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**

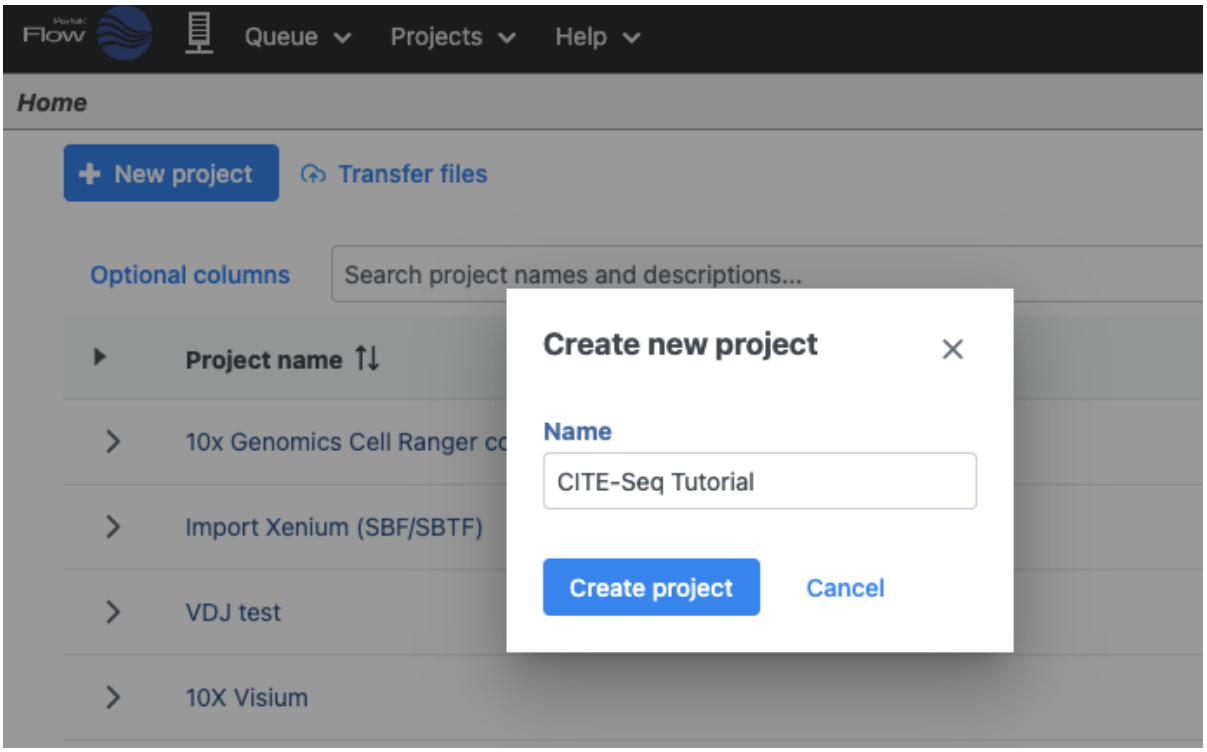

Figure 5. Create a new project and give it a meaningful name (e.g. CITE-Seq tutorial)

