# Getting Started in Terra: Importing Reads, Metadata, Workflows, and More

| Document TG-TER-03, Version 4 | |
|---|---|
| Date: | Workflow Versions: |
| 5/1/2025 | PHB v3.0.0 |

## 1. PURPOSE/SCOPE

To standardize the process of uploading next generation sequencing (NGS) data from local storage or the Sequencing Reads Archive (SRA) and creating and uploading a results metadata table using the online Terra platform for downstream Theiagen workflow analysis. Additional instructions are provided for importing workflows and adding workspace data elements and files. Acceptable NGS data types include Illumina, Oxford Nanopore Technology (ONT), ClearLabs, and FASTA file formats. Read the comprehensive workflow documentation here.

## 2. REQUIRED RESOURCES

- Computer
- Internet connection: at least 10 and 5Mbps for download and upload speeds, respectively
- Internet browser
    - Google Chrome, Firefox, or Edge
- Google account
- Terra account, linked to Google account.

**IMPORTANT NOTES**

Metadata column headers and workflow input text indicated in **gray** in this SOP are customizable; **black** is required text.

## 3. RELATED DOCUMENTS

| Document Number | Document Name |
|---|---|
| TG-TER-04 | Linking BaseSpace and Importing BaseSpace Reads to Terra Workspace |

## 4. PROCEDURE

### 4.1 IMPORTING LOCAL RAW READS

1. *Sign in* to https://app.terra.bio/ using a Gmail account and Google Authentication (Figure 1)
2. Click on the *hamburger icon* in the top left and navigate to *Workspaces* (Figure 2)
3. *Open the workspace* designated for analysis
4. In the data tab, click *Import data* and select *Open data uploader* (Figure 3**Error! Reference source not found.**)
5. For new data sets, click *Create a New Collection* (Figure 4**Error! Reference source not found.**)
    a. *The following nomenclature may be useful: YYYYMMDD_# (do not include spaces)*
6. Click *Upload* or *drag and drop* raw sequencing reads into the data table

*Figure 1*

7. When upload is complete, files will populate on this page with *file names hyperlinked* to their corresponding Google Bucket location (Figure 5)
8. Continue to section 4.2 to upload sample metadata.

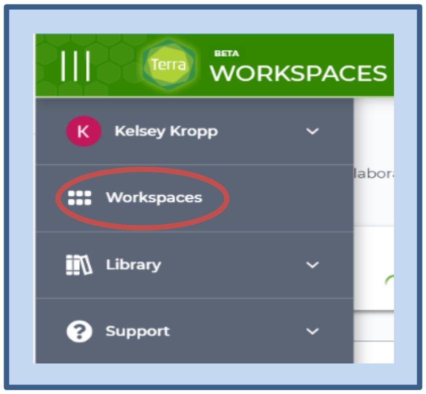


*Figure 2*

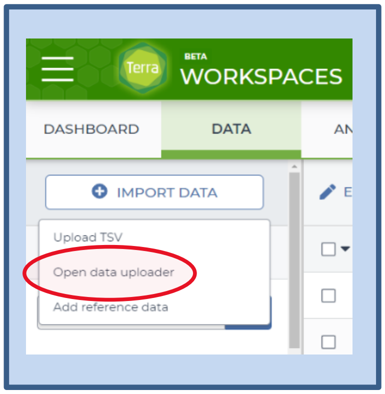
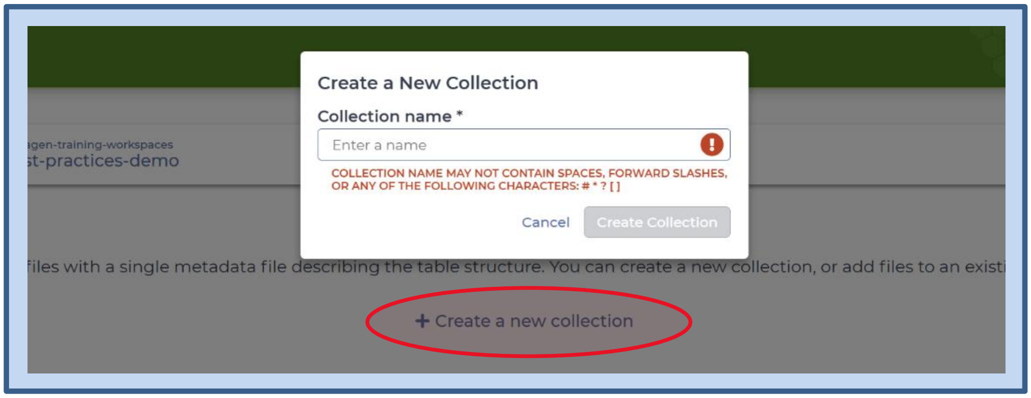


*Figure 3*



gen-training-workspaces
st-practices-demo

COLLECTION NAME MAY NOT CONTAIN SPACES, FORWARD SLASHES, OR ANY OF THE FOLLOWING CHARACTERS: # * ? [ ]

files with a single metadata file describing the table structure. You can create a new collection, or add files to an existi

