



NATIONAL CANCER INSTITUTE
Center for Cancer Research

10x Genomics Xenium Analyzer

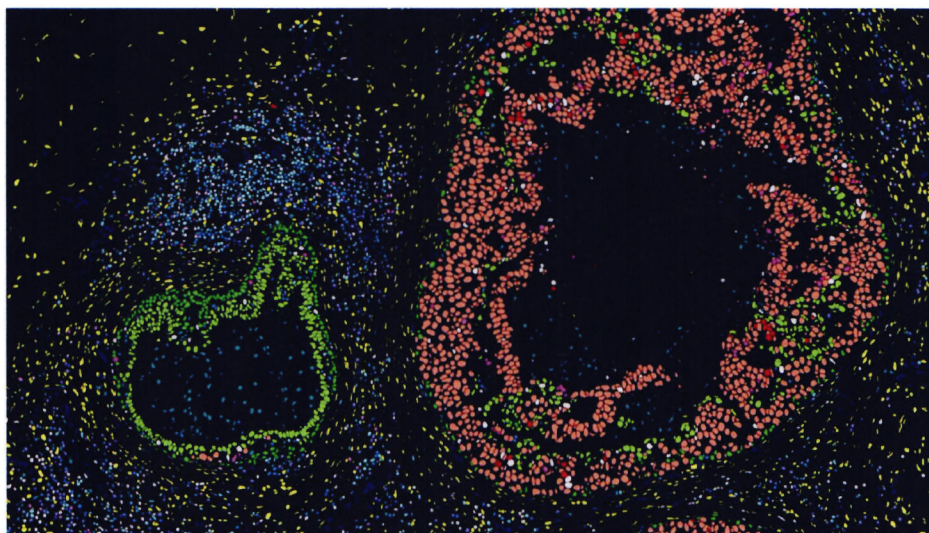
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/ 10x Genomics Xenium Analyzer

What is Xenium?

Xenium is a high-resolution, imaging-based in situ spatial profiling technology from 10x Genomics that allows for simultaneous expression analysis of RNA targets (currently in range of 100's) within the same tissue section. This assay can identify the location of target transcripts within the tissue, providing a single cell resolution map of expression patterns of all genes that are included in the selected probe panel. Researchers can choose between off-the-shelf panels of genes designed to identify cell types and interrogate specific phenotypes, add on 50-gene or 100-gene panels to these off-the-shelf panels, or design a full custom standalone panel to specifically tailor for their tissue and research questions.

The current version of the assay uses DAPI nuclear stain as the tissue morphology marker to inform on platform segmentation of individual cell borders, but data can be re-processed using third-party segmentation tools, and soon will also leverage additional morphology markers. The number of targets is current limited to approximately 500 genes, though future panels are promised at 1000 or 5000-plex and will also allow simultaneous profiling of protein expression targets as well. Data is easily viewable with provided desktop tools, and compatible with a rapidly developing array of downstream third-party analysis tools.



Key Features

- **Single-Cell Resolution:** Spatial information at the single-cell level post-segmentation.
- **Sensitive and Accurate Chemistry:** Padlock probe and rolling circle amplification promote greater specificity and allow better sensitivity.
- **Speed:** Short sequencing time and onboard image data processing provide viewable data quickly.

How Does it Work?

Xenium starts with FFPE or fresh frozen sections on specific Xenium slides. The section tissue is processed and selected probes hybridized to the RNA targets within the tissue. Bound probes are ligated, forming a circular template that allows rolling circle amplification of the probe and a unique barcode. On the Xenium platform, the tissue with amplified probe products are sequenced through a series of cycles and onboard image data processing that allow identification and location of each transcript target. Resulting data is immediately viewable and is compatible with a easy to use data viewer and with many third-party downstream analysis tools, which continue to rapidly develop.

