

10X Genomics Spatial Transcriptomic Services

Genomics Spatial Transcriptomics.

Product Overview

Capturing the spatial organization of gene expression across tissue has traditionally been difficult to attain at high resolution. Broad Clinical Labs' **10X Genomics Spatial Profiling Technology** services bring spatial context into sharp focus, resolving RNA expression within intact tissue and enabling researchers to better understand how distinct cell types interact, respond to therapeutic intervention, and contribute to disease progression.

Our team of experts is available for consultation and experimental design ahead of project initiation to determine the best spatial technology for your application.

Working with either FFPE or Frozen Tissue, padlock target probe pairs bind to target RNA molecules *in situ*. After proximal ligation, the complex undergoes rolling circle amplification, forming a fluorescent, imaggable amplicon which is read out via multiple cycles of probe binding, imaging, and cleavage. Additionally, DAPI-based and multimodal segmentations are performed to identify nuclear and cellular boundaries for higher-resolution transcript assignment.

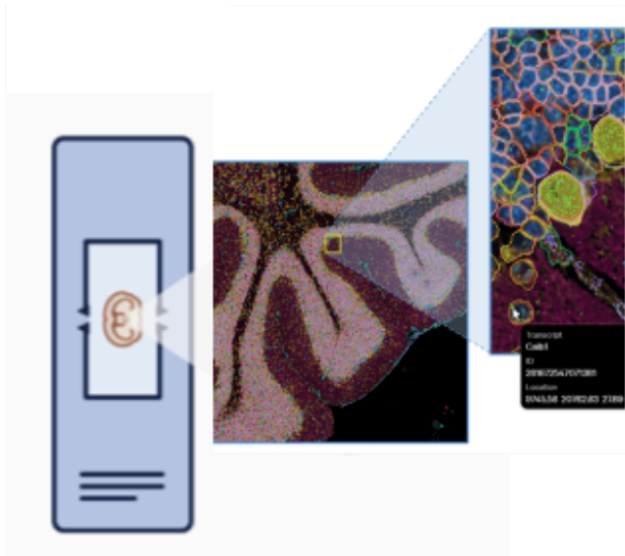


Figure 1. High-level view of cell segmentation and transcript identification from 10X

Alongside our **10X Xenium V1** and **Xenium Prime** services, Broad Clinical Labs is excited to begin offering the **10X Atera**, delivering whole transcriptome scale data at high sensitivity. **Inquire today at BCLServices@broadinstitute.org.**

	10X Xenium - V1	10X Xenium - Prime	10X Atera
Genes targeted	50-480	5,000	>18,000
Imaging area	2.35 cm ²	2.35 cm ²	>5 cm ²
Tissue Types	FFPE or Fresh Frozen Tissue	FFPE or Fresh Frozen Tissue	FFPE or Fresh Frozen Tissue
Supported Species	Human, Mouse	Human, Mouse	Human

What's Included

- Project consultation and design services
- Sample receipt and incoming visual QC
- Pre-processing histology services to section tissue and affix to slides (optional)
- 10X Xenium v1, Xenium Prime 5k, or Atera sample preparation
- Imaging readouts of 50-5,000 genes (Xenium) or whole transcriptome (Atera) using standard or custom panels
- Post-processing H&E imaging or slide return (optional)
- Data processing, QC, delivery to customer-owned cloud environment, or hosted within our partner Trusted Research Environment, Manifold

Input Requirements

- FFPE or Fresh Frozen tissue, sliced onto appropriate slides, or provided embedded in paraffin or OCT, respectively
- Minimal sample metadata

Data Deliverable

- OME-TIFF image files
- Cell-by-gene matrices
- Cell and nucleus segmentation files
- Transcript quality/localization Parquet files
- QC metric files
- H&E staining images (optional add-on)