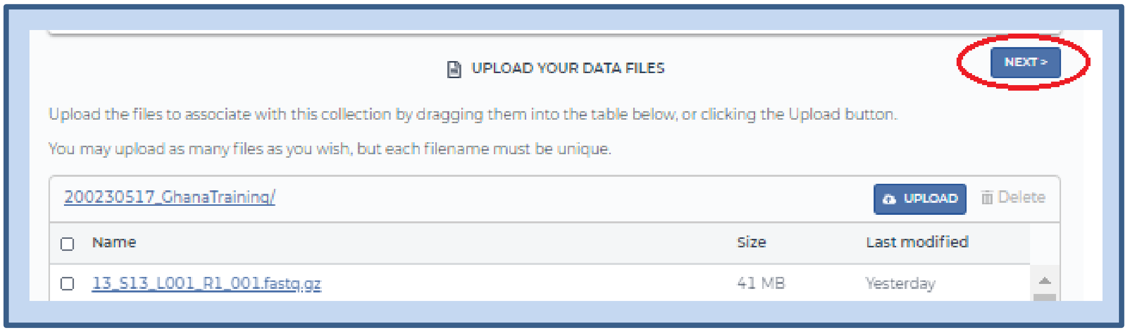
*Figure 4*

## 4.2 IMPORTING SAMPLE METADATA (TSV FILE) AFTER CREATING COLLECTION OF READ FILES

1. Once files have successfully uploaded, click *Next* (Figure 5)
2. Import the associated sample metadata file or drag and drop from file explorer (Figure )
    a. *See appendix 10.1 to create a sample metadata file*
    b. Alternatively, use the auto-generation option and carefully review

        *i.* When using this function, the collection name should be the desired table name
3. Click *create table* (Figure )

4. View the uploaded read data and metadata in the Terra data table by clicking *View the…table in the workspace* at the bottom of the screen
5. In the data tab, all read files and metadata are now populated for each sample in the associated table (e.g. *illumina_pe_specimen* table)
    a. Open the data table by clicking on the table name in the sidebar (Figure 8)



UPLOAD YOUR DATA FILES

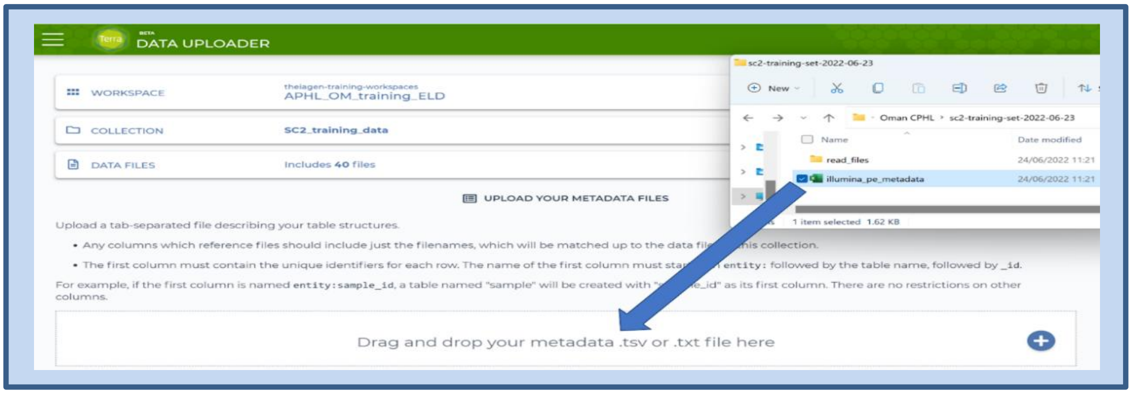
Upload the files to associate with this collection by dragging them into the table below, or clicking the Upload button.

You may upload as many files as you wish, but each filename must be unique.

200230517_GhanaTraining/

| ☐ | Name | Size | Last modified |
|---|---|---|---|
| ☐ | 13_S13_L001_R1_001.fastq.gz | 41 MB | Yesterday |

*Figure 5*



| | Name | Date modified |
|---|---|---|
| | read_files | 24/06/2022 11:21 |
| ☑ | illumina_pe_metadata | 24/06/2022 11:21 |

1 item selected 1.62 KB

WORKSPACE theiagen-training-workspaces APHL_OM_training_ELD

COLLECTION SC2_training_data

DATA FILES Includes **40** files

UPLOAD YOUR METADATA FILES

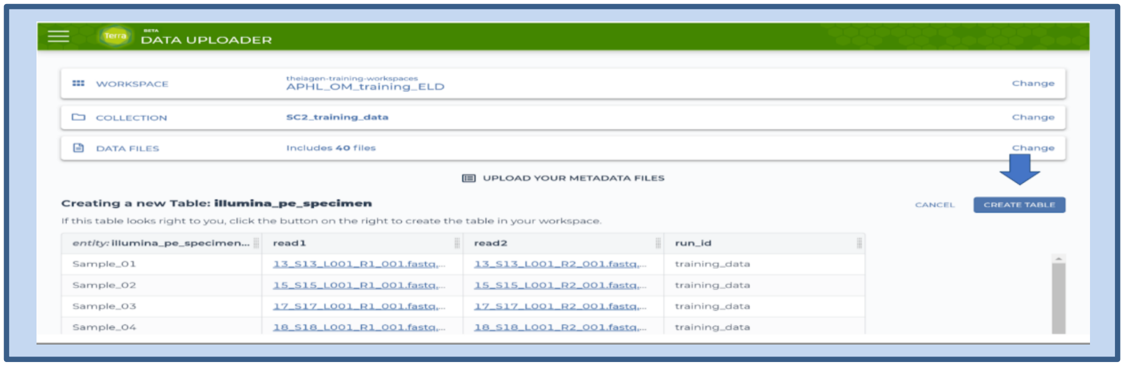
Upload a tab-separated file describing your table structures.

- Any columns which reference files should include just the filenames, which will be matched up to the data fil his collection.
- The first column must contain the unique identifiers for each row. The name of the first column must sta `entity:` followed by the table name, followed by `_id`.

For example, if the first column is named `entity:sample_id`, a table named "sample" will be created with " e_id" as its first column. There are no restrictions on other columns.

