Linking BaseSpace and Importing BaseSpace Reads to Terra Workspace

Document TG-TER-04, Version 4	
Date:	Written for Workflow Version:
1/21/2026	PHB v4

1. PURPOSE/SCOPE

To standardize the process of uploading next generation sequencing (NGS) data from BaseSpace into Terra. See appendix 10.2 for details on initial setup to link BaseSpace and Terra accounts. Acceptable data types include Illumina raw sequencing file formats. Read the 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
- BaseSpace account, linked to Terra account; see Appendix 10.2 for details on linking accounts

IMPORTANT NOTES

- Metadata column headers and workflow input text indicated in *gray* in this SOP are customizable; *black* is required text
- 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
- Filter for workspace data and files in workflow input dropdowns using the prefix *workspace.*

3. RELATED DOCUMENTS

Document Number	Document Name
None	None

4. PROCEDURE

Initial Setup Required! Labs using BaseSpace Fetch for the first time must begin by importing the BaseSpace_Fetch_PHB wofkflow and using command line to provide BaseSpace credentials to Terra to pull read files. **Start with appendices 10.1 and 10.2.**

4.1 DOWNLOAD BASESPACE SAMPLE SHEET AND IMPORT TO TERRA

1. *Login to the BaseSpace* account where samples were run at https://basespace.illumina.com/
2. In the runs tab, *select the run* to be analyzed (Fig 1)
3. Within the files tab, scroll to the bottom and *download the sample sheet* (Fig 2 and 3)

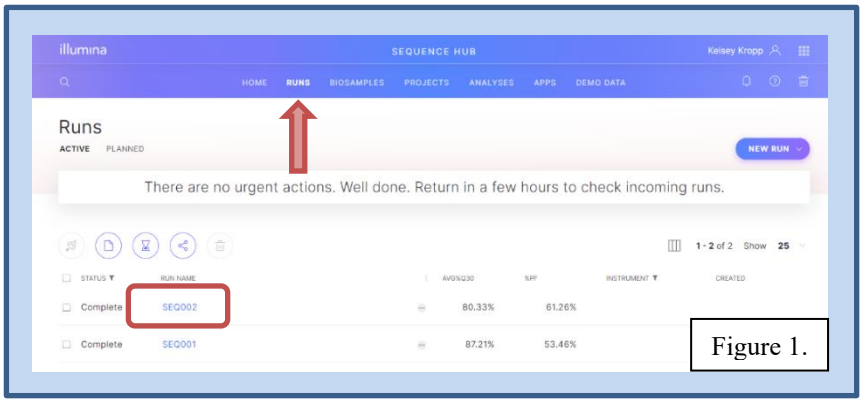


Figure 1.

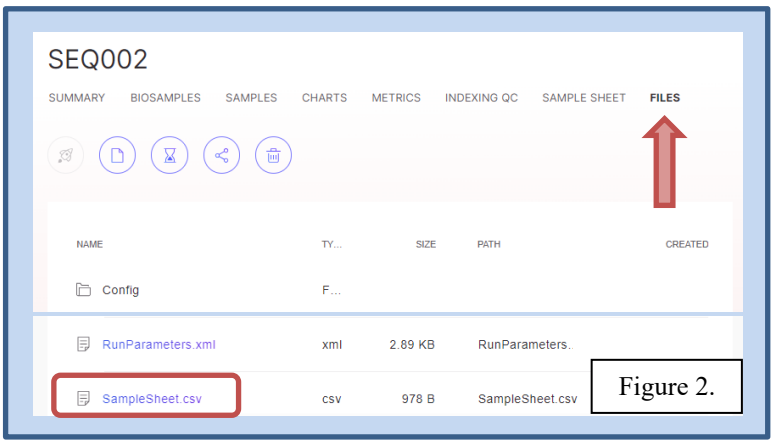


Figure 2.

Figure 3.

4. *Open the sample sheet* in excel
5. Click the plus symbol at the bottom of the window to *open a new sheet* or open a new workbook (Fig 4)

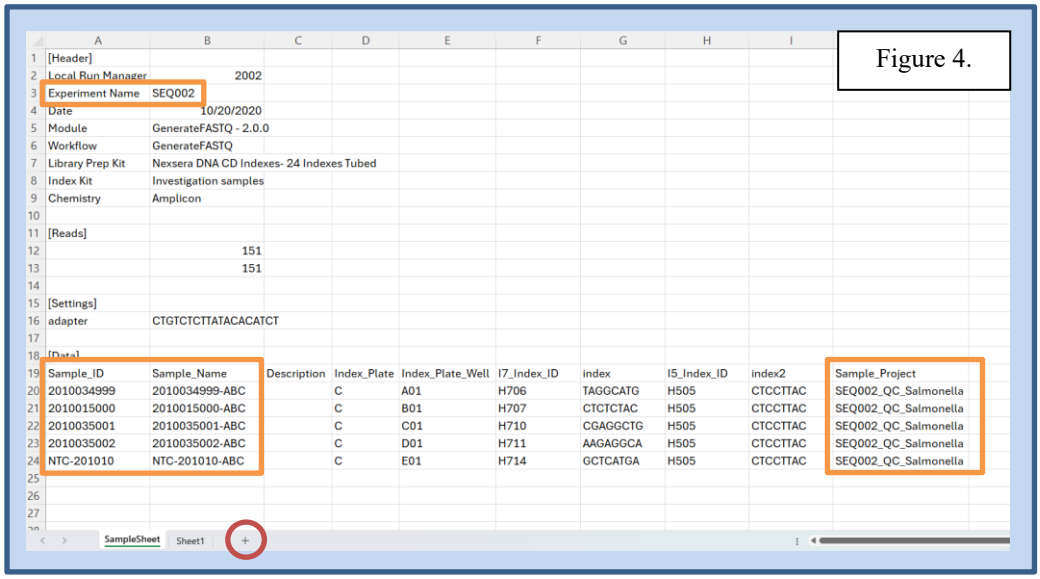
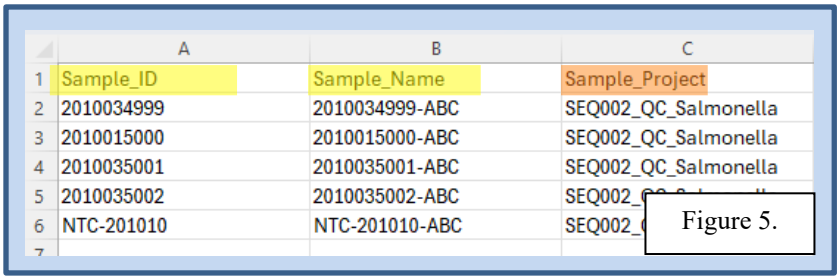


Figure 4.

