Importing Feature Barcoding Data

Create a new Project

Let's start by creating a new project.

- On the *Home page*, click **New project** (Figure 1)
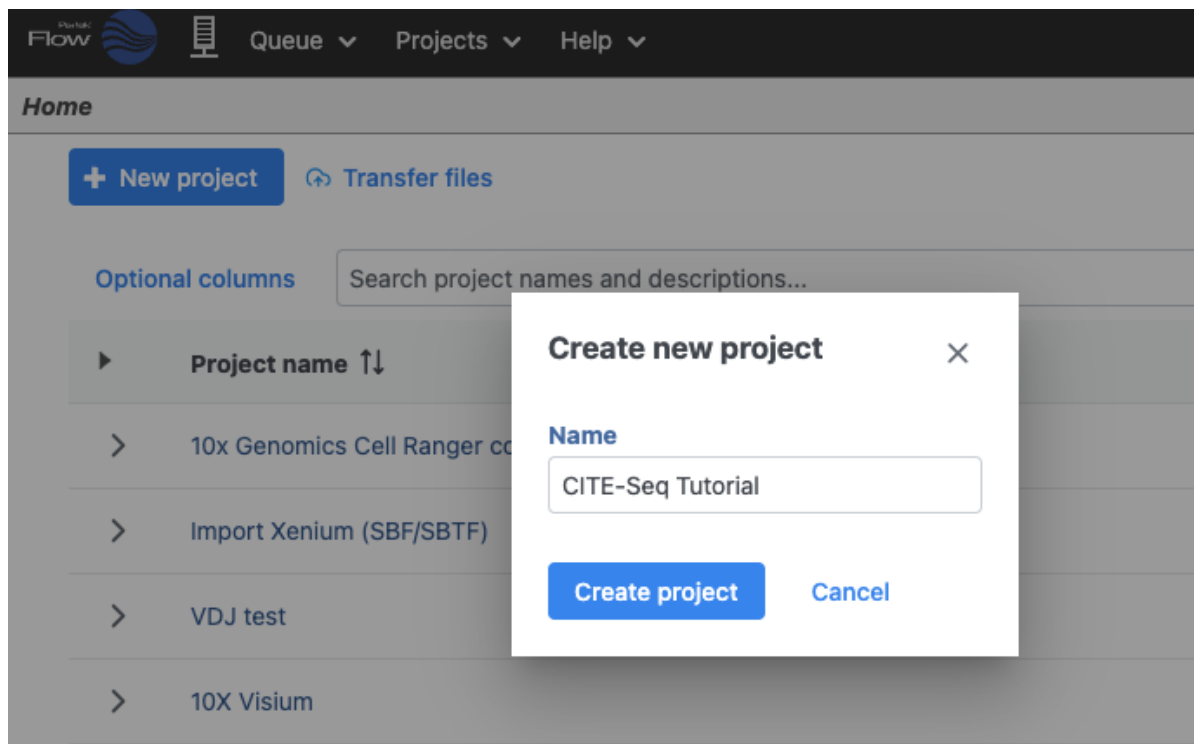- Give the project a name
- Click **Create project**

Figure 5. Create a new project and give it a meaningful name (e.g. CITE-Seq tutorial)

Import data

- In the Analyses tab, click **Add data**
- Click **10x Genomics Cell Ranger counts h5** (Figure 2)
- Choose the filtered HDF5 file for the MALT sample produced by Cell Ranger

scRNA-Seq   Spatial transcriptomics   scATAC-Seq   V(D)J   Flow/Mass Cytometry

Select the format

○ **Import scRNA count feature-barcode-mtx**
This sparse matrix output is common for 10x Genomics, Fluent Biosciences and Parse Biosciences. Each sample has 3 files (two .csv with one .mtx or two .tsv with one .mtx for each sample).

● **10x Genomics Cell Ranger counts h5**
This compressed binary format is preferred for 10x Genomics Cell Ranger output. There is 1 filtered .h5 file per sample and multiple files can be selected

○ **Full count matrix**
This rectangular cell–by-feature count matrix is common for BD Rhapsody. There is one file for one or more samples (txt, csv, tsv, txt.gz, csv.gz, tsv.gz)

○ **Seurat Rds**
This R object is for data processed by Seurat (.rds)

○ **h5ad**
This AnnData object in the h5ad file format is for data processed by Scanpy

○ **fastq**
The fastq format is used for unaligned reads. Acceptable file types are fastq, fastq.gz, fastq.bz2, fq, fq.gz, fq.bz2

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Figure 6. Import options for CITE-Seq tutorial data

Move the .h5 file to where Partek Flow is installed using **➕ Transfer files** , then browse to its location.

File select

Transfer files to the server

Current directory ⓘ

/home/flow/FlowData/CITE-Seq   Goto

	CITE-Seq
>	CR_h5_scRNA
>	Generic_count
>	library_files
>	library_files_local
>	Parse_f-b-m_format
>	Parse_res

Don't see your folder?   Refresh folder list

1 files selected

☑	Name	Size
☑	malt_10k_protein_v3_filtered_feature_bc_matrix.h5	18.75 MB

Valid files are: txt, csv, tsv, .h5, .loom, fcs or gz

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Figure 7. Import options for CITE-Seq tutorial data

Note that Partek Flow also supports the feature-barcode matrix output (barcodes.tsv, features.tsv, matrix.mtx) from Cell Ranger. The import steps for a feature-barcode matrix are identical to this tutorial.

- Click **Next**
- Name the sample **MALT** (the default is the file name)
- Specify the annotation used for the gene expression data (here, we choose **Homo sapiens (human) - hg38** and **Ensembl Transcripts release 109**). If Ensembl 109 is not available from the drop-down list, choose **Add annotation** and download it.
- Check **Features with non-zero values across all samples** in the *Report* section
- Click **Finish** (Figure 3)

Sample names

	Sample name	Files	Cells	Features
☑	MALT	malt_10k_protein_v3_filtered_feature_bc_matrix.h5	8412	33555

Feature annotation

☑ **Use annotation file**
Select the file that has been used to generate the feature counts (e.g. gene or protein information).

Assembly

[Homo sapiens (human) - hg38　∨]

Annotation model

[Ensembl Transcripts release 109 (Matt Luberti)　∨]

Primary feature identifier

⦿ Feature name (Values: MIR1302-2HG, FAM138A, OR4F5, AL627309.1, AL627309....)

◯ Feature ID (Values: ENSG00000243485, ENSG00000237613, ENSG00000186092,...)

Deduplication method

If the feature ID is not unique, the feature will be summarized by the selected method.

⦿ Mean ◯ Maximum ◯ Sum

Count value format

⦿ Raw count ◯ Normalized count with log base [None ∨]

Report

◯ All features ⦿ Features with non-zero values across all samples

☑ **Cells with total read count at least**
A low total read count threshold will result in a large number of cells which might take a long time to import

[400　⌃⌄]

[Back] [Finish]

Figure 8. File format options for MALT data set

A *Single cell counts* data node will be created under the *Analyses* tab after the file has been imported. We can move on to processing the data.

« Analyzing CITE-Seq Data　Data Processing »

Additional Assistance

If you need additional assistance, please visit our support page to submit a help ticket or find phone numbers for regional support.

Your Rating: ☆☆☆☆☆   Results: ★★★★★ 7 rates