

Single Cell/Nuclei Sequencing and Spatial Transcriptomics

NYGC's Technology Development lab provides comprehensive single-cell, spatial, and multi-omics genomics expertise to support complex research projects. As an early adopter of the 10x Genomics portfolio, NYGC has deep expertise across a broad range of single-cell and multi-omics applications, including single-cell RNA sequencing, single-nucleus RNA sequencing, Single Cell Multiome (ATAC + gene expression), CITE-seq, ECCITE-seq, ASAP-seq, DOGMA-seq, DLP+ amplification-free single-cell whole-genome sequencing, and long-read single-cell sequencing.

NYGC also offers expertise in spatial genomics technologies, including 10x Genomics Visium and Xenium platforms. Through close collaboration between Technology Development, Computational Biology, and research investigators, NYGC develops integrated analytical strategies and multimodal approaches to extract meaningful biological insights from complex genomic datasets.

Due to the project-specific nature of single-cell and spatial genomics offerings, and the variability that comes from tissue types and sample storage methods, project planning typically begins with an initial consultation involving our Technology Development and Project Management teams. Pricing and turnaround times are customized based on the scope and scale of the project and are provided following discussion with our teams.

10x Single Cell/Nuclei Sequencing

Submission Requirements

To support high-quality single-cell data generation, samples should meet the following minimum requirements:

- **Sample type:** Fresh frozen tissue or live cell suspension
- **Viability:** Greater than 90% viability as measured by Trypan Blue staining (for live cell suspensions)
- **Cell input:**
 - Minimum of 100,000 cells per sample for multiplexed experiments (up to 10 samples)
 - Up to 1 million cells for single-sample experiments

Standard Analysis

- Alignment of raw reads to human or mouse genome, if applicable
- Quality control summary metrics
- Gene quantification

- Additional analyses specific to assay

Standard Deliverables

- FASTQ files
- Aligned data
- Count matrix (gene-cell UMI count matrix)
- Additional assay-specific deliverables

10x Spatial Transcriptomics

NYGC offers end-to-end 10x Genomics Xenium spatial transcriptomics services, enabling highly sensitive, targeted RNA profiling at subcellular resolution in fresh frozen, fixed then frozen, and FFPE tissues. 10X Genomics offers a variety of pre-designed tissue specific ~350 target genes Xenium V1 panels, as well as the 5000 genes Xenium Prime panel. Custom panels of up to 100 additional genes can be added on to either Xenium V1 or Xenium Prime panels. Fully custom panels of up to 480 target genes can also be designed. Supported Xenium applications include oncology, spatial cell typing, tumor microenvironment, developmental biology, etc.

Submission Requirements

High-quality tissue preparation is essential for successful Xenium spatial profiling. NYGC works with researchers during project planning to review sample characteristics and recommend the appropriate workflow.

Compatible sample types include:

- Fresh frozen tissue
- Formalin-fixed, paraffin-embedded (FFPE) tissue

Tissue requirements:

- Tissue sections should be prepared on compatible Xenium slides
- Recommended section thickness:
 - Fresh frozen tissue: approximately 10 µm
 - FFPE tissue: approximately 5 µm
- Tissue quality should be suitable for preservation of RNA integrity and spatial morphology

For FFPE samples, tissue quality assessment prior to submission is recommended. Samples with lower RNA quality or challenging tissue characteristics may require additional review to determine suitability for Xenium analysis.

Standard Analysis

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Standard Deliverables

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Frequently Asked Questions – Single Cell/Nuclei Sequencing and Spatial Transcriptomics

What information is needed to start a project?

To begin planning a library sequencing project, we typically request:

- Species and tissue type or cell source
- Assay requirements, including whether additional modalities such as CITE-seq, ECCITE-seq, or cell hashing
- Target number of cells and desired final cell recovery
- Required timeline
- Data delivery requirements
- Any planned downstream analyses

How are projects initiated?

Once project scope and service requirements have been finalized with your NYGC Project Manager, NYGC will provide a formal service quote outlining the agreed-upon deliverables, pricing, and project details. To begin project execution and submit samples, NYGC requires a signed copy of the quote and an approved purchase order (PO). For large-scale projects, additional discussions regarding customized terms and conditions may be accommodated.

What is the expected turnaround time?

All turnaround times can be found on our '[main research services page](#)'.

How should samples be submitted?

Materials submitted for single cell, single nuclei, and spatial transcriptomics projects, including FFPE and fresh frozen tissue, and cell suspensions, can be shipped directly to NYGC. Your Project Manager will provide the appropriate shipping address and an electronic sample manifest to complete prior to shipment. Please provide at least 24 hours' advance notice before shipping samples to ensure proper receipt and processing. To maintain sample integrity and ensure successful delivery, samples should arrive during NYGC business hours, as the laboratory is closed on weekends and holidays. For those in the NYC area, dropping off samples directly may also be advisable.

Do you offer downstream alignment and analysis services?

Depending on the library type and species, yes, for an additional cost. See more about Bioinformatics and Data Analysis Services on [‘main research services page’](#).

How is data returned?

We support data delivery to a variety of client-managed endpoints and storage environments. Before delivery, we can perform a test transfer to confirm connectivity and ensure efficient transfer of large sequencing datasets.