

# RNA & Spatial Profiling Shared Resource

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## Overview

The RNA & Spatial Profiling SR has the Chromium X, CytAssist, and Xenium platforms from 10x Genomics and can provide investigators with single-cell RNA, single-cell ATAC library preparation of single cells isolated from live cultures or fixed tissues and cells (including FFPE). We can also perform library preparation for Visium SD and HD spatial transcriptomics on FF and FFPE tissue sections using the CytAssist. High-plex spatial in situ profiling at the subcellular level can be performed using the Xenium platform.

## Key Services

- Single cell library preparation for:
  - Single-cell gene expression
    - Life or fixed cells
    - FFPE blocks and FF tissues
  - Single-cell ATAC sequencing
  - Single-cell multiome ATAC and gene expression
  - Single-cell multiome CRISPR perturbation and gene expression
  - Single-cell multiome CRISPR perturbation and cell surface proteins
  - Single-cell multiome gene expression and cell surface proteins
- Spatial transcriptomics library preparation for Visium SD and HD
- Spatial in-situ RNA hybridization using Xenium
  - Up to 5000 genes at subcellular levels
- Assay design consulting

## Major Equipment /Technologies

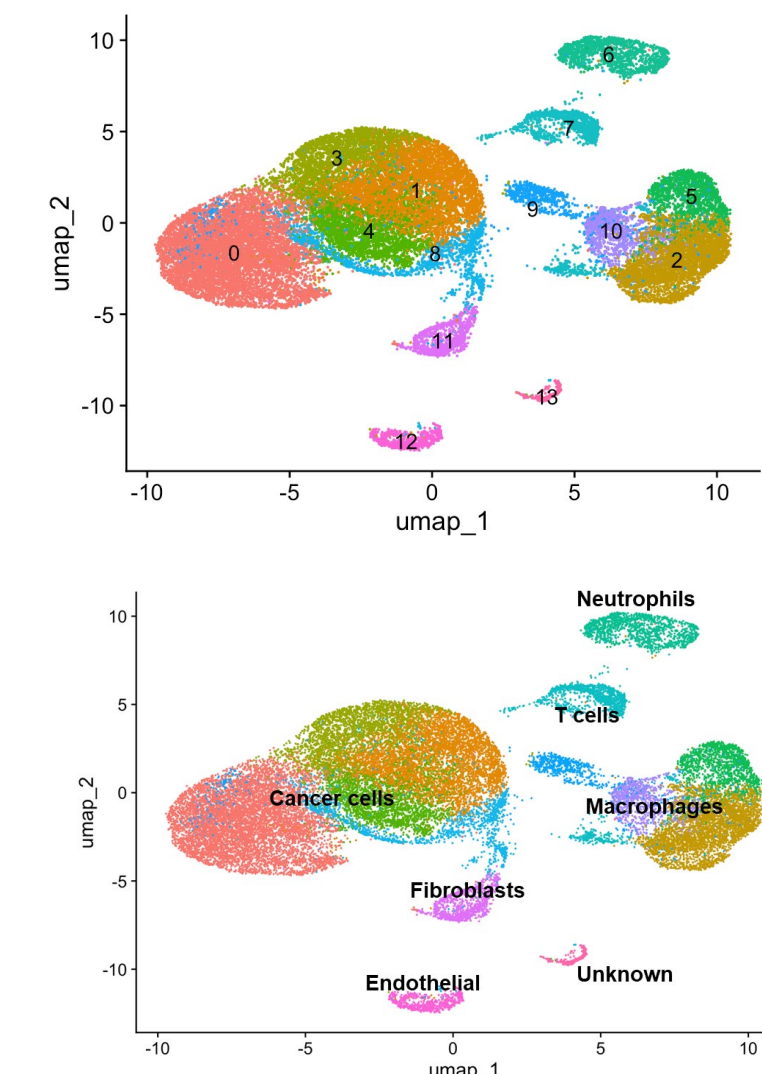
- High-throughput full-range Chromium X to profile single-cell:
  - mRNA: Flex assay; 3' and 5'
  - immune profiling
  - CRISPR perturbations
  - chromatin accessibility
- Visium CytAssist
- Xenium in situ
- 3x Biorad Thermocyclers: hybridization and amplification steps

