

Step into a New Era of **Spatial** Omics
with **SeekSpace**: Achieving True
Physical **Single-Cell** Resolution



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Envision the Future

Part 1 - Introduction of SeekSpace

SeekSpace Single Cell Spatial Transcriptome-seq Technology



SeekSpace, independently developed by SeekGene BioSciences, is an advanced **spatial single-cell** technology. It employs cleavable spatial probes to label individual cells and utilizes the SeekOne® Digital Droplet (**SeekOne® DD**) microfluidic platform for independent cell nucleus capture. By integrating the shared cell barcodes, SeekSpace effectively correlates single-cell expression data with spatial information, overcoming the limitations of

conventional spatial transcriptomics, which cannot achieve true single-cell resolution. Accompanied by the SeekSpace Tools, an analysis software, this technology provides a comprehensive solution for spatial single-cell transcriptomics. SeekSpace is a powerful tool for studying tumor microenvironment cell interactions, tracking cell developmental trajectories, and exploring the mechanisms of disease occurrence and progression.

Part 2 - Technical Highlights

Physical Single-Cell Resolution

- Achieve **precise spatial localization** of individual cells.
- Ensure accurate cell identity determination.
- Ideal for analyzing regions with diverse cell types.

User-Friendly Operation and Analysis

- Simultaneous detection of **single-cell gene expression** and **spatial** information from the **same tissue** slice.
- No need** for **permeability** condition exploration or deconvolution analysis.

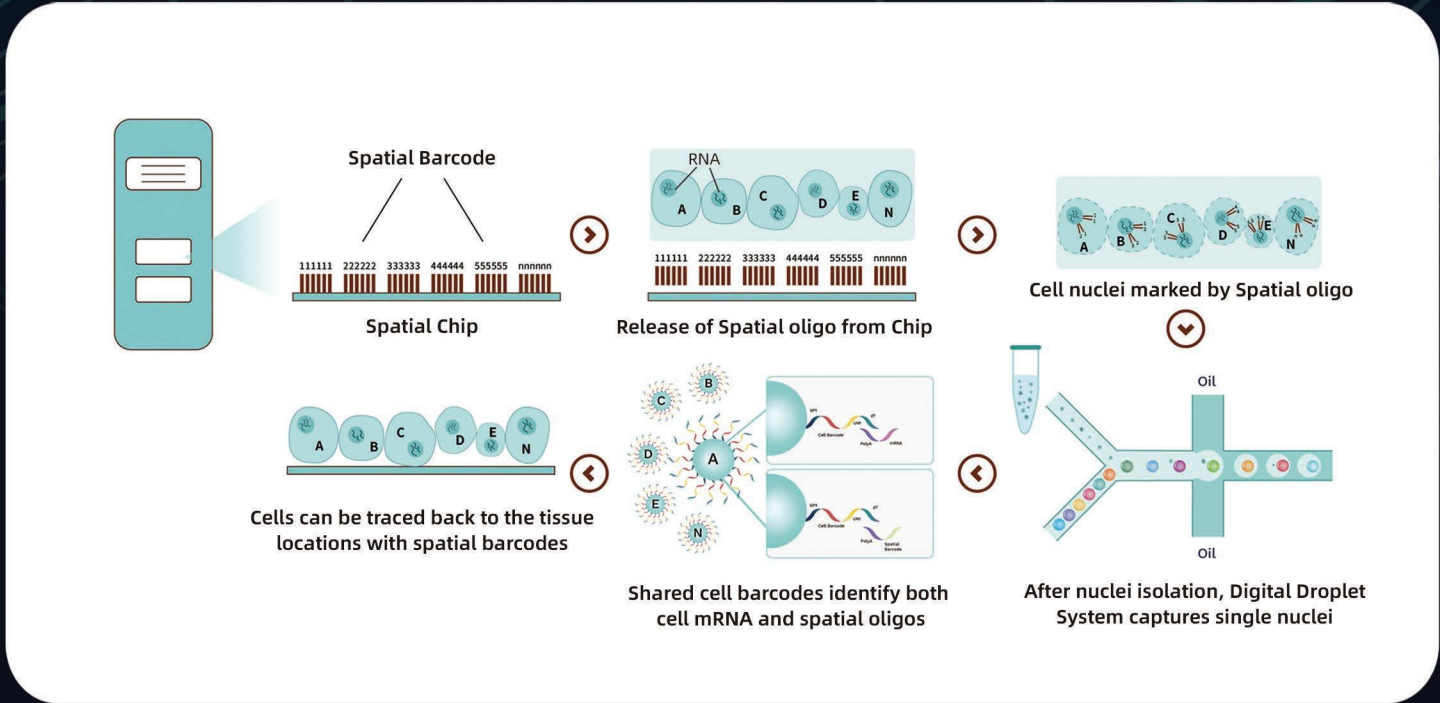
Exceptional Throughput and Sensitivity in Gene Detection

- Process up to **30,000** cells per sample.
- Median UMI count around **1,000** for robust data quality.