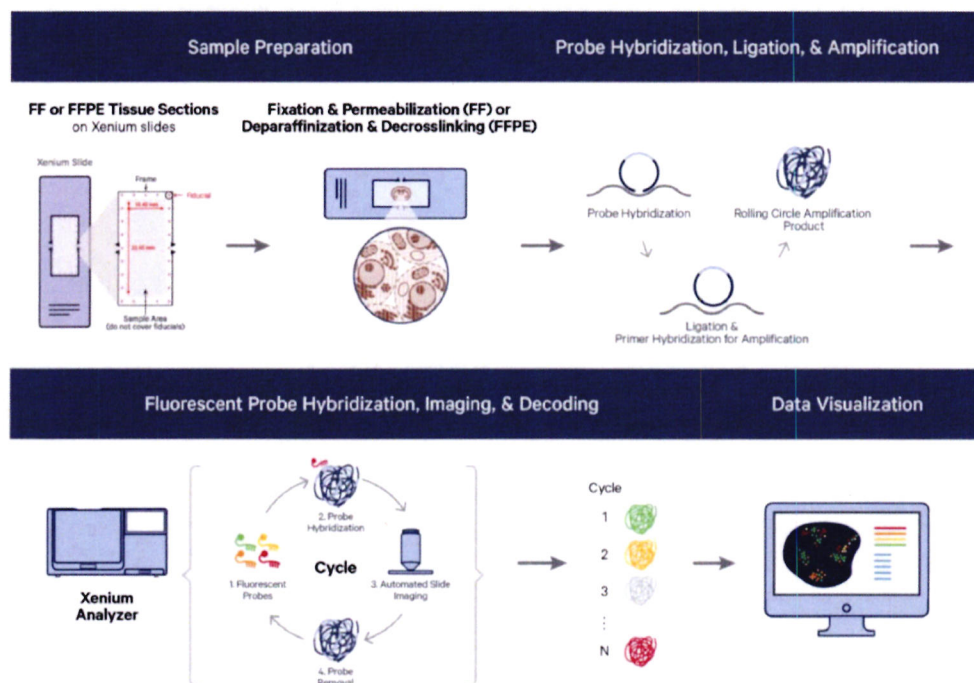


Figure 1 – Xenium General Workflow (Diagram from 10x Genomics)

