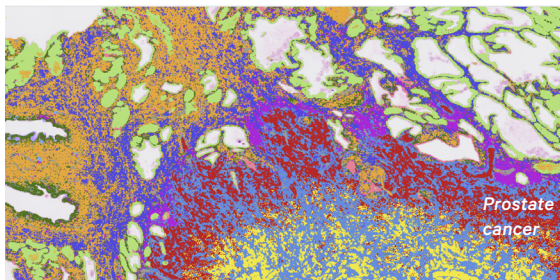


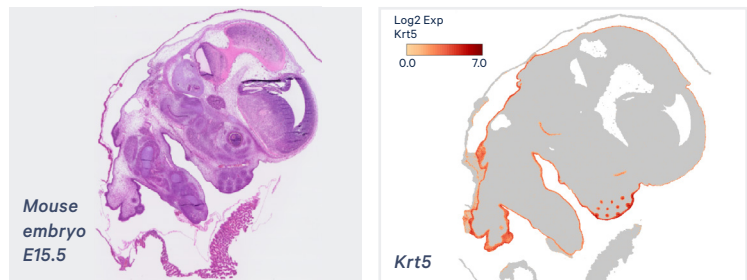
Whole transcriptome spatial discovery at the resolution you need

Visium HD Spatial Gene Expression

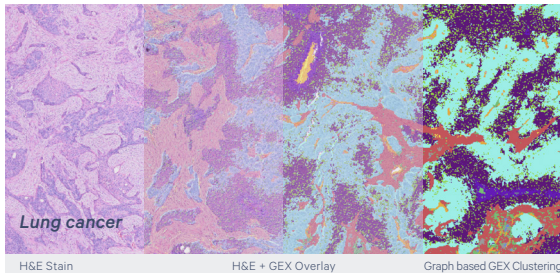
Visium HD empowers a new era of spatial discovery, enhancing proven whole transcriptome spatial analysis with single cell-scale resolution, enabling continuous tissue coverage, and delivering best-in-class data with innovative probe-based chemistry and a Visium CytAssist-enabled workflow.



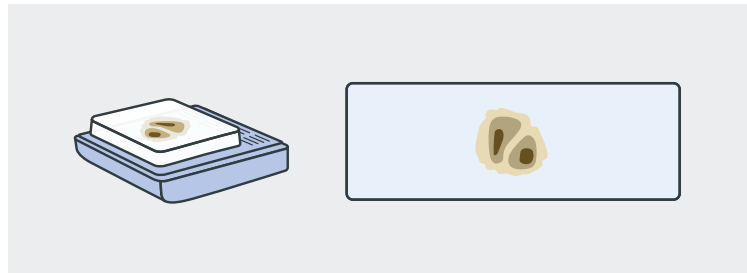
Whole transcriptome, single cell scale, continuous coverage



Precise transcript localization enabled by Visium CytAssist

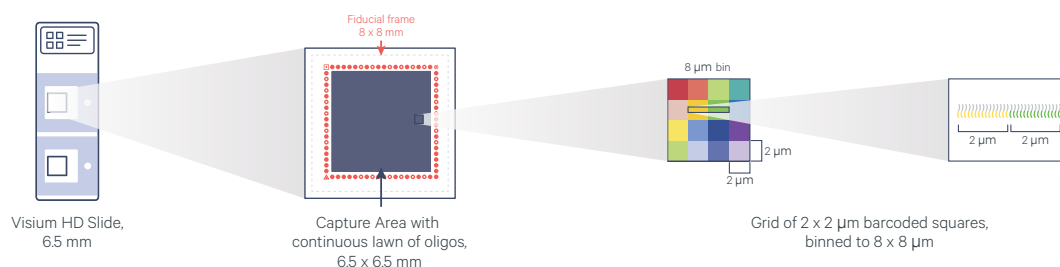


Enhancing H&E- or IF-imaged samples with high-resolution spatial transcriptomics



Powerful data from FFPE blocks or pre-sectioned slides

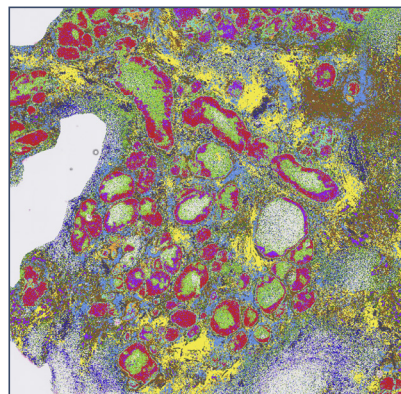
Next-generation slide architecture enables single cell-scale resolution



