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Oct 18, 2021

Titan Clear Labs SARS-CoV-2 Strain Characterization Workflow for the Terra Platform V.1

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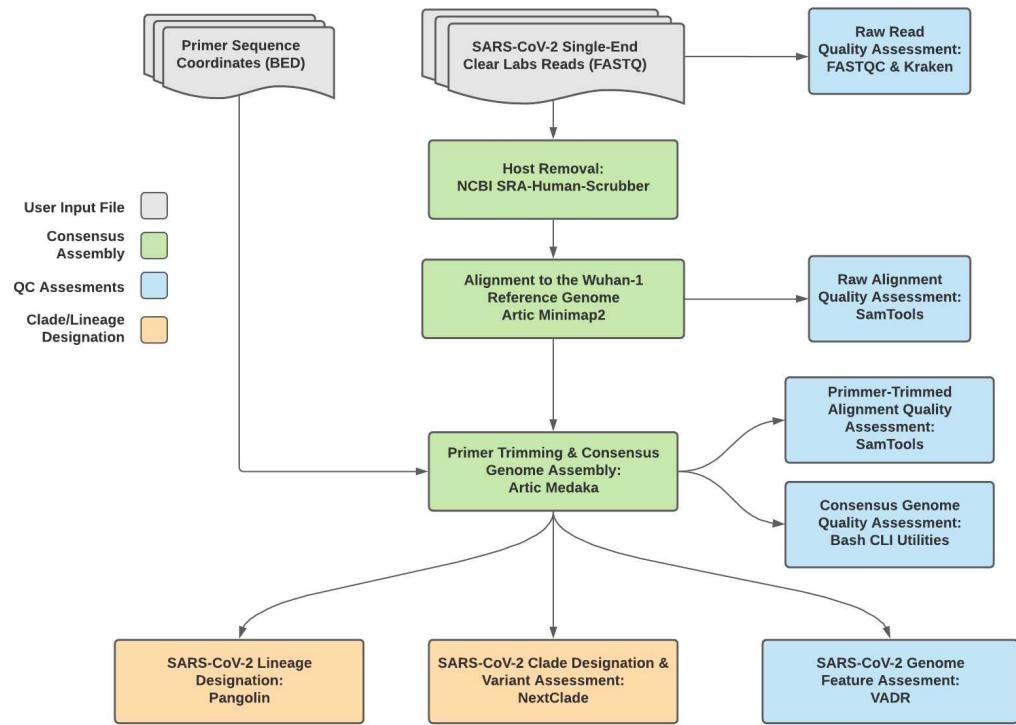
protocol .

Frank Ambrosio

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The Titan_ClearLabs workflow is a part of the Public Health Viral Genomics Titan series for SARS-CoV-2 genomic characterization. Titan_CleanLabs was written to process Clear Labs read data for SARS-CoV-2 ARTIC V3 amplicon sequencing. Upon initiating a Titan_ClearLabs run, input read data provided for each sample will be processed to perform consensus genome assembly, infer the quality of both raw read data and the generated consensus genome, and assign lineage or clade designations as outlined in the Titan_ClearLabs data workflow below.

Additional technical documentation for the Titan_ClearLabs workflow is available at:
https://public-health-viral-genomics-theiagen.readthedocs.io/en/latest/titan_workflows.html#titan-clearlabs



Titan workflow for use with Clear Labs sequencing read data

Required input data for Titan_ClearLabs:

Cear Labs FASTQ read files (single FASTQ file per sample)

Primer sequence coordinates of the PCR scheme utilized in BED file format

Video Instruction:

Theiagen Genomics: Titan Genomic Characterization

<https://www.youtube.com/watch?v=zP9I1r6TNrw>

Theiagen Genomics: Titan Outputs QC

<https://www.youtube.com/watch?v=AmB-8M71umw>

For technical assistance, please contact us at: **TOAST@cdc.gov**

Titan_ClearLabs.png

Frank J Ambrosio, Jill V Hagey, Kevin Libuit, Technical Outreach and Assistance for States Team 2021. Titan Clear Labs SARS-CoV-2 Strain Characterization Workflow for the Terra Platform. [protocols.io](https://protocols.io/view/titan-clear-labs-sars-cov-2-strain-characterization-bu5eny3e)

<https://protocols.io/view/titan-clear-labs-sars-cov-2-strain-characterization-bu5eny3e>

ONT, Nanopore, SARS-CoV-2, MinION, GridION, PromethION, MK1C, Pangolin, Genomics, Analysis, Virology, Bioinformatics, RNA, DNA, Clear Labs, Covid, Computational Biology, Sequencing, Clear Labs, Hamilton

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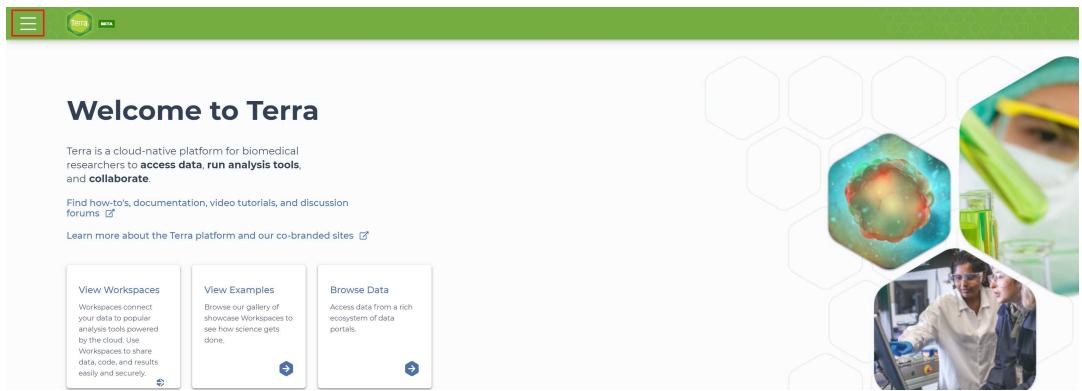
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Setup Terra and Google Cloud Accounts

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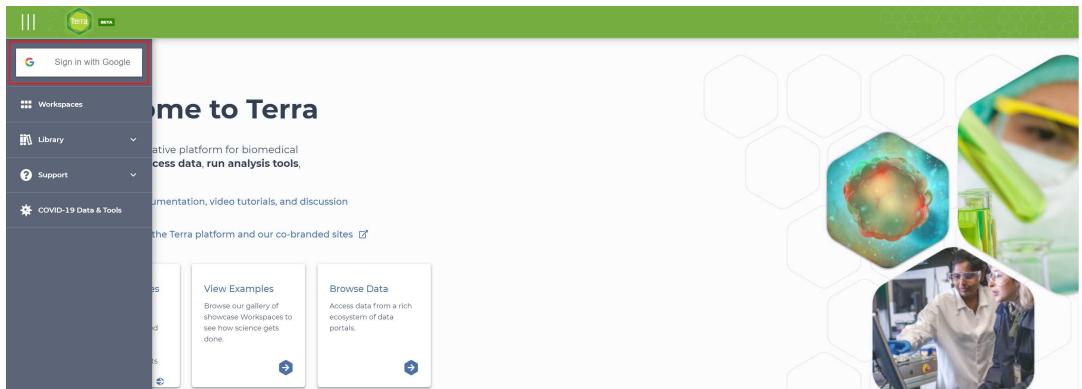
The Terra platform registration requires a Google account. If you have a Google account you can sign in using the Terra login page:

<https://app.terra.bio/>



Welcome page for Terra.bio.

Click on the three parallel lines in the top left-hand corner and click the 'Sign in with Google' button.



Terra.bio welcome page with selection panel open.

If you do not have Google email you can set up a Google account with a non-Google email. The steps to do this are described in the following link:
<https://support.terra.bio/hc/en-us/articles/360029186611>

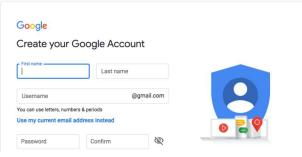
Setting up a Google account with a non-Google email

By Allie Hajian · 2 months ago · Updated

The Terra platform requires a Google account, either a Gmail account, an institutional Google Apps account, or a Google Apps account that you create. Using your institutional email address will allow you to receive notifications via your institutional email and helps Broad Project managers more easily coordinate data access and delivery.

If your institution uses CSuite, your account will already be a Google account and you can proceed directly to register on Terra. If not, you can follow these steps to create a Google account that is associated with your non-Gmail, institutional email address:

1. Go to the Google sign-up page (<https://accounts.google.com/SignUp>):



01. How to register for a Terra account
02. Setting up a Google account with a non-Google email
03. Set up billing with \$300 Google credits to explore Terra
04. How to set up billing in Terra
05. How to change the Google Billing account funding a Terra Billing project

The Terra platform uses the Google Cloud to run workflows and store data. The following documentation will describe how to set up a Google Cloud account:
<https://support.terra.bio/hc/en-us/articles/360046295092>

Terra Support > Documentation > Account and billing setup & admin (including security)

Set up billing with \$300 Google credits to explore Terra

Allie Hajian · 11 days ago · Updated · Follow

If you've never logged into the Google Cloud Platform console to set up billing, you are eligible for \$300 in free GCP credits you can use for working in Terra. Read on for step-by-step instructions for how to access the credits in Terra and FAQs about using the credits on Terra.

For more information about Google's free credits and Free Tier, see their documentation here.

Contents

Three steps to get \$300 CCP credits to use in Terra

1. Set up a CCP Billing account and accept \$300 free trial credits
2. Link Terra to your CCP Billing account
3. Create a Terra Billing project

Next - Try a template analysis
GCP free credits FAQs

Three steps to get \$300 GCP credits to use in Terra

The first step is to set up a GCP Billing account using your Terra user ID in the CCP console. Note that you will need to give some additional information to Google, as well as verify your Billing account with a credit card or bank account. Google will

01. How to register for a Terra account
02. Setting up a Google account with a non-Google email
03. Set up billing with \$300 Google credits to explore Terra
04. How to set up billing in Terra
05. How to change the Google Billing account funding a Terra Billing project

To link your Terra platform account with your Google Cloud account follow the instructions provided in the following link:

<https://support.terra.bio/hc/en-us/articles/360026182251-How-to-set-up-billing-in-Terra>

Scroll down to Section 3 titled "Create a Terra Billing Project" and follow the instructions. **It is important to note that the name you give to your Terra Billing Project must be unique across all Google Billing Projects.** If the name provided is not unique, it won't immediately throw an error, but instead will not complete the process of associating the Google Billing account with the Terra Billing Project. If this occurs, cancel the process and set up a new Terra Billing Project.

Terra Support > Documentation > Account and billing setup & admin (including security)

How to set up billing in Terra

Anton Kovalsky · 2 months ago · Updated · Follow

Terra runs on the Google Cloud Platform (CCP), so you'll pay for all storage and analysis costs through a Google account linked to Terra. Once you set up your billing structure, Terra takes care of interfacing with the Google billing account. This article goes over step-by-step instructions for how to set up billing in Terra for different scenarios. To learn more about the structure of billing in Terra, including what costs money to do and who pays for costs, see this article.

There is never a charge for administration or security services covered by the Terra platform or for support, and the community forum is available 24/7 free of charge to help you. The costs are the standard GCP fees for storing and moving data as well as executing an analysis (bulk workflow or interactive Jupyter notebook). Billing account owners can check your spend at any time on the Google Cloud Platform billing console.

