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 fresh frozen 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. Easily incorporate spatial transcriptomics into standard methods of tissue sectioning and hematoxylin and eosin (H&E) or immunofluorescence (IF) 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 biomarkers by examining histology, protein, and mRNA from the same fresh frozen 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

- Explore the spatial relationship between cells within normal and diseased tissue

- Examine gene and protein expression heterogeneity and how it contributes to your system
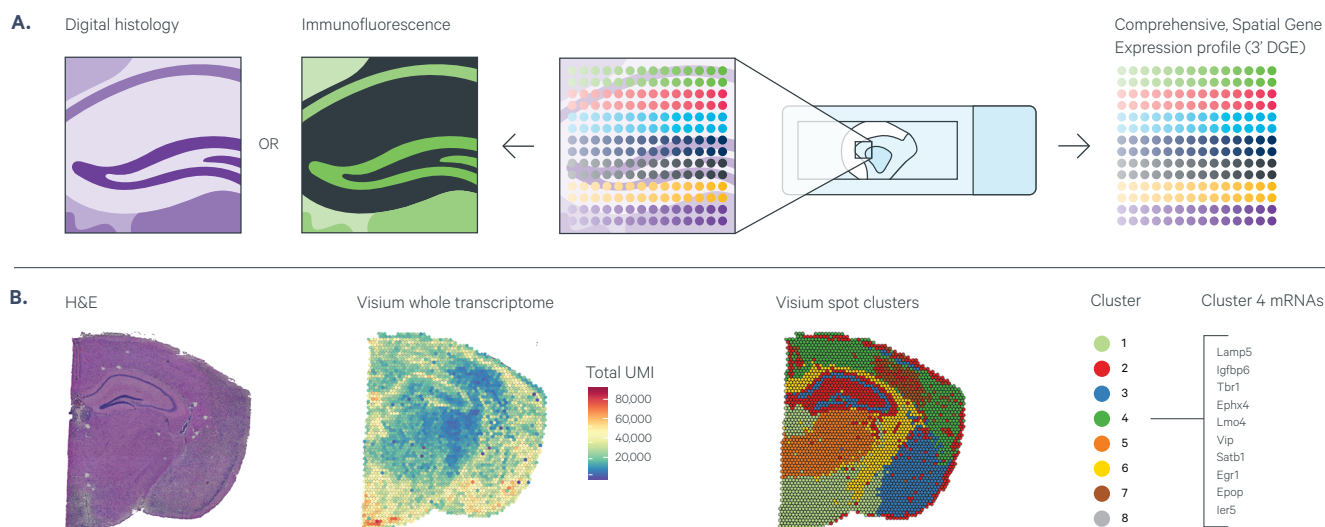

Figure 1. Gain high-resolution characterization of gene and protein expression in the tissue context. A. Visium Spatial Gene Expression provides unbiased or targeted gene expression readout in intact sections from fresh frozen tissue. The workflow is compatible with H&E to provide morphological context and IF staining to co-detect protein from the same tissue section. **B.** Shown on the left is an H&E image for a coronal mouse brain section, 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.

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

- Experience unparalleled insights—full tissue coverage, high resolution, increased sensitivity, and greater depth
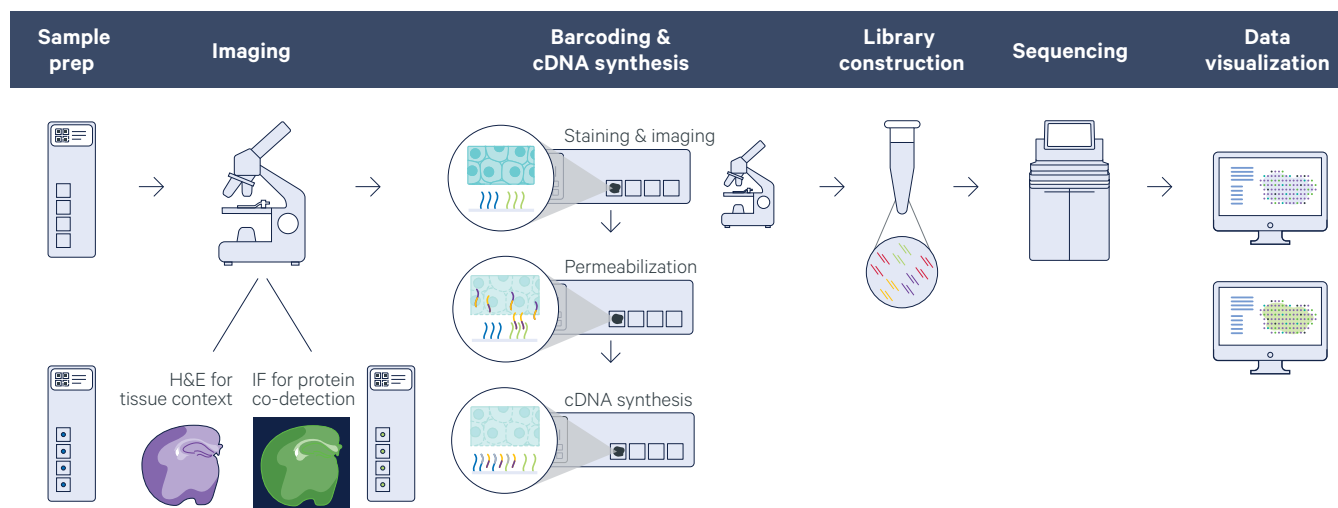

