Linking BaseSpace and Importing BaseSpace Reads to Terra Workspace

Document TG-TER-04, Version 3

Date:	Workflow Versions:
5/1/2025	PHB v3

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

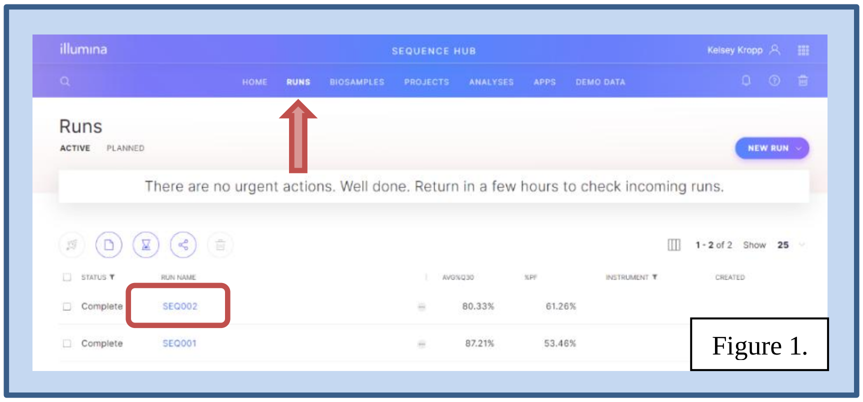
Document Number	Document Name
None	None

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

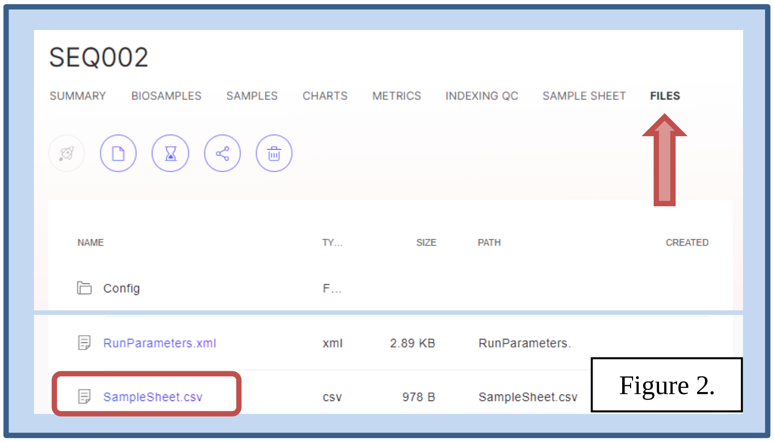
1. *Login to the BaseSpace* account where samples were run at https://basespace.illumina.com/
2. In the runs tab, *select the run* to be analyzed (Fig 1)
3. Within the files tab, scroll to the bottom and *download the sample sheet* (Fig 2 and 3)



There are no urgent actions. Well done. Return in a few hours to check incoming runs.

STATUS	RUN NAME	AVG%Q30	%PF	INSTRUMENT	CREATED
Complete	SEQ002	80.33%	61.26%		
Complete	SEQ001	87.21%	53.46%		

Figure 1.



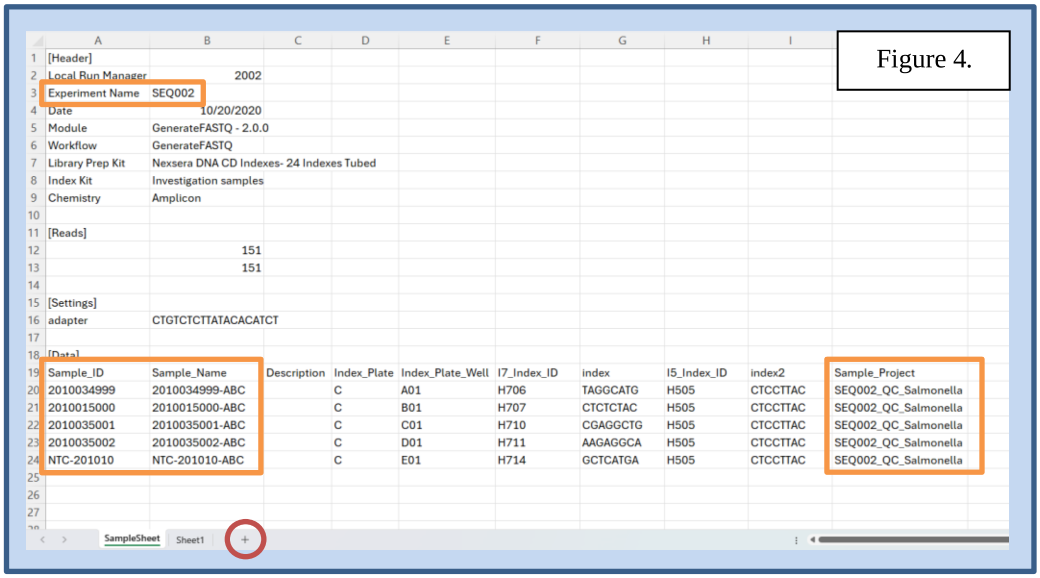
NAME	TY...	SIZE	PATH	CREATED
Config	F...			
RunParameters.xml	xml	2.89 KB	RunParameters.	
SampleSheet.csv	csv	978 B	SampleSheet.csv	

Figure 2.

```
[Header]
Local Run Manager Analysis Id,2002
Experiment Name,SEQ002
Date,2020-10-20
Module,GenerateFASTQ - 2.0.0
Workflow,GenerateFASTQ
Library Prep Kit,Nextera DNA CD Indexes - 24 Indexes Tubed
Description,
Chemistry,Amplicon

[Reads]
```

Figure 3.