Visium HD Spatial Gene Expression slides contain two 6.5 x 6.5 mm Capture Areas with a continuous lawn of oligonucleotides arrayed in ~11 million 2 x 2 μm barcoded squares without gaps, achieving single cell-scale spatial resolution. The data is output at 2 μm, as well as multiple bin sizes. The 8 x 8 μm bin is the recommended starting point for visualization and analysis.

Boundless discovery potential in every micron

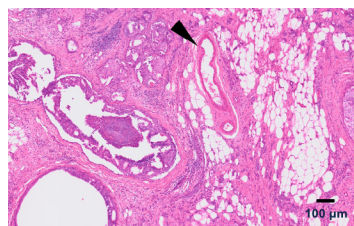
Spatially mapped GEX clustering



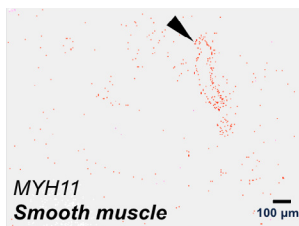
- Breast glandular cells
- Breast myoepithelial cells
- Endothelial cells
- Adipocytes
- T cells
- B plasma cells
- Fibroblasts

Visium HD analysis of this FFPE ductal carcinoma in situ human breast cancer sample builds an unbiased, whole transcriptome map, and identifies major cell types and states in the tumor microenvironment.

H&E staining

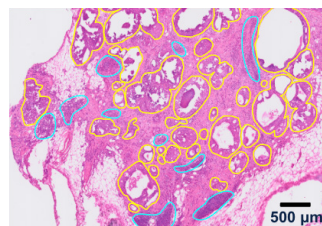


Visium HD gene expression data

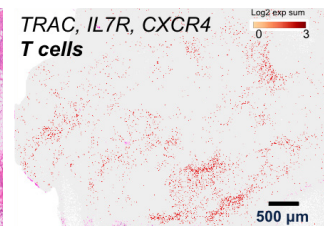


Confidently map the spatial organization of cell types in small biological structures, such as blood vessels.

H&E staining with pathology annotations of cancer (yellow) and immune rich (cyan) regions

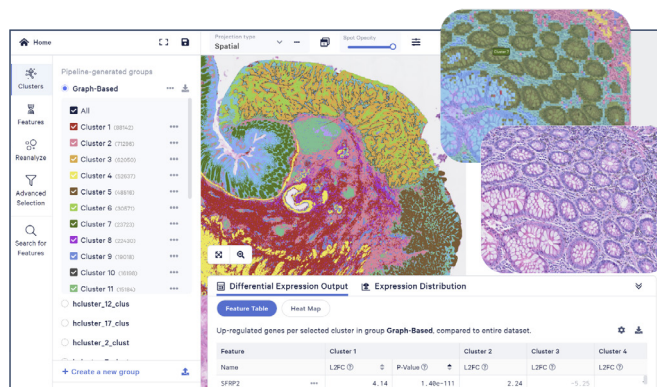


Visium HD gene expression data



Localize tissue-resident cell populations, including immune or cancer cells, to discover their interactions and contributions to disease or therapeutic response.

Intuitive data exploration accelerates discovery



Visium HD data is output at 2 µm, as well as multiple bin sizes. Above data visualized at 8 µm.

- Process Visium HD spatial gene expression data with bright-field and fluorescence microscope images using Space Ranger, a set of analysis pipelines
- Visualize and explore your data with Loupe Browser
- Continue analysis of Visium HD data with the growing ecosystem of R and Python community-developed tools

10xgen.com/visiumhd

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SAM000733 - Rev A - Visium HD Flyer - Whole transcriptome spatial discovery at the resolution you need