

Visium Spatial Gene Expression Solution

Gene Expression. Visualized.

The relationship between cells and their organization within tissue is critical to understanding normal development and disease pathology. The Visium Spatial Gene Expression Solution allows for the investigation of spatially resolved whole transcriptome mRNA expression, while capturing histological information in the same tissue section. Using this solution, gene expression profiles can be mapped back to their original location, providing a new view of tissue and gene expression complexity as it applies to the study of cancer, immuno-oncology, neuroscience, developmental biology, and beyond.

THE VISIUM SPATIAL GENE EXPRESSION SOLUTION ALLOWS YOU TO:

- Combine spatially resolved whole transcriptome analysis with morphological context, complementing single cell gene expression information
- Gain a complete view of disease complexity by mapping where all gene activity is occurring
- Discover novel targets with unbiased analysis

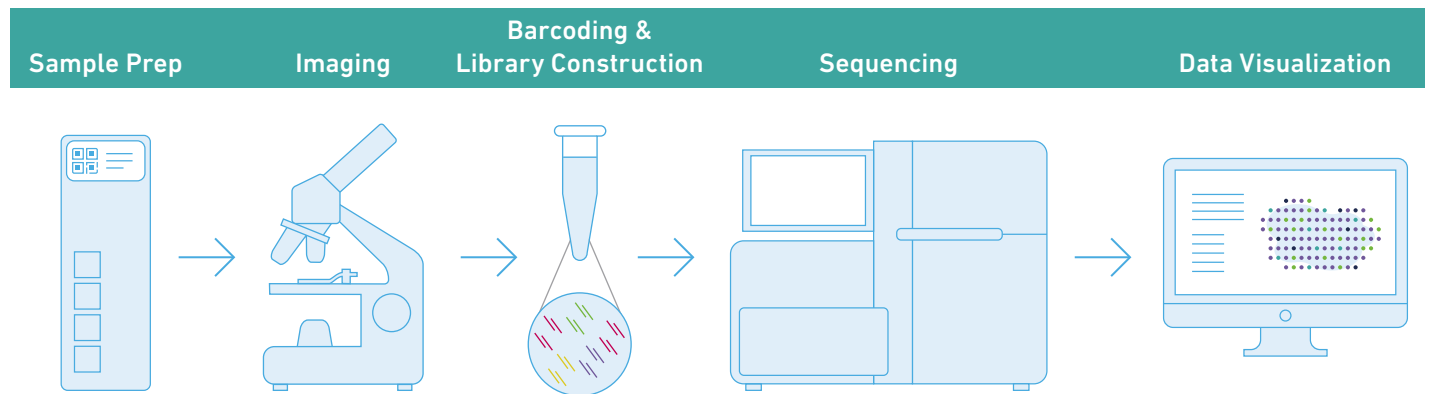


Figure 1. Workflow diagram for the Visium Spatial Gene Expression Solution. Fresh-frozen tissue is sectioned, placed onto a library preparation slide, then fixed, stained, and permeabilized, releasing mRNA which binds to spatially barcoded capture probes, allowing for the capture of gene expression information. cDNA is then synthesized from captured mRNA and sequencing libraries prepared. The libraries are then sequenced and data visualized. The workflow from sample to library prep can be completed in < 1 day.

