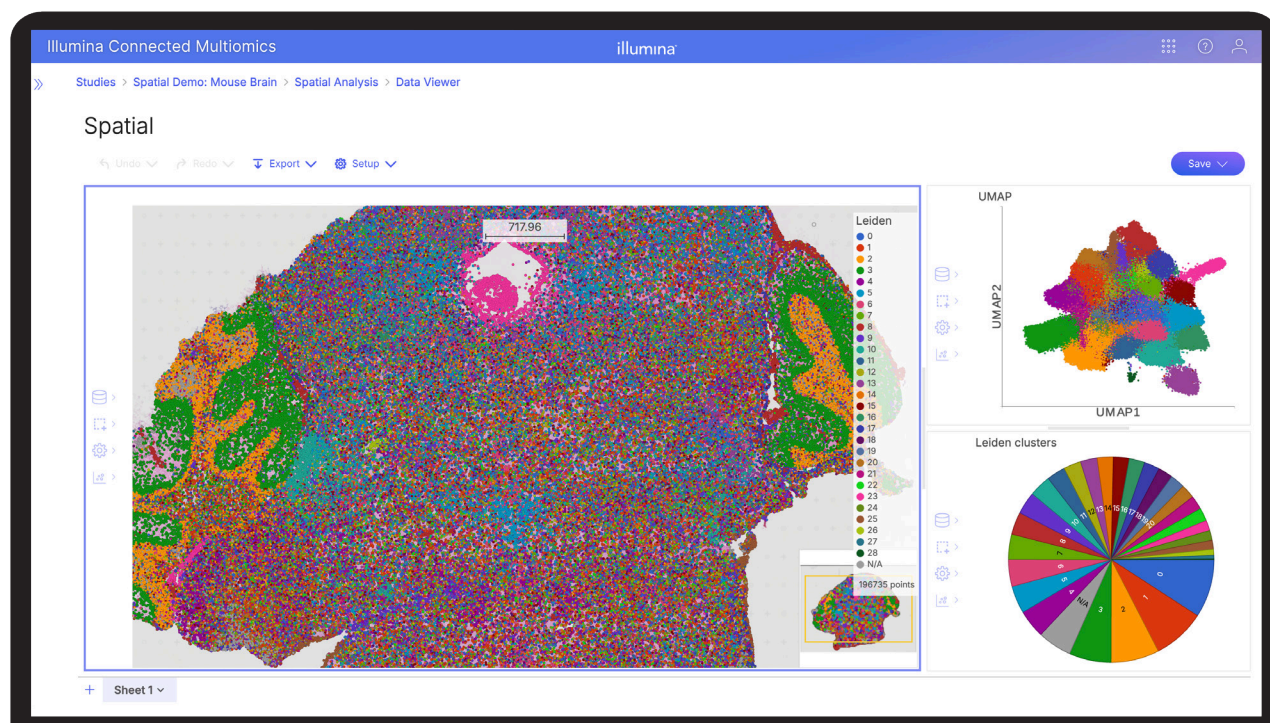# Accurate spatial exploration at scale
with Illumina Connected Multiomics

Powerful, intuitive, scalable multiomic analysis

Illumina Connected Multiomics enables researchers to intuitively analyze large and complex spatial transcriptomics data at scale. Easily combine spatial data with other omics data and modalities—no advanced bioinformatics expertise needed.