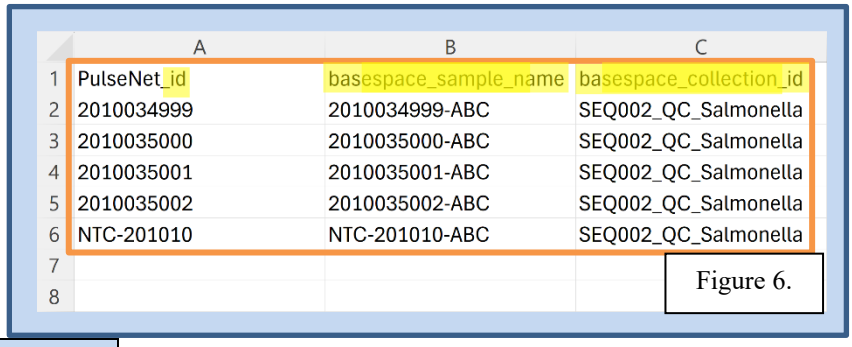
6. *Copy the lists of sample IDs and Names* (beginning with cell A19) including the headers "Sample_ID" and "Sample_Name" (Fig 4)
7. *Paste* into the new sheet (Fig 5)
8. *Copy + paste the "Sample_Project"* column into new sheet (Fig 4 and 5)
   a. If no "Sample_Project" listed, use "Experiment Name" for this value



	A	B	C
1	Sample_ID	Sample_Name	Sample_Project
2	2010034999	2010034999-ABC	SEQ002_QC_Salmonella
3	2010015000	2010015000-ABC	SEQ002_QC_Salmonella
4	2010035001	2010035001-ABC	SEQ002_QC_Salmonella
5	2010035002	2010035002-ABC	SEQ002_QC_Salmonella
6	NTC-201010	NTC-201010-ABC	SEQ002_QC_Salmonella

Figure 5.

9. *Rename the column headers* in the new sheet (Fig 6):
   a. Column A: *PulseNet_id* (previously "Sample_ID")
      i. where *PulseNet* is the unique name of **your** designated Terra data table
   b. Column B: *basespace_sample_name* (previously "Sample_Name")
   c. Column C: *basespace_collection_id* (previously "Project_Name")



	A	B	C
1	PulseNet_id	basespace_sample_name	basespace_collection_id
2	2010034999	2010034999-ABC	SEQ002_QC_Salmonella
3	2010035000	2010035000-ABC	SEQ002_QC_Salmonella
4	2010035001	2010035001-ABC	SEQ002_QC_Salmonella
5	2010035002	2010035002-ABC	SEQ002_QC_Salmonella
6	NTC-201010	NTC-201010-ABC	SEQ002_QC_Salmonella
7			
8			

Figure 6.

10. *Select and copy all cells* containing text, e.g. A1 to C6 (Fig 6)
11. In the Terra workspace where data will be uploaded, click *import data* and *upload tsv* (Fig 7)
12. Click *text import*; *paste into the text box* within the pop-up window; click *start import job* (Fig 8)

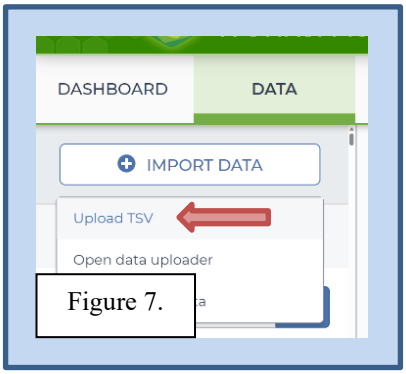


Figure 7.

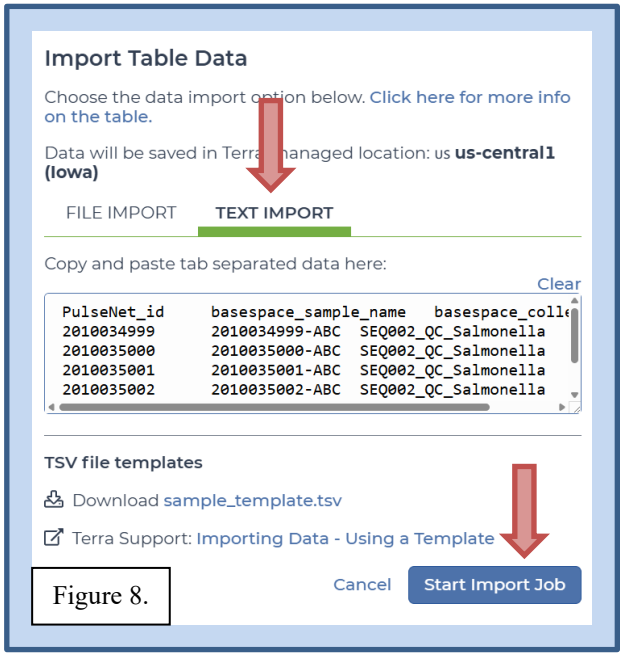


Figure 8.