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

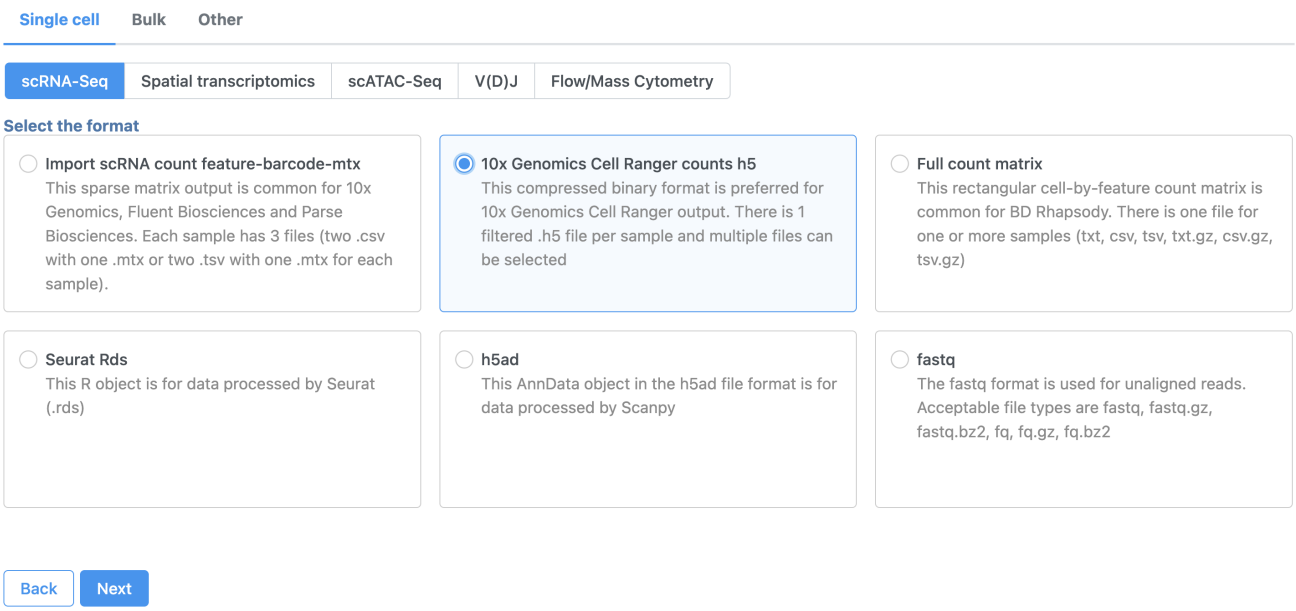

Figure 6. Import options for CITE-Seq tutorial data

Move the .h5 file to where Partek Flow is installed using 

, then browse to its location.

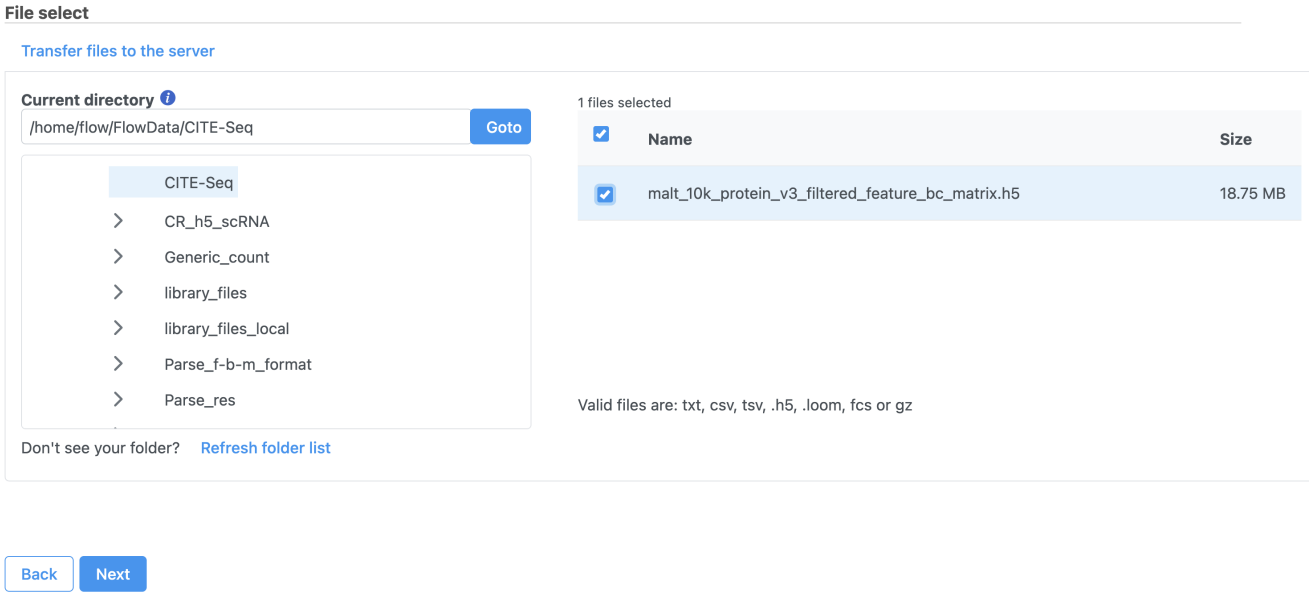

Figure 7. Import options for CITE-Seq tutorial data

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)

