run and including the flow-cell ID and date in the history name.

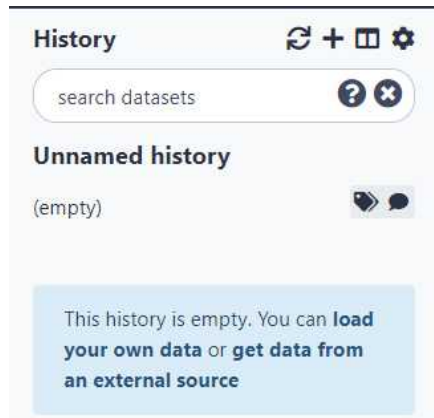
Save your MicroRunQC output here and any other relevant analyses, like serotyping, or AMR detection.

After all the analysis output from this run is saved to your internal data network or computer, older histories should be purged/deleted so as not to occupy the limited storage space in your account. In some cases it may be useful to save, for a limited time, multiple histories or to run analyses concurrently in multiple histories. In these cases you need to pay attention to your % usage bar (shows % used of allocated storage space) in the upper right corner of the GalaxyTrakr page. If you need additional space you can contact [galaxytrakrsupport@fda.hhs.gov](mailto:galaxytrakrsupport@fda.hhs.gov) and request additional storage.

#### 3.1 Click on the + icon in the upper right History panel



#### 3.2 Name your new History by clicking on the "Unnamed history" text, type in desired name, and hit Enter. We recommend including the run cell ID and the date the run was started.



## Upload data

- 4 **This section will describe the process for uploading raw fastq files into your active History panel.** After the files have been uploaded they will stay in your account until they are deleted.

- 4.1 Click on the Upload Data icon on the top of the left web page to start an upload process.



- 4.2 Select "**Type (set all):auto-detect.**" Click "**Choose local files**" button and navigate to the desired fastq files, then click "**Start**" to upload files. These files should be paired (two per sample/isolate).

Download from web or upload from disk

Regular Composite Collection Rule-based

You added 4 file(s) to the queue. Add more files or click 'Start' to proceed.

| Name              | Size     | Type        | Genome          | Settings | Status |
|-------------------|----------|-------------|-----------------|----------|--------|
| CFSAN074382_S15_L | 151.8 MB | Auto-det... | unspecified (?) |          | 0%     |
| CFSAN074382_S15_L | 152.5 MB | Auto-det... | unspecified (?) |          | 0%     |
| CFSAN074384_S20_L | 172.6 MB | Auto-det... | unspecified (?) |          | 0%     |
| CFSAN074384_S20_L | 181.2 MB | Auto-det... | unspecified (?) |          | 0%     |

1. Type (set all): Auto-detect  Genome (set all): unspecified (?)

2.  Choose local file  Choose FTP file  Paste/Fetch data Pause Reset Start  Close

As the file uploads complete, each row will turn green. Samples in yellow are still in process.

- 4.3 You have just upload a set of forward and reverse reads. For further analysis, these files need to be paired properly so the platform knows which R1 and R2 files go together. GalaxyTrakr does this by creating a **List of Dataset Pairs**.

Within your newly created History panel, click the check box, then select all the files you just uploaded by clicking "All" or by individually selecting the ones you want to pair.





**Screenshot of History panel showing recently uploaded files.** Note the way the files are named, using R1 and R2 to identify the paired reads. This will be important in the next step. Some naming conventions can be slightly different.

#### 4.4 Click "For all selected" and choose "Build List of Dataset Pairs"



#### 4.5 A new window will open to help you pair the fastq files properly. Note how your paired reads are named.

First, click on the drop down arrow and choose “\_R1,” if that is the naming convention your files follow. This automatically populates the corresponding “\_R2” in the next box.

Create a collection of paired datasets

Could not automatically create any pairs from the given dataset names. You may want to choose or enter different filters and try auto-pairing again. **cancel** and reselect new elements.

