

10x Genomics Spatial Transcriptomics Services

Overview

MGC offers 10x Genomics Visium Spatial Gene Expression and Visium HD Spatial Transcriptomics services using the CytAssist platform.

These technologies enable genome-wide transcriptomic profiling while preserving the spatial organization of cells within intact tissue sections.

Project Consultation

Q: Is a pre-submission consultation required?

A: Yes. All spatial transcriptomics projects require consultation with MGC staff before sample collection and submission.

During the consultation, we will discuss:

- Tissue type and preservation method
- Embedding and sectioning strategies
- Assay compatibility
- Experimental design
- Sequencing requirements
- Data analysis plans

Important: Tissue collection, preservation, embedding, and sectioning procedures should be discussed with MGC before samples are generated. Improper sample handling is the most common cause of project failure and may result in poor RNA quality, tissue detachment, or reduced spatial resolution.

Supported Sample Types

Q: What tissue types are compatible with Visium assays?

A: Commonly supported sample types include:

- Fresh-frozen tissue sections
- FFPE tissue sections
- OCT-embedded tissues

Animal, plant, and microbial samples may also be compatible, but feasibility should be evaluated during project consultation.

Some tissues require assay optimization prior to processing.

Tissue Preparation Requirements

Q: What are the tissue quality requirements?

A: Successful spatial transcriptomics experiments depend heavily on tissue quality.

Recommended practices include:

- Preserving tissue promptly after collection
- Maintaining high RNA integrity
- Minimizing tissue folding, tearing, or detachment
- Providing complete sample metadata
- Retaining adjacent sections for histological validation

Investigators should provide information regarding:

- Tissue origin
- Preservation method
- Embedding medium
- Experimental objectives

Sequencing Requirements

Q: How much sequencing is required?

A: Sequencing depth depends on assay type, tissue complexity, capture area, and project goals.

Project-specific recommendations will be provided during consultation.

Bioinformatics Support

Q: What data analysis services are provided?

A: Bioinformatics Core provides:

- Sequencing data generation
- Primary processing using Space Ranger

- Spatial image alignment
- Generation of expression matrices
- Visualization files for downstream analysis

Advanced analysis services are available upon request, including:

- Spatial clustering
- Cell-type annotation
- Differential expression analysis
- Integration with single-cell RNA-seq datasets
- Cell deconvolution
- Custom bioinformatics analyses

Additional charges may apply.

Important Considerations

Q: What factors influence project success?

A: RNA quality and tissue preservation are the most important determinants of spatial transcriptomics data quality.

Additional considerations include:

- Spatial transcriptomics measures gene expression within spatially resolved tissue regions and should not be considered equivalent to single-cell RNA sequencing.
- Tissue-specific optimization may be required for novel sample types.
- Pilot studies are strongly recommended for new tissues or experimental systems.

MGC cannot guarantee specific gene detection rates, sequencing metrics, or biological outcomes.