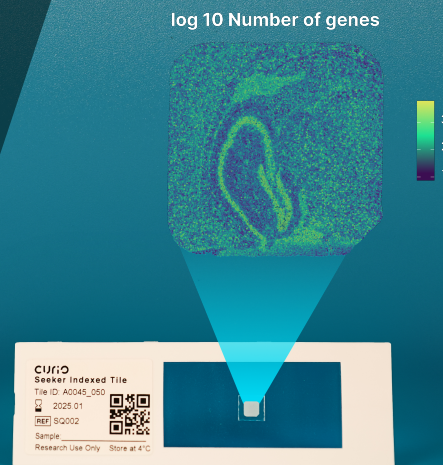# CURIO SEEKER

Whole-Transcriptome Spatial Mapping Kit

The highest resolution spatial transcriptomics workflow for fresh frozen tissue sections

Curio Seeker 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 an indexed surface composed of a monolayer of tightly packed, 10 μm 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.

log 10 Number of genes

Product Features

Feature	Curio Seeker
Resolution	10 μm
Tile Size	3 x 3 mm
Plex	Whole Transcriptome
Recommended Sequencing Depth	~200 M
Sample Type	Fresh Frozen
Duration/Hands-on time	8 hs with 2.5 hs hands-on
Specialized Hardware	None
Included analysis Software	Curio Seeker Bioinformatics Pipeline

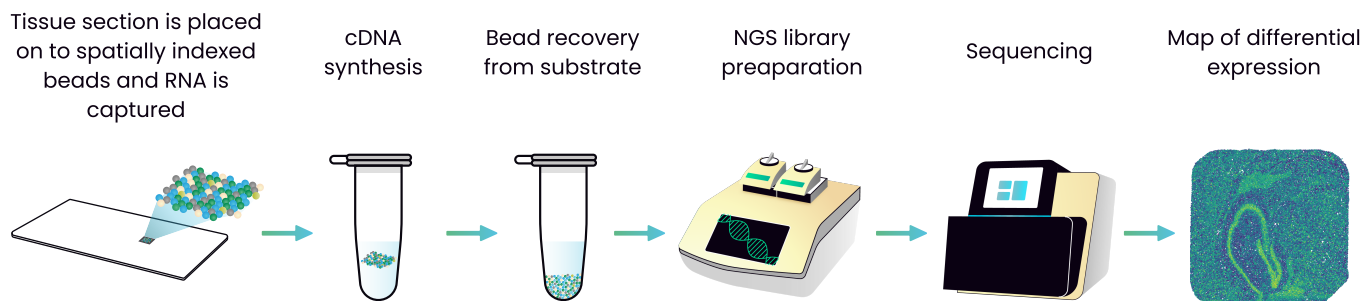Exquisite details with single-cell resolution

Close the gaps

No specialized instrumentation

Plugs into existing sequencing workflows

Curio Seeker Workflow

| Tissue section is placed on to spatially indexed beads and RNA is captured	cDNA synthesis	Bead recovery from substrate	NGS library preaparation	Sequencing	Map of differential expression