Contents

Getting started - \$300 in Google Cloud Credits
Accessing STRIDES credits on Terra
Collaborating with someone already on Terra? Some ways to share billing

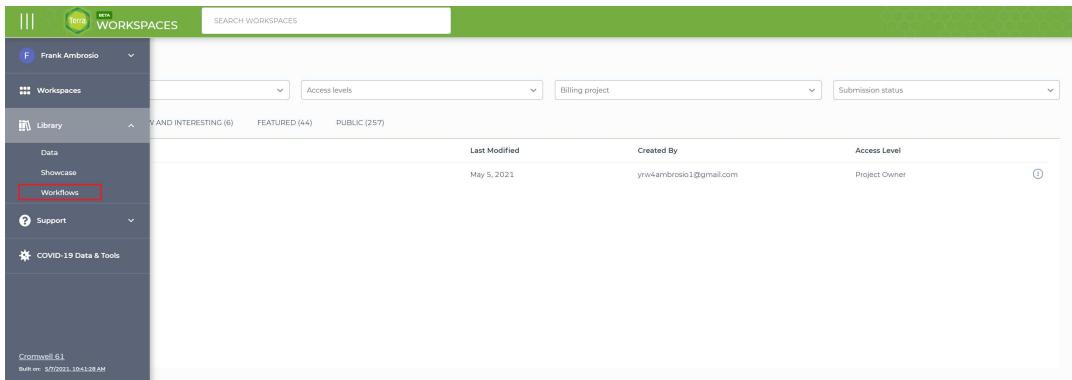
- Work in a shared workspace
- Access an existing Billing Project
- How to add or remove Billing Project users (owners)

01. How to register for a Terra account
02. Setting up a Google account with a non-Google email
03. Set up billing with \$300 Google credits to explore Terra
04. How to set up billing in Terra
05. How to change the Google Billing account funding a Terra Billing project

Import Titan Clear Labs workflow from Dockstore

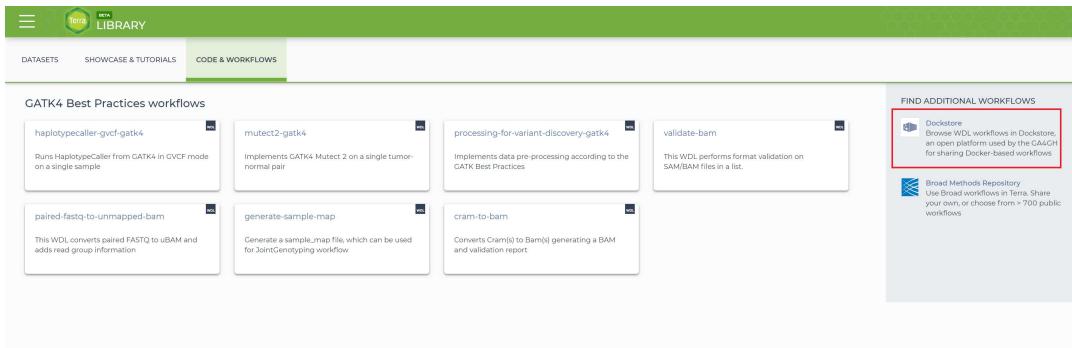
Importing the Titan Workflow from Dockstore to the User Workspace

The Titan Clear Labs workflow is hosted in the Theiagen Dockstore (<https://dockstore.org/>) repository and has to be imported into the user's Terra Workspace. Begin by clicking on the three parallel lines in the top left-hand corner, followed by clicking the 'Library' tab and finally click the 'Workflows' button.



'Workflows' button listed under the 'Library' tab in the selection panel

In the 'Workflows' panel, under 'Find Additional Workflows' click on the 'Dockstore' link in the grey box on the right side of the page.



Workflows panel with link to Dockstore

On the left side of the Dockstore page search for theiagen/public_health_viral_genomics/Titan_ClearLabs in the pull-down search bar.

The screenshot shows the Dockstore search interface. A search bar at the top contains the query "theiagen/public_health_viral_". Below it, a search panel has a red border around its search input field. To the right, a search result for "theiagen/public_health_viral_genomics/Titan_ClearLabs" is displayed, showing a table with one item. The table columns include Name, Verified, Author, Format, Project Links, and Stars. The item listed is "theiagen/public_health_viral_genomics/Titan_ClearLabs" with "n/a" in all other columns.

Search result for theiagen/public_health_viral_genomics/Titan_ClearLabs

Click the '[theiagen/public_health_viral_genomics/Titan_ClearLabs](#)' link. This will take you to a page where you can import the workflow into your workspace.

This screenshot shows the workflow details page for 'theiagen/public_health_viral_genomics/Titan_ClearLabs:main'. The left side displays workflow information like Source Code (github.com/theiagen/public_health_viral_genomics/main), TRS (Workflow GitHub URL), Checker Workflow, Descriptor Type (WDL), and DOI (n/a). The right side features a 'Launch with' section with several options, including Terra, which is highlighted with a red box. A warning message above the Terra button states: "Warning: this version of the WDL has imports, which are not supported by DNAstack. Make sure to select a version without imports in DNAstack".

Dockstore link to terra

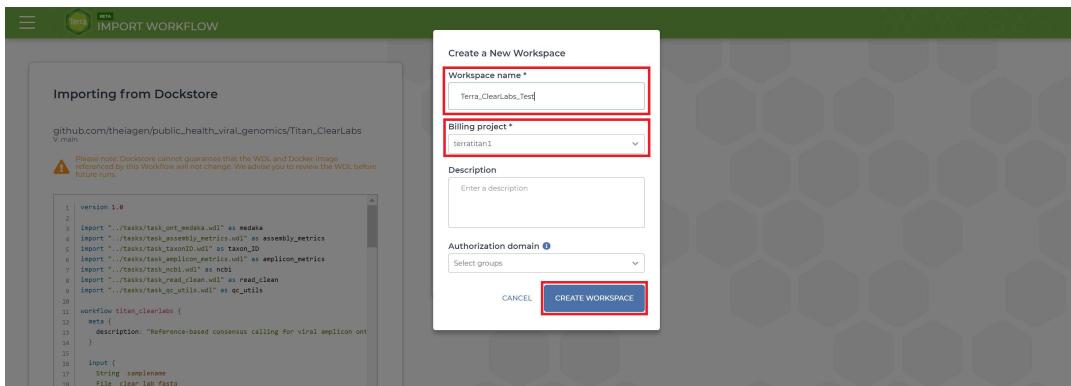
On the right-hand side of the page under the 'Launch with' window, click the 'Terra' button. It should bring you back to the Terra platform within the 'Import Workflow' page.

This screenshot shows the Terra.bio 'Import Workflow' page. On the left, there's a code editor displaying the WDL script for 'titan_clearlabs'. On the right, there are fields for 'Workflow Name' (set to 'Titan_ClearLabs') and 'Destination Workspace' (set to 'terra_ClearLabs_Test'). Below these fields is a button labeled 'Or create a new workspace' with a red box around it. At the bottom of the page, there's an 'IMPORT' button.

Terra.bio import workflow page

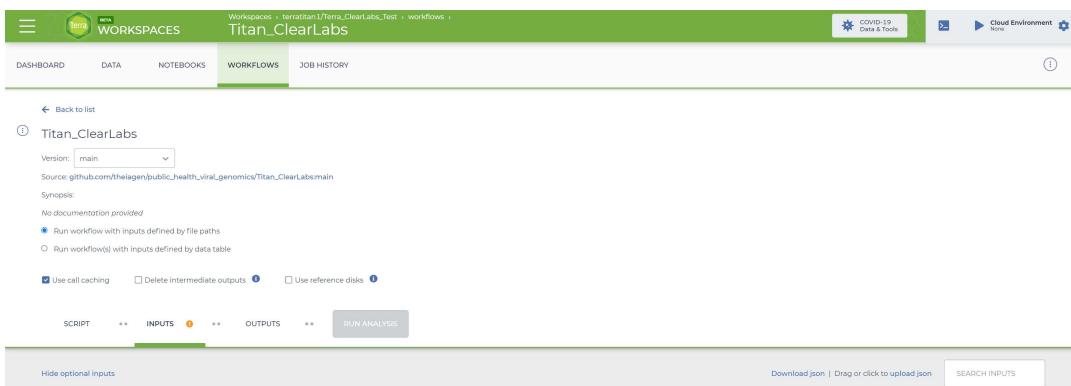
Under 'Destination Workspace,' click the 'create a new workspace' button. A pop-up window titled 'Create a New Workspace' should appear. Name your new workspace and associate it with a

billing account using the 'Billing project' drop-down menu. The Terra Billing Account you created in the previous step should be available. Finally, click the 'Create Workspace' button.



Create new workspace panel

After clicking the 'Create Workspace' button you should be automatically directed to the Titan Clear Labs workflow panel in the new workspace page that was just created.



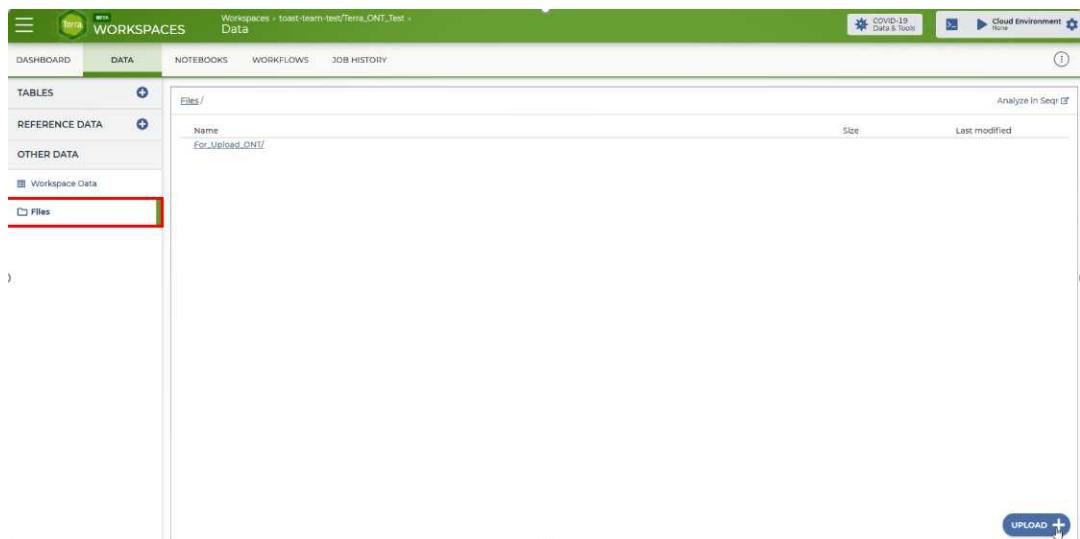
Upload Fastq Sequence Files

3 There are three options for uploading your files:

1. Upload on Terra (can only do single files).
2. Upload to Google bucket and link to Terra (can do single files or bulk files/folders).
3. Upload via '<https://app.terra.bio/#upload>' -- This is the easiest option

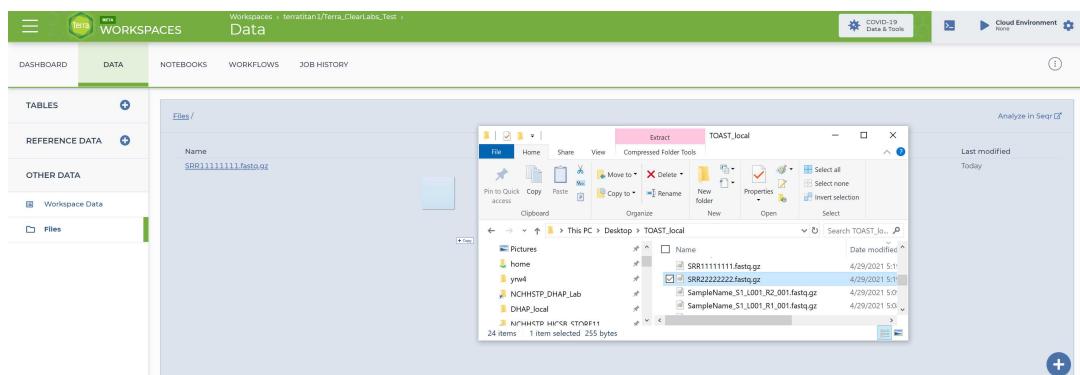
3.1 Upload fastq sequence files one at a time to be used in the analysis

Click on the 'Data' panel in the newly created workspace and then click on the 'Files' tab



The 'Files' tab within the 'Data' panel of the newly created workspace

Once in the 'Files' tab, you can either just drag and drop your files into this space or move the mouse over the blue plus sign icon in the bottom right-hand corner and click 'upload'. Upload the sequence files you'll need for this analysis. **Each fastq sequence file has to be uploaded individually using this method.**



Dragging and dropping files for upload

Once the files are uploaded, you will need to bring a table in to associate your files with their corresponding link to their google bucket location.

The Terra sample table file has to follow a specific template. We've provided the template file here [Terra_ClearLabs_Table_Upload.tsv](#) as a downloadable **tab-separated** (or .tsv) file. The tab-separated table has three columns: entity:sample_id, Reads.