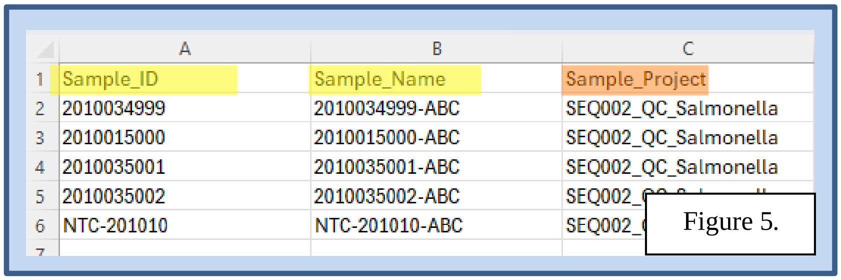
4. *Open the sample sheet* in excel
5. Click the plus symbol at the bottom of the window to *open a new sheet* or open a new workbook (Fig 4)



	A	B	C	D	E	F	G	H	I
1	[Header]								
2	Local Run Manager	2002							
3	Experiment Name	SEQ002							
4	Date	10/20/2020							
5	Module	GenerateFASTQ - 2.0.0							
6	Workflow	GenerateFASTQ							
7	Library Prep Kit	Nexsera DNA CD Indexes- 24 Indexes Tubed							
8	Index Kit	Investigation samples							
9	Chemistry	Amplicon							
10									
11	[Reads]								
12		151							
13		151							
14									
15	[Settings]								
16	adapter	CTGTCTCTTATACACATCT							
17									
18	[Data]								
19	Sample_ID	Sample_Name	Description	Index_Plate	Index_Plate_Well	I7_Index_ID	index	I5_Index_ID	index2	Sample_Project
20	2010034999	2010034999-ABC		C	A01	H706	TAGGCATG	H505	CTCCTTAC	SEQ002_QC_Salmonella
21	2010015000	2010015000-ABC		C	B01	H707	CTCTCTAC	H505	CTCCTTAC	SEQ002_QC_Salmonella
22	2010035001	2010035001-ABC		C	C01	H710	CGAGGCTG	H505	CTCCTTAC	SEQ002_QC_Salmonella
23	2010035002	2010035002-ABC		C	D01	H711	AAGAGGCA	H505	CTCCTTAC	SEQ002_QC_Salmonella
24	NTC-201010	NTC-201010-ABC		C	E01	H714	GCTCATGA	H505	CTCCTTAC	SEQ002_QC_Salmonella
25										
26										
27										

Figure 4.

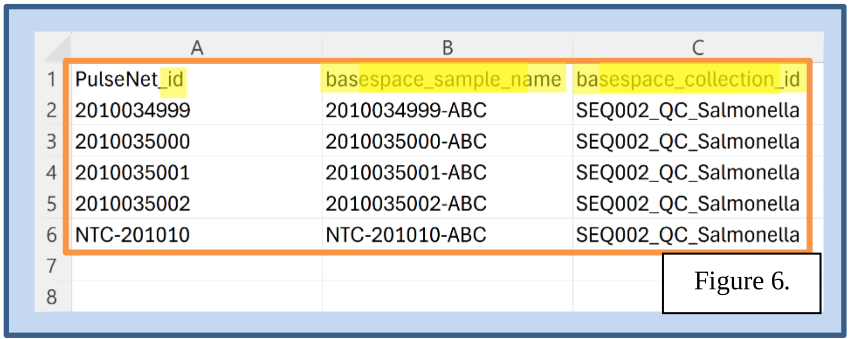
6. *Copy the lists of sample IDs and Names* (beginning with cell A19) including the headers “Sample_ID” and “Sample_Name” (Fig 4)
7. *Paste* into the new sheet (Fig 5)
8. *Copy + paste the “Sample_Project”* column into new sheet (Fig 4 and 5)
   a. If no “Sample_Project” listed, use “Experiment Name” 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_
6	NTC-201010	NTC-201010-ABC	SEQ002_

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)

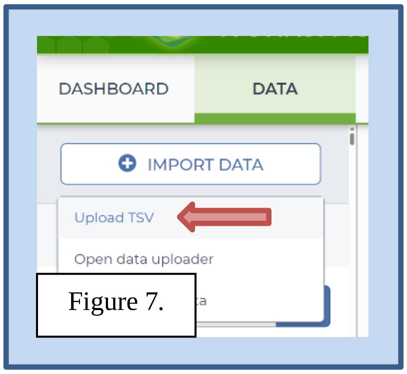
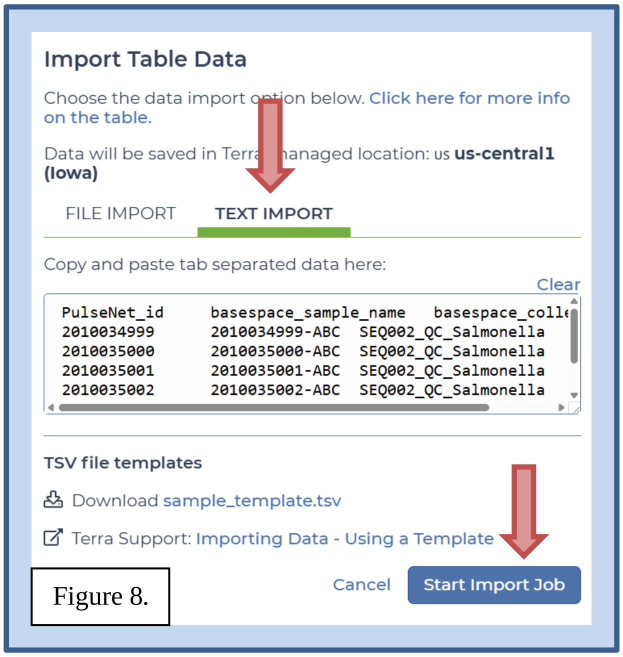


Figure 7.



