PRODUCT NOTE

Curio Trekker Single-Cell Spatial Mapping Kit

Delivering *true* single-cell spatial omics

While single-cell genomics has greatly advanced our understanding of how cells function in tissues and organs, the missing component is where cells are organized in their natural spatial context.

The Curio Trekker Single-Cell Spatial Mapping Kit elevates single-cell research by transforming standard single-cell genomics data into spatial data. Curio Trekker works by tagging each nucleus within its native tissue environment with unique spatial barcodes. These spatial barcodes are read using next-generation sequencing (NGS), allowing each nucleus to be bioinformatically positioned in its spatial coordinates. The result is a spatial map with true single-cell resolution, without the use of complex instrumentation, cell-type deconvolution, or cell segmentation.

Designed as a simple reagent kit, Curio Trekker integrates seamlessly with existing single-cell sequencing workflows and preserves the high molecular sensitivity of single-cell data. Moreover, Curio Trekker extends beyond spatial transcript-omics to other omic assays, broadening the scope of spatial analysis.

UMAP to spatial map

One-of-a-kind spatial solution designed specifically for single-cell data

True single-cell spatial resolution

Single-cell resolution every time—no deconvolution, no segmentation, no complex algorithms

Versatility

Fits in front of any single-cell sequencing workflow

Simplicity

Simple 1-hour workflow with no specialized instrumentation

Same single-cell data

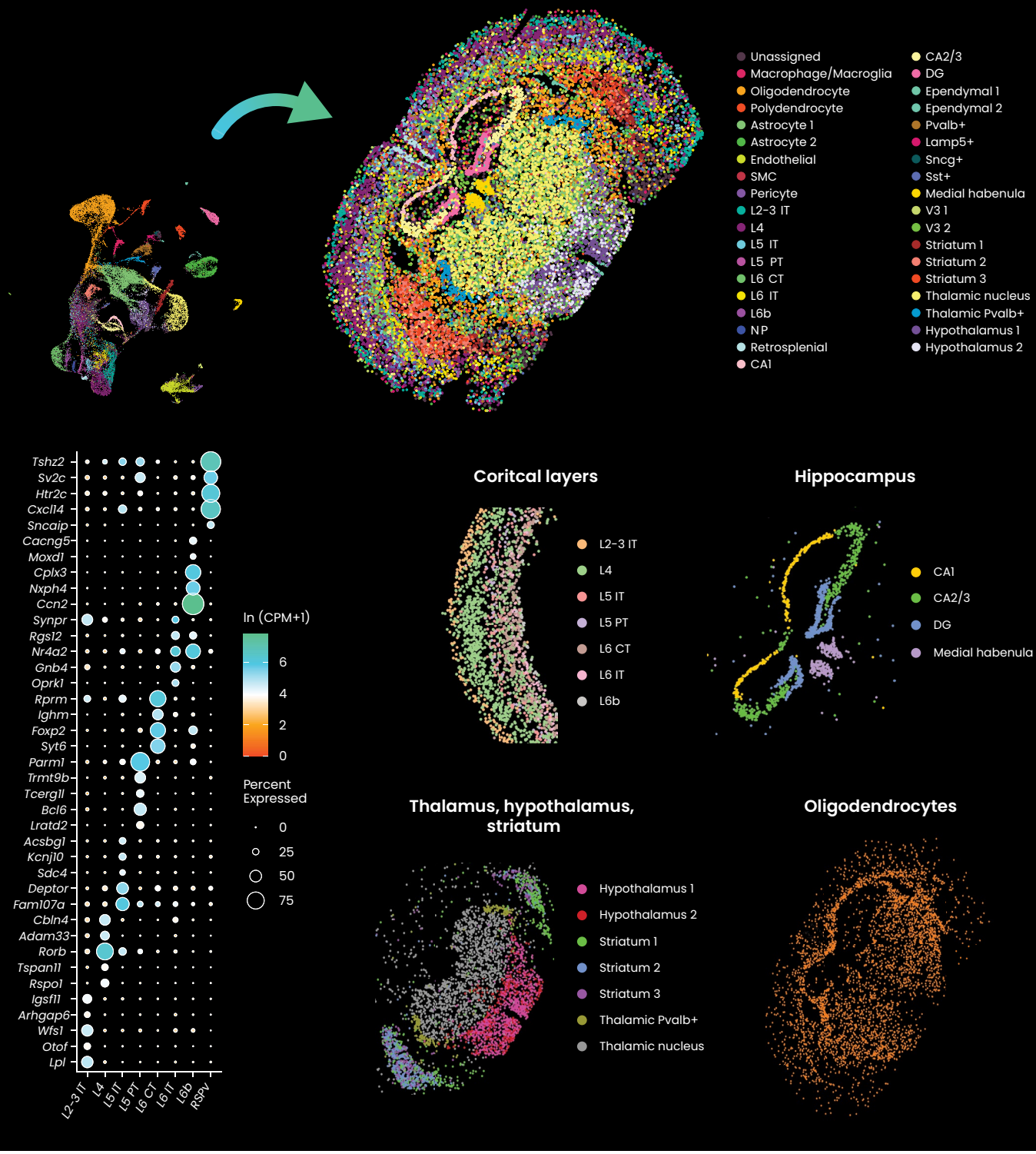
Preserve the quality and sensitivity of single-cell data