13. *A new data table should now be listed in the tables sidebar or, if adding to an existing table, data should be populated in the relevant table*

4.2 RUNNING THE BASESPACE WORKFLOW

1. In the Terra workspace where the BaseSpace sample sheet was imported, *open the BaseSpace_Fetch_PHB* workflow within the workflows tab (Fig 9)
   a. For instructions on importing the BaseSpace_Fetch workflow, see appendix 10.1

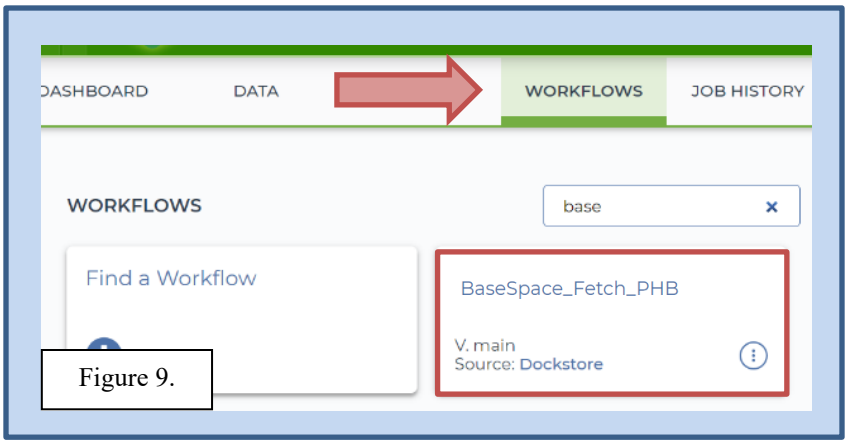


Figure 9.

2. Choose the **latest** version of the workflow in the *version dropdown field* (Fig 10, a)
3. Click the second bullet to *run workflow(s) with inputs defined by data table* (Fig 10, b)
4. Select the relevant data table name from the *select data table* dropdown, e.g. *PulseNet* (Fig 10, c)
5. Click *select data* (Fig 10, d)

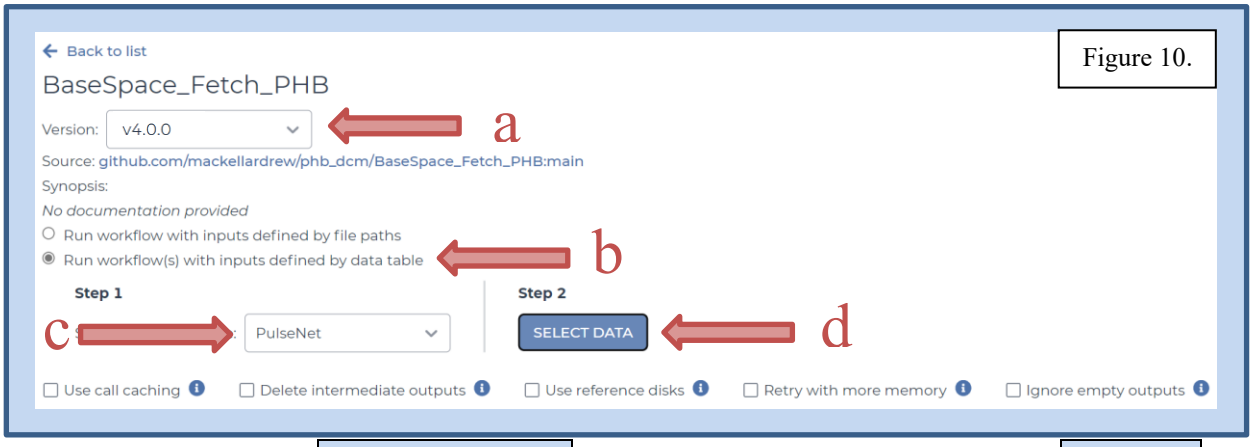


Figure 10.

6. In the pop-up window, *choose the samples* for which reads should be imported, *modify the sample set name* if desired, and click *ok* (Fig 11)
   a. Optional: to select all samples for sample sets greater than 100, click the down arrow and select all to include all samples in the table
   b. Optional: a name will be assigned to this set of samples chosen; for traceability it is useful to modify the job name to include the user's initials, e.g. BS_FetchPHB_YYYYMMDD[initials]

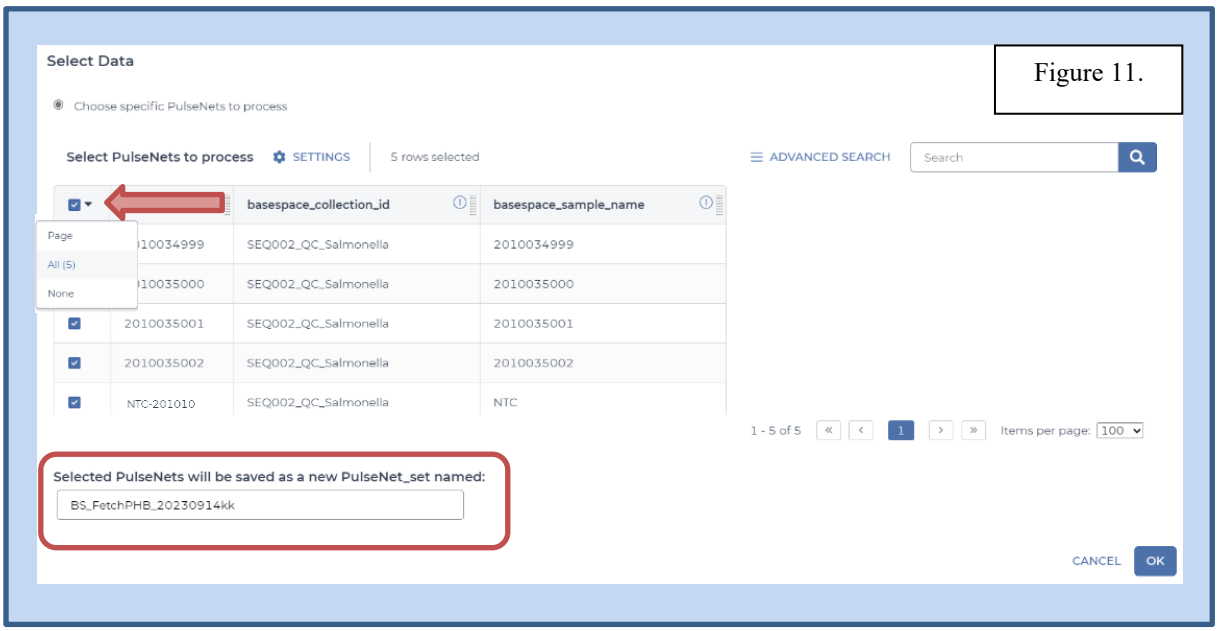


Figure 11.