Either by editing the text file or using spreadsheet software like Excel, fill in each column with the required information. The first column

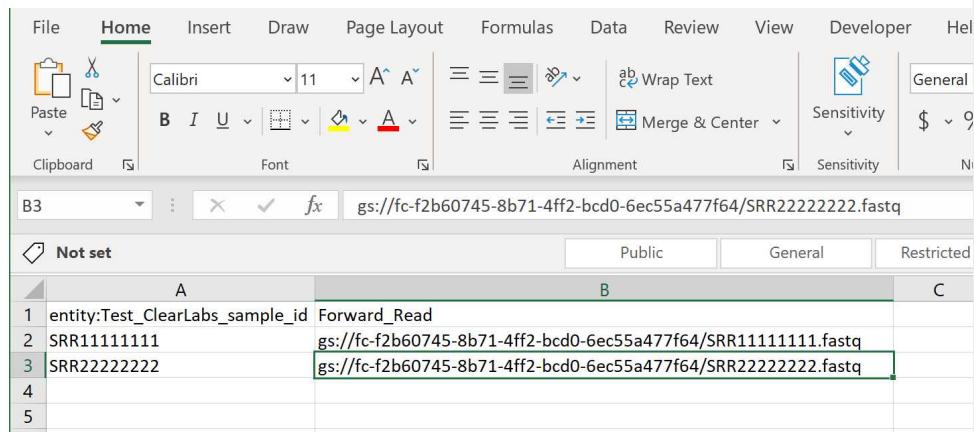
'entity:sample_id' is the sample name that is provided by the user. The second columns, Reads are the file paths where the fastq files are stored within the Google Cloud.

While you had to upload your samples individually, you can have all your samples in one datatable.

To identify the Google Cloud location, right-click on each fastq file that was uploaded in the previous step and copy the link address. The file path should look like something similar to the following:

gs://fc-b1e3191a-3d9f-43fe-9743-255551ce2f38/F_1.fastq.gz

When completed, the table should look similar to the following:



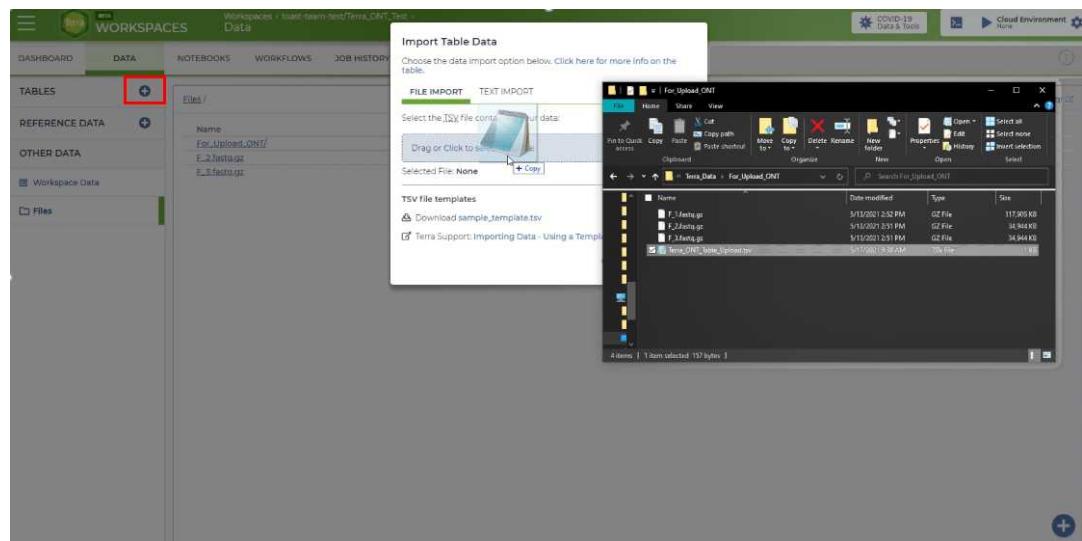
	A	B	C
1	entity:Test_ClearLabs_sample_id	Forward_Read	
2	SRR11111111	gs://fc-f2b60745-8b71-4ff2-bcd0-6ec55a477f64/SRR11111111.fastq	
3	SRR22222222	gs://fc-f2b60745-8b71-4ff2-bcd0-6ec55a477f64/SRR22222222.fastq	
4			
5			

Example Terra sample file

Once the table is filled with the required information, be sure to save it as a **tab-separated** (or tsv) file. The spreadsheet software should have an option to save as a 'tsv' file.

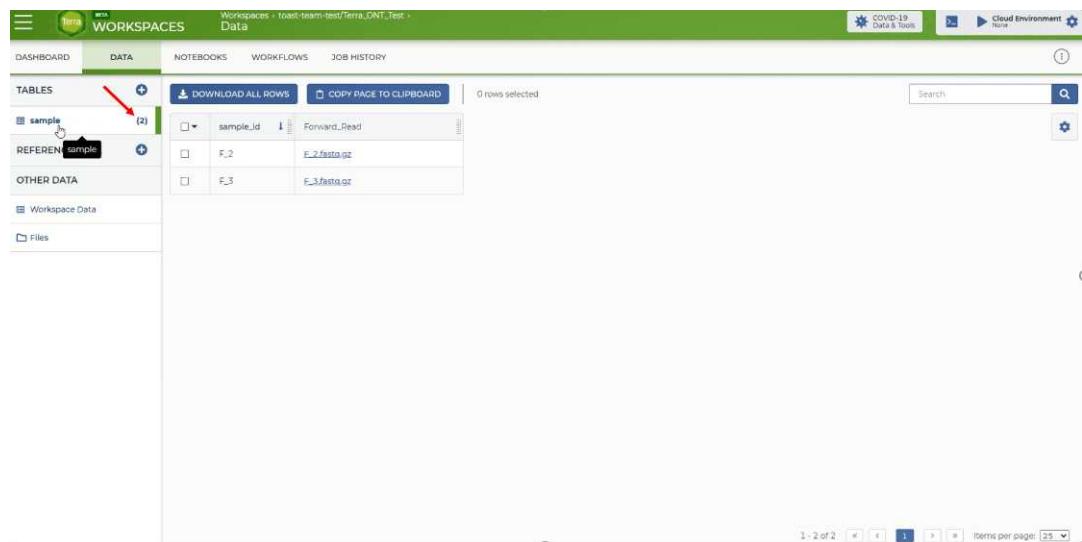
Note: When uploading additional sample table files to the same workspace, the entity types must be unique and end in "_id" (e.g. sample1_id, sample2_id etc.)

Finally, the completed Terra sample file will need to be uploaded to the newly created Cecret* workspace. On the right-hand side of the workspace 'Data' panel there is a 'Tables' tab. Click the blue plus sign icon on the right edge of the 'Tables' tab. A popup window should appear titled 'Import Table Data'. Select your completed tab-separated sample file for upload and then click the 'Upload' button.



The 'Import Table Data' window for uploading the Terra sample file

If the upload is successful then the sample file should be located under the 'Tables' tab as 'sample (#)' where # is the number of samples in your file.



The workspace 'Data' panel after successfully uploading the fastq sequence files and Terra sample file

Here is a video showing the process.

-
- 3.2** You will likely have many samples to upload and you can do this by going directly to your Google bucket.

First, go to “DASHBOARD” tab in your workspace and click “Google Bucket” at the

bottom right corner of the same page.

The screenshot shows the Terra Workspaces interface. At the top, there's a green header bar with the Terra logo and the word "WORKSPACES". Below the header, the navigation menu includes "DASHBOARD", "DATA", "NOTEBOOKS", "WORKFLOWS", and "JOB HISTORY". The main content area is titled "ABOUT THE WORKSPACE" with a note "No description added". On the right side, there's a "WORKSPACE INFORMATION" panel showing details like "Last updated 5/13/2021", "Subscribers 0", "Access level: Proj. Owner", "Cost \$0.00", and "Google Project ID: toast-team-test". Below that is an "OWNERS" section with the email "jpi@geotc.gov". Under "TAGS", there's a dropdown menu with the option "Add a tag" and a note "No tags yet". A red box highlights a "Google Bucket" entry: "Name: fc-8006b736-ce2a-4e78-8450-526cbe98230a" and "Location: us multi-region: US". There's also a link "Open in browser" with a small icon.

The Dashboard tab of your workspace.

This will direct you to your “Google Cloud Platform” page for data uploading. Click “UPLOAD FILES” in the middle of this page to upload single or multiple fastq files. You can click “UPLOAD FOLDER” to upload a folder with multiple fastq files stored inside. Or you can just drag and drop files onto the page. This will cost some google cloud credits (e.g. 4.4 Gb for \$0.75).

The screenshot shows the Google Cloud Storage interface. The left sidebar has "Cloud Storage" selected, along with "Browser", "Monitoring", and "Settings". The main area shows a bucket named "fc-8006b736-ce2a-4e78-8450-526cbe98230a". It lists objects: "F_2.fastq.gz" (34.1 MB, application/gzip) and "F_1.fastq.gz". Below these are tabs for "OBJECTS", "CONFIGURATION", "PERMISSIONS", "RETENTION", and "LIFECYCLE". A toolbar at the top has icons for "Copy", "Paste", "Delete", etc. A large central window shows a file tree with a folder "For_Upload" containing several fastq files. A status bar at the bottom says "Uploading 2 items".

Google bucket page drag and drop for uploading files and folders.

Go back to your Terra account and click “DATA” tab. The successfully uploaded fastq files will show up. If the upload is successful then the sample file should be located under the 'Tables' tab as 'sample (#)' where # is the number of samples in your file.

The screenshot shows the 'DATA' tab of a Terra workspace named 'Terra_ONT_Test'. In the left sidebar, under 'FILES', there are two files listed: 'E_1.fasta.gz' and 'E_2.fasta.gz'. A tooltip 'Recently uploaded data.' is displayed below the file list.

Recently uploaded data.

3.3 To upload via the Terra Data Uploader

Navigate to '<https://app.terra.bio/#upload>'

The landing page of the Terra Data Uploader. It displays a list of workspaces:

- terratitan1 > Terra_ONT_Test**
Last Modified: May 10, 2021
Created By: yrw4ambrosio1@gmail.com
- terratitan1 > titan-ill-pe-frank1**
Last Modified: May 5, 2021
Created By: yrw4ambrosio1@gmail.com

Landing page of the Terra Data Uploader

Select the Terra Workspace to which you would like to upload your fastq files. This will be the same workspace created in the previous step.

The workspace selection screen of the Terra Data Uploader. It shows the selected workspace:

WORKSPACE terratitan1 Terra_ONT_Test **Change**

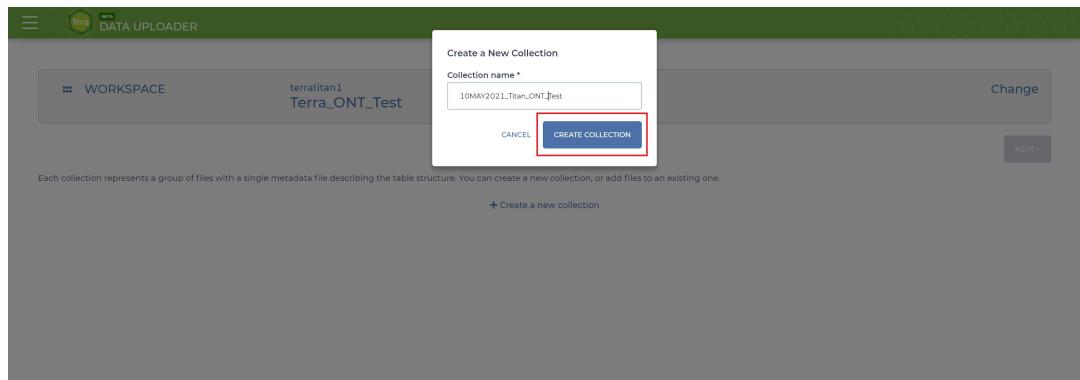
SELECT A COLLECTION +

Each collection represents a group of files with a single metadata file describing the table structure. You can create a new collection, or add files to an existing one.