Figure 2. Streamline experimentation with a ready-to-use, robust workflow for whole tissue section analysis. Fresh frozen tissue is sectioned, placed onto a library preparation slide, fixed, stained with either H&E or immunofluorescence, imaged, and permeabilized to release mRNA that binds to spatially barcoded 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.
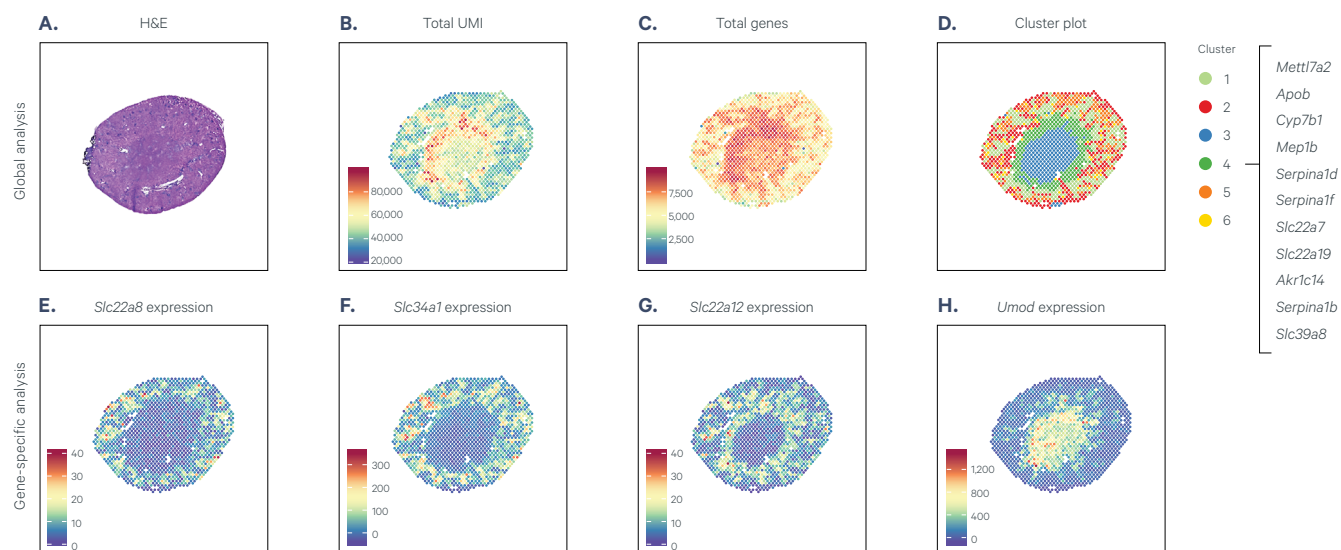
Figure 3. Spatially resolved clustering and gene expression in the mouse kidney. Top row depicts global analysis of tissue morphology, gene expression, and clustering, while the bottom row depicts gene-specific analysis of a few select genes. **A.** A coronal mouse kidney section was H&E stained, imaged, then processed through the Visium Spatial Gene Expression for fresh frozen tissue workflow. Shown are image overlays containing data for UMI counts (**B**), total gene count (**C**), and spatially naïve clustering based on total differentially expressed genes. **D.** The top 11 genes that are more highly expressed in Cluster 4 (green) than any other cluster is shown to the far right. Examples of the many mRNAs that can be analyzed in a single experiment are also depicted: Slc22a8 (**E**), Slc34a1 (**F**), Slc22a12 (**G**), and Umod (**H**), all coinciding with known expression patterns.
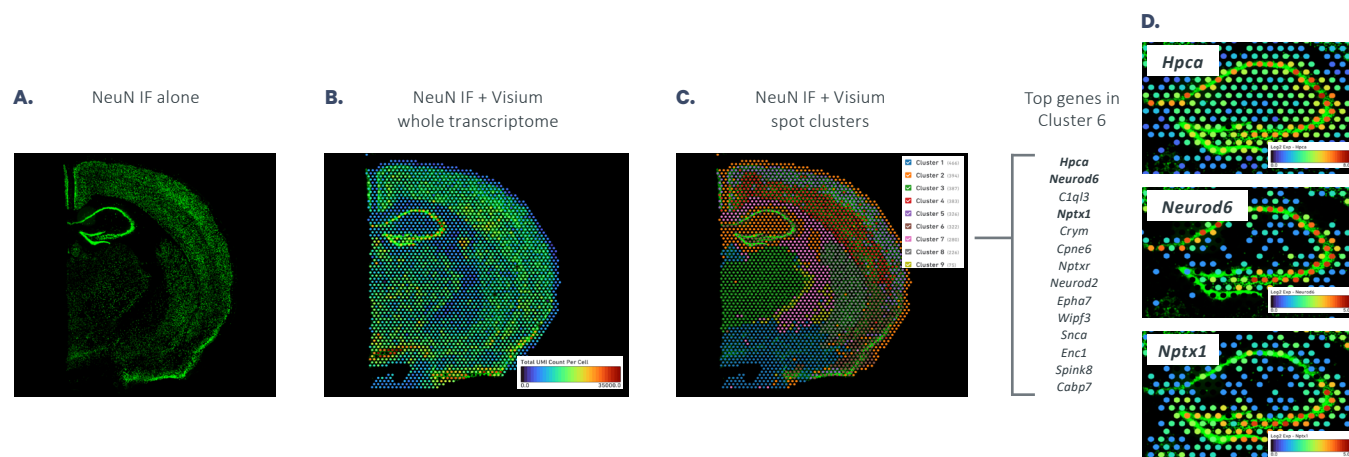