Unlock deeper biological insights
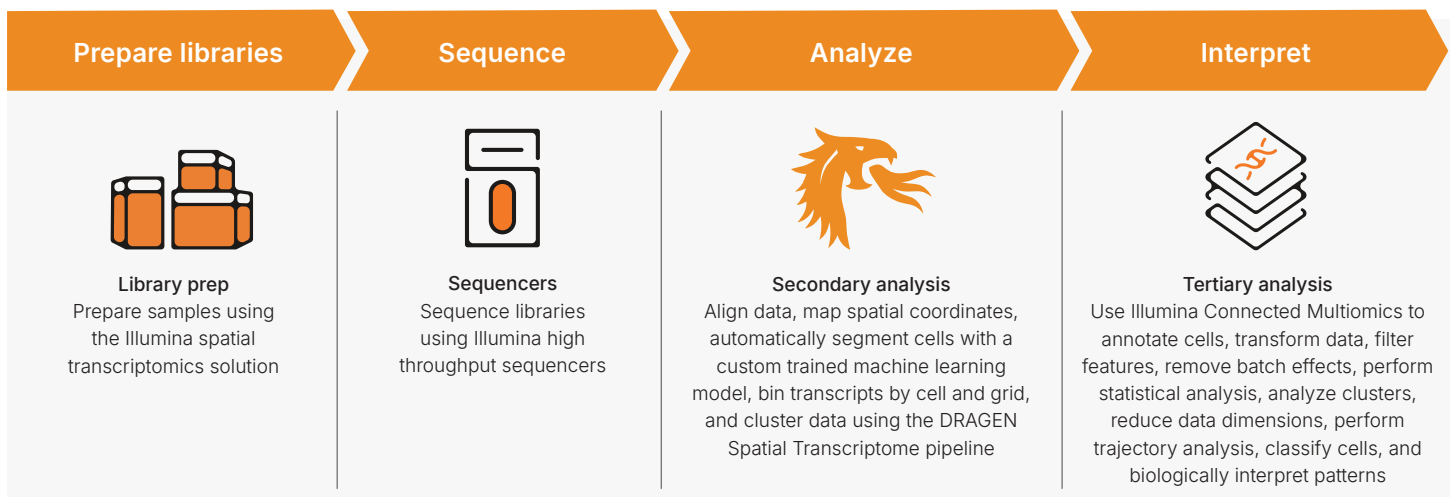

Intuitive and streamlined analysis

Scale studies with ease

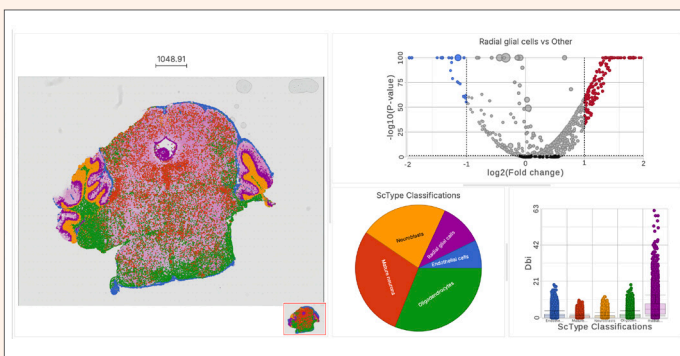**illumına**®

Connected workflow

Connected Multiomics leverages the power and accuracy of the integrated DRAGEN™ Spatial Transcriptome pipeline for secondary analysis and auto-ingests results for biological exploration. The intuitive visual interface streamlines multiomic data analysis, enabling in-depth exploration of cellular processes and spatial expression patterns through interactive plots, clustering, and high-resolution, publication-ready visualizations. Biological interpretation can be performed with the integrated Correlation Engine, one of the world's largest omics knowledgebases. Take your study from sample preparation to data interpretation within the Illumina ecosystem, and simplify your approach to spatial transcriptomics analysis.

Advanced features include:

- ⊘ QA/QC
- ⊘ Explore tissue
- ⊘ Dimensional reduction
- ⊘ Differential analysis
- ⊘ Clustering and classification
- ⊘ Normalization and batch correction
- ⊘ Biological interpretation

Prepare libraries	Sequence	Analyze	Interpret
Library prep Prepare samples using the Illumina spatial transcriptomics solution	**Sequencers** Sequence libraries using Illumina high throughput sequencers	**Secondary analysis** Align data, map spatial coordinates, automatically segment cells with a custom trained machine learning model, bin transcripts by cell and grid, and cluster data using the DRAGEN Spatial Transcriptome pipeline	**Tertiary analysis** Use Illumina Connected Multiomics to annotate cells, transform data, filter features, remove batch effects, perform statistical analysis, analyze clusters, reduce data dimensions, perform trajectory analysis, classify cells, and biologically interpret patterns

Bring your spatial data to life with interactive visualizations

Automated cell typing reveals distinct brain structures and cell populations; volcano plot highlights differential gene expression and expression levels of a signal transduction gene are shown across cell types.
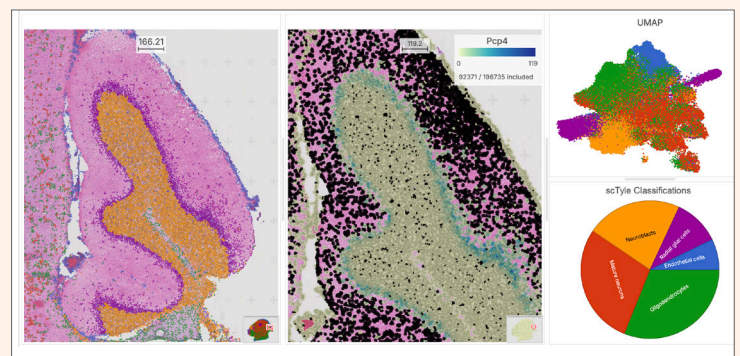
Cell types and expression of specific genes illuminate brain structures and gene expression linked to neuronal development; UMAP plot shows transcriptional similarity between cell types.

Scan or click QR code to learn more