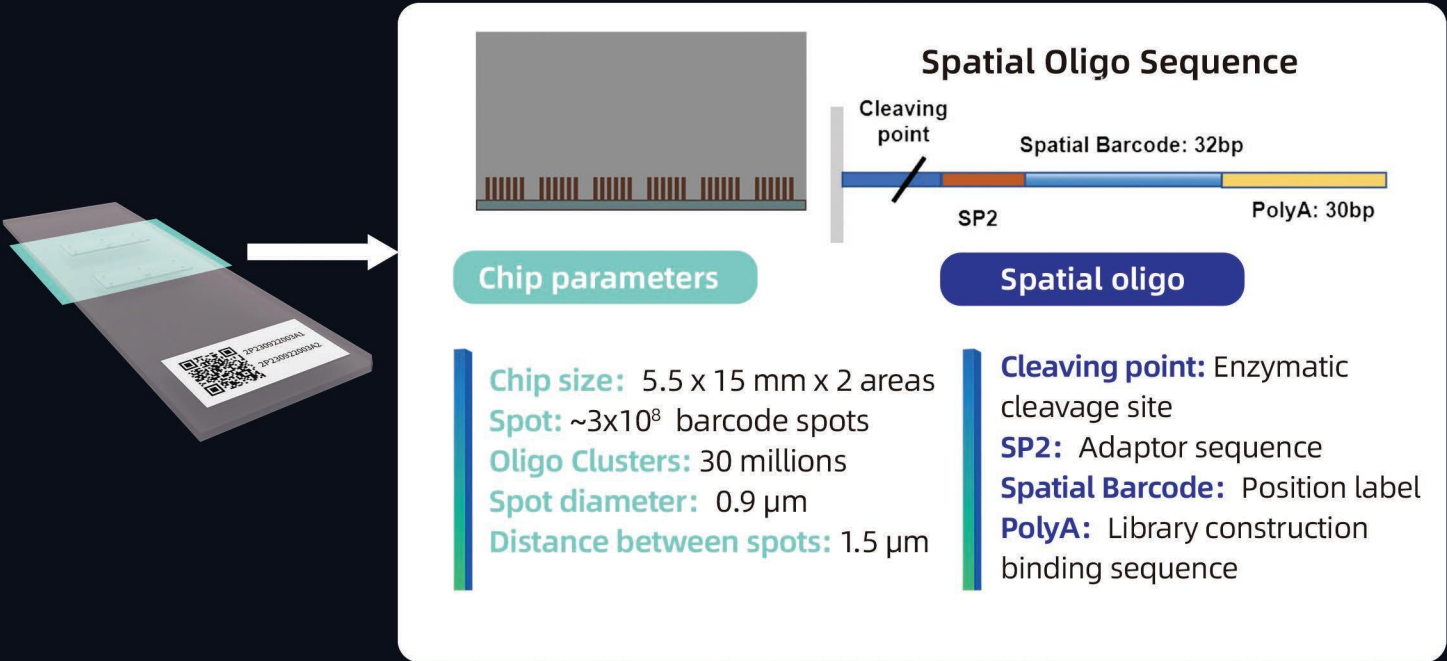
High Data Usability

- Seamlessly **integrate and compare** single-cell spatial transcriptome data with other **single-cell platforms** for comprehensive analysis.