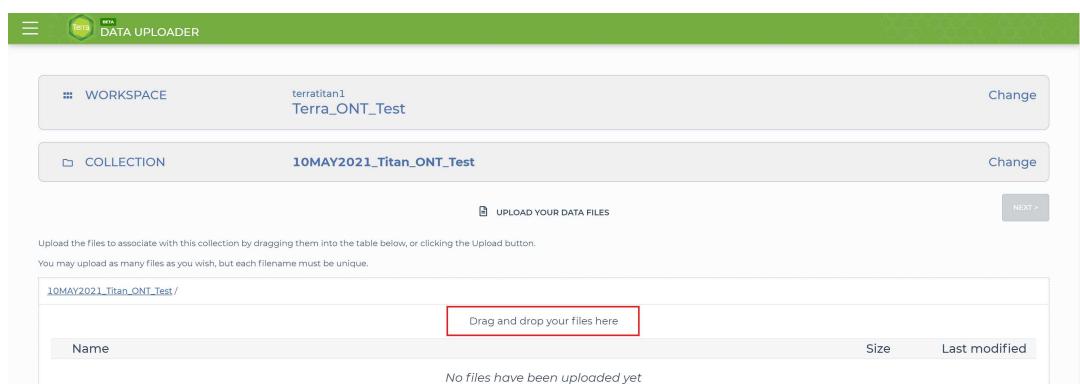
+ Create a new collection

Click the '+ Create a new collection' link and enter a name for your new collection of fastq files. **DO NOT INCLUDE SPACES IN THE COLLECTION NAME, use underscores instead. Spaces will cause an error later in the pipeline.**

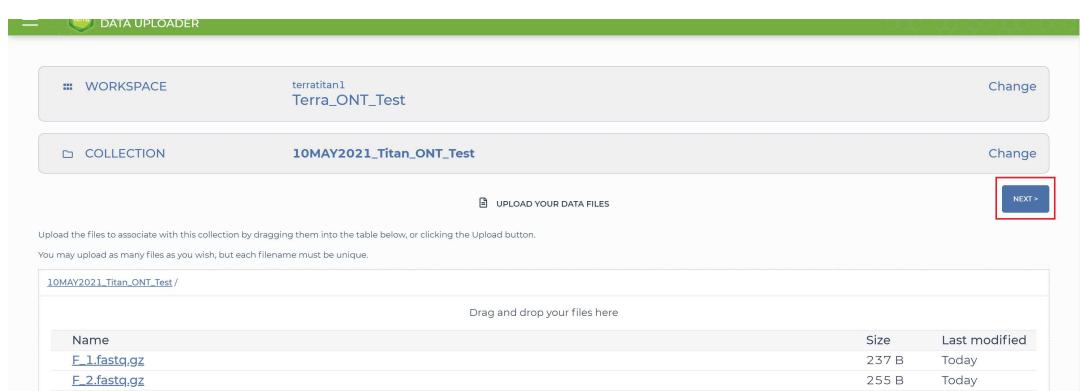
Go to step 10 to see an example error caused by spaces present in the collection name. The process will also show you how to investigate a job failure.



Click the 'Create Collection' button and you will be routed to the data uploader page where you can drag and drop fastq files directly into your browser window to initiate upload.



Drag and drop the fastq files that you would like to upload into the upload space.



Once your files have been successfully uploaded, select "NEXT>" to proceed to the metadata upload page

The screenshot shows the Terra Data Uploader interface. At the top, there's a green header bar with the Terra logo and the text "DATA UPLOADER". Below the header, there are three tabs: "WORKSPACE" (selected), "COLLECTION", and "DATA FILES". Under "WORKSPACE", it says "theagen-validations Terra_ONT_Test". Under "COLLECTION", it says "10MAY2021_Titan_ONT_TEST". Under "DATA FILES", it says "Includes 2 files". Below these tabs is a section titled "UPLOAD YOUR METADATA FILES" with instructions: "Upload a tab-separated file describing your table structures." It lists two bullet points: "Any columns which reference files should include just the filenames, which will be matched up to the data files in this collection." and "The first column must contain the unique identifiers for each row. The name of the first column must start with entity:, followed by the table name, followed by _id." There's also a note: "For example, if the first column is named entity:sample_id, a table named "sample" will be created with "sample_id" as its first column. There are no restrictions on other columns." A large text input area is labeled "Drag and drop your metadata .tsv file here" with a plus sign icon.

To upload a metadata table and create a Terra sample table in your workspace, open Excel and populate your spreadsheet with the [root entity](#) designation in A1, and "reads" in B1 as headers; underneath these headers, proceed to populate each row with the sample names in column A and the corresponding filename that was uploaded in column B.

NOTE: In this example, our root entity type is "Test_ClearLabs_sample_id" so, in cell A1, we have written "entity:Test_ClearLabs_sample_id". A "root entity" is the smallest piece of data a workflow can use as input. **The root entity is always defined with "entity:" and must always end in "sample_id"**

Important note on column names: DO NOT USE SPACES! As we did before in creating our workspace and collection names use "_" instead of spaces! The first column MUST have the start with "entity:" and end with "sample_id", you can call the other columns whatever you like, but we recommend you use something that denotes that the column contains a reads file for clarity.

The screenshot shows an Excel spreadsheet with the following data:

A	B
1 entity:Test_ClearLabs_sample_id	Forward_Read
2 SRR1111111	gs://fc-f2b60745-8b71-4ff2-bcd0-6ec55a477f64/SRR1111111.fastq
3 SRR2222222	gs://fc-f2b60745-8b71-4ff2-bcd0-6ec55a477f64/SRR2222222.fastq
4	
5	

An example minimal metadata file

You can have as many columns as you want in addition to the "entity:sample_id" and "reads" columns. Some examples you might want to include are:

- Ct value
- Sequencing run or plate ID
- Sampling or extraction dates

If you plan to use the Augur protocol or visualize your data with UShER or Auspice, consider including that metadata in the file you upload now.

Required columns for Augur are described here:

<https://docs.nextstrain.org/projects/augur/en/stable/faq/metadata.html?highlight=metadata>

and include:

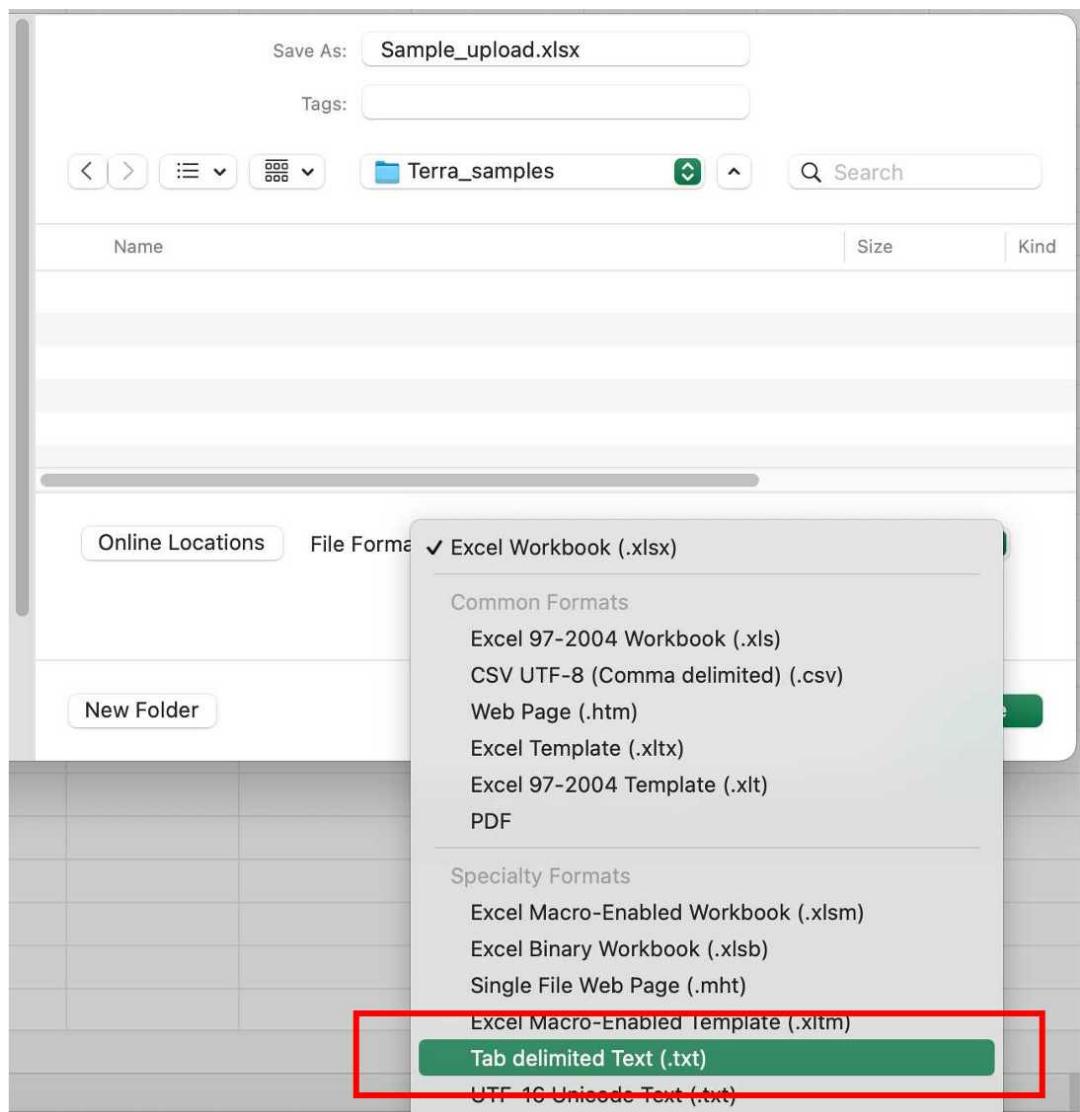
- Collection_date
- iso_country
- iso_state
- iso_continent
- iso_county

Date columns, sequencing date for example, must use the format YYYY-MM-DD.

Whatever additional columns of metadata you populate to this Terra data table will, after a Titan run, get populated to that same table as the final Titan output. You can then use this data to correlate assembly quality with CT values to determine cutoff thresholds for which samples to actually sequence in the future or identify issues that are sequence run specific.

If you plan to also use the Mercury workflow to prepare sequence and metadata for submission to public repositories (GISAID, GenBank and SRA) then populating this sheet now will make running the Mercury workflow easier.

Save this sheet as a tab delimited file text file

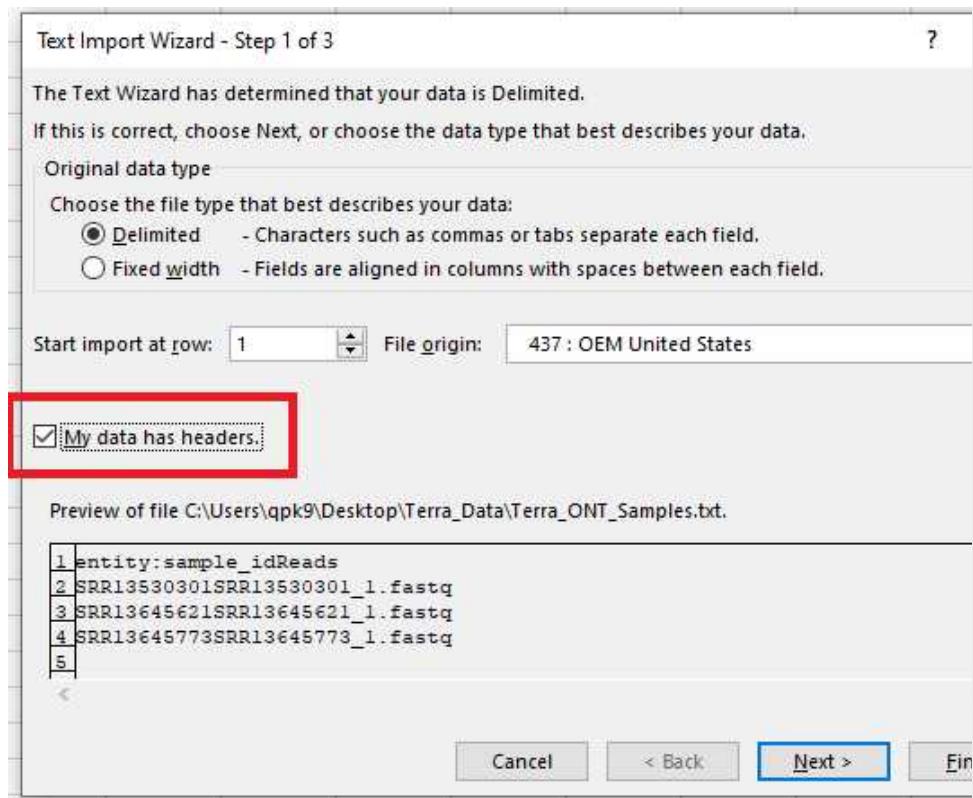


An example, metadata table is found below.

