

Importing 10x Genomics .bcl Files

Partek Flow supports .bcl files based on 10x Genomics library preparation. The following document will guide you through the steps.

To start the import, create a new project and then select **Import Data > Import bcl files**. The *Import bcl* dialog will come up (Figure 1).

The dialog box is titled "Import bcl" and contains the following elements:

- Data directory:** A text input field with the value "/home/flow/FlowData" and a "Browse" button to its right.
- Run info file:** A text input field with the value "No files selected" and a "Browse" button to its right.
- Sample sheet file:** Three radio buttons labeled "Partek Flow Server", "My Computer", and "URL". The "Partek Flow Server" radio button is selected. Below the radio buttons is a text input field with the value "No files selected" and a "Browse" button to its right.
- Advanced options:** A section header followed by an "Option set" dropdown menu showing "-- Default --" and a "Configure" link.
- Navigation:** "Back" and "Finish" buttons at the bottom left.

Figure 1. Import bcl dialog

Use the *Data directory* option to point to the location of the directory holding the data. It is located at the top level of the run directory and is typically labeled *Data*. Please see the tool tip for more info.

Use the *Run info file* option to point to the *RunInfo.xml* file. It is located at the top level of the run directory.

Use the *Sample sheet file* to point to the sample sheet file, which is usually a .csv file. Partek Flow can accept 10X Genomics' "simple" and Illumina Experiment Manager (IEM) sample sheet format, which utilize 10X Genomics' sample index set codes. Each index set code corresponds to a mixture of four sample index sequences per sample. Alternatively, Partek Flow will also accept a sample sheet file that has been correctly formatted using the [sample sheet generator](#) provided by 10X Genomics.

The click on the **Configure** link and make the following changes (Figure 2).

- *Min trimmed read length:* 8
- *Mask short adapter reads:* 8
- *Use bases mask:* see below
- *Create fastq for index reads:* OFF
- *Ignore missing bcls:* ON
- *Ignore missing filter:* ON
- *Ignore missing positions:* ON
- *Ignore missing controls:* ON

For the *Use bases mask* option, the read structure for Chromium Single cell 3' v2 prep kit is typically **Y26,I8,Y98**. The settings for Chromium Single cell 3' v3/v3.1 is typically **Y28,I8,Y91**. Please check the read structure detailed in the *RunInfo.xml* file and adjust the values to match your data.

Advanced options

Select tiles *i*

Min trimmed read length *i*

8

Mask short adapter reads *i*

8

Adapter stringency *i*

0.9

Barcode mismatches *i*

1

Use bases mask *i*

Y26,I8,Y98

Do not split fastq files by lane *i*

☒

Create fastq for index reads *i*

☐

Ignore missing bcls *i*

☒

Ignore missing filter *i*

☒

Ignore missing positions *i*

☒

Ignore missing controls *i*

☒

Save undetermined fastq *i*

☐

Apply

Save as new

Cancel

Figure 2. Setting the advanced options to import bcl files. The Use bases mask settings shown here are for Chromium v2 chemistry

Click **Apply** to accept and then **Finish** to import your files.

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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