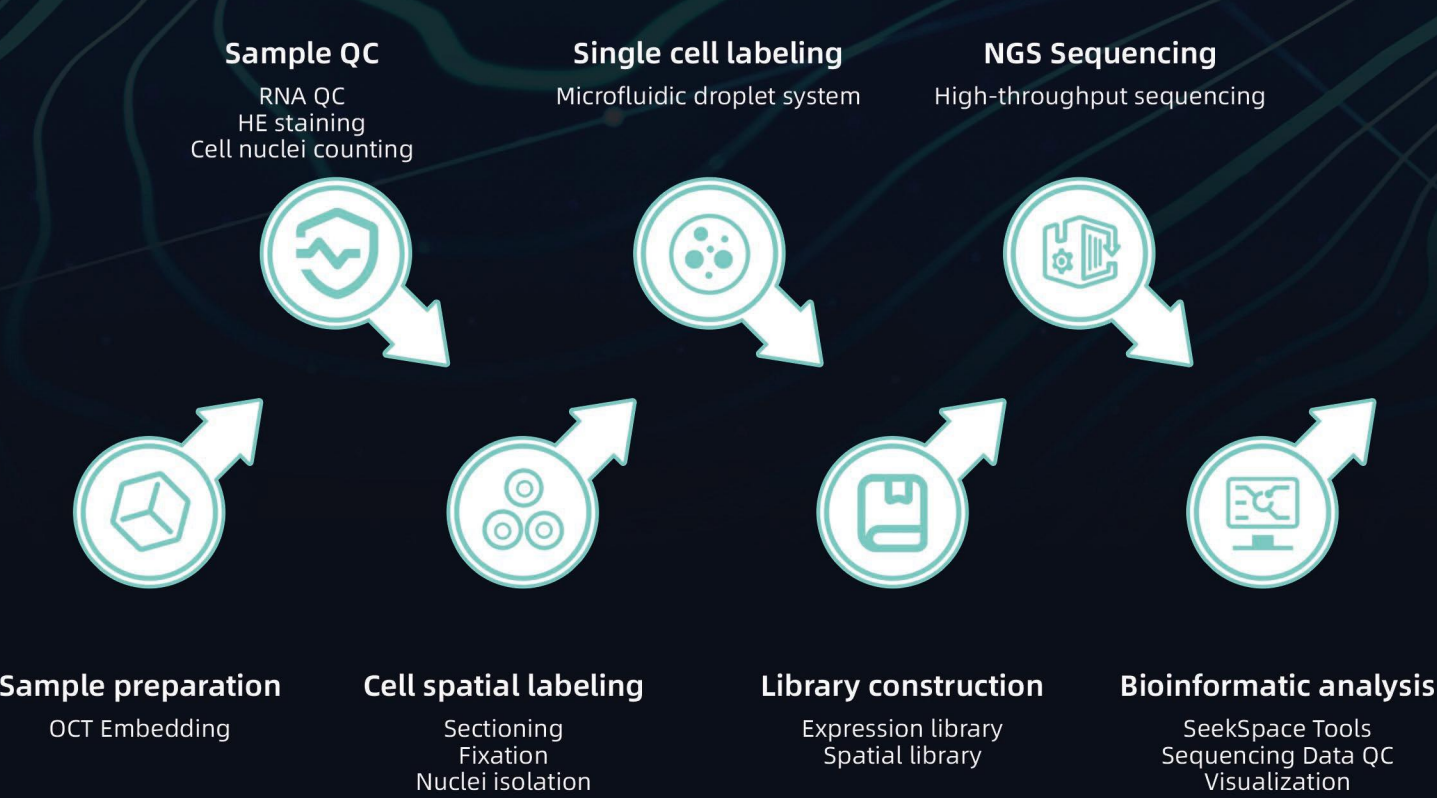
Part 3 - SeekSpace Principle



SeekSpace uses cleavable spatial probes to label individual cells, and then employs the SeekOne® DD microfluidic platform for cell labeling. By utilizing the shared cell barcodes, it matches single-cell expression information with spatial location information, truly achieving single-cell resolution spatial transcriptomic detection within the same tissue slice.



Part 4 - Workflow



Part 5 - Data Performance

Tissue Type	Estimated Number of Cells	Median Genes per Cell	Valid Barcodes	Sequencing Saturation	Reads Mapped to Genome	Total Genes Detected	Median UMI Counts per Cell
Brain	23708	732	85.09%	71.64%	84.38%	25841	1317
Breast tumor	18945	810	91.27%	72.51%	90.32%	23702	1032
Prostate	16523	951	85.47%	38.90%	86.33%	29015	1327
tumor	19501	798	89.53%	44.92%	92.04%	28668	1124
Glioma	9234	825	83.75%	58.30%	79.80%	28546	1059
Liver tumor	39356	744	85.40%	25.73%	89.13%	39515	967

Part 6 - Applications

Brain Sciences

Heterogeneity and specific roles of cells in complex brain regions.

Tumor Research

Cell populations and precise spatial locations within tumor regions.