This example file has the minimum amount of columns to be able to create a collection. Delete the sample names and populate the document with your own.

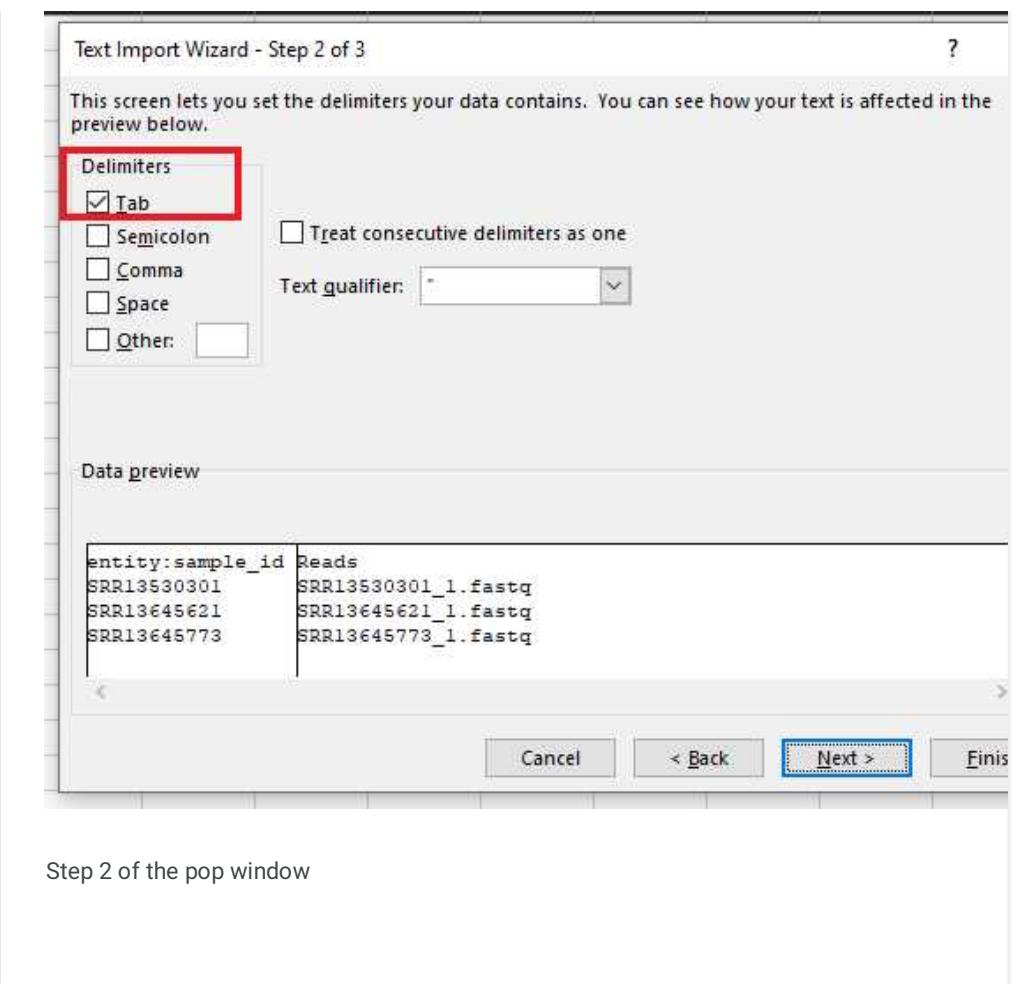
[Terra_ONT_Samples.txt](#)

When opening this file in Excel, check the box for "my data has headers" in step 1 of the text import wizard and then click "next".



Step 1 in the pop up window

In step 2, select "Tab" as the delimiter. Click "next" and then click "finish."
Now you can edit!



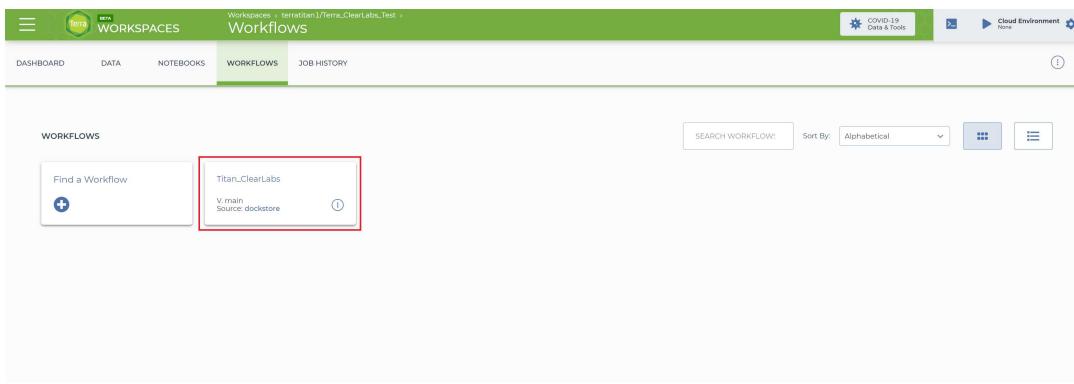
Step 2 of the pop window

Drag and drop your metadata table to the Terra #Upload page and select CREATE TABLE to complete the process

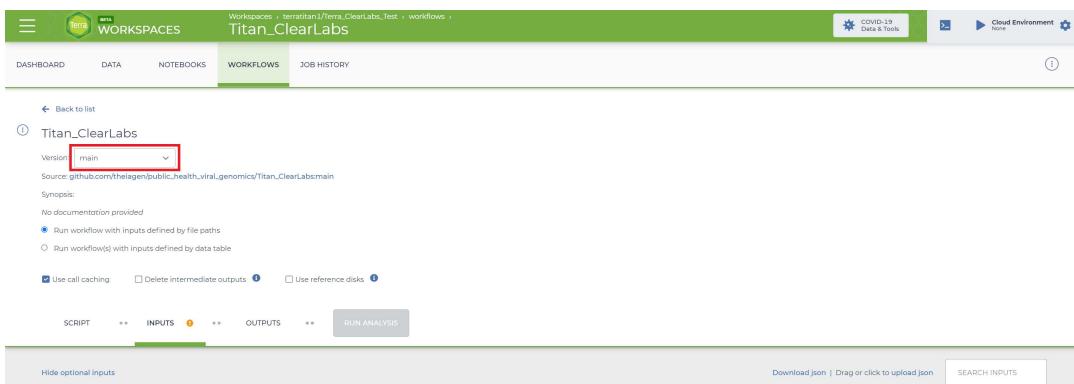


Running the Titan_ClearLabs Workflow

- To run the Titan_ClearLabs workflow, click on the 'Workflows' panel in the newly created workspace. It should bring you to your workflow page. Click on the 'Titan_ClearLabs' tile to bring up the Titan_ClearLabs assembly workflow page.

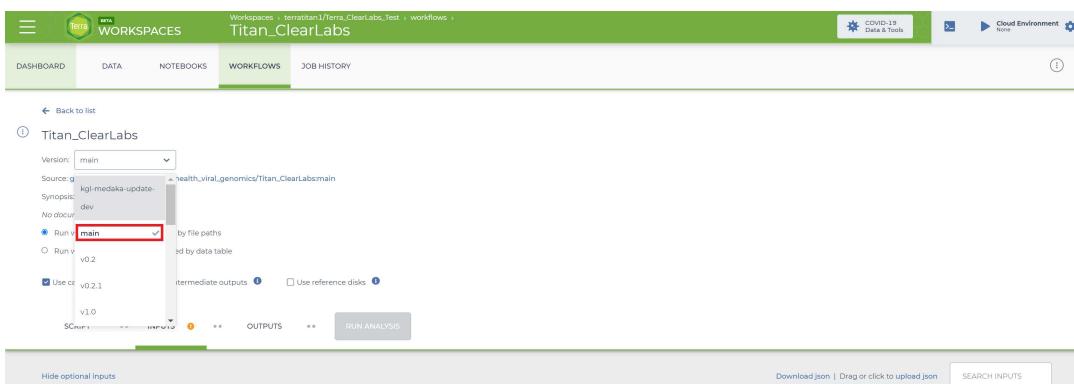


This will bring up the Titan_ClearLabs workflow page:



The Titan ClearLabs assembly workflow page

Select the version of the workflow you would like to run. **Double check that you are using the latest version of the workflow.** Alternately, you may specify another version, **but should only pick a stable version (with numbers) NOT a 'main' or 'dev' version.**



Ensure that "Run workflow(s) with inputs defined by data table" is selected and the "Use call caching" is checked and then select the root entity type for the data you wish to analyze

NOTE: Call caching allows Terra to identify and skip jobs that have been run previously; this option is by default enabled to avoid unnecessary compute costs. More information on Terra call caching, including examples of when you may want to disable this feature, is available through

the [Terra Support Documentation](#).

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Titan_ONT

Version: v1.4.2

Source: github.com/theiagen/public_health_viral_genomics/Titan_ONT:v1.4.2

Synopsis:

No documentation provided

Run workflow with inputs defined by file paths
 Run workflow(s) with inputs defined by data table

Step 1

Select root entity type: Test_ONT_sample

Use call caching Delete intermediate outputs Use reference disks

Step 2

SELECT DATA No data selected



Click "SELECT DATA" and choose the samples you wish to analyze

[← Back to list](#)

Titan_ONT

Version: v1.4.2

Source: github.com/theiagen/public_health_viral_genomics/Titan_ONT:v1.4.2

Synopsis:

No documentation provided

Run workflow with inputs defined by file paths
 Run workflow(s) with inputs defined by data table

Step 1

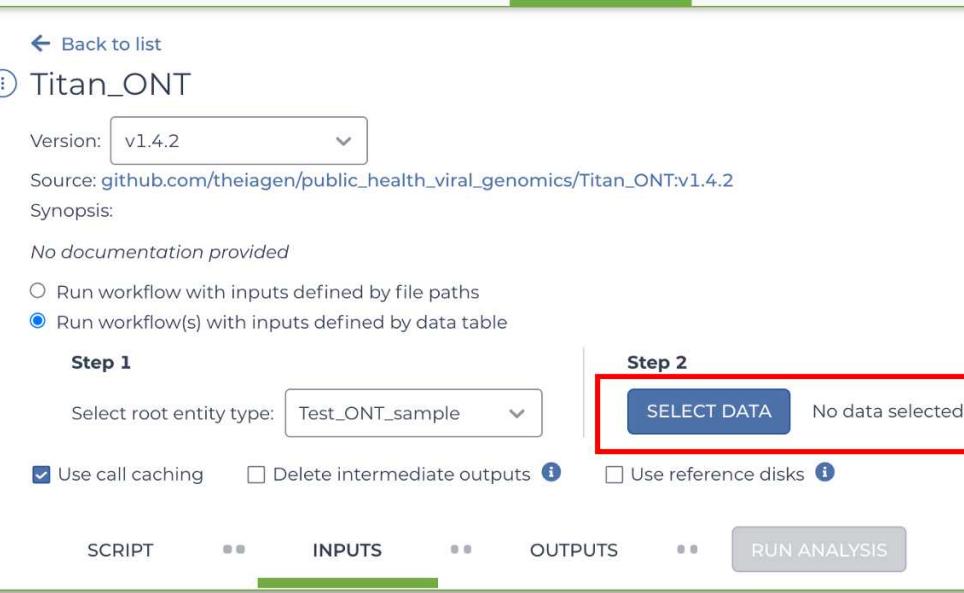
Select root entity type: Test_ONT_sample

Use call caching Delete intermediate outputs Use reference disks

Step 2

SELECT DATA No data selected

SCRIPT ... INPUTS ... OUTPUTS ... RUN ANALYSIS



Complete the INPUTS form with the appropriate attributes

The top two rows represent variables that have to be provided by the user. This was the information that we populated the sample data table with in the previous step.

In our example, for the first row, the 'demultiplex_reads' variable, we clicked on the 'Attribute' text box and wrote 'this.reads' to indicate that the 'demultiplex_reads' we wish to analyze are under the 'reads' column of our selected datatable. In the second row, the 'samplename' variable, we selected on the 'Attribute' text box and wrote 'this.Test_ONT_sample_id' to indicate the 'samplename' of each sample we are analyzing can be found in the 'Test_ONT_sample_id' column of our selected datatable.