7. Set the first five input settings as follows (Fig 12):
   a. *workspace.access_token*
   b. *this.basespace_collection_id*
   c. *this.basespace_sample_name*
   d. *this.PulseNet_id*
      i. where *PulseNet* is the unique name of your data table in Terra
   e. *workspace.api_server*

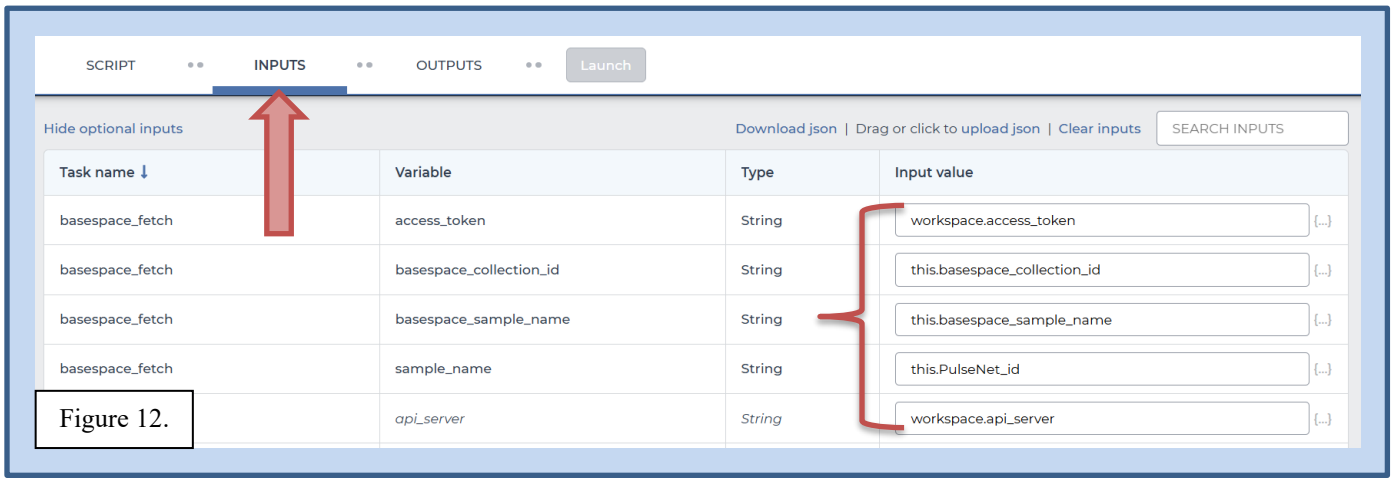


Figure 12.

8. In the outputs tab, click *use defaults* and *save* the workflow (Fig 13)
9. Then click *run analysis*, enter any comments if desired, and click *launch*

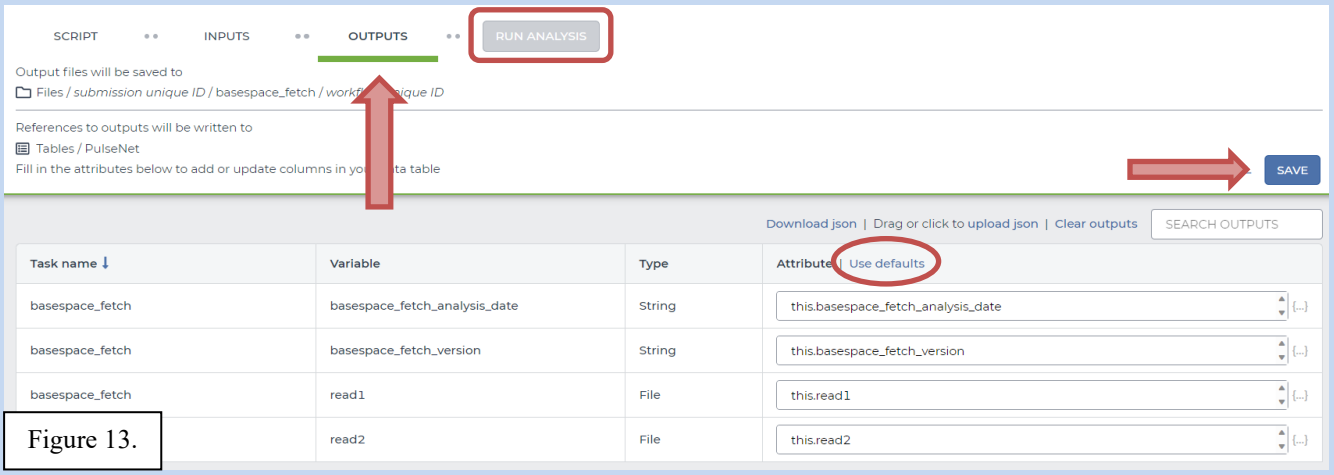


Figure 13.

5. QUALITY RECORDS

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

6. TROUBLESHOOTING

- If the first cell in the metadata table does not start 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
- 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 in workflow input dropdowns using the prefix *workspace.*
- 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

None

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 workflow documentation

9. REVISION HISTORY

Revision	Version	Release Date
Document Creation	1	9/2023
Aligning with PHB v2.0.0 release; slight format and figure changes	2	4/2024
Edits to align with Terra interface, versioning updates, and links	3	5/2025
Figure, header, and minor formatting edits	4	1/21/2026

10. APPENDICES

10.1 IMPORTING THE BASESPACE_FETCH_PHB WORKFLOW FROM DOCKSTORE

1. In the *Terra workspace* of interest, open the *workflows* tab and click *find a workflow* (Fig 14)
2. In the pop-up window, click *Dockstore.org* (Fig 15)

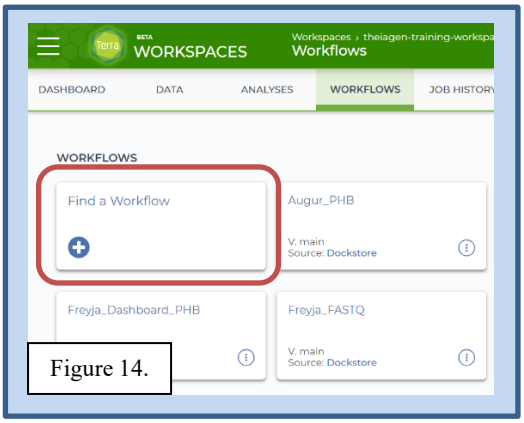


Figure 14.