Import Table Data

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

Data will be saved in Terra managed location: us **us-central1 (Iowa)**

Copy and paste tab separated data here:

```
PulseNet_id     basespace_sample_name    basespace_colle
2010034999      2010034999-ABC   SEQ002_QC_Salmonella
2010035000      2010035000-ABC   SEQ002_QC_Salmonella
2010035001      2010035001-ABC   SEQ002_QC_Salmonella
2010035002      2010035002-ABC   SEQ002_QC_Salmonella
```

TSV file templates

Download sample_template.tsv

Terra Support: Importing Data - Using a Template

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

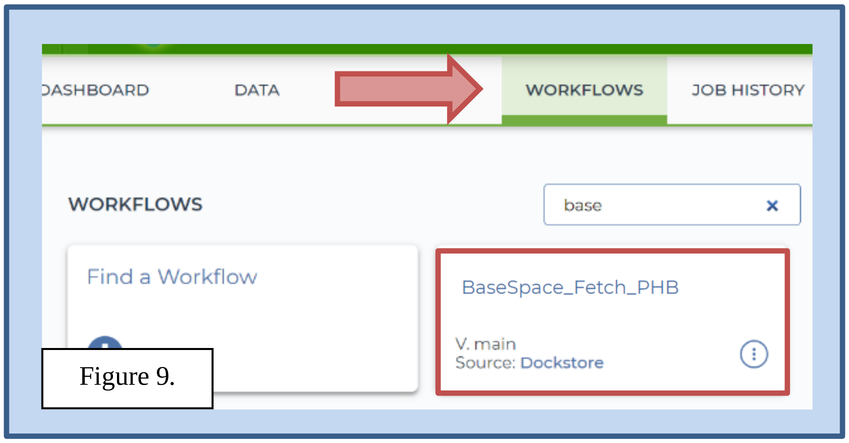
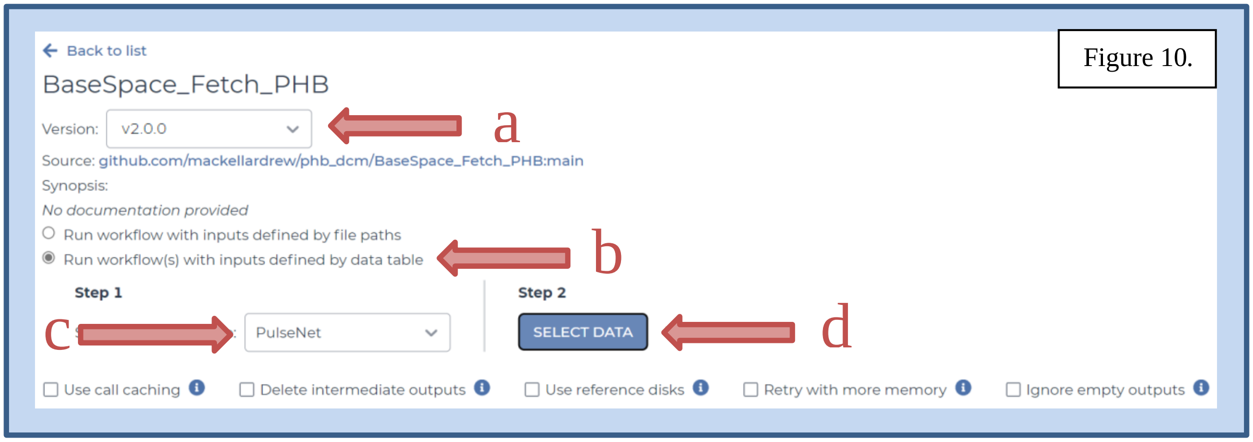


Figure 9.

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)



BaseSpace_Fetch_PHB

Version: v2.0.0

Source: github.com/mackellardrew/phb_dcm/BaseSpace_Fetch_PHB:main

Synopsis:

No documentation provided

○ Run workflow with inputs defined by file paths

● Run workflow(s) with inputs defined by data table

Step 1: PulseNet

Step 2

☐ Use call caching ☐ Delete intermediate outputs ☐ Use reference disks ☐ Retry with more memory ☐ Ignore empty outputs

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]*

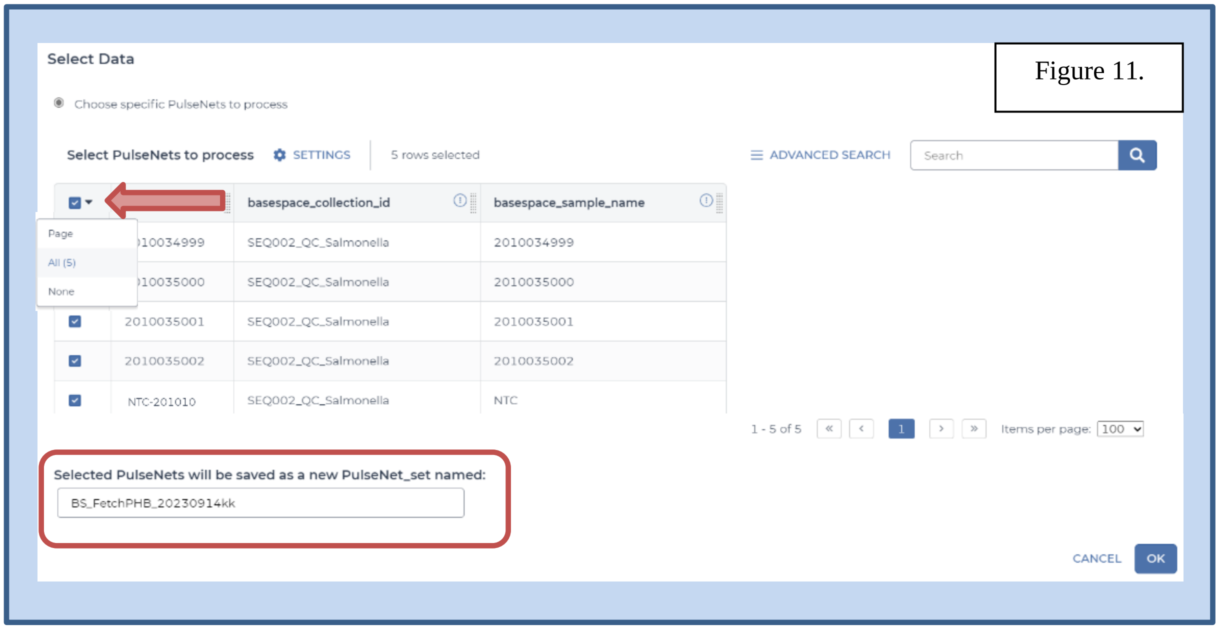


Figure 11.

