

# 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.
- Run info file:** A text input field with the value "No files selected" and a "Browse" button.
- Sample sheet file:** Radio buttons for "Partek Flow Server" (selected), "My Computer", and "URL". Below them is a text input field with the value "No files selected" and a "Browse" button.
- Advanced options:** A section with a dropdown menu for "Option set" set to "-- Default --" and a "Configure" link.
- Navigation:** "Back" and "Finish" buttons at the bottom.

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 <span style="font-size: 0.8em; color: #4a7ebb;">i</span>	<input style="width: 100%;" type="text"/>
Min trimmed read length <span style="font-size: 0.8em; color: #4a7ebb;">i</span>	<input style="width: 80%;" type="text" value="8"/> <span style="font-size: 0.8em;">▲▼</span>
Mask short adapter reads <span style="font-size: 0.8em; color: #4a7ebb;">i</span>	<input style="width: 80%;" type="text" value="8"/> <span style="font-size: 0.8em;">▲▼</span>
Adapter stringency <span style="font-size: 0.8em; color: #4a7ebb;">i</span>	<input style="width: 80%;" type="text" value="0.9"/> <span style="font-size: 0.8em;">▲▼</span>
Barcode mismatches <span style="font-size: 0.8em; color: #4a7ebb;">i</span>	<input style="width: 80%;" type="text" value="1"/>
Use bases mask <span style="font-size: 0.8em; color: #4a7ebb;">i</span>	<input style="width: 100%;" type="text" value="Y26,I8,Y98"/>
Do not split fastq files by lane <span style="font-size: 0.8em; color: #4a7ebb;">i</span>	<input checked="" type="checkbox"/>
Create fastq for index reads <span style="font-size: 0.8em; color: #4a7ebb;">i</span>	<input type="checkbox"/>
Ignore missing bcls <span style="font-size: 0.8em; color: #4a7ebb;">i</span>	<input checked="" type="checkbox"/>
Ignore missing filter <span style="font-size: 0.8em; color: #4a7ebb;">i</span>	<input checked="" type="checkbox"/>
Ignore missing positions <span style="font-size: 0.8em; color: #4a7ebb;">i</span>	<input checked="" type="checkbox"/>
Ignore missing controls <span style="font-size: 0.8em; color: #4a7ebb;">i</span>	<input checked="" type="checkbox"/>
Save undetermined fastq <span style="font-size: 0.8em; color: #4a7ebb;">i</span>	<input type="checkbox"/>

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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