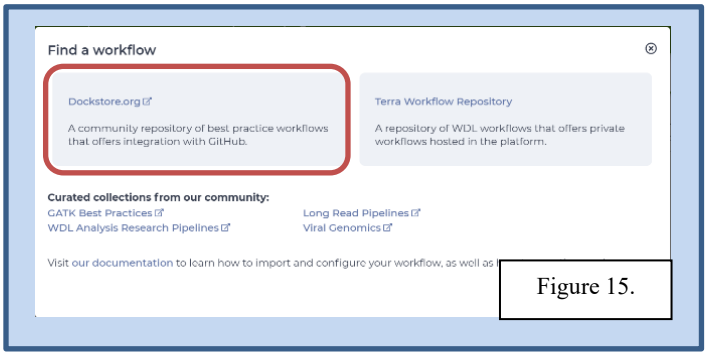


Figure 15.

3. Workflows may be retrieved in two ways:
   a. Navigate through the organization to see all available workflows (Fig 16)
      i. Click *organizations*
      ii. In the search bar type *Theiagen*
      iii. Click on the *logo*, *view*, or *# collections*
      iv. Click on collection: *Public Health Bioinformatics (PHB)* (Fig 17)
      v. Use *ctrl + F* to search for the workflow name, e.g. *basespace* (Fig 18)

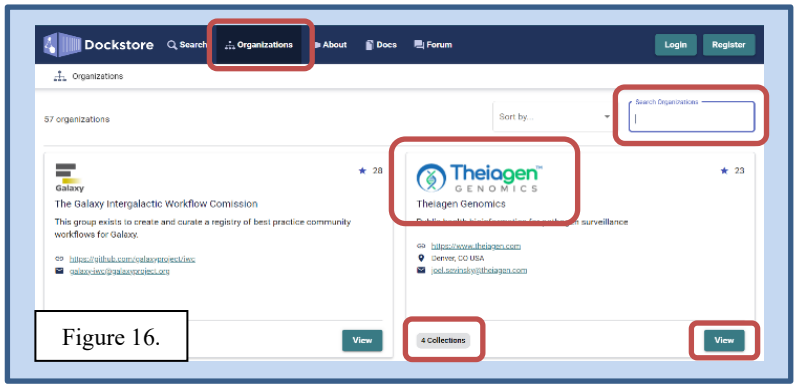


Figure 16.

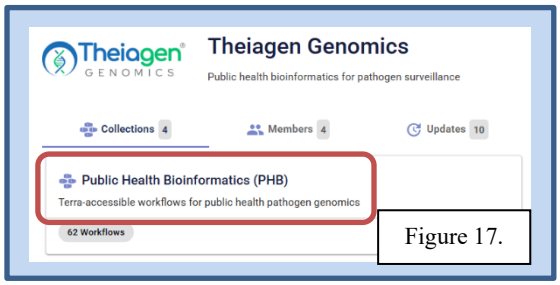


Figure 17.

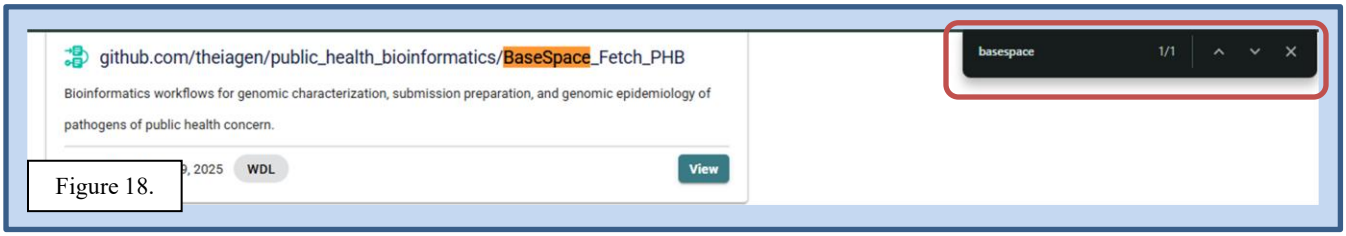


Figure 18.

b. Navigate through the search bar (Fig 19)
   i. Always select ***_PHB*** versions of Theiagen workflows