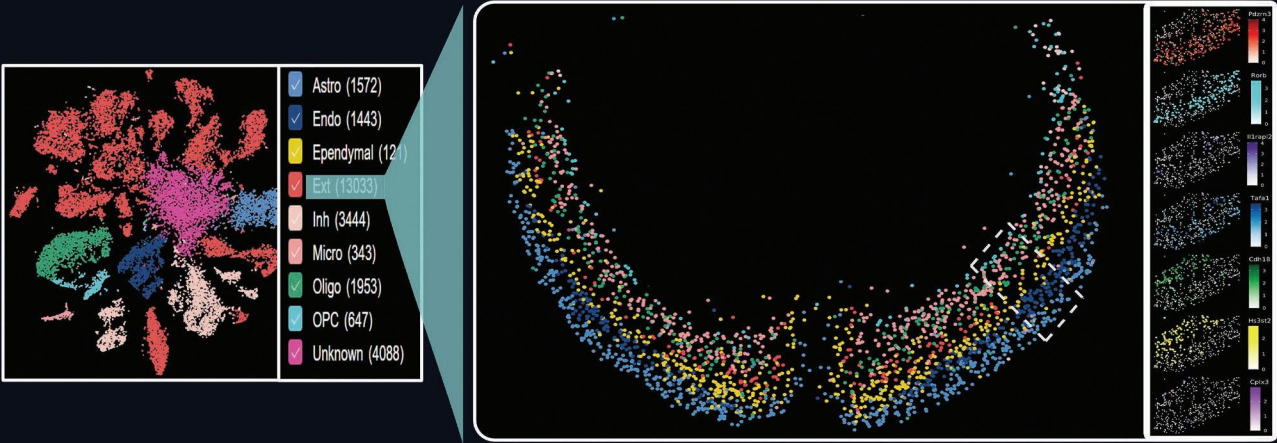
Development Studies

Evolutionary characteristics through changes in regional proportions.

Part 7 - Analysis and Features

SeekSpace achieves accurate spatial localization on the tissue

- **Independent Cell Type Annotation:**
Single-cell Spatial transcriptomics technology can distinguish different cell types without integration of other single-cell transcriptome data.
- **Direct Spatial Location Traceability:**
The spatial labels of each cell can directly trace and determine the spatial localization of cells within the tissue.
- **Cell Subpopulation Spatial Distribution:**
This technology reveals the spatial distribution of cell subpopulations within the tissue, providing a deeper understanding of cell function and interactions, eg. excitatory neurons.



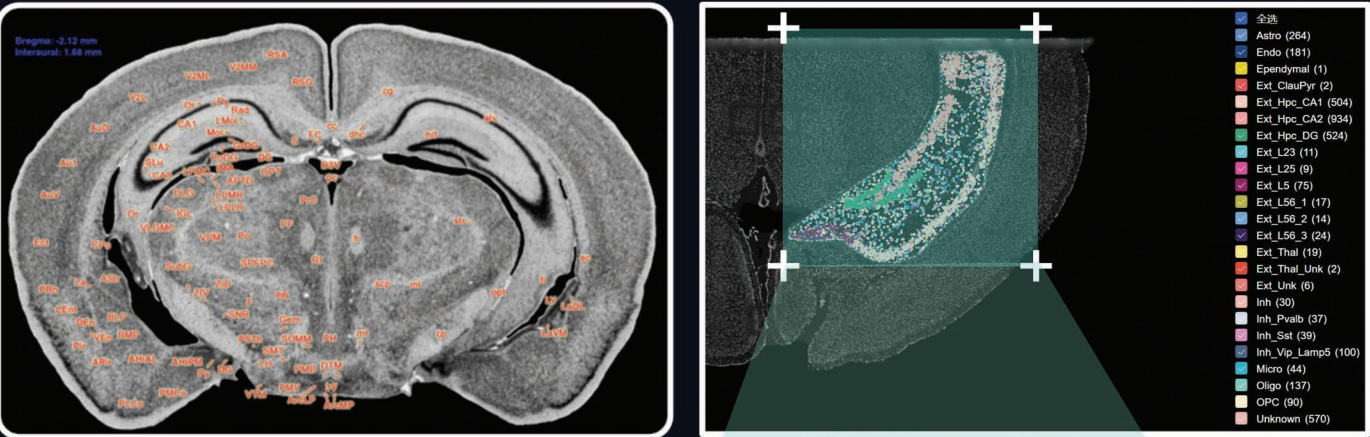
SeekSpace easily captures target cell types in specific tissue regions

Targeted Cell Type in Specific Regions

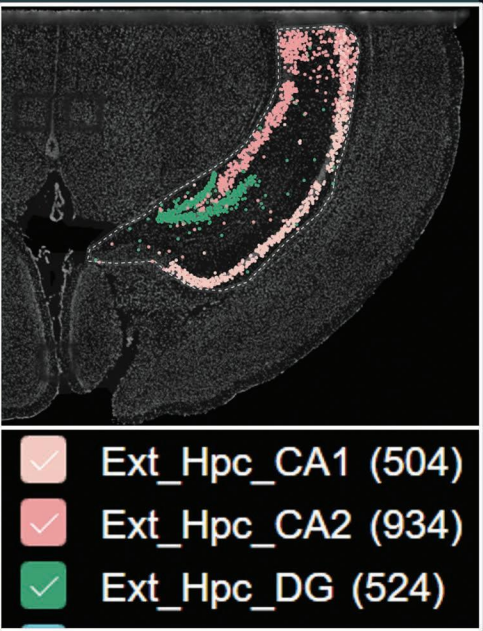
Precise spatial localization technology allows researchers to directly obtain target cell types from specific tissue regions, such as the hippocampus in the brain.

