



TELL- Seq™ BaseSpace Applications User Guide

For Research Use Only. Not for use in diagnostic procedures.

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This document describes procedures on how to upload sequencing data to BaseSpace and run Universal Sequencing Technology's Tell-Read and Tell-Link applications. Note that using BaseSpace CLI requires familiarity with working in a command line environment, and builds are available for Linux, Windows, and Mac OS X.

1. Installing BaseSpace Sequencing Hub CLI and authenticating connection to BaseSpace.

Download the latest BaseSpace Sequencing Hub Command Line Interface (CLI). Detailed instructions on how to download the latest CLI for different operating systems is described in the following link:

<https://developer.basespace.illumina.com/docs/content/documentation/cli/cli-overview>

After installation, authenticate the connection to BaseSpace using the following command:

```
% bs auth
```

This will provide a URL. Enter this URL into a Web Browser and log into BaseSpace to authenticate this account and link the BS CLI to the BaseSpace account. After authentication, existing Projects and Runs on the account can viewed at the command line with the following commands:

```
% bs project list
```

```
% bs run list
```

2. Uploading raw directory of a sequencing run to BaseSpace (optional)

Sequencing data is often uploaded to BaseSpace automatically after the run is completed. However, to manually upload the raw directory of a run, choose a name to call the run, identify the instrumentation, and upload the data using the following command:

```
% bs upload run -n <NAME_OF_RUN> -t <MACHINE> <RAW_RUN_DIR>
```

3. Creating a new Project on BaseSpace (optional)

New Projects can be created on BaseSpace using the following command:

```
% bs project create -n <NAME_OF_PROJECT>
```

The new project will be assigned an ID, which is needed when uploading reference sequences.

4. Uploading a reference fasta file to BaseSpace (optional, but often used in Tell-Read and Tell-Link)

Upload a reference fasta file to a Project in BaseSpace using the following command:

```
% bs upload dataset -p <ID_OF_PROJECT> -t common.files <FASTA>
```

5. Starting Tell-Seq Data Analysis from an uploaded run

Select the TELL-Seq Data Analysis app from the list of Apps on BaseSpace. Click on Launch the Application.

Select the Project to save the results to and select the radio button indicating Tell-Read



Configuration

Analysis Name

TELL-Seq Data Analysis 05/11/2021 9:46:02

Save Results To

[SELECT PROJECT](#)

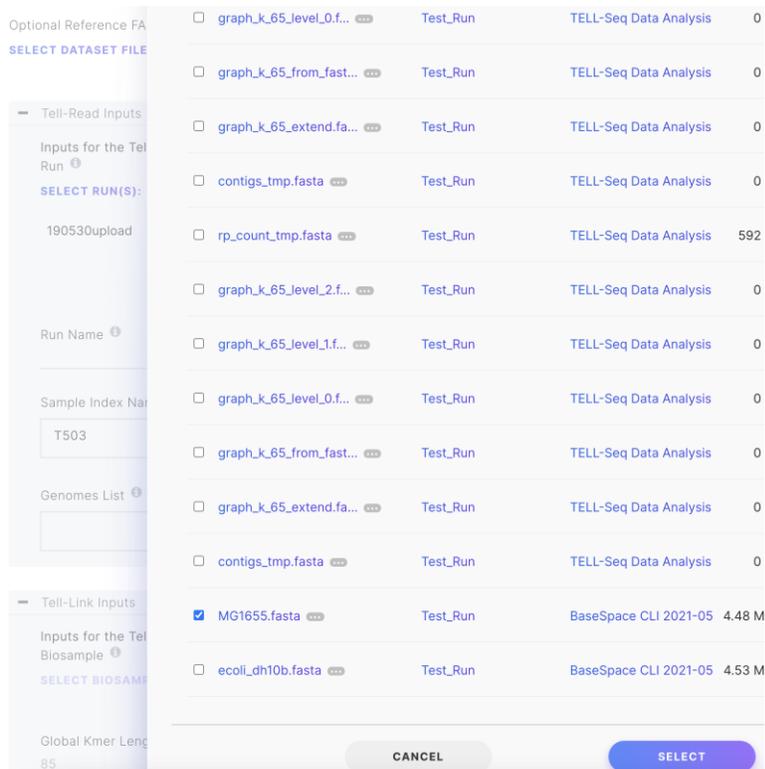
test_run_upload

x

Pipeline Configuration [?]

- Tell-Read
- Tell-Link
- Tell-Read + Tell-Link

To specify reference sequence(s) to use, click on SELECT DATASET FILE(S) and select fasta file(s) that have been already uploaded to BaseSpace.



In the section for Tell-Read Inputs, click on SELECT RUNS(S) to specify the run to be analyzed.

Specify the Run Name. The run name will be used as the prefix to the sample ID and should not contain any spaces and contain only letters, numbers, or dashes.

Specify the UST Sample Indices used, such as T501 or T502. Multiple sample indices can be separated by a comma, without usage of a space.

For each UST Sample Index used, list the corresponding genome used for the analysis. The order of the genome list must correspond with the Sample Index. The genome is the fasta file name without the .fasta suffix. For example, if two Sample indices are used and are to be analyzed using the MG1655.fasta file, the Genomes List would be MG1655, MG1655

Optional: To include Tell-Link as part of the analysis, select the radio button for “Tell-Read + Tell-Link” and specify the desired kmer Lengths in the Tell-Link Inputs Section. Note that for Tell-Link analysis, only one Reference FASTA file can be uploaded. Sequencing Runs of two different species should run Tell-Read + Tell-Link separately for both species, each utilizing different Reference FASTA files.

Click on Launch Application.

6. Viewing and Downloading Results from BaseSpace

When the Analysis is completed, click on the "FILES" link:

The screenshot shows the BaseSpace interface for an analysis titled "Analysis: TELL-Seq Data Analysis - Test Run Upload 05/11/2021 7:46:11". The "FILES" tab is selected, displaying a table of files. The table has columns for NAME, CREATED, and TYPE. Two files are listed: "TellRead" and "Logs", both created on 2021-05-11 20:31 and identified as "Dataset" type.

NAME	CREATED	TYPE
TellRead	2021-05-11 20:31	Dataset
Logs	2021-05-11 20:31	Dataset

Click on Tell-Read:

The screenshot shows the details for the "TellRead" file. The file is a "Dataset" type, created on 2021-05-11 20:31. The interface includes navigation tabs for SUMMARY, REPORTS, INPUTS, and FILES, with FILES being the active tab. Below the file information, there are icons for various actions like download, share, and delete.

The results from the Tell-Read analysis will be in this directory. Download the QC_Analysis_RUNNAME.html file to view the QC report:

 3_bwa	Folder
 4_gc_bias	Folder
 5_read_dist	Folder
 9_lambda	Folder
 benchmarks	Folder
 download	Folder
 Full	Folder
 QC_Analysis_2.Rmd	2021-05-11 20:31 Rmd
 QC_Analysis_2.md	2021-05-11 20:31 md
 QC_Analysis_test_run_upload.html	2021-05-11 20:31 html

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The instructions in this document must be followed precisely by properly trained personnel to ensure the proper and safe use of the TELL-Seq kit.

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Revision History

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