Collections of paired datasets are ordered lists of dataset pairs (often forward and reverse reads). These collections can be passed to tools and workflows in order to have analyses done on each member of the entire group...

0 unpaired forward - 6 filtered out
  0 unpaired reverse - 6 filtered out

No datasets were found

0 pairs Unpair all

☒ Hide original elements?
 ☒ Remove file extensions?

Name:

Click **Auto-pair**.

Create a collection of paired datasets

Could not automatically create any pairs from the given dataset names. You may want to choose or enter different filters and try auto-pairing again. **cancel** and reselect new elements.

Collections of paired datasets are ordered lists of dataset pairs (often forward and reverse reads). These collections can be passed to tools and workflows in order to have analyses done on each member of the entire group...

3 unpaired forward - 3 filtered out
  3 unpaired reverse - 3 filtered out

0 pairs Unpair all

☒ Hide original elements?
 ☒ Remove file extensions?

Name:

Paired reads will pair in the middle column and turn green.

Unselect "**Hide original elements,**" which is the default setting and undesired here.

Create a collection of paired datasets

Could not automatically create any pairs from the given dataset names. You may want to choose or enter different filters and try auto-pairing again. **cancel** and reselect new elements. ✕

Collections of paired datasets are ordered lists of dataset pairs (often forward and reverse reads). These collections can be passed to tools and workflows in order to have analyses done on each member of the entire group. ▾

0 unpaired forward - 0 filtered out Clear Filters Auto-pair  0 unpaired reverse - 0 filtered out

No datasets were found matching the current filters.

3 pairs Unpair all

|                                |   |                          |   |                                |   |
|--------------------------------|---|--------------------------|---|--------------------------------|---|
| CFSAN000189_N1_R1_001.fastq.gz | → | CFSAN000189_N1_001.fastq | ← | CFSAN000189_N1_R2_001.fastq.gz | ✕ |
| CFSAN000189_N2_R1_001.fastq.gz | → | CFSAN000189_N2_001.fastq | ← | CFSAN000189_N2_R2_001.fastq.gz | ✕ |
| CFSAN000189_N3_R1_001.fastq.gz | → | CFSAN000189_N3_001.fastq | ← | CFSAN000189_N3_R2_001.fastq.gz | ✕ |

Hide original elements? ☒ Remove file extensions? ☒

Name:

Clear the checkmark by "Hide original elements?" seen here by clicking on it.

Name your dataset: Example, "pairedSet-<FlowCell>-<date>"

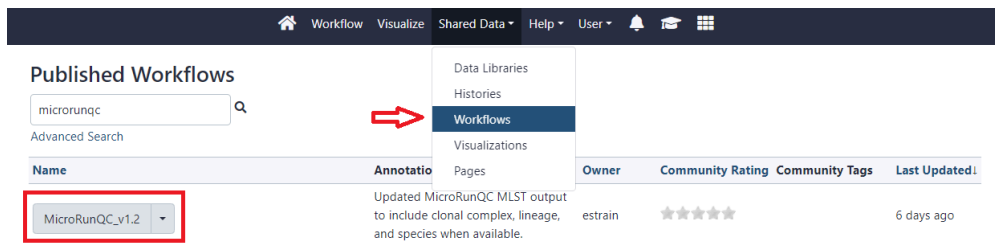
Click **Create list**.

- 4.6 This paired dataset will now be available for analysis in your history panel. You can run multiple analyses on the same dataset in a history rather than upload the same sequence data to a new history to perform additional analyses. This will help you use your allocated storage space efficiently.



## Run the MicroRunQC workflow

- 5 **Add the MicroRunQC workflow to your own "Workflows" panel.** You only have to do this step once for each new workflow you need.
- 5.1 Navigate to the **"Shared Data"** drop down menu, choose **"Workflows,"** and search for "MicroRunQC\_v1.2."