Alzheimer's Disease Gene Expression Analysis

In Alzheimer's disease research, it has been discovered that cell types related to memory and learning in the hippocampus exhibit abnormal gene expression patterns.

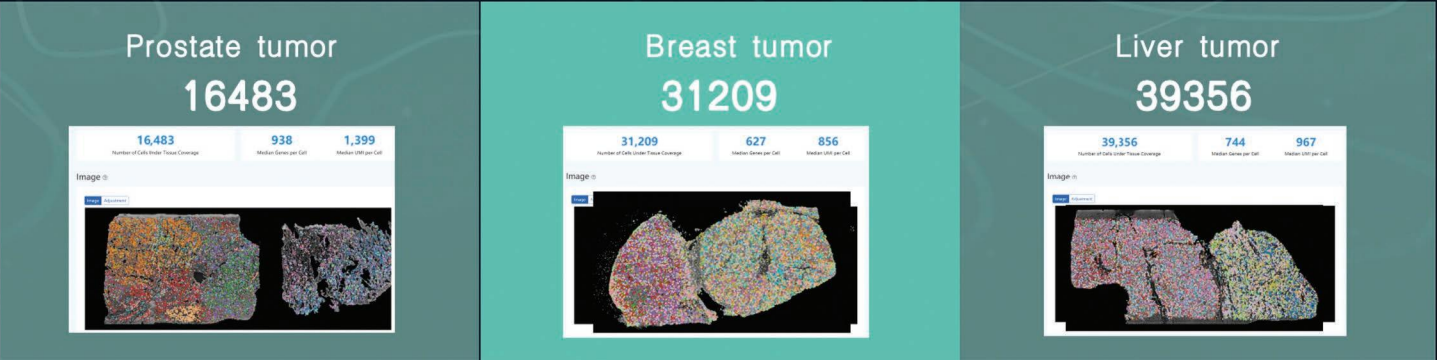


SeekSpace technology can clearly reveal the distribution of cells and their subpopulations in the hippocampus, providing essential spatial context information for analyzing cell function, cell interactions, and pseudo-time analysis.



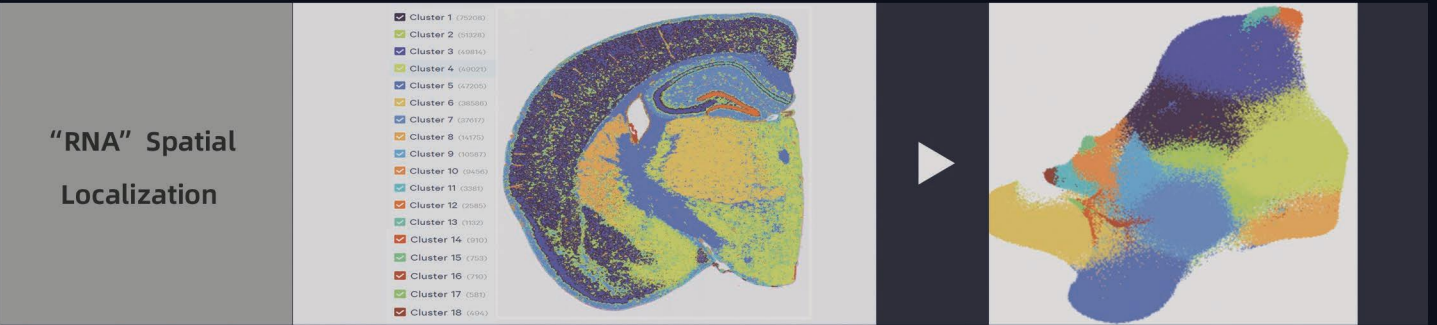
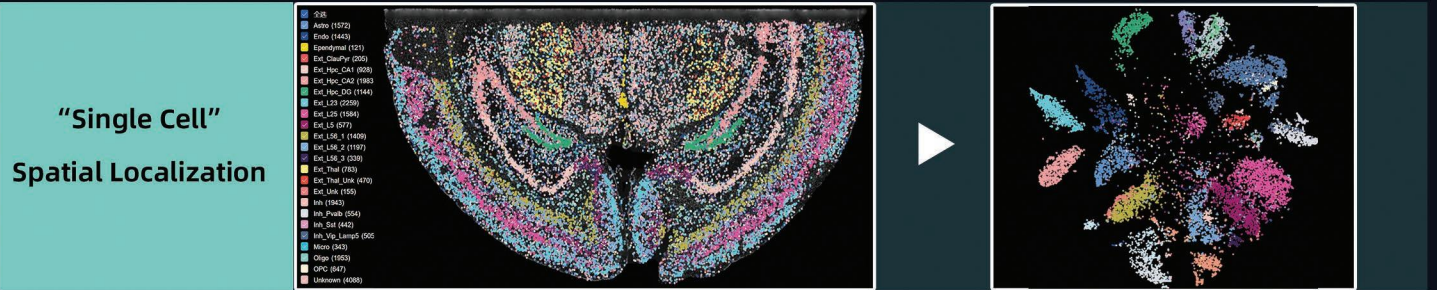
SeekSpace provides a sufficient amount of cells and gene information to support downstream analysis

