

# AtoMx Export

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# Select Study on AtoMx

Gallery

COLLECTIONS

Recreated\_SAHA\_Export  
8 Studies  
Date Modified : May 15, 2024

SAHA-TMA  
5 Studies  
Date Modified : Mar 14, 2024

Ebr-1\_7\_green | GeoMx DSP | CosMx SMI

Ebr-1\_7\_green  
Date Created : Jul 23, 2024

Ebr-1\_5\_green  
Date Created : Jul 23, 2024

FLOW CELLS AND SCANS | GeoMx DSP | CosMx SMI

(4/4) Ready for study creation  
Ebr-1\_7\_green

(4/4) Ready for study creation  
Ebr-1\_5\_green

# Method 1: Fast Export

- Works well for file transport to other institutions.
- Use fast export and then give them the login + password for them to retrieve from the Nanostring s3 bucket.
- Doesn't work at St. Jude for unknown reasons.

# Fast Export

- Select this export button.

ADD PANELS ▾

Default View ▾

SAVE VIEW

CosMx Data Analysis v1.3.2

Study details

Details and logs

Name: **EBR-1\_7\_Green**  
Number of FoVs in study: **465**  
Number of cells in study: **366385**  
Number of genes in study: **1000**  
Study created under version: **1.3.2**

EXPORT

Flow cells

FoVs

EBR-1\_7\_Green

Cell segmentation profile: Initial Segmentation (1)

☒ 1

☐ 2

☐ 3

☐ 4

☐ 5

☐ 6

☐ 7

☐ 8

☐ 9

☐ 10

☐ 11

☐ 12

☐ 13

☐ 14

☐ 15

☐ 16

☐ 17

☐ 18

☐ 19

Pipeline run

No Executed Pipelines

Pipeline structure

No pipeline selected  
Select one or use the button below to create

RUN NEW PIPELINE

DOWNLOAD LOGS

No details available for this study

# Fast Export

- Select all the files you would like to export.
- To retrieve, you can use FileZilla or other command line tools using the Hostname, Port, and Username shown in the red circle.

Export Dataset

Study detail

**Description**

This module exports raw data, standalone Seurat object, corresponding TileDB array, and/or flat csv files available for download. The exported data comprises transcript counts and locations, annotation metadata, and user-initiated data transformations performed in AtoMx SIP prior to export. All results up to the point of export will be available in the Seurat object and TileDB array. While the RNA and Protein studies share the same format, the structure of the raw files folder will vary based on the analyte.

**Warning:** To prevent the duplication of files, please export raw files only once per study. Exporting raw files from multiple pipelines within the same study may result in terabytes of duplicated files.

**Input parameters**

**Flat CSV Files:**

- ☐ Export count matrix flat csv file
- ☐ Export cell metadata flat csv file
- ☐ Export transcripts flat csv file
- ☐ Export polygons flat csv file
- ☐ Export FOV positions flat csv file

**Tertiary Analysis Objects:**

- ☐ Export a Seurat Object
  - ☐ Export Seurat contains transcript coordinates (large data)
  - ☐ Export Seurat contains polygon coordinates (large data)
- ☐ Export TileDB array

**Raw Files:**

- ☐ Export Raw Files
  - ☐ Export SpotFiles folder to redo Target Decoding (large data)
  - ☐ Export Morphology2D folder (large data)
  - ☐ Export other Miscellaneous Data Files (large data, if available)

**Output Export Access**

To download your exported data, please connect using the below SFTP information through an SFTP application such as FileZilla, WinSCP, or a Command Line. Use your regular AtoMx credentials to connect.

**Hostname:** na.export.atomx.nanostring.com

**Port:** 22

**Username:** luke.zhang@stjude.org

**Output Folder Name:** EBR-1\_7\_Green\_23\_07\_2024\_12\_37\_00\_531

CLOSE

EXPORT

# Method 2: Traditional Export

- Works at St. Jude!

# Traditional Export

- Select either Run New Pipeline or the other button in the red circle.

The screenshot displays the CosMx Data Analysis v1.3.2 interface. At the top, there are buttons for 'ADD PANELS', 'Default View', and 'SAVE VIEW'. The main content area is divided into three panels: 'Study details', 'Flow cells', and 'Pipeline run'. The 'Study details' panel shows information for 'EBR-1\_7.Green', including the number of FoVs (465), cells (366385), and genes (1000). The 'Flow cells' panel lists 19 flow cells, with the first one selected. The 'Pipeline run' panel shows 'No Executed Pipelines'. A red circle highlights the 'EXPORT' button in the 'Study details' panel. Another red circle highlights the 'RUN NEW PIPELINE' button in the 'No pipeline selected' message on the right side of the interface.