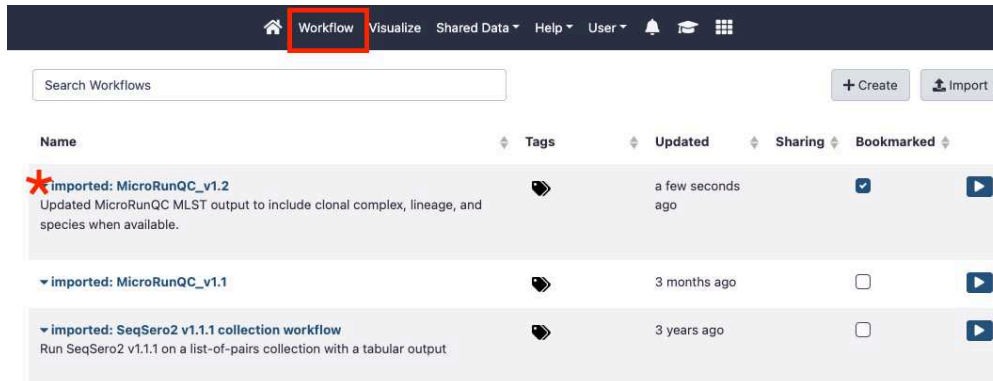


From the dropdown menu by the MicroRunQC title, select **"Import."**




5.2 To see the new imported workflow, click the **"Workflow"** tab on the top panel.



Click the box under **"Bookmarked"** to make it available in the left panel under **"Workflows"** when MicroRunQC is searched for.





5.3 From the Workflow menu on the left panel, select **MicroRunQC\_v1.2**



**GalaxyTrakr**

Tools  



 Upload Data

Metagenomics:Kraken

Metagenomics:Mitokmer

Metagenomics:Graphlan

Metagenomics:Functional Profiling

Metagenomics:Assembly

Metagenomics:Rpackages

Metagenomics:Metaphlan

Metagenomics:CPIPES

test:tools

tes

**blast\_to\_scaffold** Generate DNA scaffold from blastn or tblastx alignment of Contigs

**small\_rna\_maps**

**Clip adapter**

**Normalize By Median** Filter reads using digital normalization via k-mer abundances

**Bowtie2** - map reads against reference genome

**Trim sequences**

**NCBI EFetch** fetch records from NCBI

**Unique** occurrences of each record

**QIIME**

**kraken2**

**QualiMap BamQC** Tool to to facilitate the quality control of alignment sequencing data and its derivatives like feature counts.

**NGS:Simulator**

**WORKFLOWS**

All workflows

**imported: MicroRunQC\_v1.2**



## 5.4 Select paired list dataset you created earlier.

Click **Run Workflow**. This can take some time depending on the number of samples you are analyzing. If you choose to you can log out of GalaxyTrakr and log back in at a later time to see if the job is completed.

### Note

If you see an orange box at the top of the workflow before running it that states that the tool is out of date or contains errors, please go back to **Step 4.1** of this protocol and import the version of the tool with the most current "Last Updated" date. The version number on the MicroRunQC workflow does not increment when only the MLST database is updated, meaning that though the version number of the workflow may remain the same, re-import may be necessary for the most up-to-date analysis of your genomes.

Some tools in this workflow may have changed since it was last saved or some errors were found. The workflow may still run, but any new options will have default values. Please review the messages below to make a decision about whether the changes will affect your analysis.

