

Visualize Gene Expression within Tissue Organization

Spatial Gene Expression

The complex organization of tissue has made it difficult to discern tissue function at the molecular level in a high-throughput manner. While Immunohistochemistry and H&E staining are foundational tools to understand tissue architecture based on protein expression and morphology of cells, recent advances in spatial transcriptomic technology combine the benefits of traditional histology technologies with the massive throughput of RNA sequencing. The ability to layer on gene expression information provides a clearer, more thorough picture of the biology captured on a tissue slide. Our Visium Spatial Gene Expression Solution makes it easy to implement spatial transcriptomics technology into standard methods of tissue sectioning and staining.

The Visium Spatial Gene Expression Solution measures total mRNA in intact tissue sections and maps where that gene activity is occurring. Easily adoptable within existing lab infrastructure, this solution enables spatially resolved visualization of gene expression in a wide variety of tissues, without the need for target pre-selection. Preserving spatial context while identifying distinct groups of cells offers critical information to understand the relationship of cellular function, phenotype, and location in tissue microenvironments. Now characterize tissue with RNA and morphology in the same sample with very simple, complementary workflows and solutions.

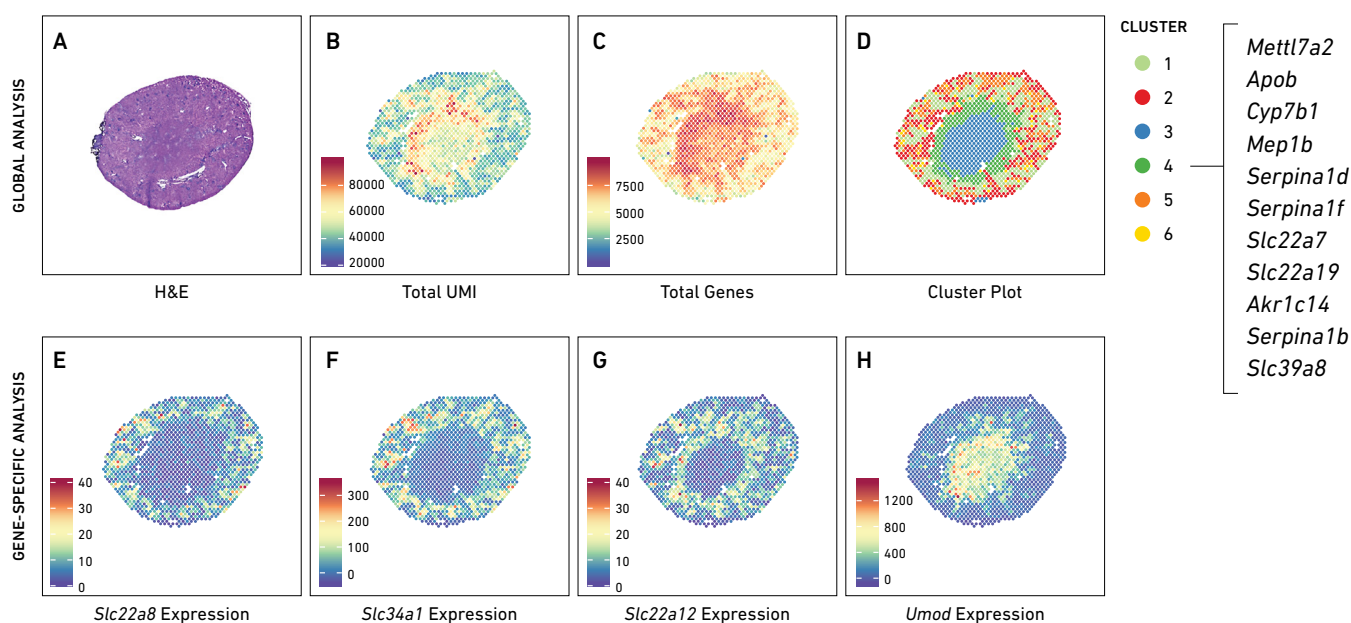


Figure 1. Spatially resolved clustering and gene expression in the mouse kidney. Top row depicts global analysis of tissue morphology, gene expression, and clustering while the bottom row depicts gene-specific analysis of a few select genes. A. A coronal mouse kidney section was H&E stained, imaged, then processed through the Visium Spatial Gene Expression workflow. Shown are image overlays containing data for UMI counts (B), total gene count (C), and spatially naive 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.