Drag and drop your metadata .tsv or .txt file here

*Figure 6*



WORKSPACE theiagen-training-workspaces APHL_OM_training_ELD

COLLECTION SC2_training_data

DATA FILES Includes **40** files

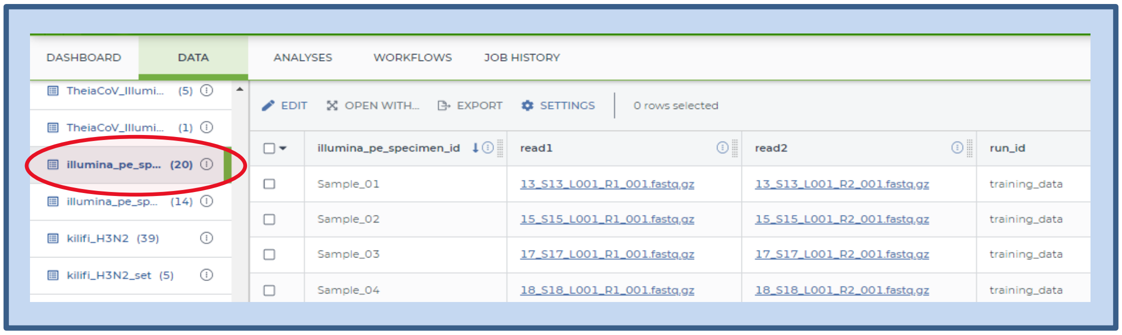
UPLOAD YOUR METADATA FILES

**Creating a new Table: illumina_pe_specimen**

If this table looks right to you, click the button on the right to create the table in your workspace.

| *entity:* illumina_pe_specimen... | read1 | read2 | run_id |
|---|---|---|---|
| Sample_01 | 13_S13_L001_R1_001.fastq,... | 13_S13_L001_R2_001.fastq,... | training_data |
| Sample_02 | 15_S15_L001_R1_001.fastq,... | 15_S15_L001_R2_001.fastq,... | training_data |
| Sample_03 | 17_S17_L001_R1_001.fastq,... | 17_S17_L001_R2_001.fastq,... | training_data |
| Sample_04 | 18_S18_L001_R1_001.fastq,... | 18_S18_L001_R2_001.fastq,... | training_data |

*Figure 7*



| ☐ | illumina_pe_specimen_id | read1 | read2 | run_id |
|---|---|---|---|---|
| ☐ | Sample_01 | 13_S13_L001_R1_001.fastq.gz | 13_S13_L001_R2_001.fastq.gz | training_data |
| ☐ | Sample_02 | 15_S15_L001_R1_001.fastq.gz | 15_S15_L001_R2_001.fastq.gz | training_data |
| ☐ | Sample_03 | 17_S17_L001_R1_001.fastq.gz | 17_S17_L001_R2_001.fastq.gz | training_data |
| ☐ | Sample_04 | 18_S18_L001_R1_001.fastq.gz | 18_S18_L001_R2_001.fastq.gz | training_data |

*Figure 8*

## 4.3 IMPORTING SAMPLE METADATA (TSV FILE) WITHOUT CREATING A READ COLLECTION

1. To upload the metadata file to Terra, return to the *Terra workspace* containing data of interest
2. In the *data* tab, click *import data*, and *upload TSV* (Figure )
3. In the pop-up window, *drag and drop* the file in the gray box or *click to select* the metadata file, then click *start import job* (Figure 10)
    a. *See appendix 10.1 to create a sample metadata file*
    b. *If adding metadata to samples in an existing data table, ensure the data table name indicated in the TSV file in cell A1 contains the same data table name listed in Terra (e.g. [DATATABLE_NAME]_id)*
4. All samples and metadata should now be populated in the corresponding Terra data table (Figure 8)

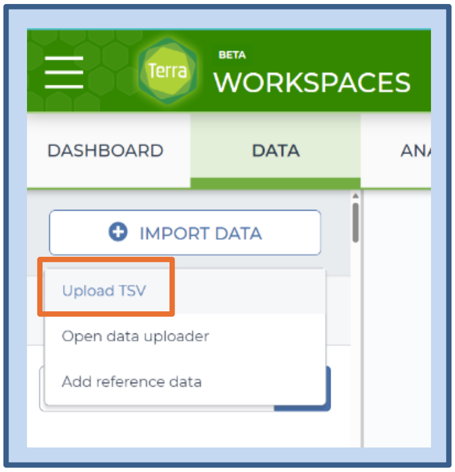
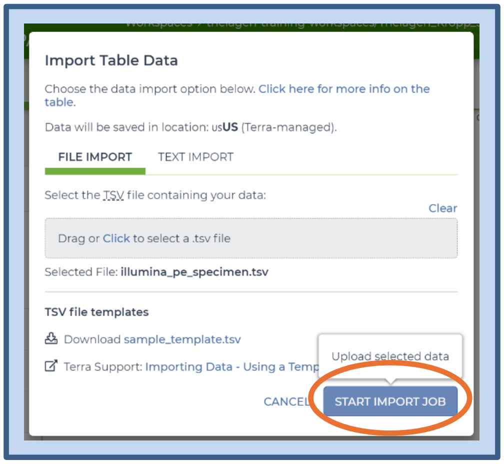


*Figure 9*



Import Table Data

Choose the data import option below. Click here for more info on the table.

Data will be saved in location: usUS (Terra-managed).

Select the TSV file containing your data:

Selected File: illumina_pe_specimen.tsv

TSV file templates

Download sample_template.tsv

Terra Support: Importing Data - Using a Temp

*Figure 10*

## 4.4 IMPORTING RAW READS USING SRA_FETCH

1. Navigate to the Terra workspace that will be used to import reads
2. In the data tab, click on *import data* and *upload TSV* (Figure )
3. Import a TSV file containing the table of SRA accession numbers for desired samples: *select* or *drag and drop* the file, then click *start import job* (Figure 4)
   a. *A template TSV file can be downloaded from this pop-up; follow appendix 10.1 to create a metadata/TSV file (for SRA Fetch, the TSV file does not need read1 or read2 columns, only sra_accession)* (Figure 5)

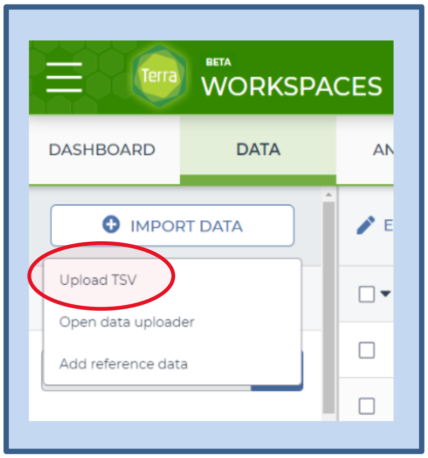


*Figure 11*


Import Table Data

Choose the data import option below. Click here for more info on the table.