Workflow: imported: MicroRunQC\_v1.2

✓ Run Workflow

#### History Options

Send results to a new history

☐ No

#### 1: Input dataset collection

45: Nevada\_Clearlabs\_Validation

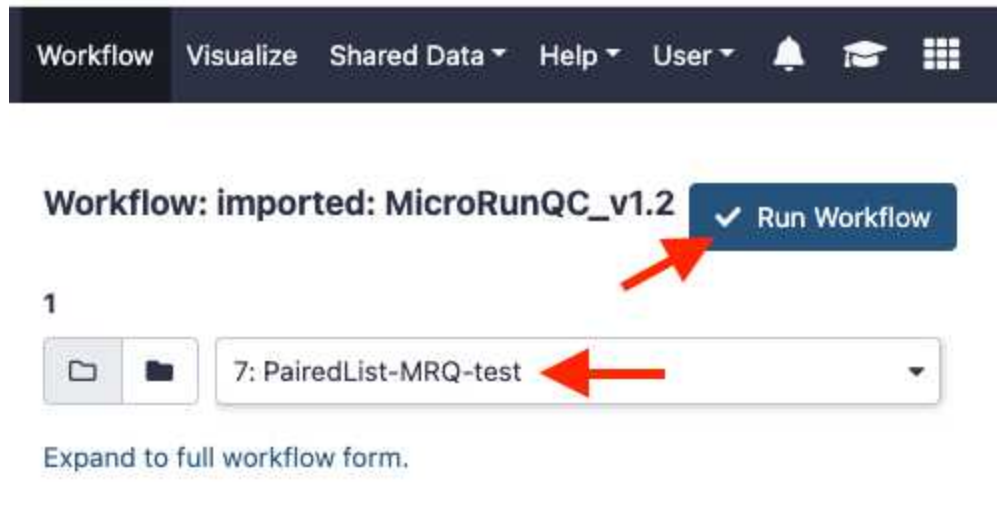
2: Trimmomatic (Galaxy Version 0.36.4)

3: microrunqc (Galaxy Version 1.0.1)

4: Concatenate multiple datasets (Galaxy Version 0.3)

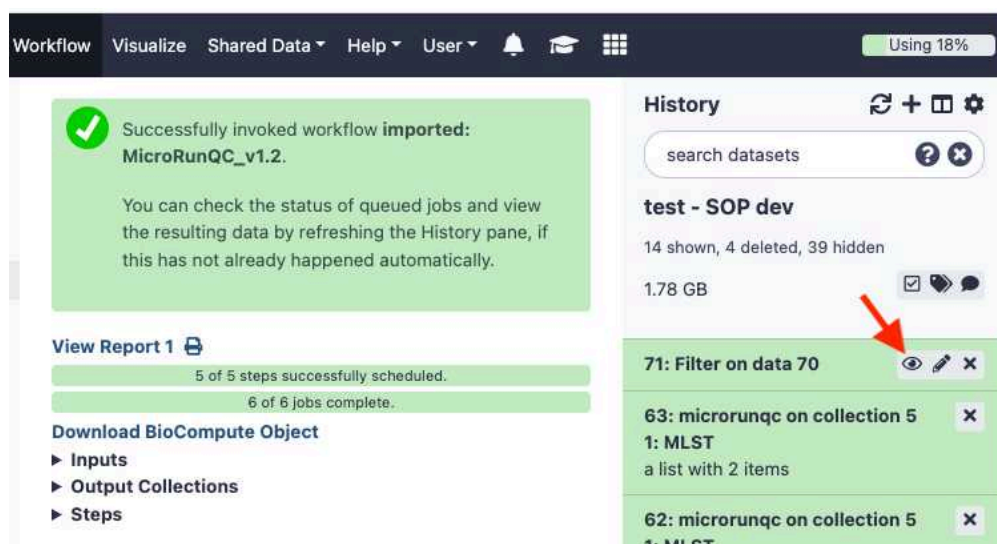
5: Filter (Galaxy Version 1.1.1)

Example of warning box



5.5 Upon completion of the pipeline all tiles in the History pane will be green.

In the “**Filter on Data ##**” tile, click on the “Eye” icon to view the output table in the GalaxyTrakr window.