High cell count: up to 30,000+, with a median UMI count around 1,000



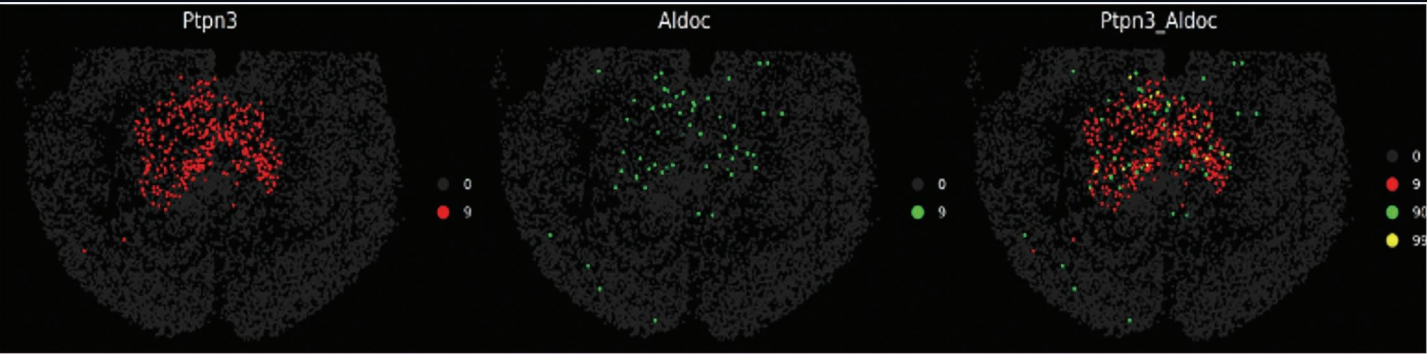
SeekSpace achieves clear cell clustering in the spatial dimension

Accurate annotation of cell types serves as the cornerstone of single-cell and spatial analysis research. This process is pivotal not only for studying cell differentiation but also for deepening our understanding of how cells respond to specific ligands and signaling molecules. Precise cell annotation plays a crucial role in uncovering the intricate interaction networks between cells, thereby advancing our knowledge of the mechanisms that regulate cell fate and function.



SeekSpace allows easier analysis of complex cell compositions within specific brain regions

The thalamic region poses a longstanding challenge in brain science due to its complex cell composition and irregular distribution patterns. This area features diverse cell types and significant spatial heterogeneity, presenting difficulties in precise cell type annotation and functional analysis. SeekSpace technology addresses these challenges by employing **precise spatial localization, thereby illuminating the distribution of various cell types within this intricate region.** This capability enhances our comprehension of thalamic function and cellular heterogeneity at a deeper level.

