Visualize Gene Expression within the Tissue Context

Spatial Gene Expression

The complex organization of tissue makes it difficult to discern tissue function at the molecular level and at scale. While immunohistochemistry and H&E staining provide a window into tissue architecture based on protein expression and cell morphology, recent advances in spatial transcriptomic technology combine the benefits of traditional histology techniques with the throughput of next-generation sequencing. The ability to visualize gene expression using either whole transcriptome analysis or targeted gene expression panels provides a clearer, more complete picture of the biology captured on a tissue slide. Easily implement spatial transcriptomics technology into standard methods of tissue sectioning and staining with Visium 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 envision the spatial organization of newly discovered cell types, states, and biomarkers. To validate your discoveries or hone in on all relevant genes and pathways, pair Visium with pre-designed oncology, immunology, or neuroscience

Highlights

- Examine histology, protein, and mRNA from the same tissue section and discover new tissue biomarkers
- Envision the spatial organization of newly discovered cell types, states, and biomarkers with whole transcriptome analysis
- Validate discoveries or hone in on all relevant genes and pathways with 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 this contributes to your biological system

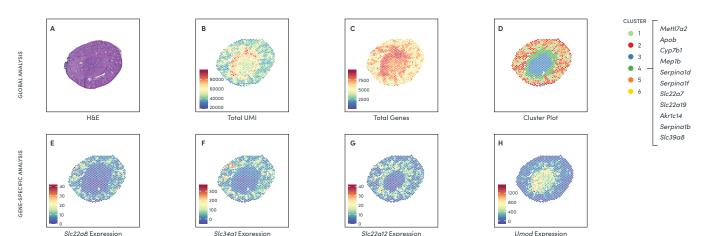


Figure 1. Spatially resolved clustering and gene expression in the mouse kidney Top row depicts global analysis of tissue morphology, gene expression, and clustering while the bottom row depicts gene-specific analysis of a few select genes. A. A coronal mouse kidney section was H&E stained, imaged, then processed through the Visium Spatial Gene Expression workflow. Shown are image overlays containing data for UMI counts (B), total gene count (C), and spatially naïve clustering based on total differentially expressed genes (D). The list of top 11 genes that are more highly expressed in cluster 4 (green) than any other cluster is shown to the far right. Examples of 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.



targeted gene panels, or design your own custom panels. Visium can also be combined with immunofluorescence for simultaneous visualization of protein and gene expression.

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. 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 and solutions.

Solution Benefits

- Spatially map global gene expression using whole transcriptome analysis or focus on your genes of interest using targeted gene expression panels*
- Ready-to-use, robust workflow for whole tissuesection analysis
- Easy to integrate with current laboratory methods and tools for tissue analysis
- Avoid the need to dissociate the sample to conduct gene expression studies
- Broaden your reach beyond predefined regions of interest to analyze the entire tissue section at once

Solution Features

- Compatible with fresh-frozen samples from most tissue types, including human, mouse, and rat tissue types such as brain, tumor, kidney, intestine, heart, and more
- 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)
- End-to-end workflow from section to imaging to library within one working day
- Compatible with immunofluorescence
- Compatible with targeted panels for focusing on the genes that matter most to you
- Easy-to-use and convenient software with Space Ranger analysis and Loupe Browser visualization

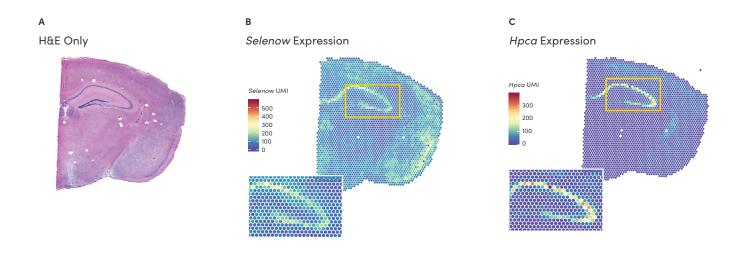


Figure 2. Spatially resolved gene expression in the mouse brain. A. H&E stained coronal mouse brain section. Spatial mRNA expression data from Selenow (B) and Hpca (C) are shown as examples of genes with known expression patterns in the brain, with predominant hippocampal expression. Expression in the 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
- Safety and Toxicology
- Pre-Clinical and Translational Research
- Tissue Engineering and Regenerative Medicine
- Pathology

Applications

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

Additional resources

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go.10xgenomics.com/spRNA/pubs

Datasets

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Seminar

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Technical Support

go.10xgenomics.com/spRNA/support

Demonstrated Protocols

support.10xgenomics.com/spatial-gene-expression

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
Dual Index Kit TT Set A, 96 rxns	1000215
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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^{*}Optimized protocol, support, and software for targeted panels with spatial gene expression coming September 2020.

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