Solution Benefits

- Obtain unbiased and high-throughput gene expression analysis for intact tissue sections in a wide variety of sample types
- Examine histological and mRNA profiles from the same tissue section and discover new tissue biomarkers
- Unravel the biological architecture and understand how localized cells interact within normal and diseased tissue
- Avoid the need to dissociate the sample to conduct gene expression studies
- Characterize cell populations without prior knowledge of cell subtypes or cell markers
- Analyze and understand gene expression heterogeneity and how this contributes to your biological system
- Confirm, characterize, or reject morphological conclusions by adding gene expression information

Solution Features

- Ready-to-use, robust workflow, including compatible tissues tested in-house
- Compatible with most tissue types, multiple mouse, rat, and human tissue types such as brain, tumor, kidney, intestine, heart and more.
- End-to-end workflow from section to library within one entire working day
- Optimized on fresh-frozen samples
- 4 capture areas each containing 5000 barcoded mRNA capture spots on a 6.5mm² area (average 1–10 cells captured per spot dependent on tissue type)
- Easy-to-use and convenient software with Space Ranger and Loupe Browser visualization
- Integrates easily with current laboratory methods and tools for tissue analysis
- High resolution and sensitivity

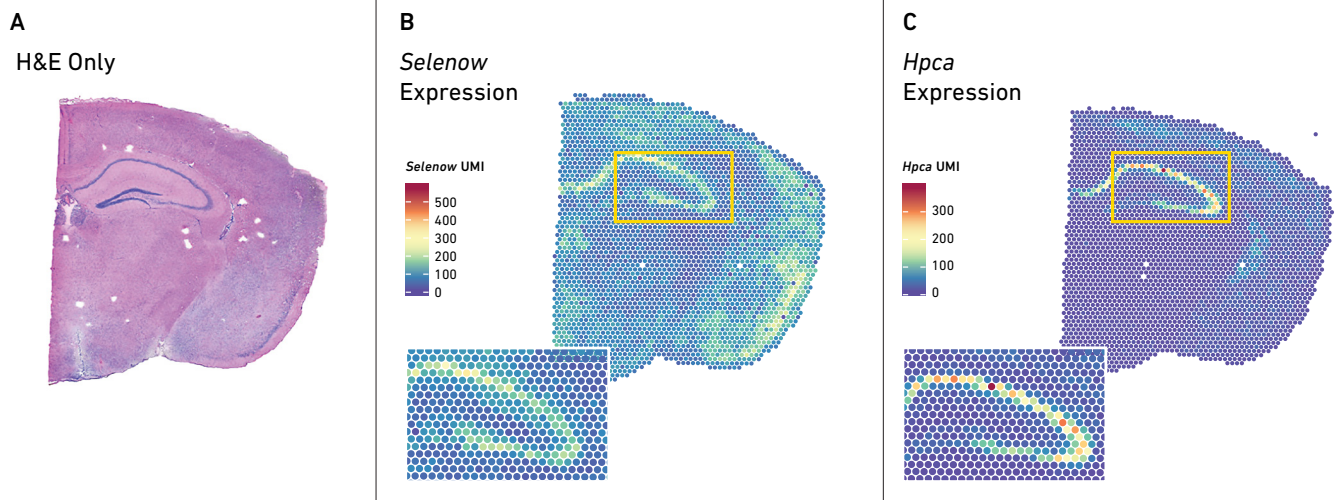


Figure 2. Spatially-resolved gene expression in the mouse brain. A. H&E stained coronal mouse brain section. Spatial mRNA expression data from Selenow (B) and Hpca (C) are shown as examples of genes with known expression patterns in the brain, with predominant hippocampal expression. Expression in the hippocampus is highlighted and coincides with known expression patterns (note that spot size is not to scale).

Research Areas

- Cancer Biology
- Neuroscience
- Immuno-oncology
- Tumor Microenvironment
- Immunology
- Developmental Biology
- Stem Cell Biology
- Toxicology
- Tissue Engineering and Regenerative Medicine
- Pathology

Applications

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

Additional Resources

Datasets	go.10xgenomics.com/spRNA/datasets
Seminars	go.10xgenomics.com/spRNA/videos
Application Notes	go.10xgenomics.com/spRNA/app-notes
Technical Support	go.10xgenomics.com/spRNA/support
Publications	go.10xgenomics.com/spRNA/pubs

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 Accessory Kit	1000194
Visium Spatial Gene Expression Starter Kit, 16 rxns	1000200

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Contact Us

10xgenomics.com

10x Genomics	+1 925 401 7300
6230 Stoneridge Mall Road	+1 800 709 1208
Pleasanton, CA 94588-3260	info@10xgenomics.com

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