Select Data

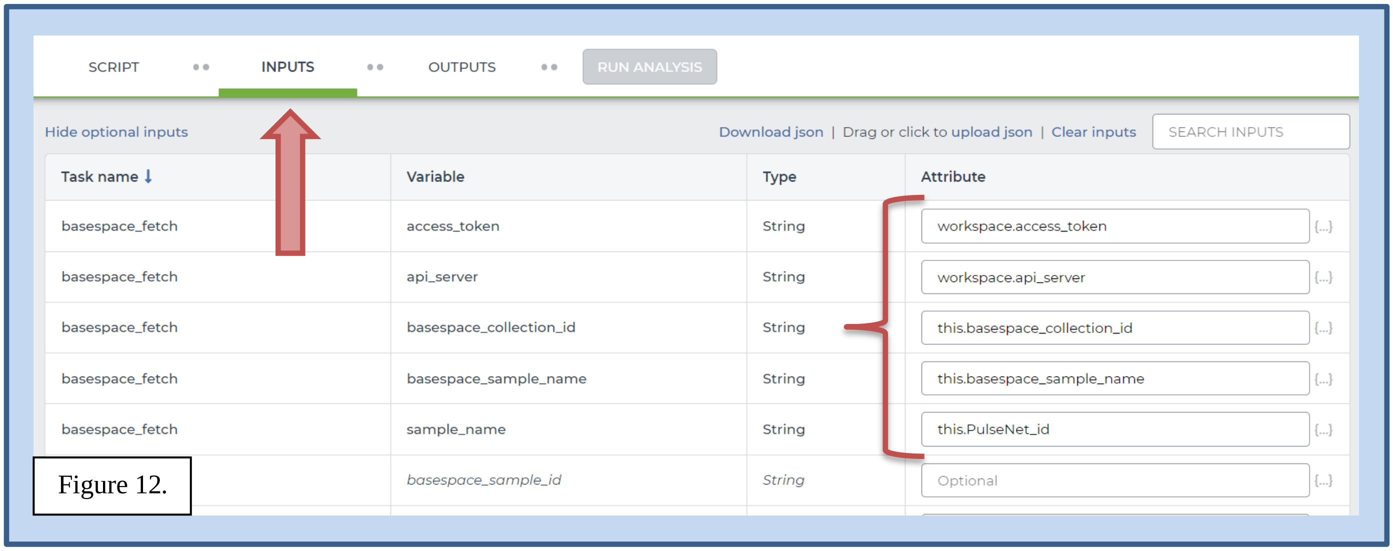
● Choose specific PulseNets to process

Select PulseNets to process · SETTINGS · 5 rows selected · ADVANCED SEARCH · Search

☑		basespace_collection_id	basespace_sample_name
	10034999	SEQ002_QC_Salmonella	2010034999
	10035000	SEQ002_QC_Salmonella	2010035000
☑	2010035001	SEQ002_QC_Salmonella	2010035001
☑	2010035002	SEQ002_QC_Salmonella	2010035002
☑	NTC-201010	SEQ002_QC_Salmonella	NTC

Selected PulseNets will be saved as a new PulseNet_set named: BS_FetchPHB_20230914kk

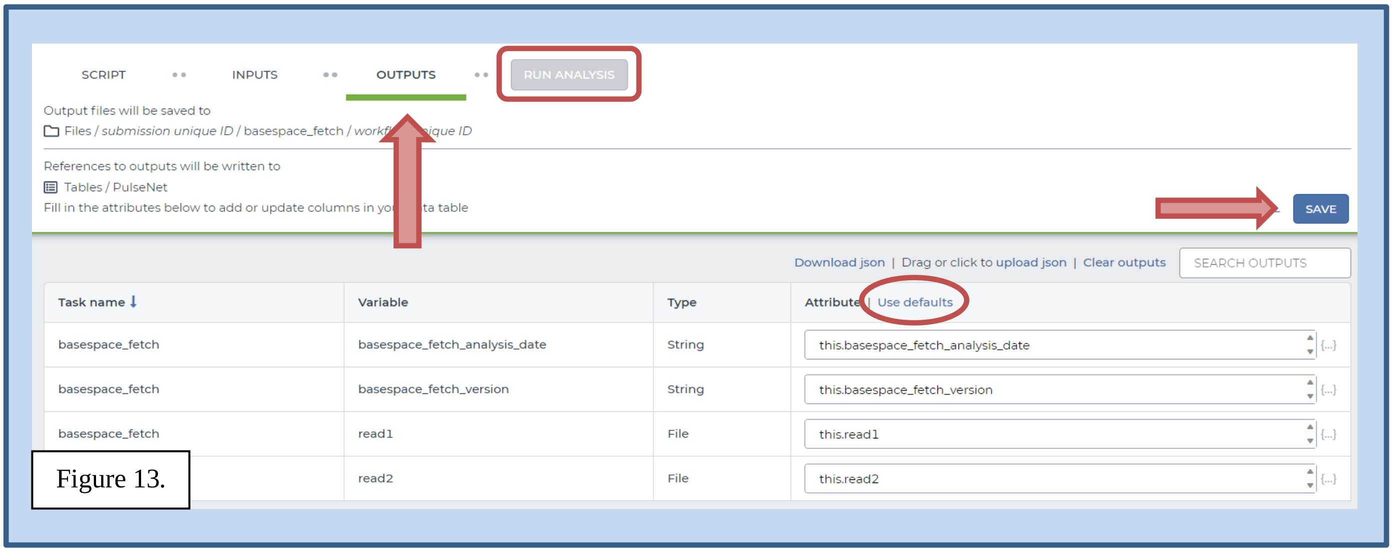
7. Set the first five input settings as follows (Fig 12):
   a. *workspace.access_token*
   b. *workspace.api_server*
   c. *this.basespace_collection_id*
   d. *this.basespace_sample_name*
   e. *this.PulseNet_id*
      i. where *PulseNet* is the unique name of your data table in Terra