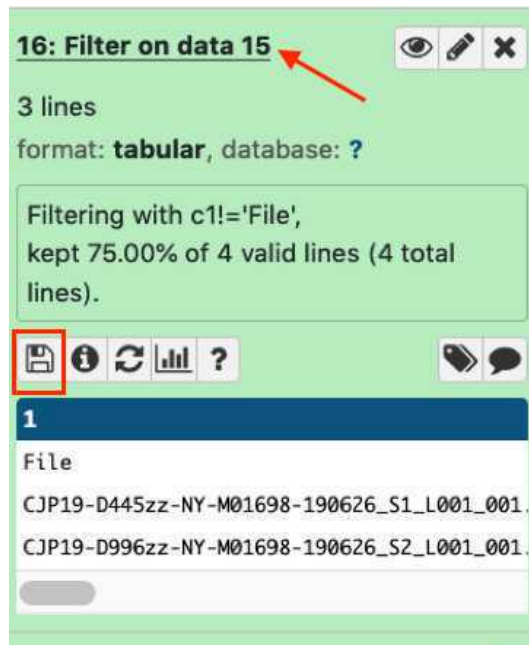


## Interpret the results

6 **Download and interpret the results:**



- 6.1 Click **Filter on data ##** and then the floppy disc icon. The tabular file can be opened in a text reader or converted to a format (.txt) that can be opened in Excel.



- 6.2 The MicroRunQC output file includes the following columns:

|  | A                    | B            | C  |
|--|----------------------|--------------|--|
|  | <b>Parameter</b>     | <b>Input</b> | <b>Description</b>   |
|  | <b>Contigs</b>       | Assembly     | Number of contigs in the de-novo SKESA assembly. Contigs smaller than 200 base-pairs (bp) are not counted.   |
|  | <b>Length</b>        | Assembly     | Total length of all contigs > 200bp. This should approximate the size of the genome for the target organism. |
|  | <b>EstCov</b>        | Assembly     | Mean coverage for contigs in the SKESA assembly.   |
|  | <b>N50</b>           | Assembly     | Sequence length of the shortest contig at 50% of the total genome length                                     |
|  | <b>MedianInsert</b>  | Read         | Distance between forward and reverse reads. Calculated by mapping reads to SKESA assembly using bwa.         |
|  | <b>MeanLength_R1</b> | Read         | Mean length of forward read  |

|  | A                    | B        | C  |
|--|----------------------|----------|--|
|  | <b>MeanLength_R2</b> | Read     | Mean length of reverse read  |
|  | <b>MeanQ_R1</b>      | Read     | Mean Q-score of forward read   |
|  | <b>MeanQ_R2</b>      | Read     | Mean Q-score of reverse read   |
|  | <b>Scheme</b>        | Assembly | PubMLST scheme name (output from mlst application that scans contig files against traditional PubMLST typing schemes). |
|  | <b>ST</b>            | Assembly | Sequence Type  |
|  | <b>MLST extra</b>    | Assembly | e.g. Listeria clonal complex info  |
|  | <b>Loci</b>          | Assembly | gene (allele number) – for example aroC(118)   |

**MicroRunQC output table headers.** This table lists the summary metrics for sequence quality, number of contigs, and estimated genome size, along with other common metrics for reads (Median Insert Size and Mean Length) and assemblies (N50). Additionally, if the Multi-Locus Sequence Type (MLST) for the isolate is available from pubmlst, the workflow also reports Sequence Type (ST) and the associated alleles.

**\*MLST extra:** Additional data fields reported when available in Sequence Type definition files (not available for all species)

1. clonal\_complex – sequences grouped by similarity to central allelic profile (e.g., *Campylobacter* ST-21 complex)
2. CC – clonal\_complex – Abbreviation used for organism like *Listeria*, ST profiles are maintained by different groups
3. Lineage – *Listeria monocytogenes* lineage (I,II,III, and IV), *Listeria* species also reported here (e.g.L.innocua)
4. species – e.g., *Vibrio alginolyticus*

**\*\*This output should be saved either to your LIMS or to a spreadsheet linked to the sequencing run and samples.**

### 6.3 Example output for 1 *Salmonella* and 5 *Listeria* isolates.

| A                   | B                       |
|---------------------|-------------------------|
| <b>Srain ID</b>     | <b>Lab Confirmation</b> |
| FDA1216271-C001-001 | Listeria mono           |
| FDA817806-S073-001  | Listeria mono           |
| FDA746634           | Listeria mono           |

|                     |                  |
|---------------------|------------------|
| A                   | B                |
| FDA1213377-C001-002 | Listeria grayi   |
| FDA933376-S060-005  | Listeria innocua |
| FDA1213835-C001-001 | Salmonella       |

