

# Curio Seeker Spatial Mapping Kit

Curio Seeker Spatial Mapping Kit enables whole transcriptome, spatial mapping of fresh frozen tissue sections at industry-leading resolution and plugs directly into existing sequencing workflows.

The Curio Seeker tile preserves spatial information of the tissue transcriptome by capturing RNA on a monolayer of tightly-packed, spatially-indexed, 10  $\mu\text{m}$  beads.

Once captured, the RNA undergoes reverse transcription, library preparation, and sequencing. The sequencing data is then reconstructed bioinformatically into a continuous, whole transcriptome map of your region of interest.



## Single-cell resolution

A tightly-packed monolayer of beads delivers a continuous view of your region of interest at 10  $\mu\text{m}$  resolution.



## Flexible

Amenable to a wide range of tissues and species with no optimization required.



## Whole transcriptome

Whole transcriptome analysis that is not limited by predetermined targets or throughput, enabling true unbiased discovery.



## Sized to meet your needs

Conveniently offered in 3 mm x 3 mm or 10 mm x 10 mm tile sizes without sacrificing resolution.



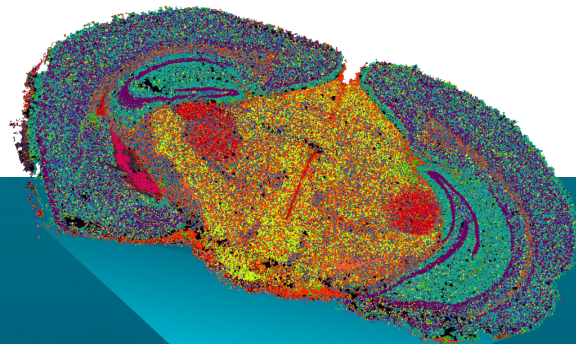
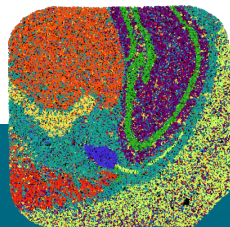
## Simple workflow

Leverages standard molecular biology techniques and instrumentation; no new specialized instrumentation or microscopy expertise needed.

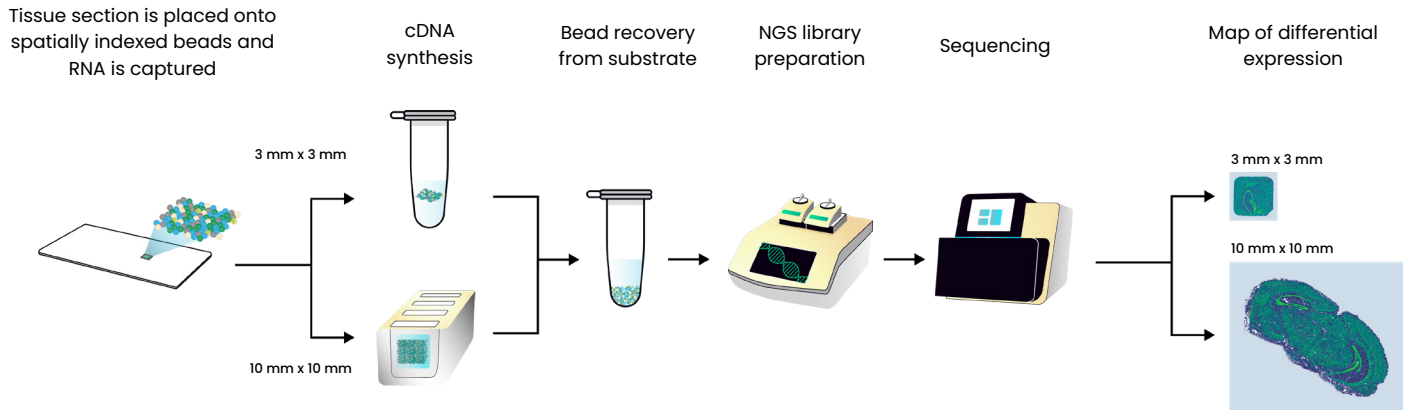


## Fast time to results

Multiple tissue samples can be prepared for sequencing in just one day.



