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Intuitive analysis of spatial transcriptomics data

Visualize transcriptional activity within intact tissue at high resolution with user-friendly tools from Partek™ Flow™ software

Spatial transcriptomics enables measuring and mapping of the location of gene activity in a tissue sample. This innovative approach expands the gene expression context provided by bulk and single-cell RNA-Seq techniques and adds important morphological context to the transcriptional profile of cells in their native state. Partek Flow software offers a user-friendly bioinformatics solution to analyze and visualize spatial transcriptomics data.

Point-and-click analysis
Analyze data easily with a user-friendly, context-sensitive interface

Advanced visualization tools
Create informative, publication-ready visualizations with just a few clicks

Powerful statistics
Use industry-standard statistical algorithms for results you can trust

Customizable workflows
Build custom analysis pipelines visually and share with collaborators

Powerful analysis and visualization tools

Whether you are creating maps of complex tissues, studying cellular development, mapping the immune repertoire, or identifying drug targets and biomarkers, Partek Flow software has the tools to help you analyze and visualize your spatial transcriptomics data easily.

Cross-platform integration for multiomic insights

Analyzing multiple omics data sets in parallel is a powerful way to identify molecular mechanisms underlying phenotypes. Easily integrate data sets from multiple assays, including single-cell RNA-Seq, CITE-Seq, antibody capture sequencing, cell hashing data, and more, with Partek Flow software for a comprehensive view of differential gene expression in regions of interest.

Steps in the **spatial transcriptomics analysis workflow**

QA/QC

Explore tissue

Normalization and batch correction

Dimension reduction

Clustering and classification

Differential analysis

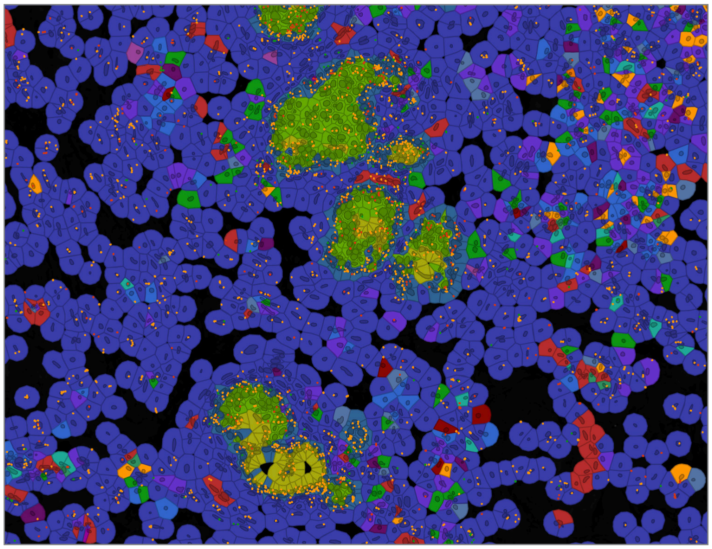
Biological interpretation

What can you do with **Partek Flow software**?

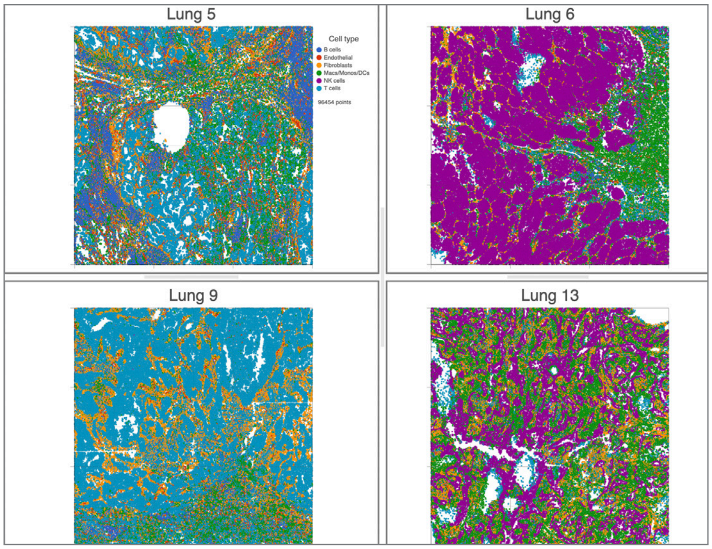
- Analyze and visualize gene expression spatially
- Perform dimension reduction and clustering techniques
- Explore clusters interactively in their spatial context
- Analyze multiple samples together or independently
- Discover biomarkers that define a tissue or cluster
- Find differentially expressed genes using industry-standard statistical methods
- Perform biological interpretation with GSEA, gene-specific analysis, and pathway analysis
- Assess relationships between different omics layers using correlation