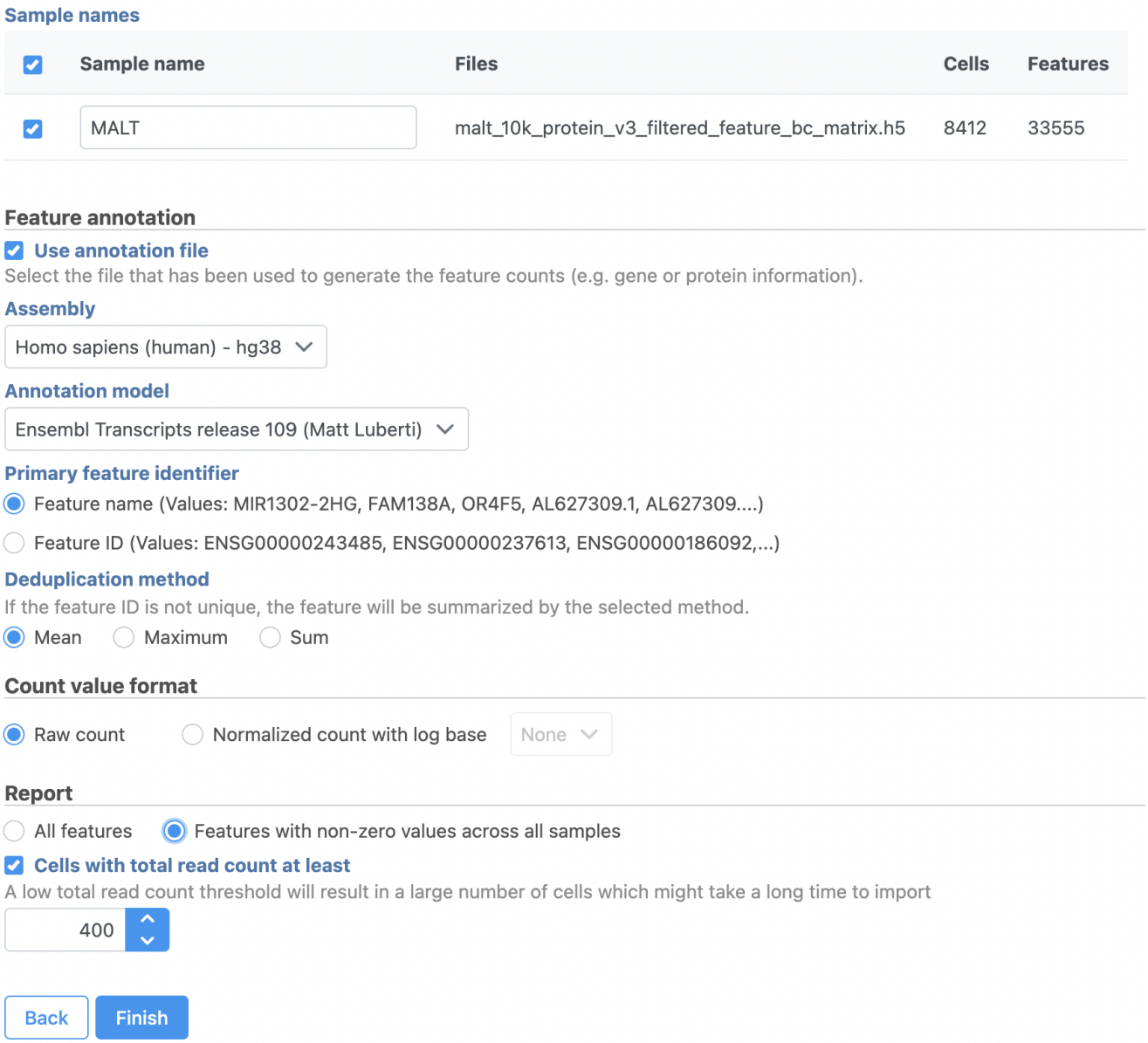

Figure 8. File format options for MALT data set

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.

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