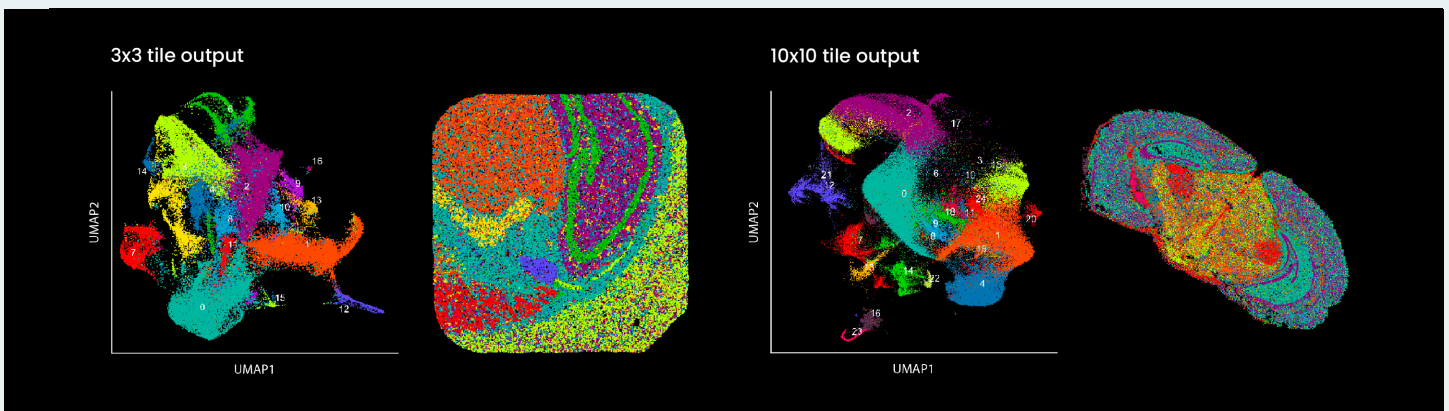
## Curio Seeker workflow



Once your tissue section is placed on the Curio Seeker tile, mRNA is captured and hybridized on the spatially-indexed beads before reverse transcription. The indexed beads are then dissociated from the tile and the tissue digested, followed by second strand synthesis and cDNA amplification.

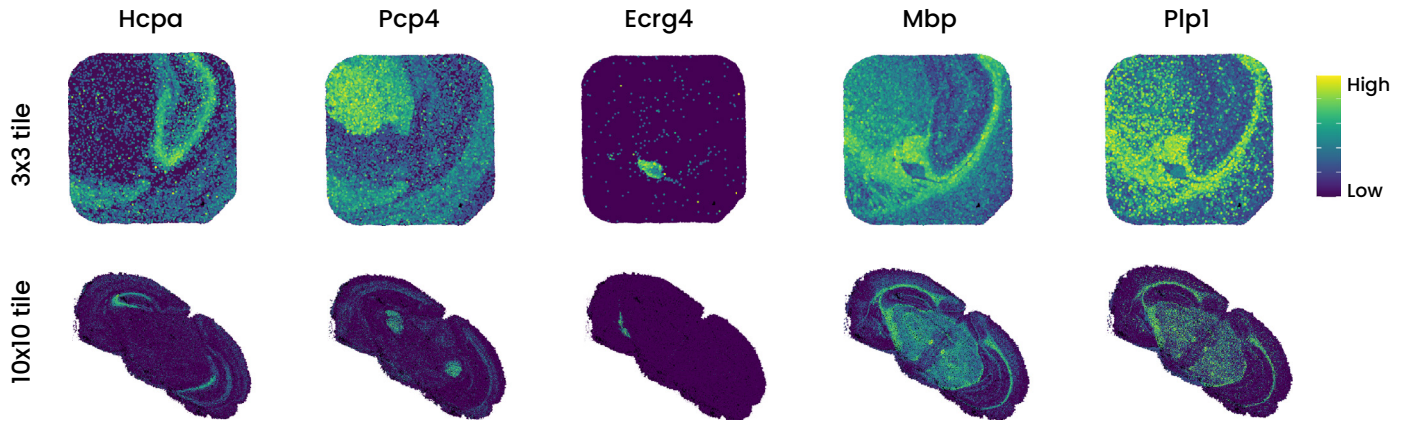
After purification and quantification, the cDNA undergoes NGS library preparation and is sequenced on an Illumina sequencer. Lastly, the resulting FASTQ files are processed by the Curio Seeker bioinformatics pipeline to create a detailed spatial transcriptomic map of your tissue section.