Task name	Variable	Type	Attribute
basespace_fetch	access_token	String	workspace.access_token
basespace_fetch	api_server	String	workspace.api_server
basespace_fetch	basespace_collection_id	String	this.basespace_collection_id
basespace_fetch	basespace_sample_name	String	this.basespace_sample_name
basespace_fetch	sample_name	String	this.PulseNet_id
	basespace_sample_id	*String*	Optional

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*



Output files will be saved to
Files / *submission unique ID* / basespace_fetch / *workf* *ique ID*

References to outputs will be written to
Tables / PulseNet
Fill in the attributes below to add or update columns in yo ta table

Task name ↓	Variable	Type	Attribute | Use defaults
basespace_fetch	basespace_fetch_analysis_date	String	this.basespace_fetch_analysis_date
basespace_fetch	basespace_fetch_version	String	this.basespace_fetch_version
basespace_fetch	read1	File	this.read1
	read2	File	this.read2

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

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)

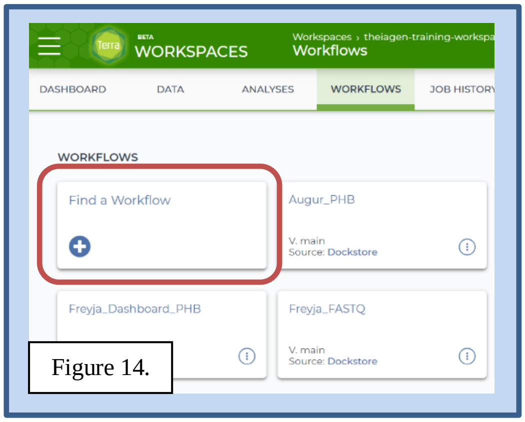
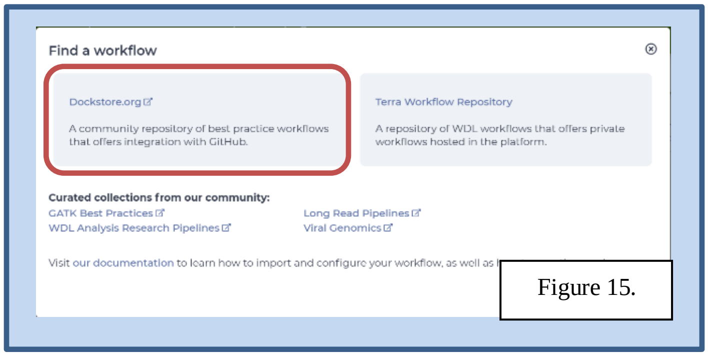


Figure 14.



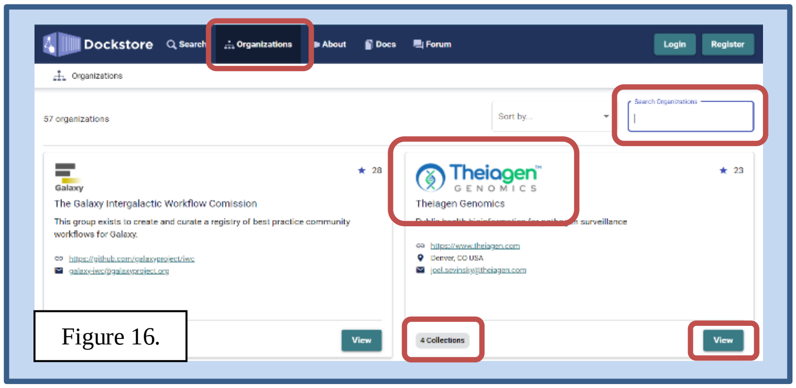
A community repository of best practice workflows that offers integration with GitHub.

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

Visit our documentation to learn how to import and configure your workflow, as well as

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*

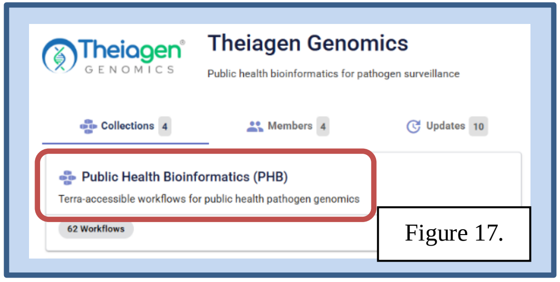


This group exists to create and curate a registry of best practice community workflows for Galaxy.

Public health bioinformatics for pathogen surveillance

Figure 16.

      iv. Click on collection: *Public Health Bioinformatics (PHB)* (Fig 17)

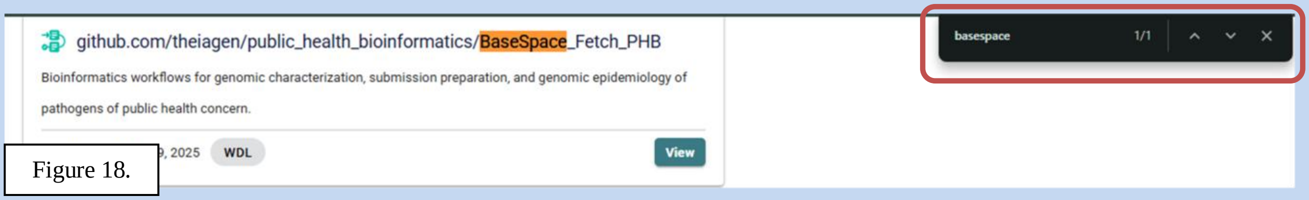


Public health bioinformatics for pathogen surveillance

Terra-accessible workflows for public health pathogen genomics

Figure 17.

v. Use *ctrl + F* to search for the workflow name, e.g. *basespace* (Fig 18)



