# 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
- Fibrolasts

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 brightfield 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



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