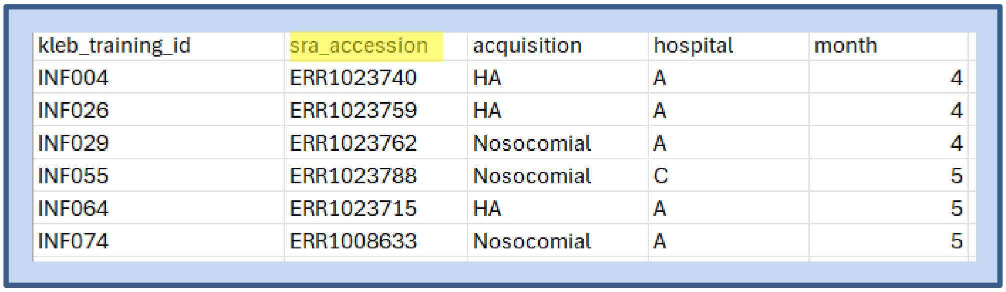
Data will be saved in location: us**US** (Terra-managed).

Select the TSV file containing your data:

Drag or Click to select a .tsv file

Selected File: **None**

*Figure 42*

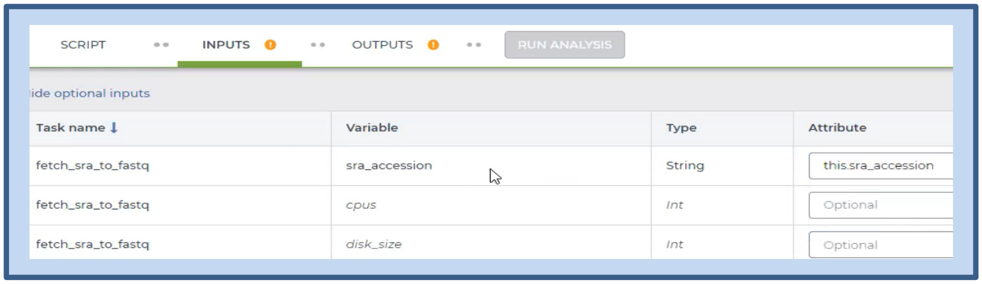


| kleb_training_id | sra_accession | acquisition | hospital | month |
|---|---|---|---|---|
| INF004 | ERR1023740 | HA | A | 4 |
| INF026 | ERR1023759 | HA | A | 4 |
| INF029 | ERR1023762 | Nosocomial | A | 4 |
| INF055 | ERR1023788 | Nosocomial | C | 5 |
| INF064 | ERR1023715 | HA | A | 5 |
| INF074 | ERR1008633 | Nosocomial | A | 5 |

*Figure 13*

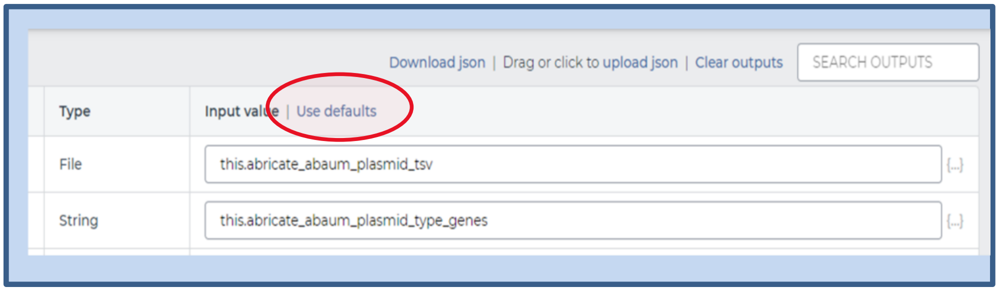
4. In the workflows tab, click *SRA_Fetch_PHB*
   a. Refer to appendix 10.2 for how to import a workflow into a workspace
5. Set the workflow *version* to the latest version, or the workflow version used for internal validations
6. Choose the second bullet to *run workflow(s) with inputs defined by data table*
7. Select the sample table to use under *select data table*
   a. *Do not choose the "set" table version*

8. Click *select data* and *mark the checkboxes* to specify which sample reads to import
9. Set the first input setting to *this.sra_accession*, where *sra_accession* is the TSV file column name containing SRA numbers (Figure 7)
10. In the outputs tab, click *use defaults* (Figure 6) and *save* the workflow
11. Then click *run analysis*, enter any comments if desired, and click *launch*
12. Fetched reads will be populated in the *read1* and *read2* columns of the data table



| Task name ⬇ | Variable | Type | Attribute |
|---|---|---|---|
| fetch_sra_to_fastq | sra_accession | String | this.sra_accession |
| fetch_sra_to_fastq | *cpus* | *Int* | Optional |
| fetch_sra_to_fastq | *disk_size* | *Int* | Optional |

*Figure 74*



| Type | Input value \| Use defaults |
|---|---|
| File | this.abricate_abaum_plasmid_tsv |
| String | this.abricate_abaum_plasmid_type_genes |

*Figure 65*

## 4.5 IMPORTING RAW READS FROM BASESPACE

1. Command line steps are required for the initial setup between BaseSpace and Terra. Refer to the following sites for details on initial setup and the import process:
    a. Theiagen's BaseSpace Fetch Documentation
    b. Document TG-TER-04, Version 3