## Key Personnel

RNA & spatial profiling Director Petra den Hollander, PhD

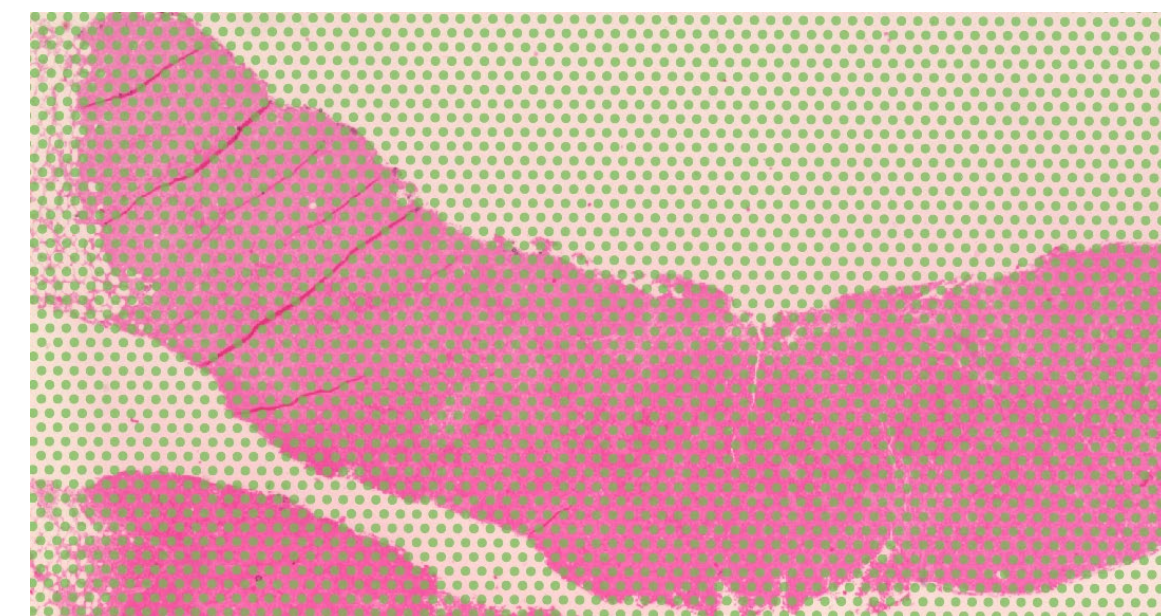
## Examples of Scientific Impact

### Chromium



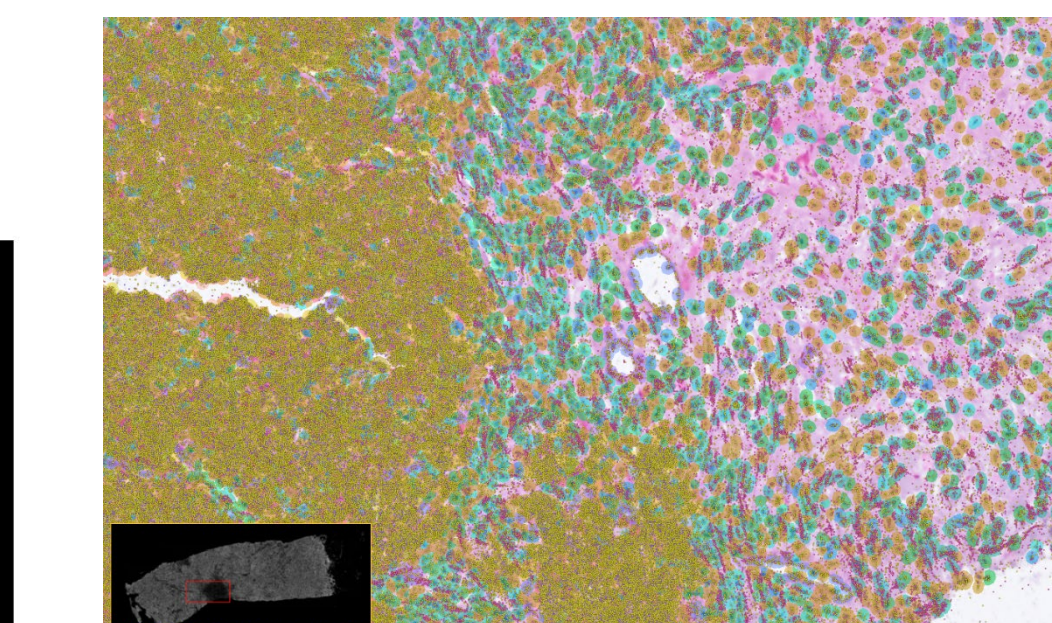
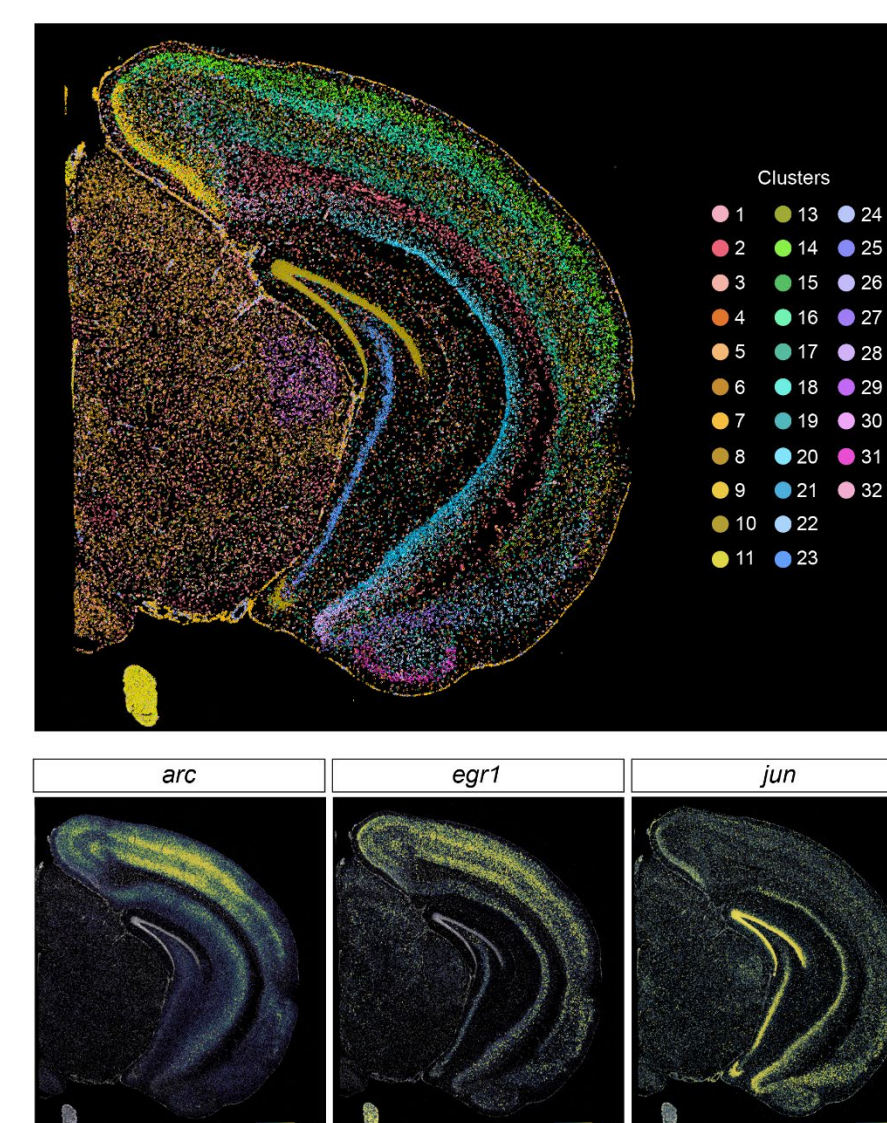
- Species agnostic single-cell RNA sequencing of fresh tissues and cells
- Single-cell RNA sequencing archival tissue from human or mouse
- Chromatin accessibility changes
- Multiomic profiling of immune diversity such as BCR and TCR
- Assessment of CRISPR perturbation