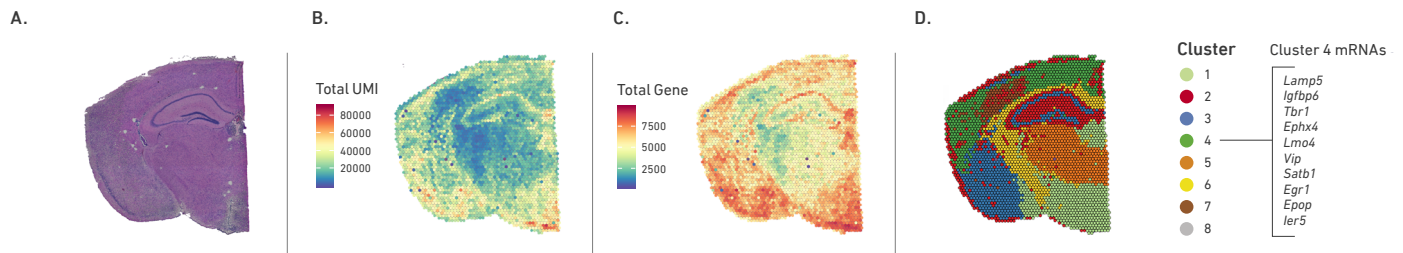


Figure 2. Spatially-resolved clustering and expression in the mouse brain. A. A coronal mouse brain section was H&E stained, imaged, then processed through the Visium Spatial Gene Expression workflow. Shown are image overlays containing data for UMI counts (B), total gene count (C), and spatially naïve clustering based on total differentially expressed genes (D). The top genes that are more highly expressed in cluster 4 (green) than any other cluster are shown to the far right.

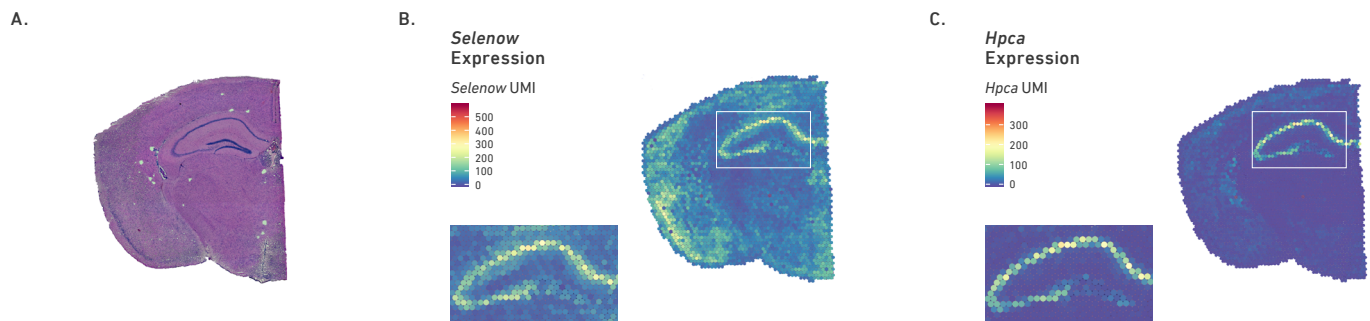


Figure 3. Spatially-resolved gene expression in the mouse brain. A. H&E stained coronal mouse brain section. Spatial mRNA expression of *Selenow* (B) and *Hpca* (C) is shown as examples of genes with known expression patterns in the brain, with predominant hippocampal expression. Expression in the hippocampus is highlighted and coincides with known expression patterns (note that spot size is not to scale).

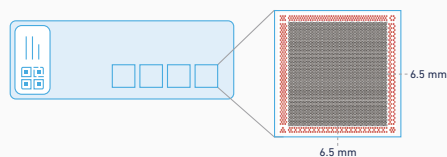
Product Configuration

VISIUM SPATIAL GENE EXPRESSION SLIDE AND REAGENT KIT

- Includes all the reagents and slides for 4 (1 slide) or 16 (4 slides) reactions
- Each slide contains 4 capture areas (6.5x6.5 mm) with 5,000 barcoded spots per capture area
- Each spot is 55 μ m in diameter (100 μ m 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



Visium Spatial Gene Expression Slide

Compatible with the Following Tissues*:

HUMAN

Heart, Kidney, Ovary, Breast, Lymph Node

MOUSE

Adipose, Brain, Small Intestine, Stomach, Liver, Brain, Quadriceps, Lung, Testes, Thyroid, Eyes, Tongue, Large Intestine, Spleen, Mammary Gland

RAT

Brain, Kidney, Heart

*Not an inclusive list; represents list of tissues tested internally to date. Tissue compatibility updates will be posted here:

go.10xgenomics.com/spRNA/tissue

10xgenomics.com/spatial-gene-expression

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