## 5. QUALITY RECORDS

- Raw read files
- Metadata results table
- Workspace elements and files

## 6. TROUBLESHOOTING

- Terra data table column headers become available as workflow inputs when running workflows, search for them in workflow input dropdowns using the prefix *this*. to filter
- For workspace data and files, search for them in workflow input dropdowns using the prefix *workspace.*
- If the first cell in the metadata table does not end with *_id*, an error message will prevent file import; adjust the metadata text in cell A1 and re-upload
- If any workflow, input, or output settings are entered incorrectly, the analysis will not run as expected; verify all settings are correct and re-launch analysis
- If analysis fails, navigate to the job history in the workspace and click on the job submission for details; for help resolving run failures, email support@theiagen.com

## 7. LIMITATIONS

N/A

## 8. REFERENCES

1. Libuit, Kevin G., Emma L. Doughty, James R. Otieno, Frank Ambrosio, Curtis J. Kapsak, Emily A. Smith, Sage M. Wright, et al. 2023. "Accelerating Bioinformatics Implementation in Public Health." Microbial Genomics 9 (7). https://doi.org/10.1099/mgen.0.001051
2. Theiagen Genomics Public Health Bioinformatics Workflow Documentation
3. Theiagen's BaseSpace_Fetch and SRA_Fetch workflow resource pages
4. Theiagen's Docker Image and Reference Materials for SARS-CoV-2
5. Theiagen's Public Health Resources

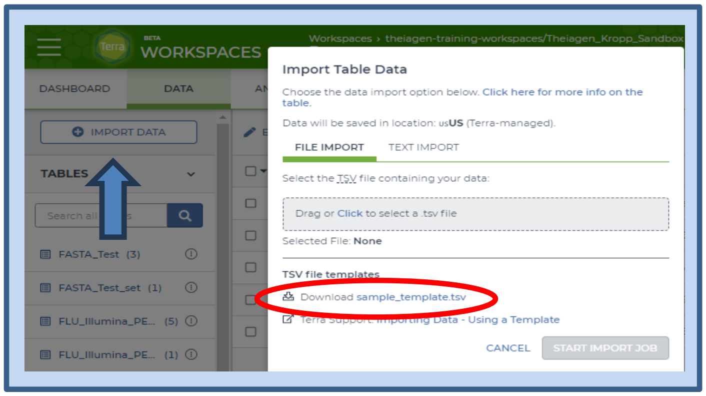
## 9. REVISION HISTORY

| Revision | Version | Release Date |
|---|---|---|
| Document Creation | 1 | 7/2023 |
| Added internet speeds recommended for up/download, important notes, section 4.5, SRA metadata info in appendix 9.1, and appendix 9.3 | 2 | 9/2023 |
| Formatting (Figure references and cross-references check), section 4.1 - 4.4 updates, inclusion of figure 15, appendix 10.1 updates | 3 | 4/2024 |
| Edits for version release, aligning with Terra interface, and formatting | 4 | 5/2025 |
|  |  |  |

## 10. APPENDICES

### 10.1 CREATING A METADATA FILE (TSV FILE)

1. Open the downloadable TSV template located in the Import Data/Upload TSV pop-up window (Figure 6)



Import Table Data

Choose the data import option below. Click here for more info on the table.

Data will be saved in location: usUS (Terra-managed).

Select the TSV file containing your data:

Drag or Click to select a .tsv file

Selected File: None

TSV file templates

Download sample_template.tsv

Terra Support: Importing Data - Using a Template

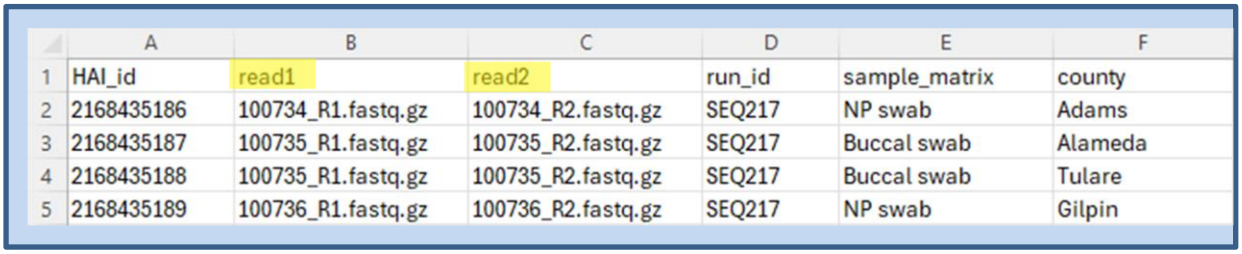
*Figure 16*

2. Cell A1 must contain the following text: *[name]_id* (Figure 17)
   - *a.* Do not include spaces or characters other than hyphens (-) or underscores (_)
   - *b.* The data table name should contain text to indicate the project name (e.g. Cell A1 may read *HAI_id* to create a table for all HAI organisms)
3. Enter all ***sample IDs*** into column 1 below cell A1
4. Label column headers for desired metadata (do not include spaces or special characters)
   - *a.* *Optional:* enter run_id as a column header and the run ID for each sample in the column
   - *b.* *Optional:* add additional metadata columns and sample information, as needed

| HAI_id | run_id | sample_matrix | county |
|---|---|---|---|
| 2168435186 | SEQ217 | NP swab | Adams |
| 2168435187 | SEQ217 | Buccal swab | Alameda |