The Curio Seeker tile captures and stabilizes mRNA from a placed tissue section on its spatially indexed beads by hybridization and reverse transcription. The indexed beads are then dissociated during tissue clearing before second strand synthesis and cDNA amplification. After purification and quantification, the cDNA library undergoes NGS library preparation and is sequenced on an Illumina sequencer. FASTQ files from the sequencing run are processed by the Curio Seeker Bioinformatics pipeline to create a detailed spatial transcriptomic map of the tissue section.
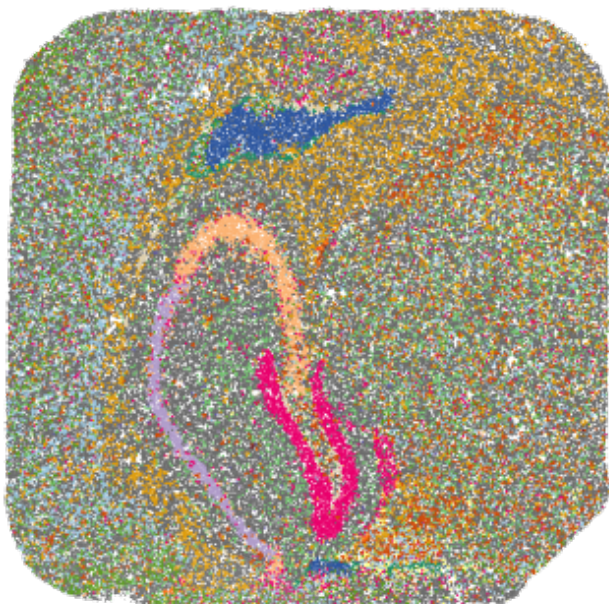
High-Resolution Spatial Expression Maps
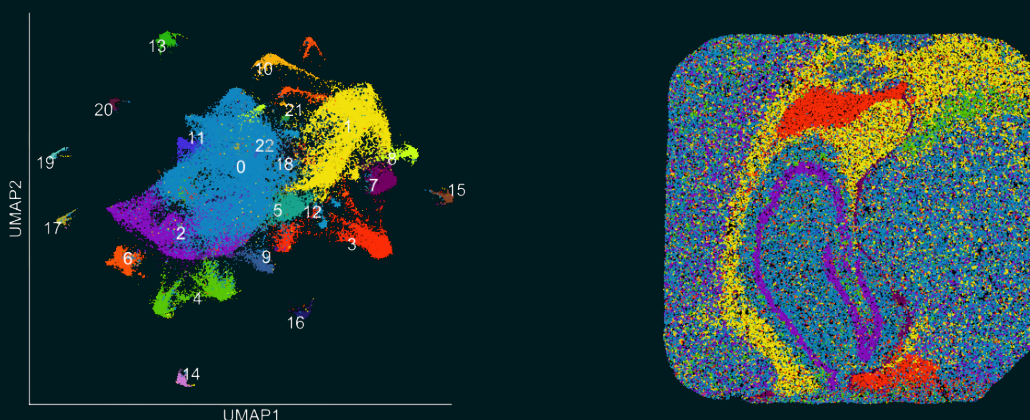
Standard html output from the Curio Seeker bioinformatics pipeline includes results from unbiased clustering and dimension reduction (left) as well as spatial map of identified clusters (right). These plots enable the end user to easily determine if the data is biologically meaningful and decide how to best move forward with their analysis.
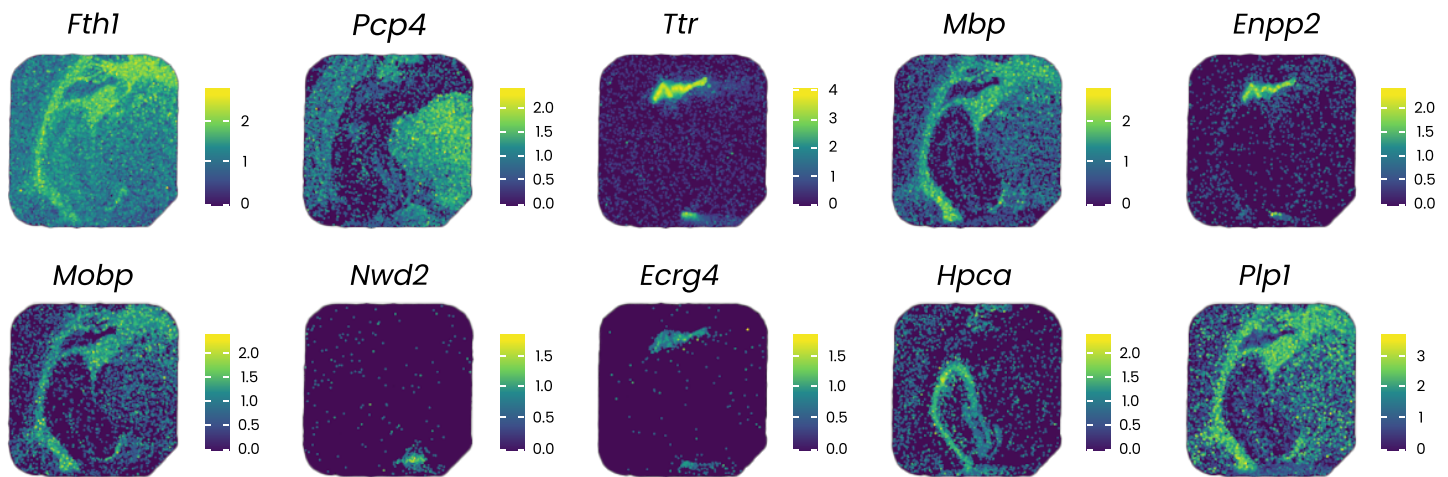
The Curio Seeker bioinformatics pipeline reconstructs spatial gene expression of a section of murine hippocampus. The expression patterns of the top ten spatially differential genes are shown here. These images highlight the sharp definition of gene expression that can be achieved on the Curio Seeker system.

Annotate cell clusters using single-cell data

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

- 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 / entorthinal cortex
- Unassigned

Ordering Information

Component	Part Number
Curio Seeker Spatial Mapping Kit	SK002
Curio Seeker Dual Indexing Kit	K003

The Curio Seeker Spatial Mapping Kit includes 8 tiles for tissue mapping, and all necessary reagents to prepare samples for library preparation and sequencing.

Additionally, we offer the Curio Seeker Dual Indexing Kit that supports 40 Curio Seeker tiles.

Necessary reagents from other manufacturers such as the Nextera XT Kit, SPRI beads and DNA LoBind tubes are not included.