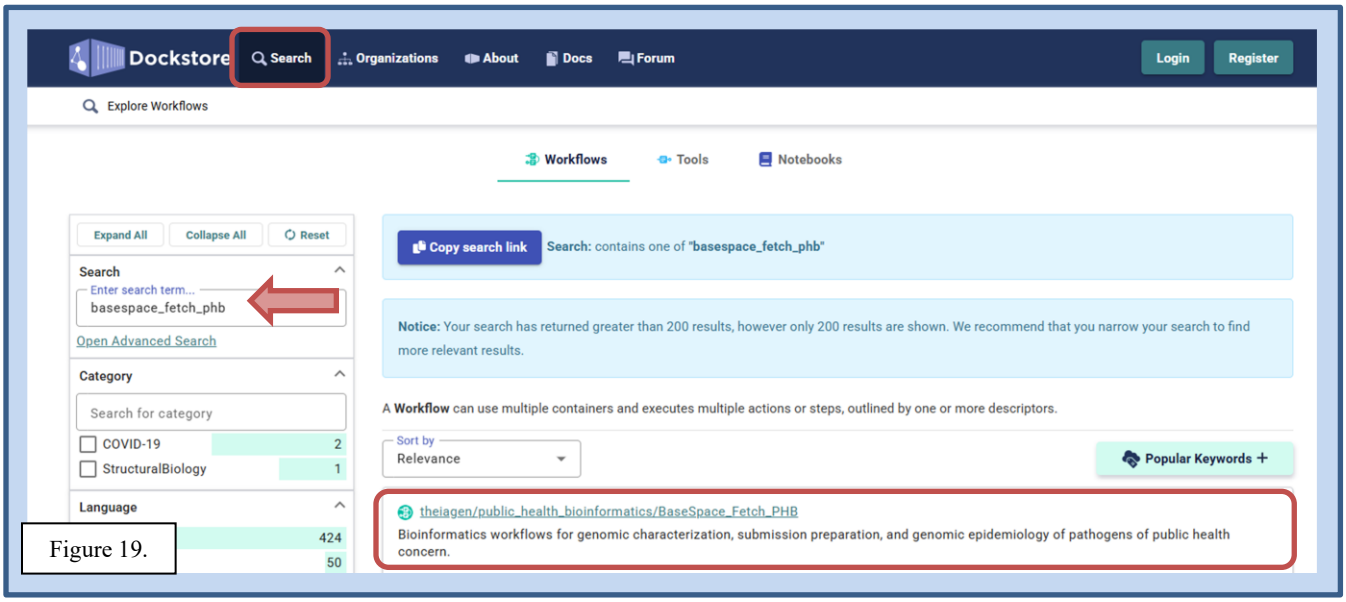


Figure 19.

4. *Open the workflow* (workflow name listed at the end of the file path)
5. Click *Terra* to launch the workflow in Terra (Figure 20)

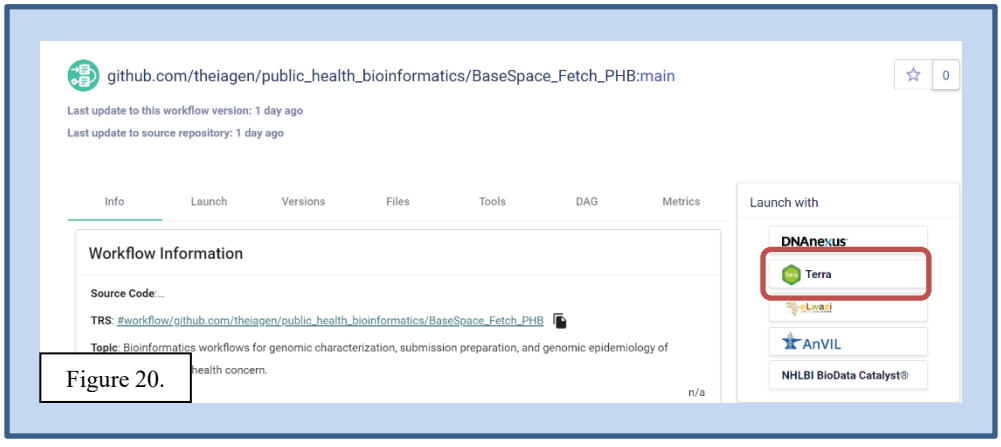


Figure 20.

6. Choose the *destination workspace* in the dropdown (Figure 21)
7. Click *import* or *create a new workspace* (Figure 21)

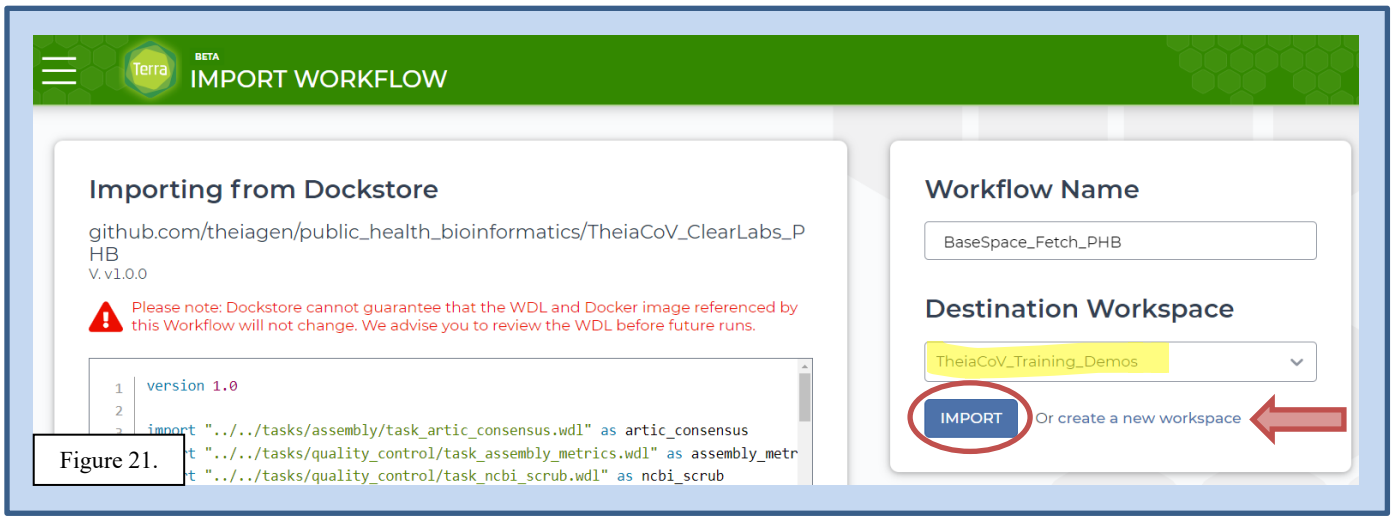


Figure 21.