*Figure 17*

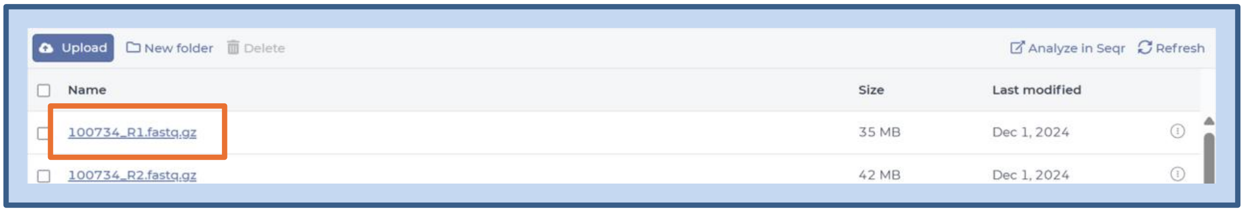
5. **For manually-uploaded reads** via the *Data Uploader*, include read columns (Figure 18)
   a. For **paired-end** (PE) sequencing: *read1* and *read2*



| | A | B | C | D | E | F |
|---|---|---|---|---|---|---|
| 1 | HAI_id | read1 | read2 | run_id | sample_matrix | county |
| 2 | 2168435186 | 100734_R1.fastq.gz | 100734_R2.fastq.gz | SEQ217 | NP swab | Adams |
| 3 | 2168435187 | 100735_R1.fastq.gz | 100735_R2.fastq.gz | SEQ217 | Buccal swab | Alameda |
| 4 | 2168435188 | 100735_R1.fastq.gz | 100735_R2.fastq.gz | SEQ217 | Buccal swab | Tulare |
| 5 | 2168435189 | 100736_R1.fastq.gz | 100736_R2.fastq.gz | SEQ217 | NP swab | Gilpin |

*Figure 18*

   b. For **single-end** (SE) sequencing: only *read1*
   c. Use the *file name* as the value for this column (e.g. 100734_R1.fastq.gz) (Figure 19)



| ☐ | Name | Size | Last modified |
|---|---|---|---|
| ☐ | 100734_R1.fastq.gz | 35 MB | Dec 1, 2024 |
| ☐ | 100734_R2.fastq.gz | 42 MB | Dec 1, 2024 |

*Figure 19*

6. **For SRA uploads:**
   a. *Label the column header* for column 2 as *sra_accession*, or similar
   b. Enter SRA accessions as the values for this column (e.g. SRR# or ERR#)

| HAI_id | sra_accession | hospital | month | year | age | run_id |
|---|---|---|---|---|---|---|
| 2168435186 | ERR1023740 | D | 4 | 2013 | 30-39 | SEQ217 |
| 4831845358 | SRR11445892 | A | 2 | 2014 | 80-89 | SEQ217 |
| 8415835241 | ERR4087740 | C | 6 | 2013 | 60-69 | SEQ217 |
| 6846813545 | SRR11842392 | A | 3 | 2013 | 80-89 | SEQ217 |

7. In Excel, click *save as* and change the file type to *Text (Tab delimited).*
8. Refer to section 4.2 to import TSV files at the same time as creating new read collections (importing files locally) and section 4.3 to import TSV files without creating read collections

## 10.2 IMPORTING A WORKFLOW FROM DOCKSTORE

1. In the *Terra workspace* of interest, navigate to the *workflows* tab and click *find a workflow* (Figure 20)
2. In the pop-up window, click *Dockstore.org* (Figure 21)
3. Workflows may be found through the search bar or by navigating through the organization if it is known
    a. To find a Theiagen workflow
        i. click *organizations* (Figure 22)
        ii. In the search bar type *Theiagen* (Figure 22)
        iii. Click on the *logo*, *view*, or *# collections.* (Figure )
        iv. Click on the collection to see available workflows: *Public Health Bioinformatics (PHB)*
4. Find and *open the workflow* (workflow name listed at the end of the file path) (Figure 24)
5. Click *Terra* to launch the workflow in Terra (Figure )
6. Choose the *destination workspace* in the dropdown
7. Click *import* or *create a new workspace* (Figure 26)

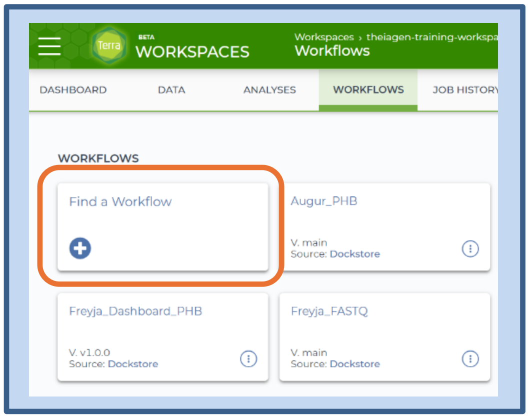
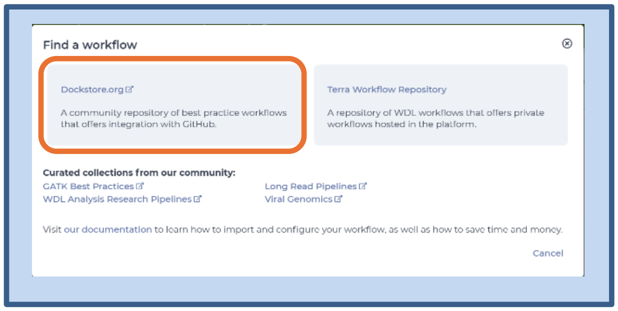


*Figure 20*



Find a workflow

Dockstore.org

A community repository of best practice workflows that offers integration with GitHub.