Lab confirmed IDs for 6 isolates

|  | A                   | B       | C       | D      | E      | F            | G                | H                | I           | J           | K             | L   | M                | N       | O       | P      | Q        | R      | S      | T        |
|--|---------------------|---------|---------|--------|--------|--------------|------------------|------------------|-------------|-------------|---------------|-----|------------------|---------|---------|--------|----------|--------|--------|----------|
|  | File                | Contigs | Length  | EstCov | N50    | MedianInsert | MeanLength<br>R1 | MeanLength<br>R2 | MeanQ<br>R1 | MeanQ<br>R2 | Scheme        | ST  | MLSTextra        |         |         |        |          |        |        |          |
|  | FDA1216271-C001-001 | 16      | 2911949 | 36.7   | 476210 | 321          | 148.4            | 148.4            | 36.4        | 34.6        | listeria<br>2 | 5   | CC=CC5,Lineage=I | abcZ(2) | bgIA(1) | cat(1) | dapE(3)  | dat(3) | ldh(1) | lhkA(7)  |
|  | FDA817806-          | 20      | 3068354 | 179.6  | 525438 | 329          | 234.7            | 235.2            | 36.7        | 31.9        | listeria<br>2 | 321 | CC=CC321,Line    | abcZ(5) | bgIA(6) | cat(8) | dapE(62) | dat(6) | ldh(7) | lhkA(34) |

|  | A   | B      | C                               | D                 | E                               | F           | G                 | H                 | I            | J            | K  | L                | M   | N   | O                                    | P                               | Q   | R                               | S                                    | T   |
|--|---|--------|---------------------------------|-------------------|---------------------------------|-------------|-------------------|-------------------|--------------|--------------|--|------------------|---|---|--------------------------------------|---------------------------------|---|---------------------------------|--------------------------------------|---|
|  | S<br>0<br>7<br>3<br>-<br>0<br>0<br>1  |        |                                 |                   |                                 |             |                   |                   |              |              |  |                  | e<br>a<br>g<br>e<br>=<br>l  |   |                                      |                                 |   |                                 |                                      |   |
|  | F<br>D<br>A<br>7<br>4<br>6<br>6<br>3<br>4   | 3<br>0 | 3<br>0<br>5<br>2<br>8<br>8<br>8 | 4<br>1.<br>4      | 2<br>9<br>3<br>9<br>4<br>7      | 3<br>2<br>0 | 1<br>4<br>8.<br>4 | 1<br>4<br>8.<br>4 | 3<br>6.<br>5 | 3<br>6       | l<br>i<br>s<br>t<br>e<br>r<br>i<br>a<br>-<br>2 | -                |   | a<br>b<br>c<br>Z<br>(<br>2<br>)           | b<br>g<br>l<br>A<br>(<br>1<br>)      | c<br>a<br>t<br>(<br>1<br>1<br>) | d<br>a<br>p<br>E<br>(<br>3<br>)           | d<br>a<br>t<br>(<br>3<br>)      | l<br>d<br>h<br>(<br>1<br>)           | l<br>h<br>k<br>A<br>(<br>~<br>7<br>)      |
|  | F<br>D<br>A<br>1<br>2<br>1<br>3<br>3<br>7<br>7<br>-<br>C<br>0<br>0<br>1<br>-<br>0<br>0<br>2 | 2<br>0 | 2<br>6<br>7<br>2<br>1<br>8<br>0 | 1<br>5<br>5<br>.1 | 4<br>7<br>3<br>1<br>8<br>1      | 2<br>7<br>0 | 1<br>4<br>7.<br>3 | 1<br>4<br>7.<br>3 | 3<br>7.<br>2 | 3<br>6.<br>1 | -  | -                |   |   |                                      |                                 |   |                                 |                                      |   |
|  | F<br>D<br>A<br>9<br>3<br>3<br>3<br>7<br>6<br>-<br>S<br>0<br>6<br>0<br>-<br>0<br>0<br>5      | 9      | 2<br>8<br>8<br>1<br>8<br>6<br>9 | 2<br>1<br>3       | 1<br>4<br>9<br>8<br>7<br>9<br>0 | 3<br>0<br>3 | 2<br>3<br>2.<br>1 | 2<br>3<br>2.<br>2 | 3<br>7       | 3<br>6.<br>2 | l<br>i<br>s<br>t<br>e<br>r<br>i<br>a<br>-<br>2 | 1<br>4<br>8<br>9 | C<br>C<br>=<br>C<br>C<br>1<br>4<br>8<br>9,<br>L<br>i<br>n<br>e<br>a<br>g<br>e<br>=<br>L<br>i<br>n<br>o<br>c | a<br>b<br>c<br>Z<br>(<br>2<br>5<br>0<br>) | b<br>g<br>l<br>A<br>(<br>2<br>1<br>) | c<br>a<br>t<br>(<br>8<br>3<br>) | d<br>a<br>p<br>E<br>(<br>2<br>9<br>8<br>) | d<br>a<br>t<br>(<br>2<br>0<br>) | l<br>d<br>h<br>(<br>4<br>5<br>8<br>) | l<br>h<br>k<br>A<br>(<br>2<br>1<br>6<br>) |