ADD PANELS Default View SAVE VIEW CosMx Data Analysis v1.3.2

**Study details** Details and logs

Name: **EBR-1\_7.Green**  
Number of FoVs in study: **465**  
Number of cells in study: **366385**  
Number of genes in study: **1000**  
Study created under version: **1.3.2**

EXPORT

**Flow cells**

FoVs

EBR-1\_7.Green  
Cell segmentation profile: Initial Segmentation (1)

☒ 1  
☐ 2  
☐ 3  
☐ 4  
☐ 5  
☐ 6  
☐ 7  
☐ 8  
☐ 9  
☐ 10  
☐ 11  
☐ 12  
☐ 13  
☐ 14  
☐ 15  
☐ 16  
☐ 17  
☐ 18  
☐ 19

**Pipeline run**

No Executed Pipelines

**No pipeline selected**  
Select one or use the button below to create



RUN NEW PIPELINE  
DOWNLOAD LOGS

No details available for this study

# Traditional Export

- Select ExportFlatFiles at the top and enter the information as follows:
- Destination S3 file path:  
`s3://na-data-export/na-stjude/`
- Destination AWS access key:  
`AKIAZ55PQIPFTDHD25X4`
- Destination AWS secret key:  
`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`
- Destination AWS region:  
`ca-central-1`

Run pipeline

Run name: EBR-1\_7\_Green    ExportFlatFiles      CUSTOM PIPELINE

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### ExportFlatFiles

Input Parameters

Module version  
Version 2

- ☒ Generate count matrix file
- ☒ Generate cell metadata file
- ☒ Generate transcripts file
- ☒ Generate cell boundaries
- ☒ Generate FOV position file
- ☒ gzip files, does not affect LoadNanostrin

Output Folder Name  
EBR-1\_7\_Green

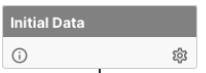
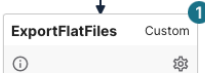
Destination S3 file path  
s3://na-data-export/na-stjude/

Destination AWS access key  
AKIAZ55PQIPFTDHD25X4

Destination AWS secret key  
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

Destination AWS region  
ca-central-1

Destination AWS session token, if configured

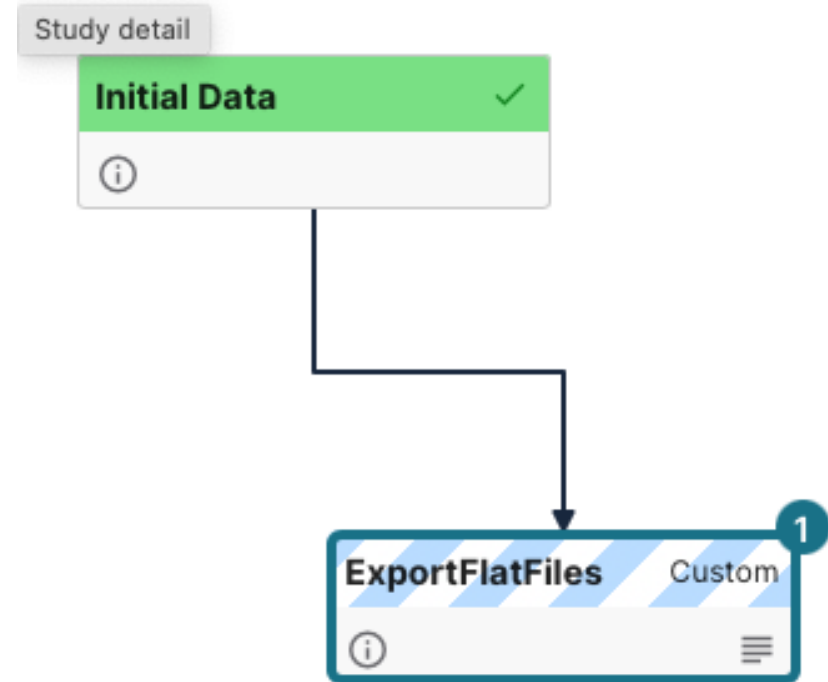
  


CLOSE    CREATE AND RUN    CREATE



# Traditional Export

- This is what it looks like once the export is running.



# Traditional Export

- To export other files (not flat files), you can export them using a different module. Select Export RAW instead of ExportFlatFiles.
- However, you may need to recreate the study to do so.

# Retrieval S3

- Use FileZilla on the server.
- Enter the following information and then download the files:
- Hostname: `s-1dcf1f5ded96458d9.server.transfer.ca-central-1.amazonaws.com`
- Username: `stjude`
- Password: `0Xkx,^4S.;j(vkquW3C6`
- Port: 22