### Visium



- Whole transcriptomic analysis in the tissue context
- Visium HD allows for single-cell level analysis

### Xenium



- Characterization of triple-negative breast cancer core-needle biopsies using Xenium
- molecular characterization of glomeruli in the mouse olfactory bulb using Xenium

## Users and Projects

- Patrycja Dubielecka Lab
  - Spatial transcriptomics analysis of AML
  - Spatial transcriptomics analysis of Lymphoma
  - Xenium analysis of Lymphoma
- Benedito A Carneiro
  - Therapy resistance in prostate cancer through senescence mechanisms using scRNA-sequencing analysis.
- Sendurai Mani Lab
  - Characterization of triple-negative breast cancer core-needle biopsies using single-cell RNA sequencing, spatial transcriptomics and Xenium
  - Characterization of PDAC using single-cell RNA sequencing and spatial transcriptomics
  - Discovery of pathways to overcome resistance to chemotherapy using single-cell RNA sequencing
  - Identification of the mechanism by which small molecule inhibitors reduce stemness and metastasis.
- Alper Uzun and Ali Amin
  - Spatial transcriptomics analysis of bladder cancer using the Visium HD platform
- Mukesh Jain Lab
  - Investigation of aortic aneurism using spatial transcriptomics
- Alexander Fleischmann Lab
  - molecular characterization of glomerular identity in the mouse olfactory bulb using Xenium
  - Spatially-resolved activity-dependent gene expression during odor place association

## Interactions with LCC Shared Resources

- Brown Genomics and spatial proteomics
- Cancer Bioinformatics
- Translational Oncology
- Single Cell Technologies
- Cancer Biospecimen Bank
- Subcellular level analysis with:
  - Predesigned panels
    - 7 Human
    - 2 Mouse
  - Prime 5K human or mouse pan tissue & pathways panel
  - Custom add-on panel of up to 100 genes
  - Custom stand-alone panel of up to 480 genes
  - Ready-to-use protein subpanels:
    - 27 human immune and TME markers