Terra Workflow Repository

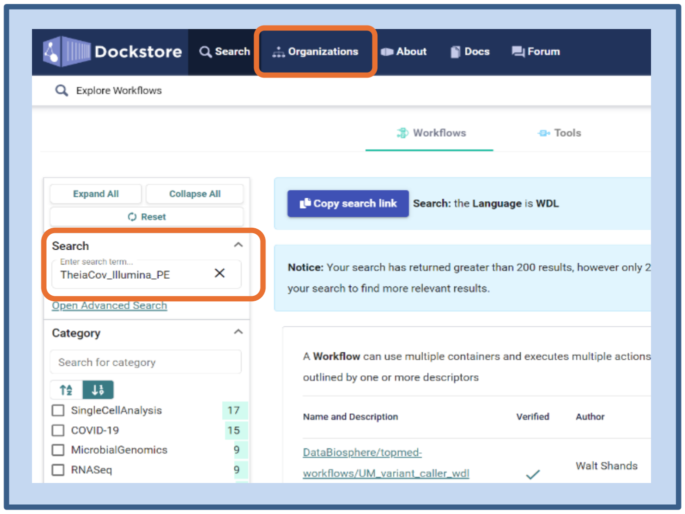
A repository of WDL workflows that offers private workflows hosted in the platform.

**Curated collections from our community:**

GATK Best Practices
WDL Analysis Research Pipelines
Long Read Pipelines
Viral Genomics

Visit our documentation to learn how to import and configure your workflow, as well as how to save time and money.

*Figure 21*



**Search:** the **Language** is **WDL**

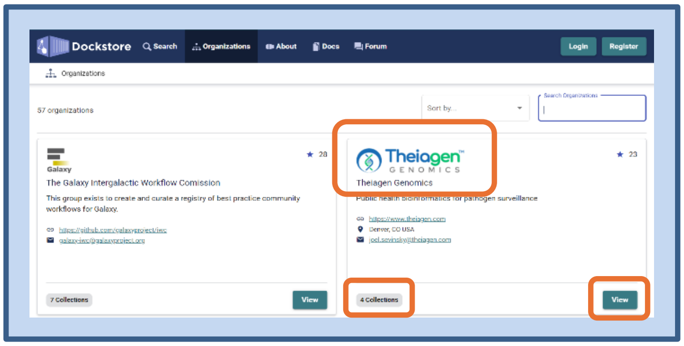
**Notice:** Your search has returned greater than 200 results, however only 2

your search to find more relevant results.

A **Workflow** can use multiple containers and executes multiple actions

outlined by one or more descriptors

*Figure 22*



This group exists to create and curate a registry of best practice community workflows for Galaxy.

Public health bioinformatics for pathogen surveillance

*Figure 23*

Terra-accessible workflows for public health pathogen genomics

Bioinformatics workflows for characterization, epidemiology and sharing of pathogen genomes.

**More information about the steps undertaken in these workflows is available via the Theiagen Public Resources Documentation.**

*Figure 24*


github.com/theiagen/public_health_bioinformatics/TheiaCoV_ClearLabs_PHB:v1.0.0

Tag created: 38 days ago

Last update to source repository: 4 hours ago

Labels theiagen-phb

Workflow Information

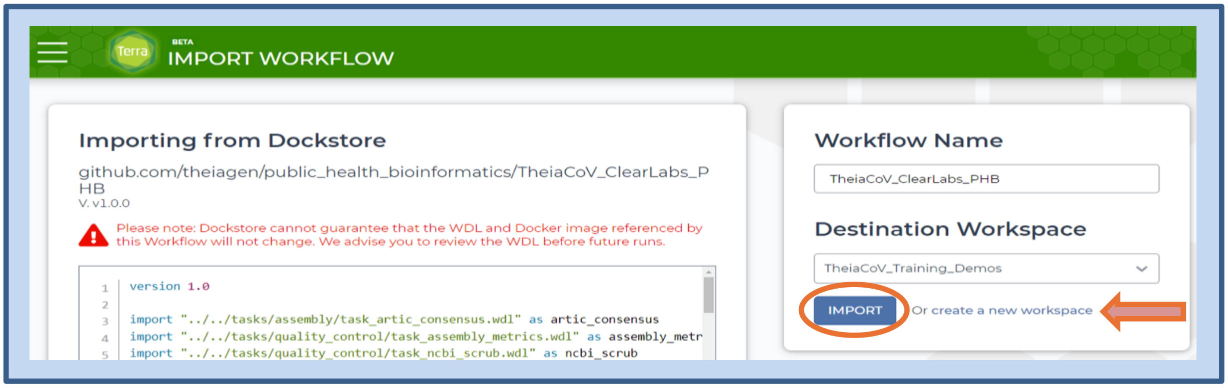
Source Code:...

TRS: #workflow/github.com/theiagen/public_health_bioinformatics/TheiaCoV_ClearLabs_PHB

Topic: Bioinformatics workflows for genomic characterization, submission preparation, and genomic epidemiology of pathogens of public health concern.

Checker Workflow: n/a

*Figure 25*



Importing from Dockstore

github.com/theiagen/public_health_bioinformatics/TheiaCoV_ClearLabs_PHB
V. v1.0.0

Please note: Dockstore cannot guarantee that the WDL and Docker image referenced by this Workflow will not change. We advise you to review the WDL before future runs.

```
version 1.0

import "../../tasks/assembly/task_artic_consensus.wdl" as artic_consensus
import "../../tasks/quality_control/task_assembly_metrics.wdl" as assembly_metr
import "../../tasks/quality_control/task_ncbi_scrub.wdl" as ncbi_scrub
```

Workflow Name: TheiaCoV_ClearLabs_PHB

Destination Workspace: TheiaCoV_Training_Demos

*Figure 26*

## 10.3 ADDING AND UPDATING WORKSPACE DATA ELEMENTS AND FILES

1. Navigate to the *Terra workspace* where analyses will be run
2. To upload local files:
    a. Open the *workspace files* tab in the right-side panel of the workspace (Figure 7).
    b. Click *upload*
    c. Following upload, click the *clipboard* or *right click* on the file name to *copy link*
3. To add workspace variables:
    a. Click the *workspace data* tab at the bottom of the left-side panel (Figure 27)
    b. Click *Edit* in the top menu (Figure 28)
    c. Click *Add Variable* (Figure 28)
    d. Click in the *key field* and *name the element* being added (Figure 9)
    e. In the value field, choose *string* as the value type
    f. Paste the file path copied above in step 2, or enter the desired file path (see below)
        i. *E.g. to add the Artic V4-1 primer bed file, the key* Artic_V4-1_primer_bed *may be used with the file path as the value* (Figure 30)
4. Docker images and tags for TheiaCoV workflows should be included in workspace variables.
    a. Ensure the docker images and dataset tags are aligned with versions used for internal validation procedures or are re-verified before use.
    b. Available in the [Docker Image and Reference Materials for SARS-CoV-2]
    c. All resources can be found on the [Theiagen Public Health Resources] page

