

# Import 10x Genomics Xenium Analyzer output

- [Obtain and add files to the project](#)

## Obtain and add files to the project

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.

<a href="#">Download in browser</a> <a href="#">Batch download</a>		
If the file size is large, we suggest using <a href="#">batch download</a> instead.		
Input Files	Size	md5sum
<a href="#">Panel (JSON)</a>	154 kB	9c0e828424fb41ff99a52e8fe99feb24
<a href="#">Supplemental: Panel (TSV)</a>	11.6 kB	24b22f15263af644b0cb0dcb5f89251b
<a href="#">Supplemental: Post-Xenium H&amp;E image (TIFF)</a>	1.7 GB	faf792e9555824c03af067b62d2a055b
<a href="#">Supplemental: Registered post-Xenium H&amp;E image (TIFF)</a>	1.43 GB	89455539ba8c1659143cef7d4528aac1
<a href="#">Supplemental: Post-Xenium IF image (TIFF)</a>	418 MB	cf8e28717304d0490c0e763b9b4b07b2
<a href="#">Supplemental: Gene Groups (CSV)</a>	6.58 kB	596ad321817d8417d452a8d07cd06a25
Output Files	Size	md5sum
<a href="#">Xenium Output Bundle</a>	9.86 GB	7d42a0b232f92a2e51de1f513b1a44fd

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).

Single cellBulkMicroarrayOther

scRNA-SeqSpatialscATAC-SeqV(D)JFlow/Mass Cytometry

Select the format

☐ 10x Genomics Visium Space Ranger output  
10x Genomics Space Ranger output can be count matrix data as 1 filtered .h5 file per sample or sparse matrix files for each sample as 3 files (two .csv with one .mtx or two .tsv with one .mtx for each sample). The spatial output files should be in compressed format (.zip). The high resolution image can be uploaded and is optional.

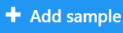

☒ 10x Genomics Xenium  
10x Genomics Xenium data should include the unzipped Xenium Output Bundle with the preferred input image file (TIFF) for each sample.

☐ NanoString CosMx  
NanoString CosMx data should include 5 files (exprMat\_file.csv, metadata\_file.csv, polygons.csv, tx\_file.csv, fov\_positions\_file.csv) and an image folder (CellComposite) per sample

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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  then use the green **Add sample**  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).

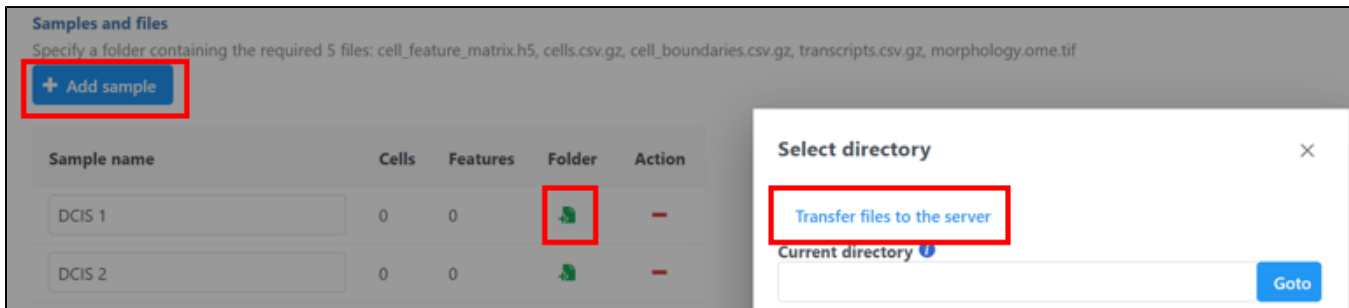


Figure 9. Transfer files using the 10x Genomics Xenium importer

- 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.

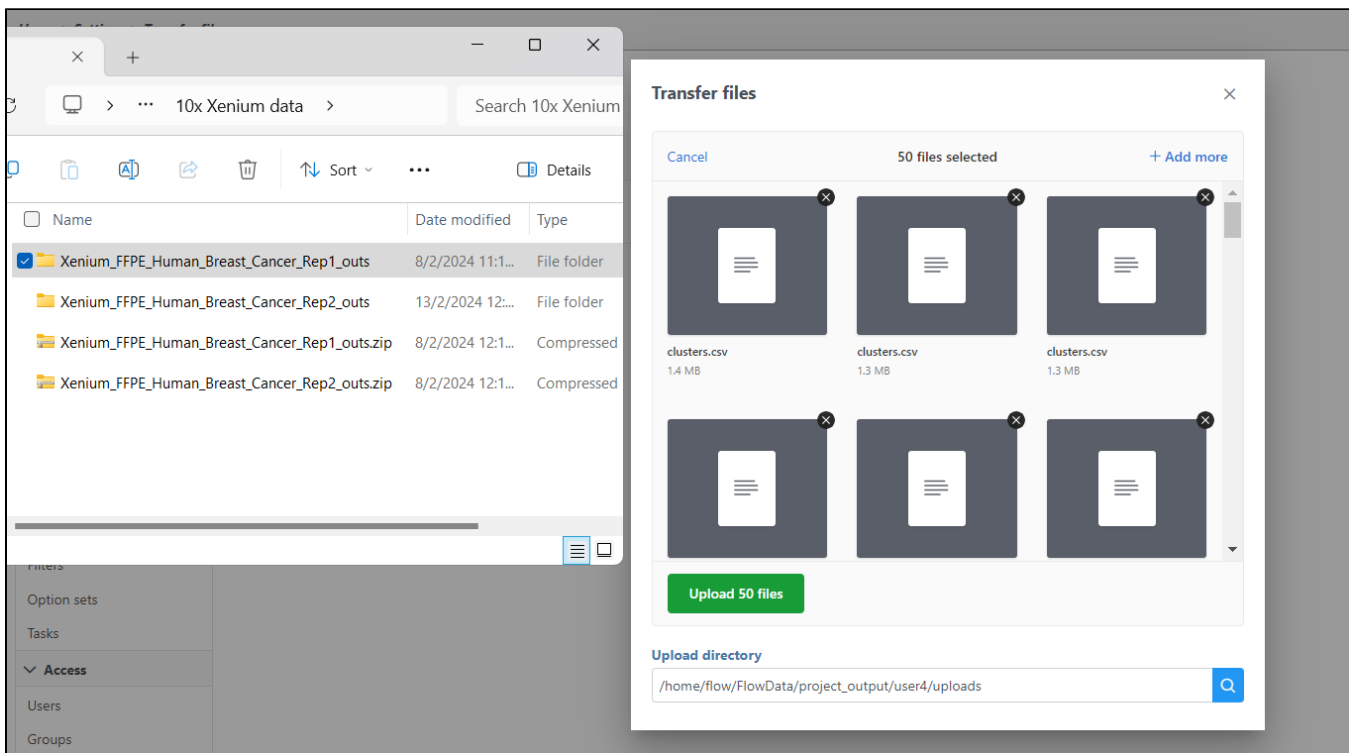


Figure 10. Drag & drop unzipped Xenium Output Bundle folder into Transfer files dialog

- Once uploaded the folder to the server, navigate to the appropriate folder for each sample using **Add sample**  (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.



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

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:  1 rates