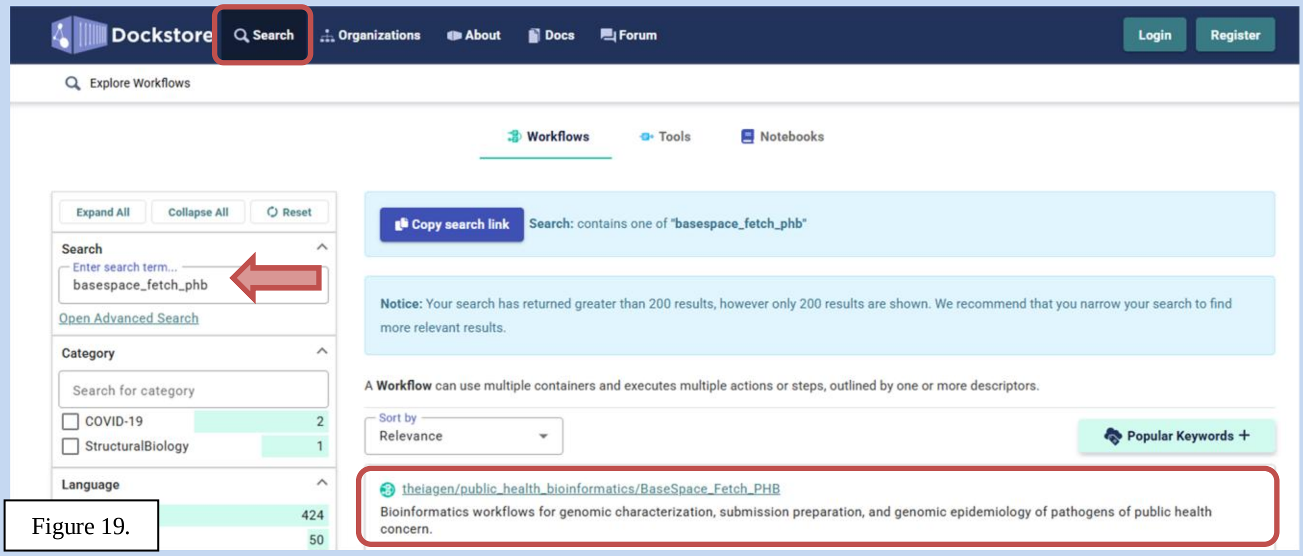
github.com/theiagen/public_health_bioinformatics/BaseSpace_Fetch_PHB

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

9, 2025

Figure 18.

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



Enter search term...: basespace_fetch_phb

Search: contains one of "basespace_fetch_phb"

Notice: Your search has returned greater than 200 results, however only 200 results are shown. We recommend that you narrow your search to find more relevant results.

A **Workflow** can use multiple containers and executes multiple actions or steps, outlined by one or more descriptors.

theiagen/public_health_bioinformatics/BaseSpace_Fetch_PHB

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

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 (**Error! Reference source not found.**20)

github.com/theiagen/public_health_bioinformatics/BaseSpace_Fetch_PHB:main

Last update to this workflow version: 1 day ago

Last update to source repository: 1 day ago

Workflow Information

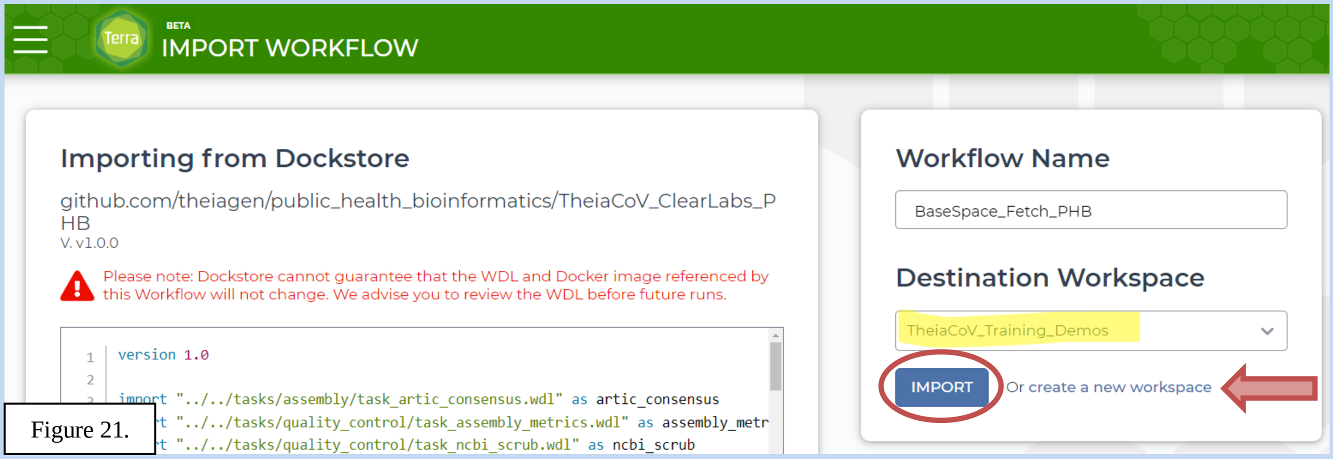
Source Code:...

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

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

Figure 20.

6. Choose the *destination workspace* in the dropdown (Fig 21)
7. Click *import* or *create a new workspace* (**Error! Reference source not found.**21)