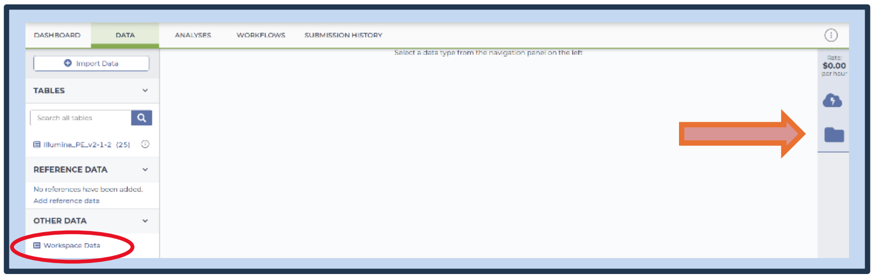


*Figure 27*

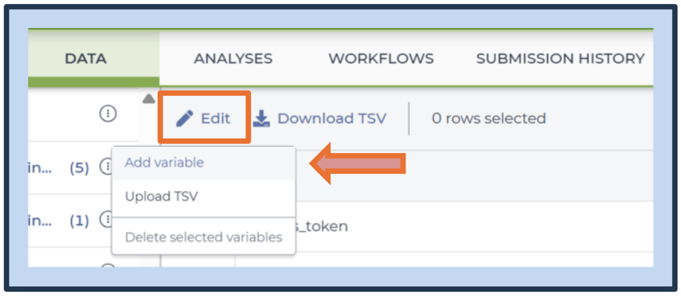
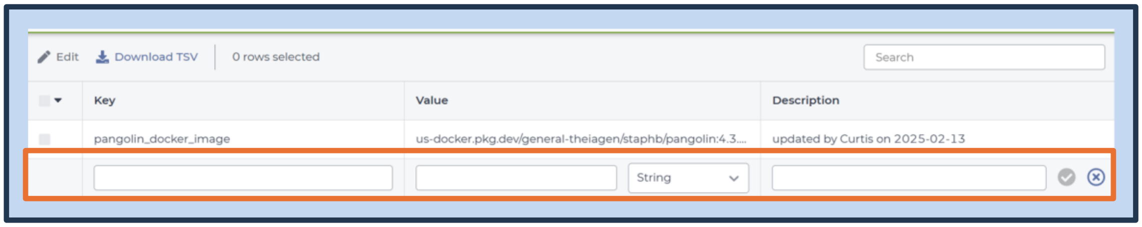
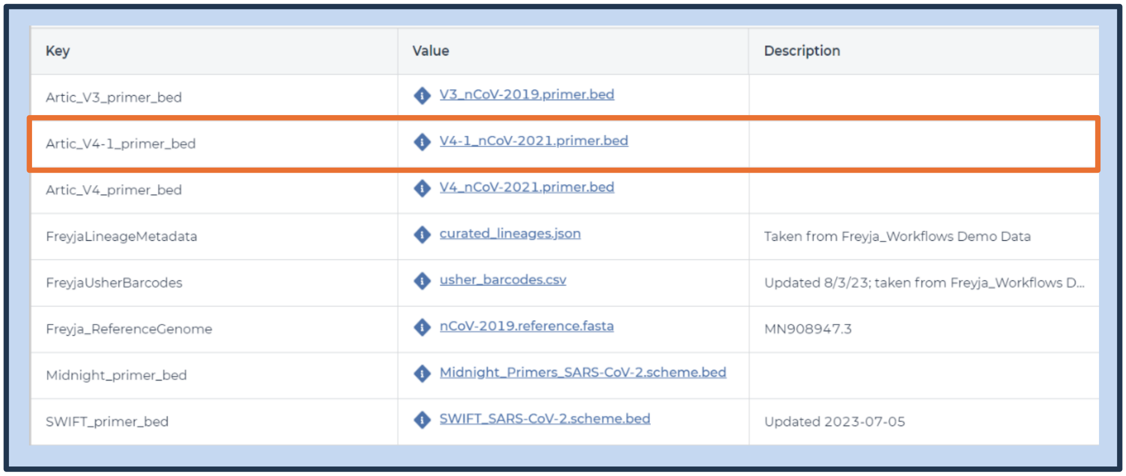


*Figure 28*



| Key | Value | Description |
|---|---|---|
| pangolin_docker_image | us-docker.pkg.dev/general-theiagen/staphb/pangolin:4.3.... | updated by Curtis on 2025-02-13 |

*Figure 29*



| Key | Value | Description |
|---|---|---|
| Artic_V3_primer_bed | V3_nCoV-2019.primer.bed | |
| Artic_V4-1_primer_bed | V4-1_nCoV-2021.primer.bed | |
| Artic_V4_primer_bed | V4_nCoV-2021.primer.bed | |
| FreyjaLineageMetadata | curated_lineages.json | Taken from Freyja_Workflows Demo Data |
| FreyjaUsherBarcodes | usher_barcodes.csv | Updated 8/3/23; taken from Freyja_Workflows D... |
| Freyja_ReferenceGenome | nCoV-2019.reference.fasta | MN908947.3 |
| Midnight_primer_bed | Midnight_Primers_SARS-CoV-2.scheme.bed | |
| SWIFT_primer_bed | SWIFT_SARS-CoV-2.scheme.bed | Updated 2023-07-05 |

*Figure 30*