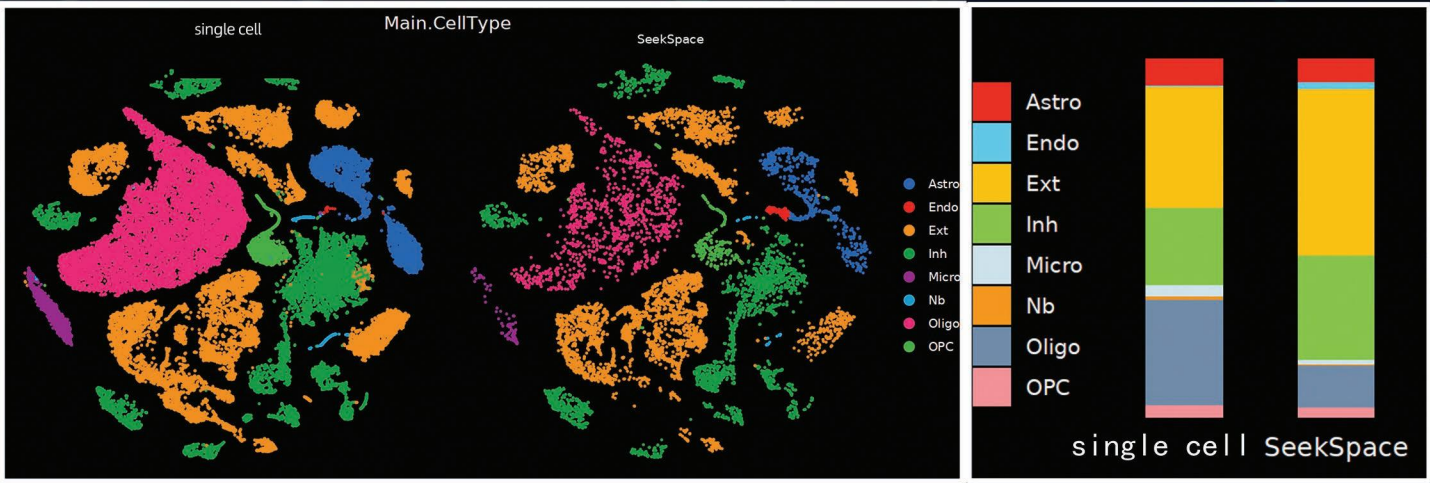


"Single-cell" spatial localization technology: SeekSpace precisely distinguishes between excitatory neurons and astrocytes in the thalamic region.



"RNA" spatial localization technology: Noise generated by permeabilization results in most units exhibiting dual-cell markers.

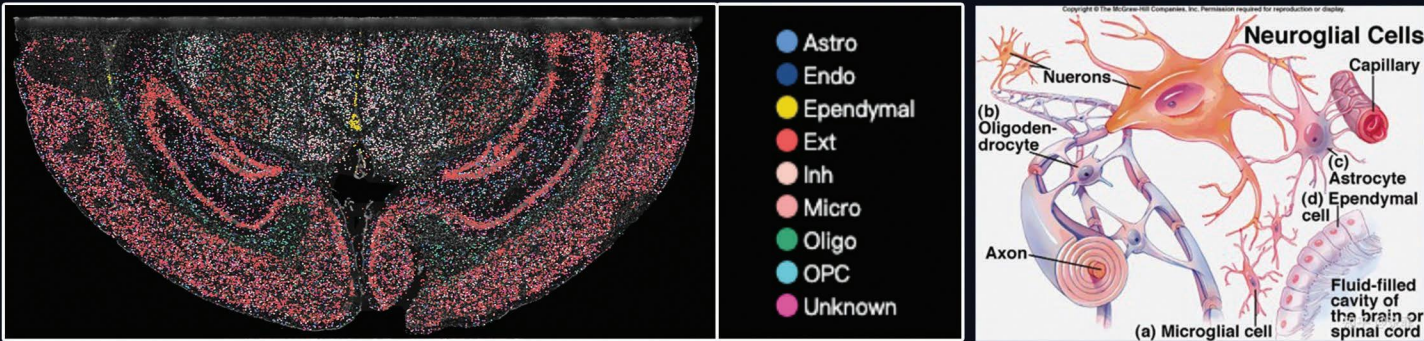
Advantages of SeekSpace Data Integration



- ① SeekSpace provides **single-cell resolution**, eliminating the need for supplementary single-cell transcriptome data to complete cell annotation.
- ② SeekSpace is "single-cell data" with spatial information, allowing for **direct integration, clustering, and comparative analysis** with single-cell transcriptome data.
- ③ Most single-cell transcriptome data related to the brain are "**single-nuclei**" data. SeekSpace also generates single-nuclei data, ensuring **higher consistency in the results.**
- ④ The detection of rare cells is improved by multiplex integration analysis, which more **truly reflects the complexity of tissue cell composition.**

SeekSpace provides a deeper understanding of complex diseases

SeekSpace demonstrates the cellular composition within the brain, revealing the spatial distribution of different cell types. This spatial image provides **a clear view of the symmetrical cellular localization of the brain structure.**



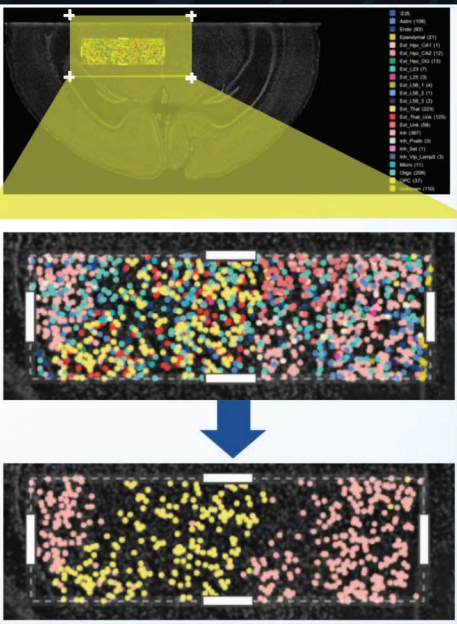
Easier analysis of complex cells and gene expression across brain regions, particularly boundaries

Cellular Dimensions

- 1. The hypothalamus hosts a diverse array of cell types, creating a complex structural landscape.
- 2. SeekSpace can comprehensively identify all cellular compositions within this intricate region.
- 3. It can pinpoint specific cell types localized to distinct regions, facilitating exploration of potential functional differences based on their spatial distribution.