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
t "../../tasks/quality_control/task_assembly_metrics.wdl" as assembly_metr
t "../../tasks/quality_control/task_ncbi_scrub.wdl" as ncbi_scrub
```

Workflow Name

BaseSpace_Fetch_PHB

Destination Workspace

TheiaCoV_Training_Demos

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.*

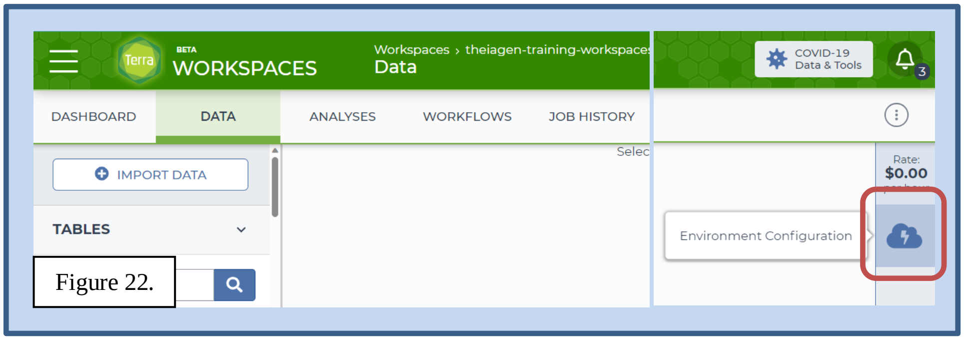


Figure 22.

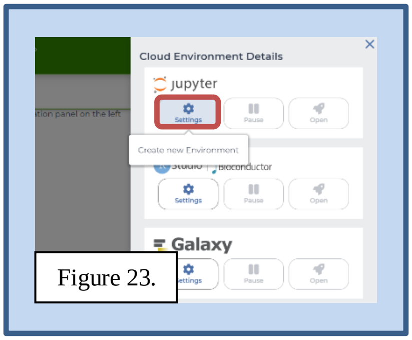
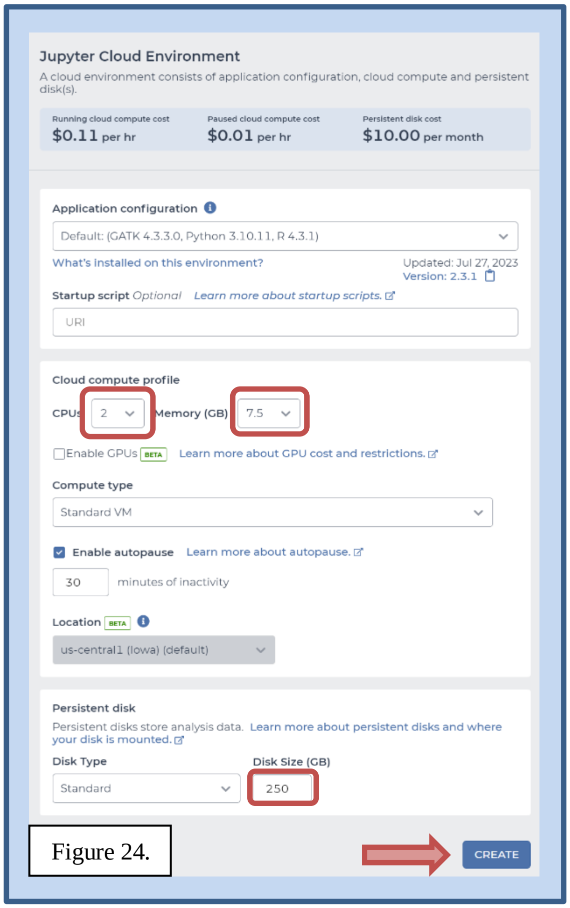


Figure 23.

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."*



Jupyter Cloud Environment

A cloud environment consists of application configuration, cloud compute and persistent disk(s).

Running cloud compute cost	Paused cloud compute cost	Persistent disk cost
$0.11 per hr	$0.01 per hr	$10.00 per month

Application configuration: Default: (GATK 4.3.3.0, Python 3.10.11, R 4.3.1)
What's installed on this environment? Updated: Jul 27, 2023 Version: 2.3.1
Startup script *Optional* *Learn more about startup scripts.*
URI

Cloud compute profile
CPUs 2 Memory (GB) 7.5
☐ Enable GPUs BETA Learn more about GPU cost and restrictions.
Compute type: Standard VM
☑ Enable autopause Learn more about autopause.
30 minutes of inactivity
Location BETA: us-central1 (Iowa) (default)

Persistent disk
Persistent disks store analysis data. Learn more about persistent disks and where your disk is mounted.
Disk Type: Standard
Disk Size (GB): 250

CREATE

Figure 24.

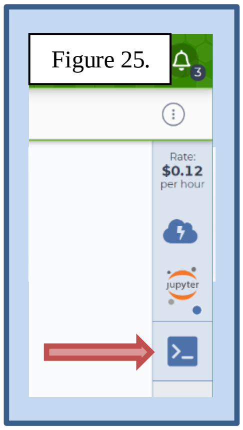
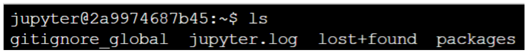


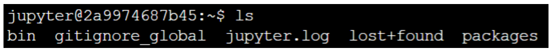
Figure 25.

6. Test to see if the terminal is working by typing *ls* and *hit enter*
    a. *Verify the output* looks like the following:



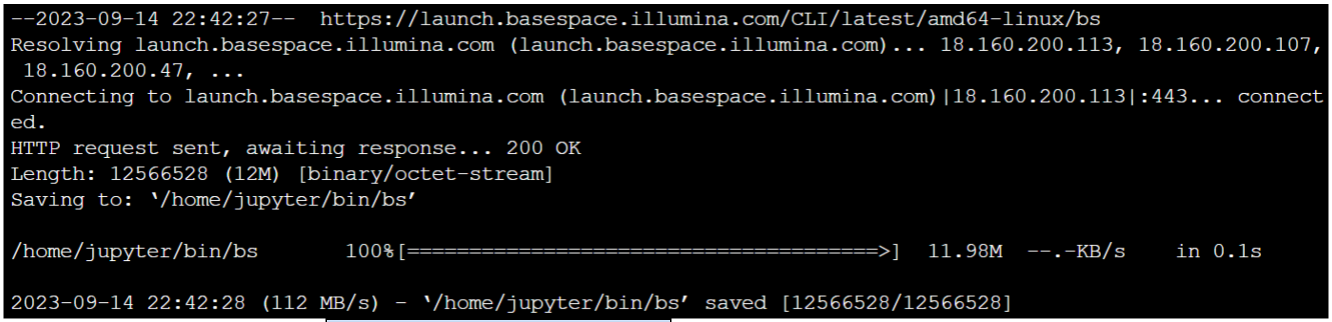
```
jupyter@2a9974687b45:~$ ls
gitignore_global  jupyter.log  lost+found  packages
```

    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:*



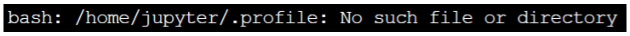
```
jupyter@2a9974687b45:~$ ls
bin  gitignore_global  jupyter.log  lost+found  packages
```

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:*



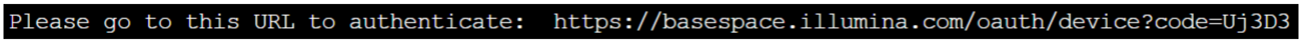
```
--2023-09-14 22:42:27--  https://launch.basespace.illumina.com/CLI/latest/amd64-linux/bs
Resolving launch.basespace.illumina.com (launch.basespace.illumina.com)... 18.160.200.113, 18.160.200.107,
 18.160.200.47, ...
Connecting to launch.basespace.illumina.com (launch.basespace.illumina.com)|18.160.200.113|:443... 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=Uj3D3
```

    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)

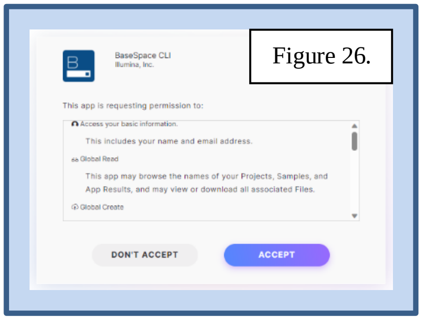


Figure 26.

BaseSpace CLI
Illumina, Inc.

This app is requesting permission to:

Access your basic information.

This includes your name and email address.

Global Read

This app may browse the names of your Projects, Samples, and App Results, and may view or download all associated Files.

Global Create

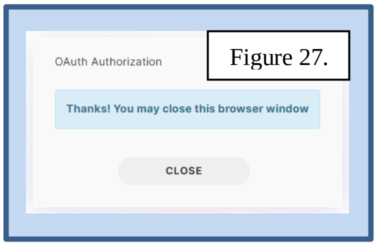
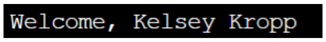


Figure 27.

OAuth Authorization

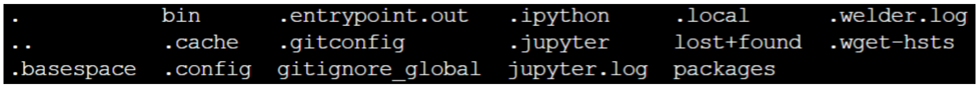
Thanks! You may close this browser window

13. *An authorization message will be received from BaseSpace (Fig 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 = b2aac9f782404625ace2c6ca83e43187
```