NOTE: If you named your columns something other than reads then just type "this." followed by whatever the column name is. We would advise naming your reads column "reads" for clarity.

Task name	Variable	Type	Attribute
titan_ont	demultiplexed_reads	File	this.reads
titan_ont	samplename	String	thisTest_ONT_sample_id
bedtools_cov	fail_threshold	String	Optional

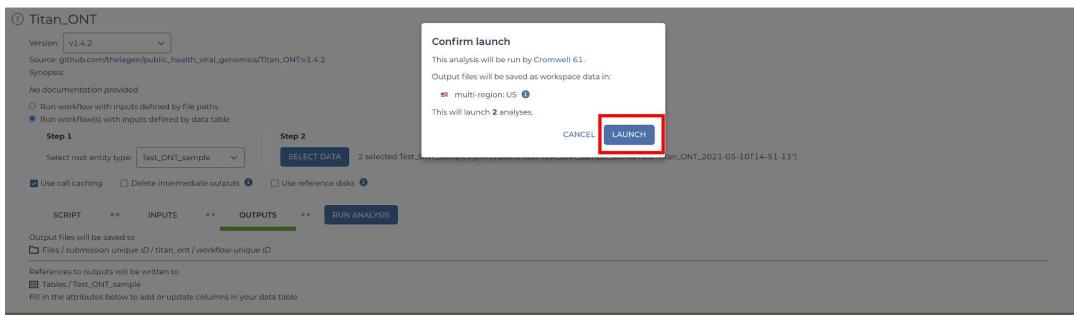
Once your input form is complete, move on to the OUTPUTS form and select "Use Defaults". Terra will then populate the OUTPUTS form with all of the default outputs options generated by the workflow. If you forget to do this you won't have easily accessible results! **Save these changes by clicking the 'Save' button.**

Task name	Variable	Type	Attribute
titan_ont	aligned_bai	File	Use defaults
titan_ont	aligned_bam	File	Use defaults
titan_ont	amp_coverage	File	Use defaults
titan_ont	artic_version	String	Use defaults
titan_ont	assembly.fasta	File	Use defaults

Once your INPUTS and OUTPUTS forms are complete, click the 'Save' button on the top right-hand side of the page. The yellow caution icons should disappear and the Run Analysis option should be made available.

The screenshot shows the 'Step 1' and 'Step 2' sections of the workflow setup. Step 1 includes fields for 'Version' (v1.4.2), 'Source' (github.com/ttheigen/public_health_viral_genomics/Titan_ONT:v1.4.2), and 'Run workflow with inputs defined by file paths' (radio button selected). Step 2 shows 'SELECT DATA' with '2 selected Test_ONT_samples' and a note about creating a new sample set. Below these are checkboxes for 'Use call caching', 'Delete intermediate outputs', 'Use reference disks', and 'Use local disk'. The 'RUN ANALYSIS' button is prominently highlighted with a red box at the bottom of the page.

You are now ready to run the Titan_ClearLabs workflow! Click on the 'Run Analysis' button to the right of the 'Outputs' tab. A popup window should appear titled 'Confirm launch'. If the 'Run Analysis' button is greyed out, you need to save your recent changes by clicking the 'Save' button.



Clicking the 'Launch' button should bring you to the 'Job History' panel where each sample will be queued for the Titan_ClearLabs analysis. The status will change from queued to submitted to running.

Data Entity	Last Changed	Status	Run Cost	Messages	Workflow ID	Links
F_1 (Test_ONT_sample)	May 10, 2021, 8:05 AM	Queued	N/A		f71ea18d-4092-47bc-85cc-fb9bcf5abecb	View Edit Delete
F_2 (Test_ONT_sample)	May 10, 2021, 8:05 AM	Queued	N/A		2aaa6f48-c719-4258-a3b4-2c759777006c	View Edit Delete

Job history screen after launching Terra job

View and Download the Titan Output Report

5

First, **verify all of the samples have completed** the analysis run by looking at the 'Workflow Status' section in the top left of the 'Job History' panel. The job has completed when all the samples have a status of 'succeeded' with a green checkmark.

Data Entity	Last Changed	Status	Run Cost	Messages	Workflow ID	Links
F_1 (Test_ONT_sample)	May 10, 2021, 11:38 AM	Succeeded	N/A		f71ea18d-4092-47bc-85cc-fb9bcf5abecb	View Edit Delete
F_2 (Test_ONT_sample)	May 10, 2021, 11:54 AM	Succeeded	N/A		2aaa6f48-c719-4258-a3b4-2c759777006c	View Edit Delete

The 'Job History' panel when the job has completed

Then go to the 'Data' panel and under the 'Tables' tab click on the sample table that you created and uploaded in step 4. It will be named 'sample (#)' where # is the number of samples in your file.

The screenshot shows the Terra workspace interface. The top navigation bar includes 'WORKSPACES' (Beta), 'Data (read-only)', 'COVID-19 Data & Tools', and 'Cloud Environment'. The main area displays a 'TABLES' section with two entries: 'Test_ONT_sample' (2 rows) and 'Test_ONT_sample_set' (1 row). Below this is a table titled 'Test_ONT_sample' with columns: aligned_bai, aligned_bam, amp_coverage, artic_version, assembly_fasta, assembly_length_unambiguous, and assembly_mean_coverage. The last column has a gear icon. The table contains four rows: F_1 and F_2 with their respective file paths and consensus sequence links.

Test_ONT_sample						
	aligned_bai	aligned_bam	amp_coverage	artic_version	assembly_fasta	assembly_mean_coverage
F_1	E_1.primertrimmed.rg.sorted.bam.bai	E_1.primertrimmed.rg.sorted.bam	amplicon_coverage.txt	Medaka via artic 1.1.3	E_1.medaka.consensus.fas	
F_2	E_2.primertrimmed.rg.sorted.bam.bai	E_2.primertrimmed.rg.sorted.bam	amplicon_coverage.txt	Medaka via artic 1.1.3	E_2.medaka.consensus.fas	

The Terra sample table with the added output attributes from the Titan ONT run

Now the Terra sample table will have the additional attributes that were added by the workflow when you specified the output names (set to default in this example). You can reduce the number of fields you want to visualize by clicking the "gear" icon in top row on the right. Select only the fields you want to see then click "Done".

This screenshot shows the 'Select columns' dialog box overlaid on the Terra workspace. The dialog lists various metrics: aligned_bai, aligned_bam, amp_coverage, artic_version, assembly_fasta, assembly_length_unambiguous, assembly_mean_coverage, assembly_length, assembly_mean, assembly_method, auspice_json, bedtools_version, consensus_flagstat, consensus_stats, and fastQC_raw. The 'assembly_mean_coverage' checkbox is checked. The 'DONE' button at the bottom right is highlighted with a red circle.

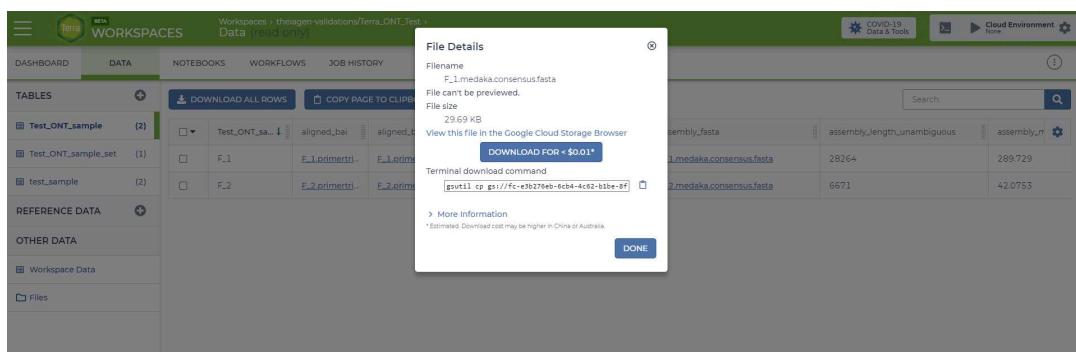
Click gear for pop up menu of outputs.

An explanation for what each output column is can be found in the [Theiagen documentation](#) under "outputs".

This screenshot shows the 'Select columns' dialog box overlaid on the Terra workspace. The dialog lists various metrics: aligned_bai, aligned_bam, amp_coverage, artic_version, assembly_fasta, assembly_length_unambiguous, assembly_mean_coverage, assembly_length, assembly_mean, assembly_method, auspice_json, bedtools_version, consensus_flagstat, consensus_stats, and fastQC_raw. The 'aligned_bai', 'aligned_bam', 'amp_coverage', 'artic_version', 'assembly_fasta', 'assembly_length_unambiguous', and 'assembly_mean_coverage' checkboxes are checked. The 'DONE' button at the bottom right is highlighted with a red circle.

Selecting only metrics we want to see.

To download the consensus sequence for a particular sample, click on the link in the 'assembly_fasta' attribute column and a popup window titled 'File Details' should appear. Click the 'Download For < \$0.01' button, which will download the consensus sequence to your local directory. This can be uploaded to NextClade to visualize if desired (see step 9).



The 'File Details' popup window for downloading consensus sequence.

The NextClade and Pangolin lineage assignments determined by the pipeline can be viewed in the Terra sample report by scrolling to the right (or just only selecting those columns using the "gear" icon). You can download or copy this report by using either the 'Download All Rows' or 'Copy Page To Clipboard' buttons at the top of the table.

Data (read only)						
TABLES	Test_ONT_sample	(2)	aligned_bai	aligned_fa	assembly.fasta	assembly_length,unambiguous
	F_1	F_1.primertr...	F_1.fasta		F_1.medaka.consensus.fasta	28264
	F_2	F_2.primertr...	F_2.fasta		F_2.medaka.consensus.fasta	6671
						42,0753

Nextclade assignments for the samples in 'nextclade_clade' column (column 2).

Data (read only)						
TABLES	Test_ONT_sample	(2)	nextclade_aa_subs	nextclade_clade	nextclade_json	nextclade_tsv
	ORFla11375f ORF1b v2223L ORF...	19B		E_1.medaka.consensus.nextclade.json	E_1.medaka.consensus.nextclade.tsv	0.14.2
	ORFla52242F ORFBL84S	19A		E_2.medaka.consensus.nextclade.json	E_2.medaka.consensus.nextclade.tsv	0.14.2
						0

Pangolin lineage assignments for the samples in 'Pangolin_lineage' column (column 1).

Note, here we have one sample that was not assigned a pangolin lineage. We will need to look at more our metrics to understand why.

Additional documentation for the Titan SARS-CoV-2 workflows and the Terra platform are available.

Titan workflows: [Theiagen Genomics Documentation](#)

Terra Platform: [Documentation – Terra Support](#)

Reviewing Quality Metrics

- 6 Ideally, at the end of this process, we would have a complete consensus assembly sequence, which represents the entirety of the RNA sequence that was present in the virion in the sample. However, often a full length sequence is not generated at the end of the protocol, but rather fragments of the genome. We can look at metrics to determine how fragmented our genome is relative to the reference sequence. There are 3 metrics in our report to help us assess this.

Assembly length unambiguous - the final count of ATCGs (i.e. unambiguous bases) within the consensus assembly.

- A higher number here will indicate a more complete consensus sequence.

The screenshot shows a Terra workspace interface. The top navigation bar includes 'WORKSPACES' (Beta), 'Data (read only)', 'COVID-19 Data & Tools', and 'Cloud Environment'. Below the navigation is a search bar and a table titled 'Test_ONT_sample' (2 rows). The table has columns: assembly_fasta, assembly_length_unambiguous, assembly_mean_coverage, assembly_method, auspice_json, and bedtools_ver. The second row, 'F_2.medaka.co...', has its 'assembly_length_unambiguous' value (6671) highlighted with a red box.

assembly_fasta	assembly_length_unambiguous	assembly_mean_coverage	assembly_method	auspice_json	bedtools_ver
F_1.medaka.co...	28264	289.729	Medaka via artic 1.1.3	F_1.medaka.consensus.nextclade.a...	bedtools v2.26.0
F_2.medaka.co...	6671	42.0753	Medaka via artic 1.1.3	F_2.medaka.consensus.nextclade.a...	bedtools v2.26.0

Assembly length unambiguous metric in the output

Here we see that the second sample has only 6,671bp that were unambiguous (A,T,C, or G), which means much of the genome was not able to be recovered through sequencing.