## High-resolution spatial expression maps



Standard html output from the Curio Seeker bioinformatics pipeline includes results from unbiased clustering and dimension reduction as well as a spatial map of identified clusters within a mouse hippocampus (left, 3 mm x 3 mm tile) and whole mouse brain (right, 10 mm x 10 mm tile). These plots enable the end user to easily determine if the data is biologically meaningful and decide how to best move forward with their analysis.

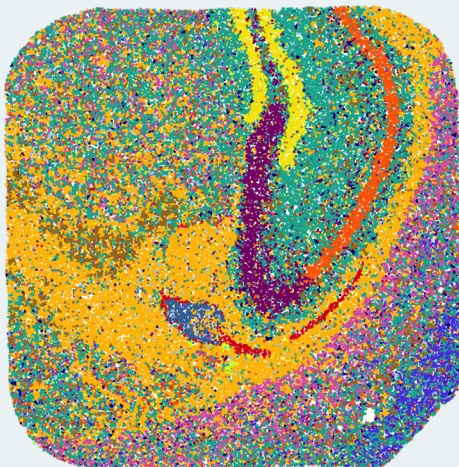
## Mapping of spatial gene expression



The Curio Seeker bioinformatics pipeline maps the spatial gene expression within a mouse hippocampus section (3 mm x 3 mm tile, top row) or whole mouse brain (10 mm x 10 mm tile, bottom row). The expression patterns of the top five spatially-variable genes are shown here. These images highlight the sharp spatial boundaries of gene expression that can be achieved on the Curio Seeker Spatial Mapping Kit.

## Annotate cell clusters using single-cell data

### 3x3 tile with cell types



- Astrocyte
- CA1 principal cell
- CA2 / CA3 principal cell
- Cajal-Retzius cell
- Choroid plexus
- Dentate principal cell
- Endothelial stalk cell
- Endothelial tip cell
- Ependymal cell
- Interneuron
- Microglial cell
- Mural cell
- Neuron
- Oligodendrocyte
- Polydendrocyte
- Subgranular zone
- Subiculum / entorhinal cortex
- NA

Secondary analysis using single-cell gene expression reference data sets and open source tools such as RCTD can accurately identify and spatially locate cell types of interest.

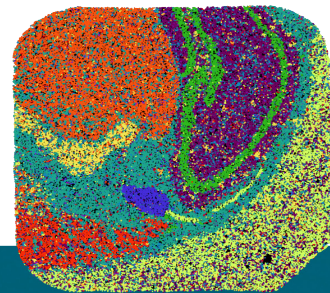
## Product features

Keep your focus with the Curio Seeker 3x3 kit or expand your horizons with the Curio Seeker 10x10 kit.

Features	Curio Seeker 3x3 kit	Curio Seeker 10x10 kit
Plex	Whole transcriptome	
Resolution	10 $\mu$ m	
Special capital equipment	None required	
Sample type	Fresh frozen	
Analysis software Included	Curio Seeker bioinformatics pipeline	
Tile size	3 mm x 3 mm	10 mm x 10 mm
Duration/hands-on time	8 hrs with 2.5 hrs hands-on time	8.5 hrs with 3 hrs hands-on time
Recommended sequencing depth	~ 400 M	~ 2 B

Curio Seeker 3x3 kit	Part number
3x3 Seeker Kit Bundle V1.1 (8 tiles)	SK004
Curio Seeker Dual Indexing Primer Kit V2	K006

Curio Seeker 10x10 kit	Part number
10x10 Seeker Kit Bundle (4 tiles)	SK003
Curio Seeker Dual Indexing Primer Kit V2	K006
Thermal Cycler Adapter	TJ002



## Sized to meet your research needs

The Curio Seeker Spatial Mapping Kit includes 8 (3x3) or 4 (10x10) tiles and reagents to prepare cDNA from your captured RNA. For indexing and multiplex sequencing, the Curio Seeker Dual Indexing Primer Kit is required and supports 40 (3x3) or 5 (10x10) Curio Seeker tiles. Together, these kits generate sequencing libraries in approximately 8.5 hours.