Figure 4. Spatially resolved clustering based on simultaneous gene expression and protein detection in the mouse brain. A mouse brain section was labeled using immunofluorescence to visualize NeuN and then processed through the Visium Spatial Gene Expression workflow. Shown are (**A**) an IF-only image, (**B**) an IF image overlaid with Visium data containing total UMI counts, and (**C**) an IF image overlaid with Visium data for spatially naïve clustering based on total differentially expressed genes. **D.** The top 10 genes that are more highly expressed in Cluster 6 are shown to the right along with example images.

Product specifications

- **Configuration:** Visium Spatial Gene Expression Slide & Reagents Kit for fresh frozen tissue includes all the reagents and slides for 2 (1 slide, 2 capture areas) 4 (1 slide, 4 capture areas) or 16 (4 slides, 16 capture areas) reactions

- **High cellular resolution:** Each capture area (6.5 x 6.5 mm) contains 5,000 barcoded spots that are 55 μm in diameter (100 μm center to center between spots providing an average resolution of 1 to 10 cells per spot)

- **Whole transcriptome analysis:** Profile entire fresh frozen tissue sections from any species

Spatial whole transcriptome profiling products	Product code
Visium Spatial Tissue Optimization Slide & Reagents Kit, 4 samples	1000193
Visium Spatial Gene Expression Slide & Reagents Kit, 4 rxns	1000187
Visium Spatial Gene Expression Slide & Reagents Kit, 16 rxns	1000184
Visium Spatial Gene Expression Accessory Kit	1000194
Visium Spatial Gene Expression Starter Kit	1000200
Visium Gateway Package, 2 rxns	1000316
Dual Index Kit TT Set A, 96 rxns	1000215

Related products	Product code
Space Ranger support.10xgenomics.com/spatial-geneexpression/software/pipelines/latest/what-is-space-ranger	Download
Loupe Browser support.10xgenomics.com/spatial-geneexpression/software/visualization/latest/what-is-loupe-browser	Download

Spatial targeted transcriptome profiling	Product code
Target Hybridization Kit, 16 rxns	1000248
Library Amplification Kit, 16 rxns	1000249
Human Pan-Cancer Panel, 4 rxns	1000260
Human Pan-Cancer Panel, 16 rxns	1000247
Human Immunology Panel, 4 rxns	1000259
Human Immunology Panel, 16 rxns	1000246
Human Gene Signature Panel, 4 rxns	1000258
Human Gene Signature Panel, 16 rxns	1000245
Human Neuroscience Panel, 4 rxns	1000277
Human Neuroscience Panel, 16 rxns	1000278

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