10.2 OPEN COMMAND LINE TERMINAL TO PROVIDE BASESPACE CREDENTIALS TO TERRA

**This setup is up only required once per BaseSpace account. Additionally, the access token and API server keys may be copied into multiple workspaces without having to re-run command line.*

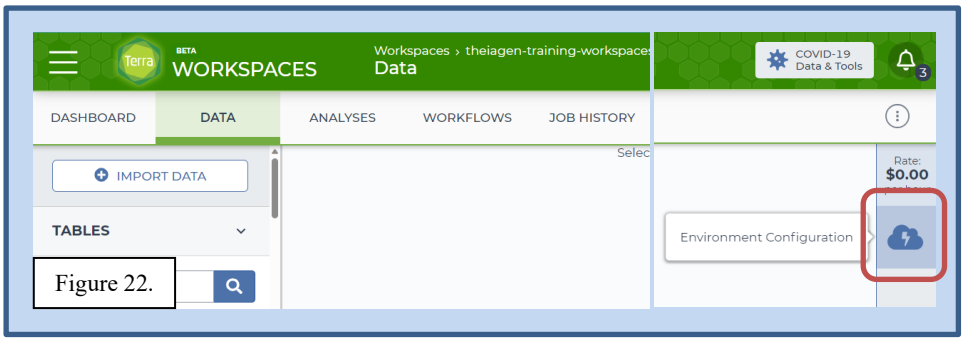


Figure 22.

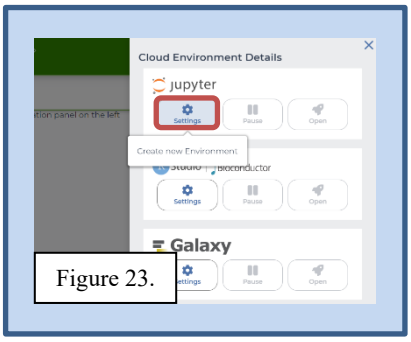


Figure 23.

1. In the workspace where BaseSpace reads will be imported, open a cloud environment in Terra by clicking on the *enivironment configuration* (Fig 22)
2. Click on the *Jupyter settings* button (Fig 23)
3. *Set environment configurations* as follows (Fig 24):
   a. Application configuration: *Default: (GATK 4.3.3.0, Python 3.10.11, R 4.3.1)*
      i. The version numbers may vary slightly as updates are incorporated into the default application configuration
   b. Cloud compute profile: CPUs *2*, Memory *7.5*
   c. Persistent disk: Disk Type *Standard*, Disk Size (GB) *250*
   d. Click *create*
4. *Click on the open terminal button* located in the right sidebar (Fig 25)
5. *A message will appear that says "Creating cloud environment. You can navigate away and return in 3-5 minutes."*

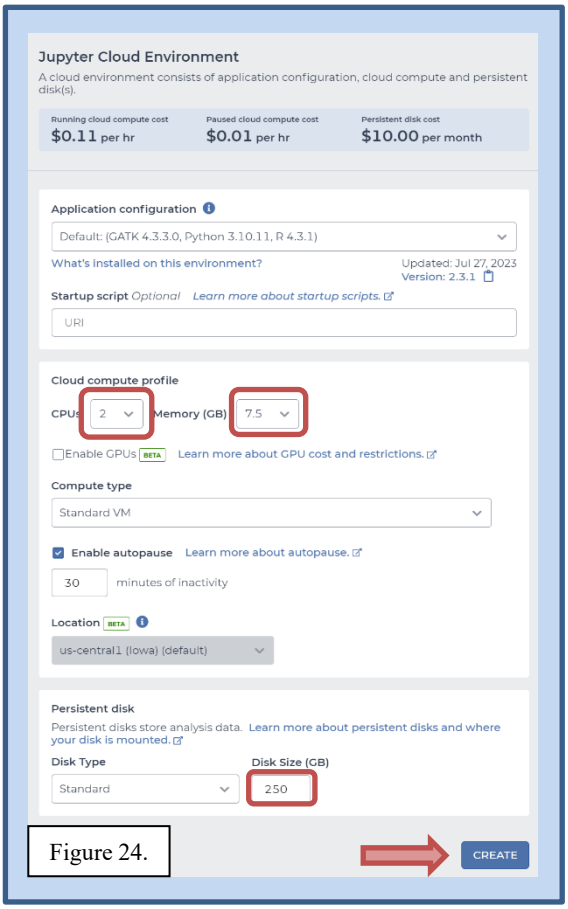


Figure 24.

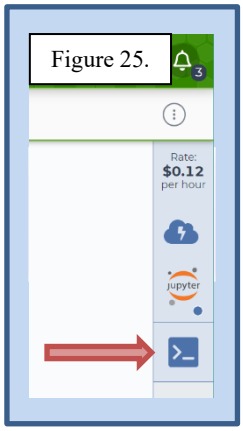


Figure 25.

6. Test to see if the terminal is working by typing *ls* and *hit enter*
   a. *Verify the output* looks like the following:
   ```
   jupyter@2a9974687b45:~$ ls
   gitignore_global  jupyter.log  lost+found  packages
   ```
   b. *If everything looks okay, proceed with the command line; if not, try closing and re-opening the terminal and re-testing the ls command*
7. Enter the following to create a bin: *mkdir ~/bin* and *hit enter*
   a. *Ctrl + c and Ctrl + v do not work in this terminal, but right clicking to copy/paste should work*
8. Type the command *ls* and *hit enter* to verify a new bin has been created; *you should see "bin" in addition to the following:*
   ```
   jupyter@2a9974687b45:~$ ls
   bin  gitignore_global  jupyter.log  lost+found  packages
   ```
9. Enter the command: *wget "https://launch.basespace.illumina.com/CLI/latest/amd64-linux/bs" -O $HOME/bin/bs*
   a. *You should get the following returned:*

```
--2023-09-14 22:42:27--  https://launch.basespace.illumina.com/CLI/latest/amd64-linux/bs
Resolving launch.basespace.illumina.com (launch.basespace.illumina.com)... 18.160.200.113, 18.160.200.107,
 18.160.200.47, ...
Connecting to launch.basespace.illumina.com (launch.basespace.illumina.com)|18.160.200.113|:443... connect
ed.
HTTP request sent, awaiting response... 200 OK
Length: 12566528 (12M) [binary/octet-stream]
Saving to: '/home/jupyter/bin/bs'

/home/jupyter/bin/bs       100%[=====================================>]  11.98M  --.-KB/s    in 0.1s

2023-09-14 22:42:28 (112 MB/s) - '/home/jupyter/bin/bs' saved [12566528/12566528]
```

10. Enter the command: *chmod u+x $HOME/bin/bs*
    a. *Nothing will be returned for this command*
11. Enter the command: *source ~/.profile*
    a. *The following will be returned:*
    ```
    bash: /home/jupyter/.profile: No such file or directory
    ```
12. Enter the command: *~/bin/bs auth*
    a. *The following will be output:*

```
Please go to this URL to authenticate:  https://basespace.illumina.com/oauth/device?code=
```

   b. *Click the link and login* to the BaseSpace account to link to Terra
      i. *If the BaseSpace account is already logged in, the login process may be skipped*
   c. *Accept the permission request* from Terra in BaseSpace (Fig 26)

Figure 26.

