Import 10x Genomics Xenium Analyzer output

- Obtain and add files to the project

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The project includes Human Breast Cancer (In Situ Replicate 1) and Human Breast Cancer (In Situ Replicate 2) files in one project.

- Obtain the **Xenium Output Bundles** (Figure 1) for each sample.

Figure 7. Obtain the Xenium Output Bundle on your machine

- Navigate the options to select **10x Genomics Xenium Output Bundle** as the file format for input. Choose to import **10x Genomics Xenium** for your project (Figure 2).

Figure 8. Transfer files using the 10x Genomics Xenium importer

- Click **Transfer files** on the homepage, under settings, or during import.

- Click the blue **+ Add sample button** [+ Add sample] then use the green **Add sample** [icon] button to add each sample's Xenium output bundle folder. If you have not already transferred the folder to the server, this can be done using **Transfer files to the server** Transfer files to the server (Figure 3).

Figure 9. Transfer files using the 10x Genomics Xenium importer

- You will need to **decompress** the Xenium Output Bundle zip file before they are uploaded to the server. After decompression, you can **drag and drop** the entire folder into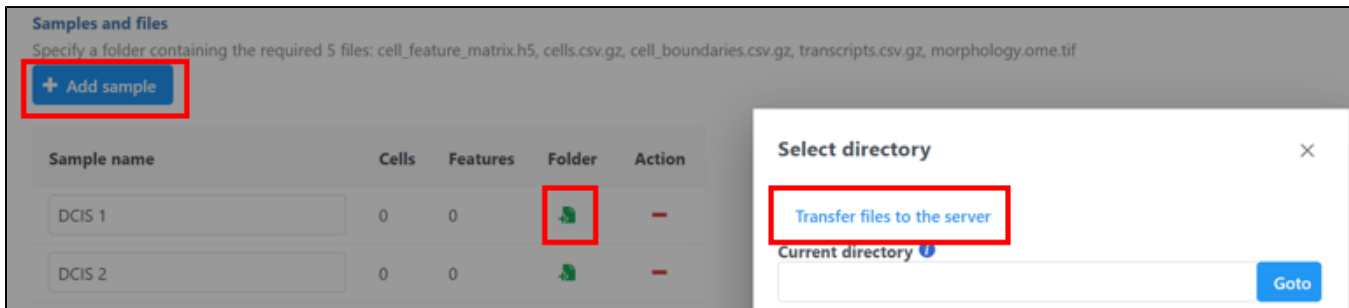 the Transfer files dialog, all individual files in the folder will be listed in the Transfer files dialog after drag & drop, with no folder structure (Figure 4). The folder structure will be restored after upload is completed.
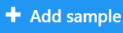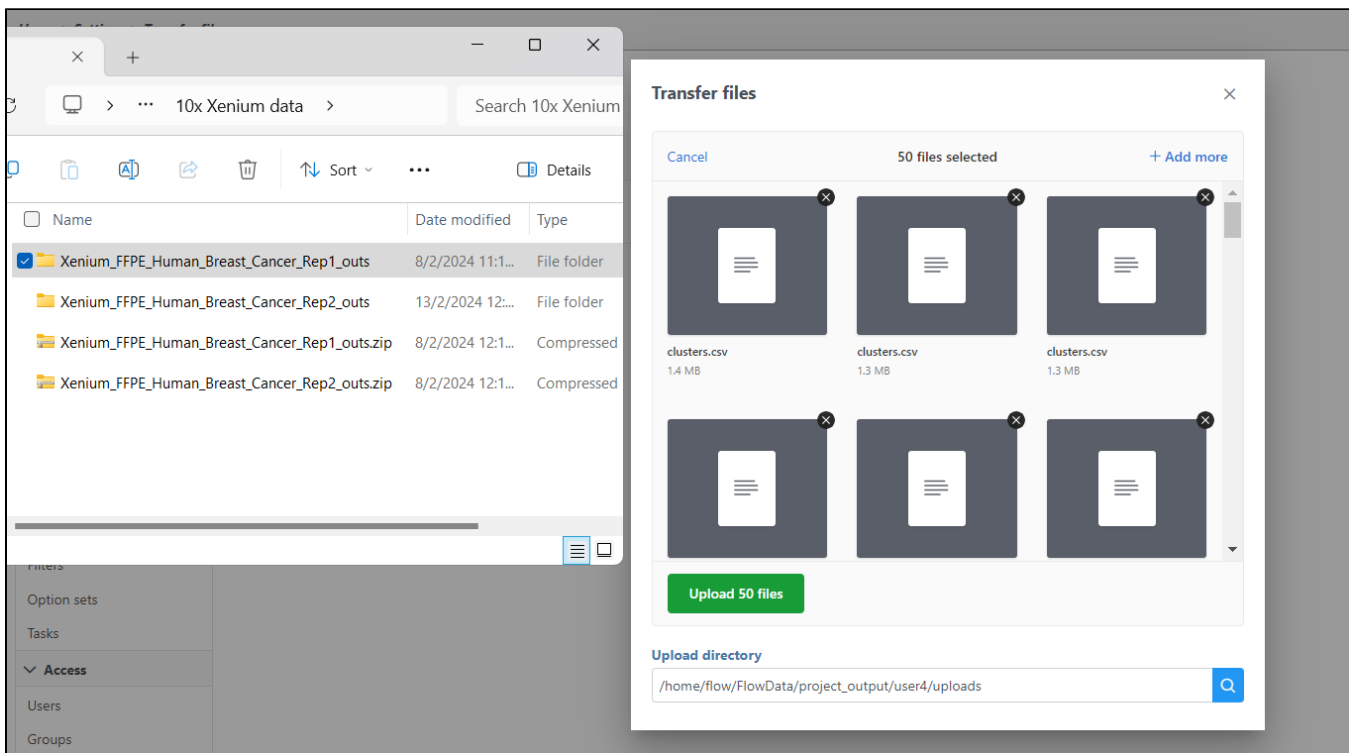

Figure 10. Drag & drop unzipped Xenium Output Bundle folder into Transfer files dialog

- Once uploaded the folder to the server, navigate to the appropriate folder for each sample using **Add sample** [icon] (Figure 5).

The Xenium output bundle should be included for each sample (Figure 5). Each sample requires the whole sample folder or a folder containing these 6 files: cell_feature_matrix.h5, cells.csv.gz, cell_boundaries.csv.gz, nucleus_boundaries.csv.gz, transcripts.csv.gz, morphology_focus.ome.tif. Once added, the *Cells* and *Features* values will update. You can choose an annotation file during import that matches what was used to generate the feature count.

Do not limit cells with a total read count since Xenium data is targeted to less features.

Figure 11. Add Xenium output bundle

Once the download completes, the sample table will appear in the *Metadata* tab, with one row per sample (Figure 6).

Figure 12. Each sample should be present in the Metadata tab

The sample table is pre-populated with one sample attributes: # Cells. Sample attributes can be added and edited manually by clicking *Manage* in the *Sample attributes* menu on the left. If a new attribute is added, click *Assign values* to assign samples to different groups. Alternatively, you can use the *Assign values from a file* option to assign sample attributes using a tab-delimited text file. For more information about sample attributes, see here. Cell attributes are found under Sample attributes and can be added by publishing cell attributes to a project.

For this tutorial, we do not need to edit or change sample attributes.

« 10x Genomics Xenium Data Analysis   Process Xenium data »

Additional Assistance

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