Number of Ns - the converse of assembly length unambiguous - It is the final count of the number of Ns (i.e. ambiguous) bases. These are *completely ambiguous bases* due to either too little signal or too much noise for the basecaller to confidently determine what base was at this position.

- If there was an "S" (basecaller couldn't tell if it was an C or G) or "W" (basecaller couldn't tell if it was an A or T) these counts are considered "semi-ambiguous" and are not included in either the number of N or assembly length unambiguous metrics.
- A higher number of Ns will mean you have a more fragmented assembly. Less Ns is a strong consensus assembly.

Percent reference coverage - Portion of the genome covered by consensus assembly. This uses the assembly length unambiguous metric to gauge how much of the reference sequence (Wu Han-1) is covered by the consensus assembly.

- Takes the #ATCG/length of SC2 reference genome (29903bp)*100

Ideally this should equal 100%, indicating that the assembly covered 100% of the reference genome length, unambiguously.

	number_N	percent_reference_coverage
F_1	1639	94.52
F_2	23232	22.31

Metrics on the number of Ns and percent reference coverage.

From these metrics we can see that there is a large number of bases that are Ns (23,232bp), which translates to only 22.31% of the reference genome covered by the sequencing in the second sample. Taken together these metrics indicate that much of the genome sequence is unknown in the second sample, which explains why we were unable to get a pangolin lineage assignment for this sample. The troubleshooting metrics can help determine what caused this.

Metrics for Troubleshooting

7 Pool 1 and 2 Representation (not available in all workflow versions)

We can look at how much read data was generated from each primer pool by looking at the pool 1 and pool 2 percentages. This will help identify if a PCR reaction failed. You want the ratio to be roughly 40:60 in either direction. If there is a 10:90 or 20:80 ratio this is a strong indication that one of the PCR reactions failed and resequencing should be considered to generate a confident consensus sequence for that sample.

pangolin_ver	percent_reference_coverage	pool1_percent	pool2_percent	reads	samtools_version
pangolin ...	94.52	53.13	46.87	E_1.fasta.gz	samtools 1.10
pangolin ...	22.31	79.41	20.59	E_2.fasta.gz	samtools 1.10

The percent of the reads in a sample that came from each pool.

The fact that in the second sample 80% of reads came from pool 1 is an indication that there was a failure to amplify pool 2 in the second sample, which led to much of the genome not being sequenced in that sample. In contrast, in the first sample there is roughly an even split of the number of reads coming from each primer pool, which is ideal.

FastQC Raw Output

These data are the number of raw reads in an input file and indicates how much sequencing occurred.

	consensus_flagstat	consensus_stats	fastqc_raw	kraken_human	kraken_report	kraken_sc2
E_1	E_1.flagstat.txt	E_1.stats.txt	242956	0.11	E_1_kraken2_report.txt	99.76
E_2	E_2.flagstat.txt	E_2.stats.txt	78804	25.37	E_2_kraken2_report.txt	54.19

Number or raw reads that resulted from the sequencing run.

These data show that the second sample had significantly fewer reads from the sequencing run. This was another reason the genome that was assembled from the second sample was so fragmented.

Percent of Reads Identified to be Human and SARS-CoV-2

These data indicate how much human read contamination is in the sequencing reads. Ideally, the number of reads containing human data should be as low as possible and the percent of reads assigned SARS-CoV-2 should be high. If the sequencing run contains greater than ~15% human reads, the concentration of SARS-CoV-2 in your original sample may be too low to generate sufficient coverage depth for a good quality assembly, or there is an issue in the wet lab protocol that is leading to the low generation of SARS-CoV-2 reads.

	kraken_human	kraken_report	kraken_sc2	kraken_version	meanbasedq_trim
E_1	0.11	E_1_kraken2_report.txt	99.76	Kraken version 2.0.8-beta	24.9
E_2	25.37	E_2_kraken2_report.txt	54.19	Kraken version 2.0.8-beta	25

Output from the program "Kraken" that identifies the number of human and SARS-CoV-2 reads in a sample.

The first sample is fairly free of contamination, with 99.76% of the sequenced reads belonging to SARS-CoV-2. However, in the second sample there is a high amount of contamination, with 25.37% of reads belonging to human and only 54.19% of reads determined to be of SARS-CoV-2 origin. Thus, there is roughly ~21% of reads that are some other source of contamination that is not human. If a lab is having consistent problem with contamination that is not identified to be of human origin with this workflow, a larger Kraken database can be used to determine the offending organism. Contact TOAST@cdc.gov if you would like assistance with this or read [Kraken2's documentation](#) for how to do this on your own. Users should refer to their lab's cut offs for quality metrics to determine if a sample requires resequencing.

Bam File

This file is generated during alignment and contains all information regarding the alignment to the WuHan-1 reference. This file is found in the 'aligned_bam' column, and we can download this file just like we did with the consensus sequence in step 5. These files can be visualized this with

[Geneious](#), [CLC workbench](#) or [IGV](#).

Submit Consensus Sequences to Public Repositories

- 8 If you plan on submitting the SARS-CoV-2 consensus sequence to either the GenBank or GISAID public repositories, please refer to the following documentation for submission criteria and minimum quality control thresholds.

GenBank Submission Criteria: [About GenBank Submission \(nih.gov\)](#)

GISAID Submission Criteria: [!\[\]\(57c18b879714b128ac3cf0d79c251988_img.jpg\) Gisaid inclusion criteria.pdf](#)

The Mercury workflows are designed to **prepare** genome assemblies and sample metadata on the Terra platform for subsequent GISAID and NCBI submission.

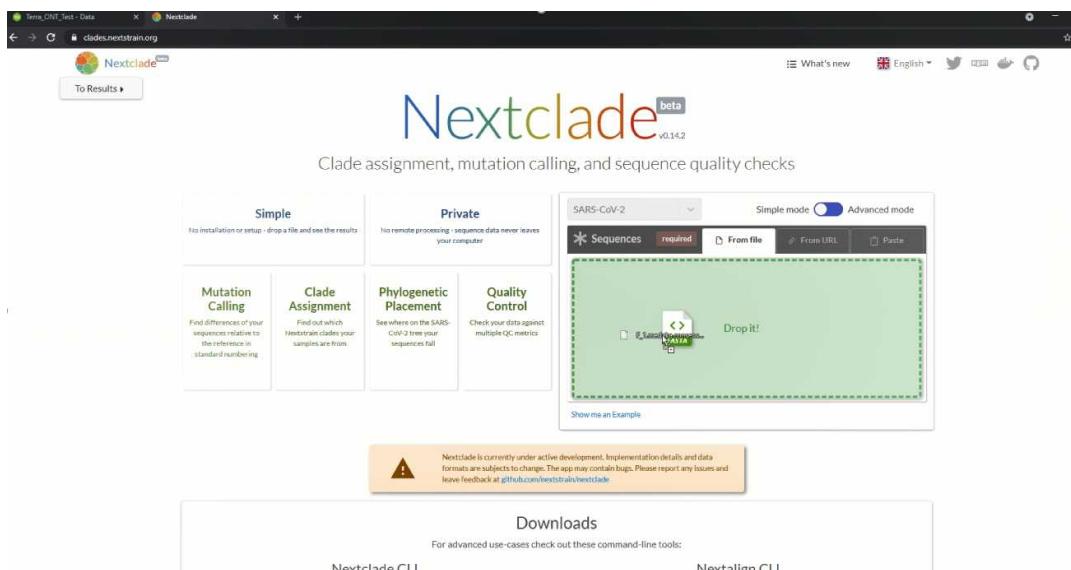
Mercury Overview: <https://www.youtube.com/watch?v=h8YASVckOrw>

After preparing consensus sequences of SARS-CoV-2 and sample metadata for submission, use the following protocols submit them to the public repositories. Completing submissions in this order allows all the sequence information to be linked together.

1. [GISAID submission protocol](#)
2. [NCBI submission to SRA, BioSample, and BioProject protocol](#)
3. [Genbank submission protocol](#)

NextClade Visualization

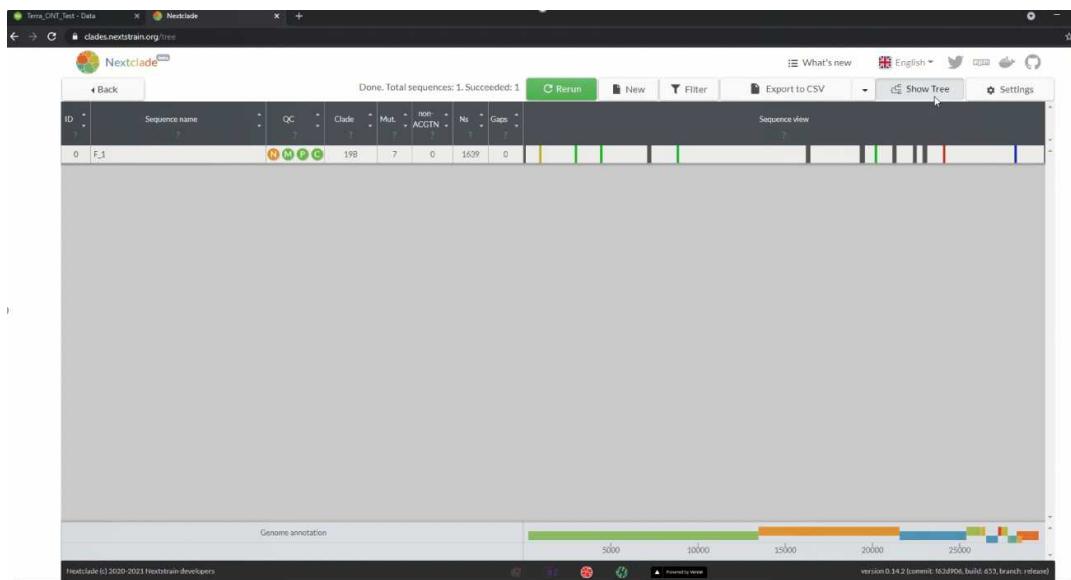
- 9 After downloading consensus sequence for a particular sample following directions in Step 5, go to the [NextClade website](#) and drag-and-drop the downloaded fasta file. The screen will automatically take you to the analysis page.



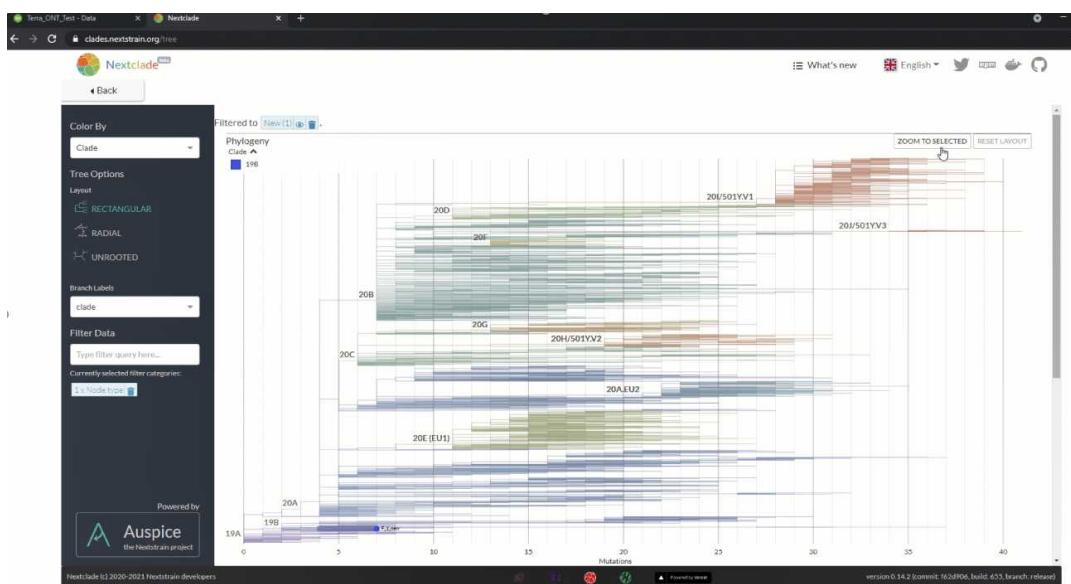
Drag and drop file for analysis

Hover over the different columns to get more information. Click on the "Show Tree" button at the

top right of the page to see where the sequence sits on the tree of other consensus sequences from SARS-CoV-2.



