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.

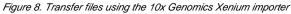
• Obtain the Xenium Output Bundles (Figure 1) for each sample.

		ad.
Input Files	Size	mo
Panel (JSON)	154 kB	9c0e828424fb41ff99a52e8fe99
Supplemental: Panel (TSV)	11.6 kB	24b22f15263af644b0cb0dcb5f8
Supplemental: Post-Xenium H&E image (TIFF)	1.7 GB	faf792e9555824c03af067b62d2
Supplemental: Registered post-Xenium H&E image (TIFF)	1.43 GB	89455539ba8c1659143cef7d452
Supplemental: Post-Xenium IF image (TIFF)	418 MB	cf8e28717304d0490c0e763b9b4l
Supplemental: Gene Groups (CSV)	6.58 kB	596ad321817d8417d452a8d07cd
Output Files 🛛 Format details	Size	md
Xenium Output Bundle	9.86 GB	7d42a0b232f92a2e51de1f513b1;

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 cell Bulk Microarray Other		
scRNA-Seq Spatial scATAC-Seq V(D)J Flow/Mass Cytometry		
Select the format 10x Genomics Visium Space Ranger output 10x Genomics 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, tc_file.csv, fov_positions_file.csv) and an image folder (CellComposite) per sample
10x Genomics Visium fastq Unaligned fastq reads (fastq, fastq,gz, fastq,bz2, fq, fq,gz, fq,bz2) can be processed using the 10x Genomics Space Ranger task. Please follow a naming convention only containing letters, digits, underscores and dashes.		
Back Next		



- 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).

mples and files secify a folder containing the requir Add sample	red 5 files: cell_fea	iture_matrix.h	5, cells.csv.g	z, cell_boundari	es.csv.gz, transcripts.csv.gz, morphology.ome.tif
Sample name	Cells	Features	Folder	Action	Select directory
DCIS 1	0	0	-8	-	Transfer files to the server
DCIS 2	0	0	-8	-	Current directory 🔮

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.

·· · · · · · · · · · · · · · · · · · ·	-				
🖯 🖵 > … 10x Xenium data >	Search	10x Xenium	Transfer files		
🖵 🛅 🖄 🖻 🗊 🔨 Sort -∕	(Details	Cancel	50 files selected	+ Add more
Name	Date modified	Туре			
Zenium_FFPE_Human_Breast_Cancer_Rep1_outs	8/2/2024 11:1	File folder	=		=
Xenium_FFPE_Human_Breast_Cancer_Rep2_outs	13/2/2024 12:	File folder			
늘 Xenium_FFPE_Human_Breast_Cancer_Rep1_outs.zip	8/2/2024 12:1	Compressed	clusters.csv	clusters.csv	clusters.csv
늘 Xenium_FFPE_Human_Breast_Cancer_Rep2_outs.zip	8/2/2024 12:1	Compressed	1.4 MB	1.3 MB	1.3 MB
			=		
Option sets			Upload 50 files		
Tasks					
✓ Access			Upload directory		
Users			/home/flow/FlowData/pr	oject_output/user4/uploads	
Groups					

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.

amples and files				
Specify a folder containing the required	6 files: cell_fea	ature_matrix.h	5, cells.csv.g	z, cell_boun
+ Add sample			5	
a Add sample				
Sample name	Cells	Features	Folder	Action
			_	
DCIS 1	0	0	4°	-
		_		
DCIS 2	0	0	÷	
Feature annotation				
Use annotation file				
Select the file that has been used to ger	ierate the featu	ure counts (e.o	g. gene or p	rotein inforr
Deduplication method				
f the feature ID is not unique, the featu	re will be sumr	marized by the	e selected m	ethod.
🖲 Mean 🔵 Maximum 🔵 Sum				
Data format				
Count value format				
Count value format				
Raw counts O Normalized co	ounts with log l	base None	\sim	
Filtering				
				🗹 Re
Features to report				
All features				
All features	; all samples			Disabl impor
	s all samples			
All features	s all samples			
All features	s all samples			

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).

Analyses Metadata Lo	g Proje	ect settings	Notebook	Data viewer	Attachmen
✓ Sample attributes				Attributes	
Manage Assign values		Sample nan	16	# Cells	
Assign values from file	1	DCIS 1	:	167780	
Add system-wide attribute	2	DCIS 2	:	118752	
\vee Cell attributes					
Manage	© S	how data files	🖪 Downlo	bad	

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 *Sam ple 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.