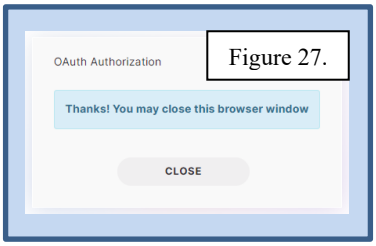


Figure 27.

13. *An authorization message will be received from BaseSpace* (Figure 27)
14. *Return to the terminal* window; *a welcome message should be returned for the authorized user similar to the following:*
```
Welcome, Kelsey Kropp
```
15. *Verify the basespace access* has been added by entering the command *ls -a*
    a. *The following should be returned – notably, the .basespace bin*
```
.           bin       .entrypoint.out   .ipython      .local       .welder.log
..          .cache    .gitconfig        .jupyter      lost+found   .wget-hsts
.basespace  .config   gitignore_global  jupyter.log   packages
```
16. Enter the following command: *cat ~/.basespace/default.cfg*
    a. *The following should be returned:*
```
apiServer    = https://api.basespace.illumina.com
accessToken  = xxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxx
```
17. *Copy the apiServer key* https://api.basespace.illumina.com; *copy by highlighting, right click, copy*
18. *Open a new Terra window* for the relevant workspace
19. Scroll to the bottom of the left sidebar and *click on workspace data* (Figure 28)

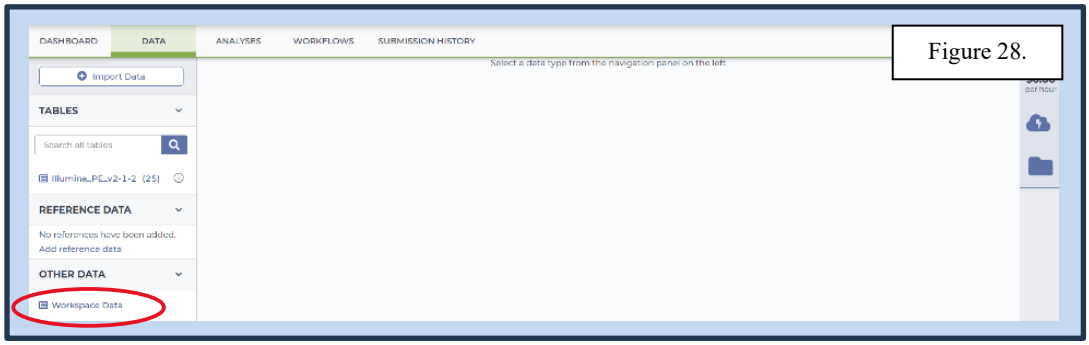


Figure 28.

20. Add a workspace data key by *clicking Edit* and *Add variable* (Fig 29)
21. Specify the following (Fig 30):
    a. Key: *api_server*
    b. Value: *paste the apiServer key* obtained above in step 16
    c. Description: optional
    d. *Click the blue checkmark* to save (Fig 30)

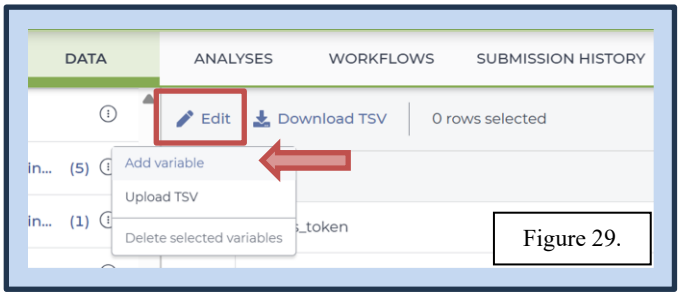


Figure 29.

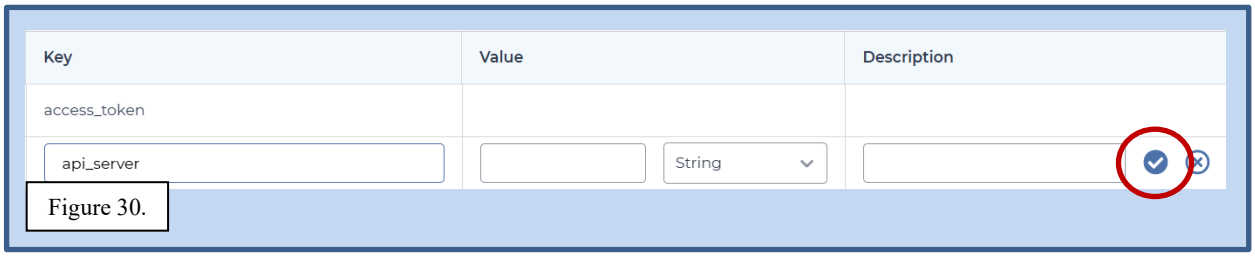


Figure 30.

22. In the terminal window *copy the accessToken* value; don't include spaces
23. Return to the Terra workspace and *add a new workspace data key* by clicking *Edit* and *Add variable* (Figure 29)
24. Specify the following, then *click the blue checkmark to save* (Figure 30):
    a. Key: *access_token*
    b. Value: *paste the accessToken* value copied from the terminal window obtained in step 16
    c. Description: optional
25. Continue with section 4.1 to download and import the BaseSpace sample sheet and section 4.2 to run the BaseSpace_Fetch_PHB workflow to import sample reads