Clicking on 'Show Tree" button



The sequence is highlighted on the tree of SARS-CoV-2 consensus sequences.

Video of the full process:

How to debug a failed run

- 10 In this example of a failed run, we will look at what an error caused by adding spaces into your collection name looks like. If there is a failure for some other reason, you can follow similar steps to understand why your job failed. Here we will be using Illumina paired-end data, but the process of debugging an error is the same.

If a run fails, you will see this indicated on the job history screen in the "status" column.

The screenshot shows the 'Job History' tab in the 'WORKSPACES' interface. A specific workflow run is selected, showing the following details:

- Workflow Statuses:** Failed: 1
- Workflow Configuration:** toast-team-test/Illumina_PE
- Submitted by:** qpk9@cdc.gov, May 13, 2021, 5:40 PM
- Data Entity:** 3015780998_ZZYGIWY sample
- Submission ID:** 97f5da29-71d1-45e8-9938-82ba0a36b788
- Total Run Cost:** N/A
- Delete Intermediate Outputs:** Disabled
- Use Reference Disks:** Disabled
- Call Caching:** Disabled

Below this, a table lists the data entity information:

Data Entity	Last Changed	Status	Run Cost	Messages	Workflow ID	Links
3015780998_ZZYGIWY (sample)	May 13, 2021, 5:46 PM	Failed	N/A		e1687504-3421-4a20-9de1-11e35422d3e3	

A mouse cursor is hovering over the 'Workflow Dashboard [alpha]' link in the 'Links' column.

Job Failure

To understand why it failed, click on the "workflow dashboard" icon in the "links" column. This will take you to a new screen and you can click the arrows next to the "message" to see what it says. Here we see there are two errors that direct us to a log file to check. To find out more click on the "execution directory" icon under the links header. This will take you to the google bucket with all the output from the run.

The 'Workflow Dashboard' screen displays the following information:

- Workflow Status:** Failed
- Workflow Timing:** Start: May 13, 2021, 5:41 PM; End: May 13, 2021, 5:45 PM
- Links:**
 - Job Manager
 - Execution Directory** (highlighted)
 - View execution log

Under 'Workflow-Level Failures', there are two entries:

- 0: {
 - message: "Workflow failed"
 - causedBy: [
 - 0: {
 message: "Workflow failed"
 causedBy: [
 0: {
 message: "Task read_QC_trim:trimomatic:N/A failed. Job exit code 1. Check gs://fc-650005cc-5856-433b-95e6-27c1fcfb07e/97f5da29-71d1-45e8-9938-82ba0a36b788/litlan_illumina_pe/e1687504-3421-4a20-9de1-11e35422d3e3/call-read_QC_trim/read_QC_trim@136a-e810-447c-3223-7cc0d2373278/call-trimomatic@stderr for more information. PAPI error code 9. Please check the log file for more details: gs://fc-650005cc-5856-433b-95e6-27c1fcfb07e/97f5da29-71d1-45e8-9938-82ba0a36b788/litlan_illumina_pe/e1687504-3421-4a20-9de1-11e35422d3e3/call-read_QC_trim/read_QC_trim@136a-e810-447c-3223-7cc0d2373278/call-trimomatic@stderr for more information. PAPI error code 9. Please check the log file for more details: gs://fc-650005cc-5856-433b-95e6-27c1fcfb07e/97f5da29-71d1-45e8-9938-82ba0a36b788/litlan_illumina_pe/e1687504-3421-4a20-9de1-11e35422d3e3/call-read_QC_trim/read_QC_trim@136a-e810-447c-3223-7cc0d2373278/call-trimomatic@stderr for more information. PAPI error code 9. Please check the log file for more details: gs://fc-650005cc-5856-433b-95e6-27c1fcfb07e/97f5da29-71d1-45e8-9938-82ba0a36b788/litlan_illumina_pe/e1687504-3421-4a20-9de1-11e35422d3e3/call-fastqc@raw.log"
- 1: {
 - message: "Task read_QC_trim:fastqc:raw:N/A failed. Job exited without an error, exit code 0. PAPI error code 9. Please check the log file for more details: gs://fc-650005cc-5856-433b-95e6-27c1fcfb07e/97f5da29-71d1-45e8-9938-82ba0a36b788/litlan_illumina_pe/e1687504-3421-4a20-9de1-11e35422d3e3/call-fastqc@raw.log"

Job failure messages

Follow the file path in the google bucket to the log files that were referenced in the error messages (in red/orange text in the above photo).

Click on log file referenced in the error message.

Click on the "Authenticated URL" link that will take you to a text file.

Authenticated URL link

In the text file, we can see that there was an error that cause by there being a space between "Bad" and "Sample" in our file path that was created when we made "Bad Sample" rather than "Bad_Sample" as our collection name.

```
2021/05/13 21:42:55 Starting container setup.
2021/05/13 21:42:57 Done container setup.
2021/05/13 21:43:01 Starting localization...
2021/05/13 21:43:10 Localizing input grar/fc-650035cc-5856-433b-95e6-27c1f5cfbb7e/uploads/bad_Sample/3015700998_2ZVQHMY_S29_L001_41_001.fasta.gz --> /cromwell_root/fc-650035cc-5856-433b-95e6-27c1f5cfbb7e/uploads/bad_Sample/3015700998_2ZVQHMY_S29_L001_41_001.fasta.gz
2021/05/13 21:43:10 Localizing input grar/fc-650035cc-5856-433b-95e6-27c1f5cfbb7e/uploads/bad_Sample/3015700998_2ZVQHMY_S29_L001_41_001.fasta.gz --> /cromwell_root/fc-650035cc-5856-433b-95e6-27c1f5cfbb7e/uploads/bad_Sample/3015700998_2ZVQHMY_S29_L001_41_001.fasta.gz
[0/1] [0/1] [0/1] [0/1] [0/1] [0/1] [0/1] [0/1] [0/1] [0/1] [0/1]
2021/05/13 21:43:14 Localizing input grar/fc-650035cc-5856-433b-95e6-27c1f5cfbb7e/9775da29-71d1-45e8-9938-82ba0a36078e/titan_illumina_pe/e1687504-3421-4a20-9d61-11e35422d3e3/call-read_QC_trim/read_QC_trim/61d4230a810-447c-9223-7cd82373278/fastqc/raw/fastqc_new.log --> /cromwell_root/fc-650035cc-5856-433b-95e6-27c1f5cfbb7e/9775da29-71d1-45e8-9938-82ba0a36078e/titan_illumina_pe/e1687504-3421-4a20-9d61-11e35422d3e3/call-read_QC_trim/read_QC_trim/61d4230a810-447c-9223-7cd82373278/fastqc/raw/fastqc_new.log
FastQC v0.11.8
Fixed up: /cromwell_root/fc-650035cc-5856-433b-95e6-27c1f5cfbb7e/9775da29-71d1-45e8-9938-82ba0a36078e/titan_illumina_pe/e1687504-3421-4a20-9d61-11e35422d3e3/call-read_QC_trim/read_QC_trim/61d4230a810-447c-9223-7cd82373278/fastqc/raw/fastqc_new.log
/cromwell_root/fc-650035cc-5856-433b-95e6-27c1f5cfbb7e/9775da29-71d1-45e8-9938-82ba0a36078e/titan_illumina_pe/e1687504-3421-4a20-9d61-11e35422d3e3/call-read_QC_trim/read_QC_trim/61d4230a810-447c-9223-7cd82373278/fastqc/raw/fastqc_new.log which didn't exist, or couldn't be read
Appending: /cromwell_root/fc-650035cc-5856-433b-95e6-27c1f5cfbb7e/9775da29-71d1-45e8-9938-82ba0a36078e/titan_illumina_pe/e1687504-3421-4a20-9d61-11e35422d3e3/call-read_QC_trim/read_QC_trim/61d4230a810-447c-9223-7cd82373278/fastqc/raw/fastqc_new.log
/cromwell_root/fc-650035cc-5856-433b-95e6-27c1f5cfbb7e/9775da29-71d1-45e8-9938-82ba0a36078e/titan_illumina_pe/e1687504-3421-4a20-9d61-11e35422d3e3/call-read_QC_trim/read_QC_trim/61d4230a810-447c-9223-7cd82373278/fastqc/raw/fastqc_new.log which didn't exist, or couldn't be read
Appending: /cromwell_root/fc-650035cc-5856-433b-95e6-27c1f5cfbb7e/9775da29-71d1-45e8-9938-82ba0a36078e/titan_illumina_pe/e1687504-3421-4a20-9d61-11e35422d3e3/call-read_QC_trim/read_QC_trim/61d4230a810-447c-9223-7cd82373278/fastqc/raw/fastqc_new.log
[0/1] [0/1] [0/1] [0/1] [0/1] [0/1] [0/1] [0/1] [0/1] [0/1] [0/1]
2021/05/13 21:43:24 Starting delocalization...
2021/05/13 21:43:24 Delocalization script execution started...
2021/05/13 21:43:24 Delocalizing output /cromwell_root/9775da29-71d1-45e8-9938-82ba0a36078e/titan_illumina_pe/e1687504-3421-4a20-9d61-11e35422d3e3/call-read_QC_trim/read_QC_trim/61d4230a810-447c-9223-7cd82373278/fastqc/raw/fastqc_new.log --> grar/fc-650035cc-5856-433b-95e6-27c1f5cfbb7e/9775da29-71d1-45e8-9938-82ba0a36078e/titan_illumina_pe/e1687504-3421-4a20-9d61-11e35422d3e3/call-read_QC_trim/read_QC_trim/61d4230a810-447c-9223-7cd82373278/fastqc/raw/fastqc_new.log
2021/05/13 21:43:24 Delocalizing output /cromwell_root/stderr --> grar/fc-650035cc-5856-433b-95e6-27c1f5cfbb7e/9775da29-71d1-45e8-9938-82ba0a36078e/titan_illumina_pe/e1687504-3421-4a20-9d61-11e35422d3e3/call-read_QC_trim/read_QC_trim/61d4230a810-447c-9223-7cd82373278/fastqc/raw/fastqc_new.log
2021/05/13 21:43:24 Delocalizing output /cromwell_root/stdout --> grar/fc-650035cc-5856-433b-95e6-27c1f5cfbb7e/9775da29-71d1-45e8-9938-82ba0a36078e/titan_illumina_pe/e1687504-3421-4a20-9d61-11e35422d3e3/call-read_QC_trim/read_QC_trim/61d4230a810-447c-9223-7cd82373278/fastqc/raw/fastqc_new.log
2021/05/13 21:43:24 Delocalizing output /cromwell_root/stderr --> grar/fc-650035cc-5856-433b-95e6-27c1f5cfbb7e/9775da29-71d1-45e8-9938-82ba0a36078e/titan_illumina_pe/e1687504-3421-4a20-9d61-11e35422d3e3/call-read_QC_trim/read_QC_trim/61d4230a810-447c-9223-7cd82373278/fastqc/raw/fastqc_new.log
2021/05/13 21:43:24 Delocalizing output /cromwell_root/stdout --> grar/fc-650035cc-5856-433b-95e6-27c1f5cfbb7e/9775da29-71d1-45e8-9938-82ba0a36078e/titan_illumina_pe/e1687504-3421-4a20-9d61-11e35422d3e3/call-read_QC_trim/read_QC_trim/61d4230a810-447c-9223-7cd82373278/fastqc/raw/fastqc_new.log
2021/05/13 21:43:24 Delocalizing output /cromwell_root/stderr --> grar/fc-650035cc-5856-433b-95e6-27c1f5cfbb7e/9775da29-71d1-45e8-9938-82ba0a36078e/titan_illumina_pe/e1687504-3421-4a20-9d61-11e35422d3e3/call-read_QC_trim/read_QC_trim/61d4230a810-447c-9223-7cd82373278/fastqc/raw/fastqc_new.log
Required file output /cromwell_root/3015700998_2ZVQHMY_S29_L001_41_001.fasta.html does not exist.
```

fastqc_raw.log file showing the error.



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Video of the whole process.

Contact **TOAST@cdc.gov** for assistance with error messages and debugging job failures.