Multiple ways to **explore spatial transcriptomics data**

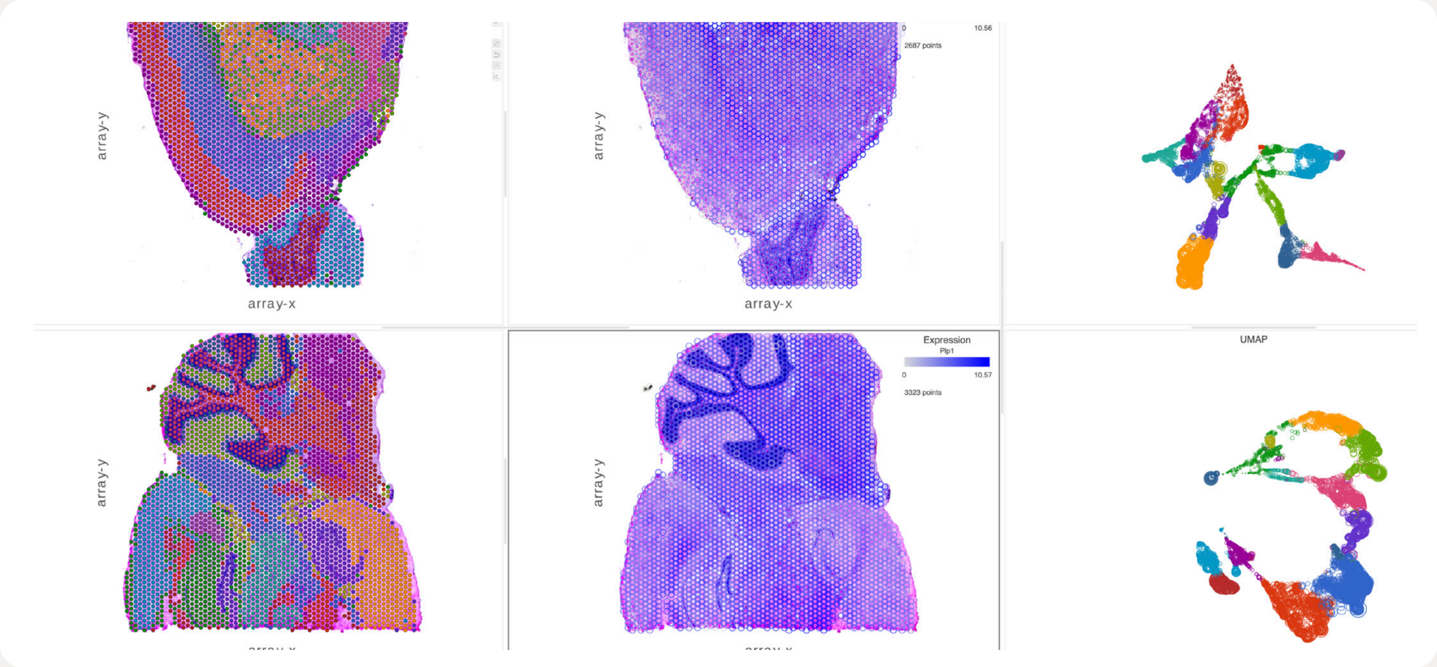
Transform spatially resolved gene expression data into interactive figures and maximize biological insights from your transcriptomics studies. Access all the tools that you need to generate publication-ready visualizations on a single platform with Partek Flow software.



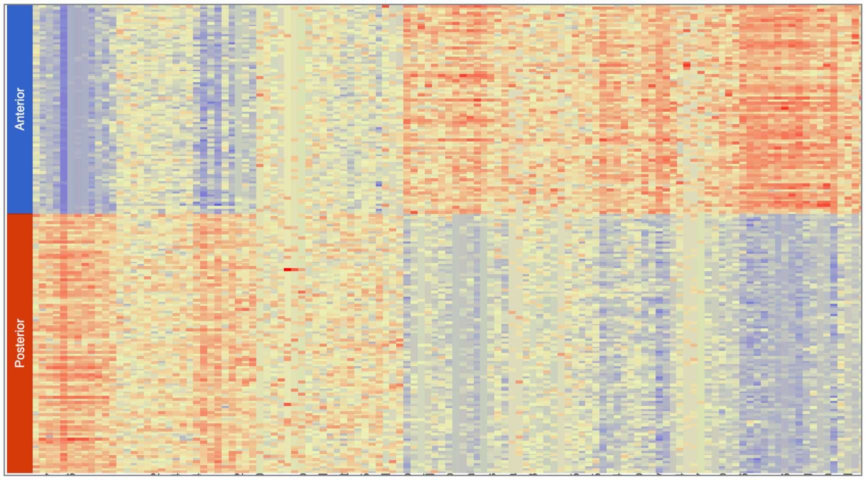
Identify differential gene expression based on cell type within intact tissue. Human Ductal Carcinoma In Situ (DCIS) sample using 10x Genomics Xenium technology. The cells are colored by cell type.



Analyze and visualize multiple samples together. Four human lung tissue samples were profiled using NanoString CosMx Spatial Molecular Imager. Cells are colored by cell type.



Integrate tissue and transcriptomics data with side-by-side visualizations. (Left) Graph-based clustering of gene expression data overlaid on tissue spots, (center) tissue spots are colored by the expression levels of the *Plp1* gene, (right) UMAPs based on gene expression data of the rostral and caudal brain sections where the colors represent graph-based clusters.



Study differential gene expression using heat maps. Rows represent gene expression signatures of tissue regions and columns represent individual genes.

Learn more

Partek Flow software

Request a demo

Abbreviations: CITE-Seq, cellular indexing of transcriptomes and epitopes by sequencing; GSEA, gene set enrichment analysis; QA, quality assurance; QC, quality control; RNA-Seq, RNA sequencing; UMAP, uniform manifold approximation and projection

illumina®

1.800.809.4566 toll-free (US) | +1.858.202.4566 tel
techsupport@illumina.com | www.illumina.com