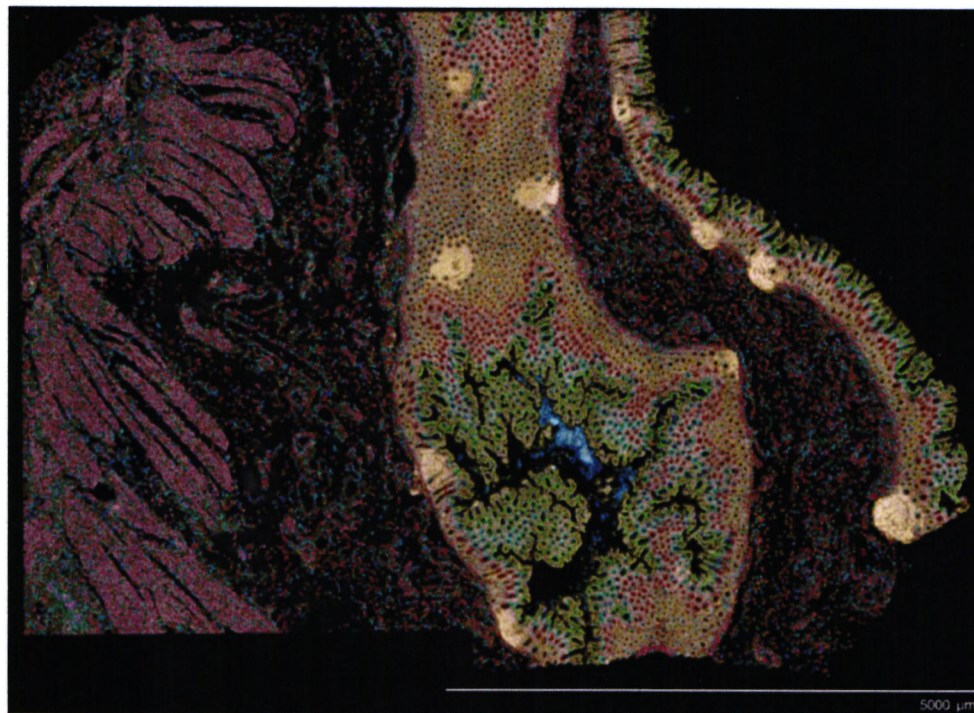


Figure 2 – Colon tissue sample analyzed with an off-the-shelf predesigned panel, with segmented cells color coded based on their gene expression profiles. (Data from 10x Genomics)

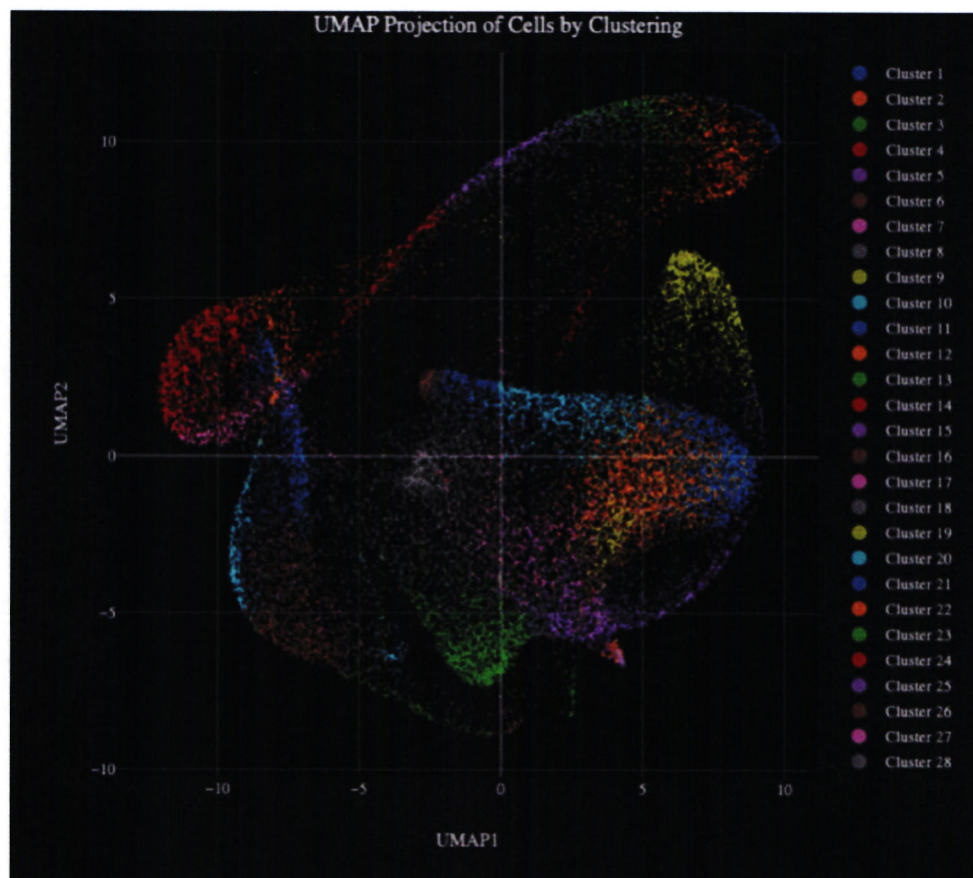


Figure 3 – UMAP plot of resulting Xenium data from sample shown in Figure 2, with cluster designations and UMAP showing differences in gene expression. (Data from 10x Genomics)

Project Support

To get more information or to discuss a potential supported project at CCR, please contact the Single Cell Analysis Facility (SCAF).

[Contact SCAF](#)

Disclaimer: The information provided here is based on the latest available data and may be subject to updates.

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