Visualize gene expression within the tissue context

Spatial Gene Expression

Visium Spatial Gene Expression measures either the whole transcriptome or a defined set of transcripts in intact tissue sections and maps where gene activity is occurring. With whole transcriptome analysis, discover and reveal the spatial organization of cell types, states, and biomarkers. Focus on specific genes or pathways of interest with our pre-designed oncology, immunology, or neuroscience targeted gene panels. Combine with immunofluorescence for simultaneous visualization of protein and gene expression. Visium Spatial Gene Expression makes it easy to incorporate spatial transcriptomics technology into standard methods of tissue sectioning and H&E or immunofluorescence staining. Never before have you been able to scale characterization of tissue sections with RNA, protein, and morphology in the same sample with simple, complementary workflows.

Highlights

- Discover new tissue biomarkers by examining histology, protein, and mRNA from the same tissue section
- Reveal the spatial organization of newly discovered cell types, states, and biomarkers with whole transcriptome analysis
- Validate discoveries or hone in on all relevant genes with pre-designed targeted gene panels
- Unravel the biological architecture and understand the spatial relationship between cells within normal and diseased tissue
- Analyze and understand gene and protein expression heterogeneity and how it contributes to your system

Figure 1. Gain high-resolution characterization of gene and protein expression in the tissue context. A. Visium Spatial Gene Expression provides unbiased or targeted gene expression readout in intact tissue sections. The Visium Spatial Gene Expression workflow is compatible with H&E to provide morphological context and immunofluorescence staining to provide both gene and protein expression patterns from the same tissue section. B. Spatially resolved gene expression and spot clustering are demonstrated in a coronal mouse brain section. Shown on the left is an H&E image, followed by an overlay of Visium data for total unique molecular identifiers (UMIs) for whole transcriptome analysis or spatially naïve spot clustering based on total differentially expressed genes. Listed on the far right are the most highly expressed genes in Cluster 4.
Fresh-frozen tissue is sectioned, placed on a library preparation slide, fixed, stained with either H&E or immunofluorescence, imaged, and permeabilized to release mRNA that binds to spatially defined capture spots on the slide. cDNA is synthesized from captured mRNA and washed off the slide before sequencing library construction. Whole transcriptome or targeted gene expression libraries are sequenced and data can be analyzed and visualized using Space Ranger and Loupe Browser, our easy-to-use data analysis and visualization software. Loupe Browser enables direct comparison of gene expression with histology or immunofluorescence protein data. The entire workflow, from sample to sequencing-ready library, can be completed in one day.

Figure 2. Streamline experimentation with a ready-to-use, robust workflow for whole tissue section analysis. Fresh-frozen tissue is sectioned, placed onto a library preparation slide, fixed, stained with either H&E or immunofluorescence, imaged, and permeabilized to release mRNA that binds to spatially defined capture probes, allowing for the capture of gene expression information. cDNA is synthesized from captured mRNA and then washed off the slide before sequencing library construction. Whole-transcriptome or targeted gene expression libraries are sequenced and data can be analyzed and visualized using Space Ranger and Loupe Browser, our easy-to-use data analysis and visualization software. Loupe Browser enables direct comparison of gene expression with histology or immunofluorescence protein data. The entire workflow, from sample to sequencing-ready library, can be completed in one day.

Figure 3. Get more from a single tissue section with immunofluorescence, histology, and targeted or whole transcriptome gene expression in the same section. A. Human breast cancer tumor section stained for CD3 by immunofluorescence, overlaid with Visium data containing total UMI counts, and pathologist annotations for regions of morphological interest. On the right are listed the most highly expressed genes in Cluster 4, which overlaps with a region of high CD3 protein detection. B. Shown is a human breast cancer section with H&E staining overlaid with pathologist annotations for regions of morphological interest; pathologist annotations converted to Visium data for direct concordance with gene expression spots; total UMIs from Visium gene expression data for 196 breast cancer–related genes selected from the Human Pan-Cancer Panel, and expression level of ERBB2, a specific breast cancer–related gene.

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Product configuration

Visium Spatial Gene Expression Slide And Reagent Kit
- Contains all the slides and reagents to optimize up to 4 tissue types
- Includes all the reagents and slides for 4 (1 slide) or 16 (4 slides) reactions
- Each slide contains 4 capture areas (6.5 x 6.5mm) with 5,000 barcoded spots per capture area
- Each spot is 55 µm in diameter (100 µm center to center between spots)

Visium Spatial Tissue Optimization Slide And Reagent Kit
- Contains all the slides and reagents to optimize up to 4 tissue types
- Includes all the reagents and slides for 4 (1 slide) or 16 (4 slides) reactions

Compatible with the following tissues
- Human
  - Brain, Breast, Breast cancer, Heart, Kidney, Large intestine, Lung, Lung cancer, Lymph node, Ovary, Spleen, Spinal cord
- Mouse
  - Brain, Eyes, Heart, Knee, Large intestine, Liver, Lungs, Ovary, Quadriceps, Small intestine, Spleen, Stomach, Testes, Thyroid, Tongue
- Rat
  - Brain, Heart, Kidney

*Not an inclusive list; represents list of tissues tested internally to date, but other tissues may be compatible. Tissue compatibility updates will be posted to the support site.

Sample prep
- Imaging
- Barcoding & cDNA synthesis
- Library construction
- Sequencing
- Data visualization

Imaging
- H&E for tissue context
- IF for protein co-detection

Barcoding & cDNA synthesis
- cDNA synthesis
- Permeabilization
- Staining & imaging

Library construction

Sequencing

Data visualization

Product features
- Integrate easily with your current laboratory methods and tools for tissue analysis, letting you start your Spatial Gene Expression experiments immediately
- Avoid the need for dissociating your samples before conducting gene expression studies to retain spatial context
- Broaden your reach beyond predefined regions of interest to analyze the entire tissue section at once so you don’t miss out on unanticipated results
- Combine with immunofluorescence staining and imaging to gain multiomic characterization in the spatial context
- Combine with Targeted Gene Expression Panels to focus on the genes that matter most and accelerate your studies into actionable insights

Product Sheet

10x Genomics
**Research areas**

- Cancer Biology
- Immuno-oncology
- Molecular Pathology
- Cell and Gene Therapies
- Neurodegenerative Disease
- Brain Injury
- Neurodevelopment
- Immunobiology
- Infectious Disease
- Inflammation
- Stem Cell and Developmental Biology

**Applications**

- Tumor Heterogeneity
- Tissue Morphology
- Mechanisms of Tissue Development
- Response to Therapeutic Interventions
- Biomarker Discovery
- Cell Atlasing

**Products**

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<th>Products</th>
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**Space Ranger**

[download](https://support.10xgenomics.com/spatial-gene-expression/software/pipelines/latest/what-is-space-ranger)

**Loupe Browser**

[download](https://support.10xgenomics.com/spatial-gene-expression/software/visualization/latest/what-is-loupe-browser)