|  | A   | B      | C                               | D            | E                          | F           | G           | H           | I            | J            | K  | L           | M      | N                                | O                                    | P                                    | Q                                | R                               | S                                    | T                                    |
|--|---|--------|---------------------------------|--------------|----------------------------|-------------|-------------|-------------|--------------|--------------|--|-------------|--------|----------------------------------|--------------------------------------|--------------------------------------|----------------------------------|---------------------------------|--------------------------------------|--------------------------------------|
|  |   |        |                                 |              |                            |             |             |             |              |              |  |             | u<br>a |                                  |                                      |                                      |                                  |                                 |                                      |                                      |
|  | F<br>D<br>A<br>1<br>2<br>1<br>3<br>8<br>3<br>5<br>-<br>C<br>0<br>0<br>1<br>-<br>0<br>0<br>1 | 3<br>7 | 4<br>8<br>3<br>2<br>3<br>6<br>5 | 3<br>4<br>.4 | 2<br>9<br>4<br>9<br>3<br>6 | 3<br>5<br>4 | 1<br>4<br>9 | 1<br>4<br>9 | 3<br>6.<br>6 | 3<br>5.<br>7 | s<br>e<br>n<br>t<br>e<br>r<br>i<br>c<br>a<br>-<br>a<br>c<br>h<br>t<br>m<br>a<br>n<br>2 | 2<br>1<br>4 |        | a<br>r<br>o<br>C<br>(1<br>4<br>) | d<br>n<br>a<br>N<br>(<br>7<br>2<br>) | h<br>e<br>m<br>D<br>(<br>2<br>1<br>) | h<br>i<br>s<br>D<br>(1<br>2<br>) | p<br>u<br>r<br>E<br>(<br>6<br>) | s<br>u<br>c<br>A<br>(<br>1<br>9<br>) | t<br>h<br>r<br>A<br>(<br>1<br>5<br>) |

MicroRunQC example report showing mlst ST results for different *Listeria* species.

The mlst *Listeria* database includes multiple species, including *Listeria monocytogenes* and *L. innocua*. When available, the *Listeria* clonal complex (CC) or *L. monocytogenes* lineage is listed alongside the ST.

- 6.4
- For quality control threshold guidelines for the GenomeTrakr surveillance network,  
[go to step #1](#) These are also relevant for NARMS and VetLIRN contributors.

\*MicroRunQC users should follow QC threshold guidelines established by their respective surveillance coordinating body(s).