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* (Fig 28)

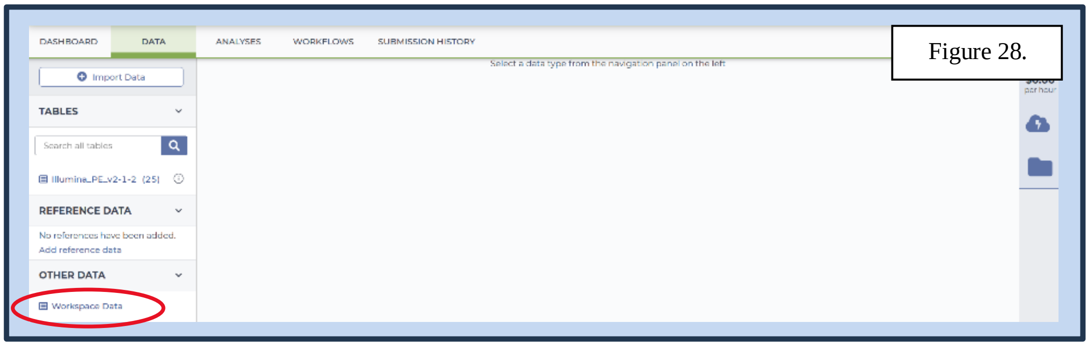


Figure 28.

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
22. *Click the blue checkmark* to save (Fig 30)

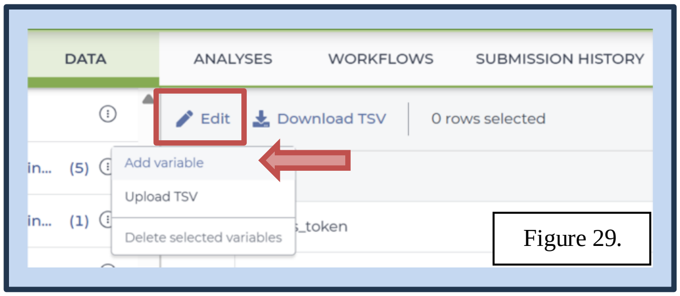
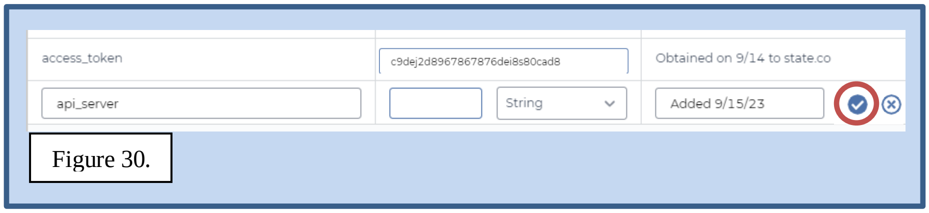


Figure 29.



access_token	c9dej2d8967867876dei8s80cad8	Obtained on 9/14 to state.co
api_server	String	Added 9/15/23

Figure 30.

23. In the terminal window *copy the accessToken* value; don’t include spaces
24. Return to the Terra workspace and *add a new workspace data key* by clicking *Edit* and *Add variable* (Fig 29)
25. Specify the following, then *click the blue checkmark to save* (Fig 30):
    a. Key: *access_token*
    b. Value: *paste the accessToken* value copied from the terminal window obtained in step 16
    c. Description: optional
26. 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