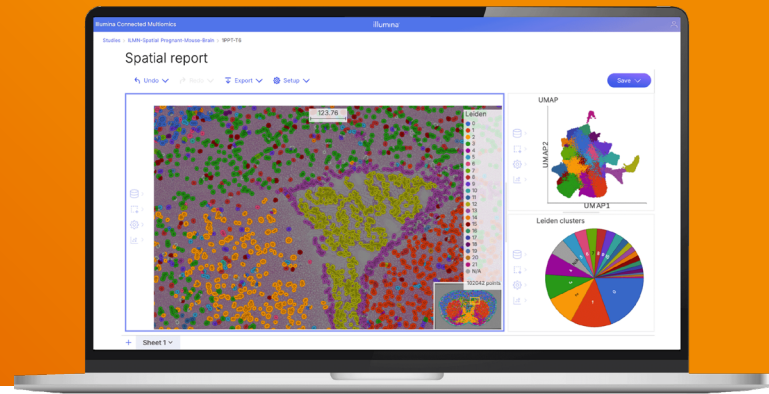




Accurate spatial exploration at scale

with Illumina Connected Multiomics

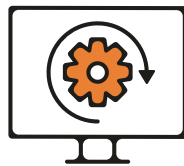


Illumina Connected Multiomics enables researchers to intuitively analyze large and complex spatial transcriptomic data at scale. Combine spatial data with other omics data and modalities easily—no bioinformatic expertise needed.

Connected Multiomics leverages the power and accuracy of the integrated Illumina DRAGEN™ Spatial Transcriptome pipeline for secondary analysis and auto launches 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 visualizations. Take your study from sample preparation to data interpretation all within the Illumina ecosystem and simplify how you approach spatial transcriptomic analysis.



**Unlock deeper
biological insights**

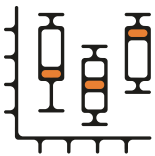


**Streamline analysis
with intuitive software**



**Scale your studies
with ease**

Confidently analyze spatial data



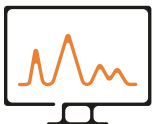
Interactive visualizations

Explore gene expression and cell populations in spatial context with information rich and publication ready visualizations



Powerful analysis

Attain results you can trust with robust statistical methods



Multimodal and multiomic analysis

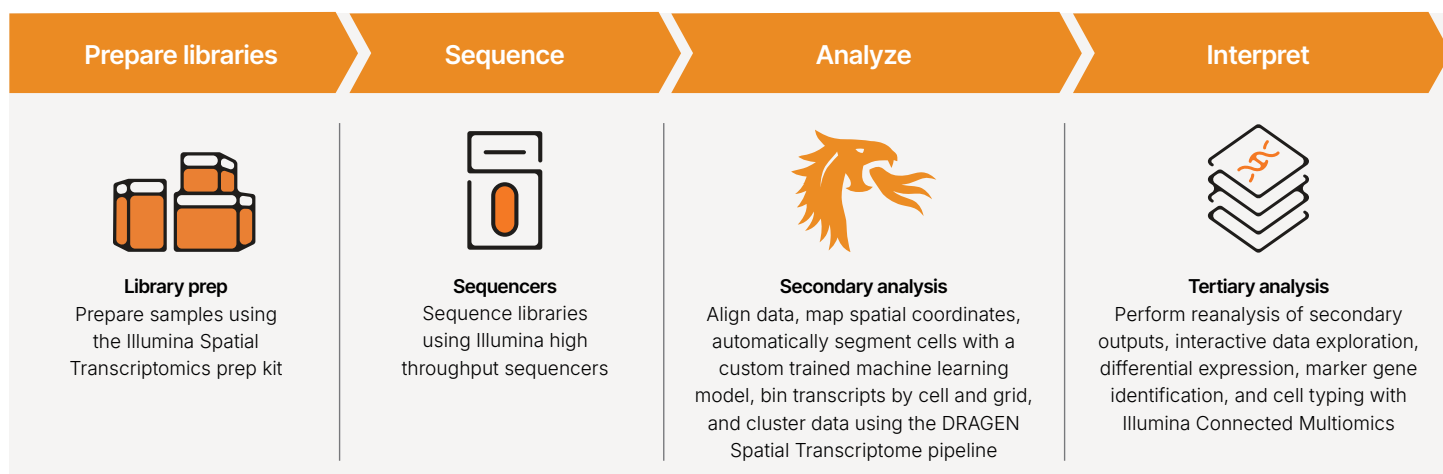
Analyze multiple omics datasets together to identify molecular mechanisms underlying phenotypes



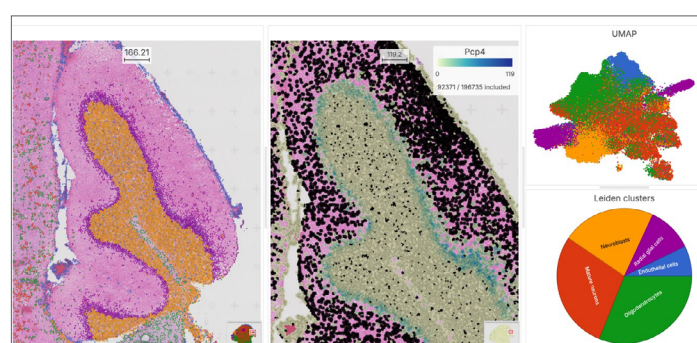
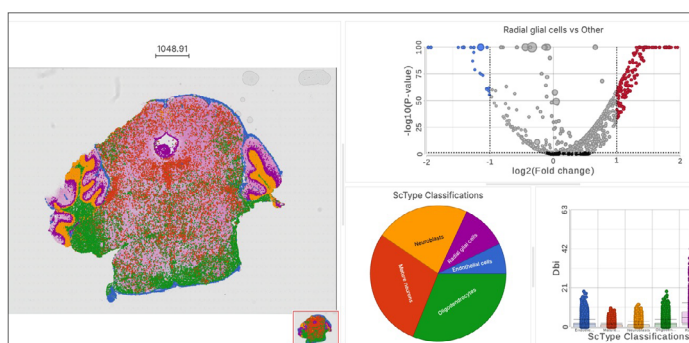
Security-first infrastructure

Protect the privacy of your data with industry-leading global and local security standards

A spatial workflow that integrates with the Illumina Spatial Transcriptomics prep kit and sequencers to take biological studies from sample preparation to data interpretation.



Bring your spatial data to life with interactive visualizations



Advanced features include:

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

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Learn more



Request demo

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