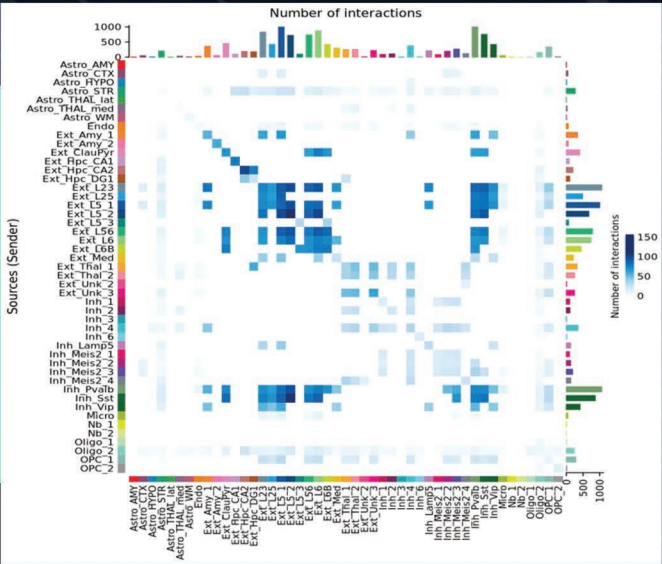
Gene Dimensions

- 1.The cell subpopulation of **Inh 2 (pink)** is predominantly distributed bilaterally across the hypothalamic region.
- 2.The cell subpopulation of **Ext_Thal1 (yellow)** is primarily concentrated in the central part of the hypothalamic region.



More accurate cell interaction analysis to precisely identify targets and markers

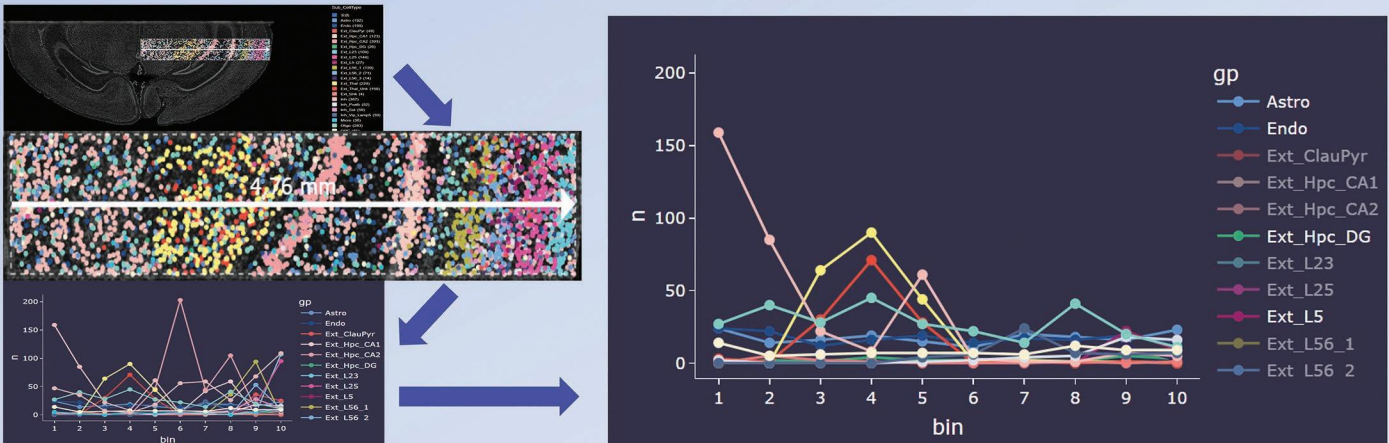
The effective range for cell-cell interactions is 0-200 μ m. SeekSpace assigns a precise position coordinate to each cell, facilitating **accurate analysis of cell interactions** through ligand-receptor analysis. By filtering out false positive data based on distance, SeekSpace enhances the identification of **meaningful interaction information**. This capability provides a solid foundation for delving into functional mechanisms in greater depth.



Part 8 - Order Information

Gradient distribution of expression features across subcellular genes of the brain

SeekSpace can accurately capture changes in cell composition along gradients from the cortical to the thalamic areas, enabling targeted functional analysis of specific regions and cell types.



Product	Specifications	Product code
SeekSpace Single Cell Spatial Transcriptome-seq Kit	8 tests/Kit	K02501-08
SeekOne® Digital Droplet System	1	M001A
SeekSpace High-Frequency Ultrasonic Device	1	M005A
SeekSpace Chip Holder	1	SP00054