Beyond spatial transcriptome

Venture into spatial single-cell multi-ome analysis

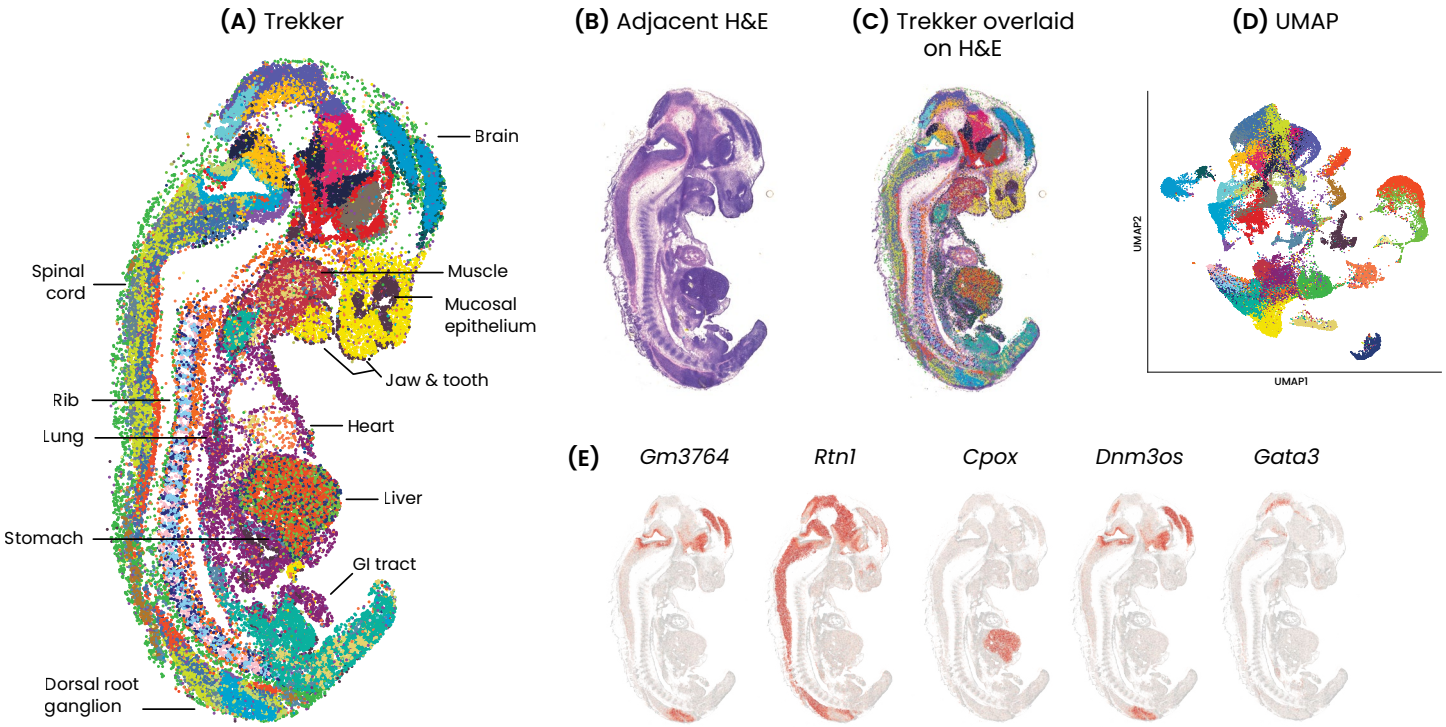
Spatialize your single-cell data today

Transform a single-cell UMAP to a spatial map



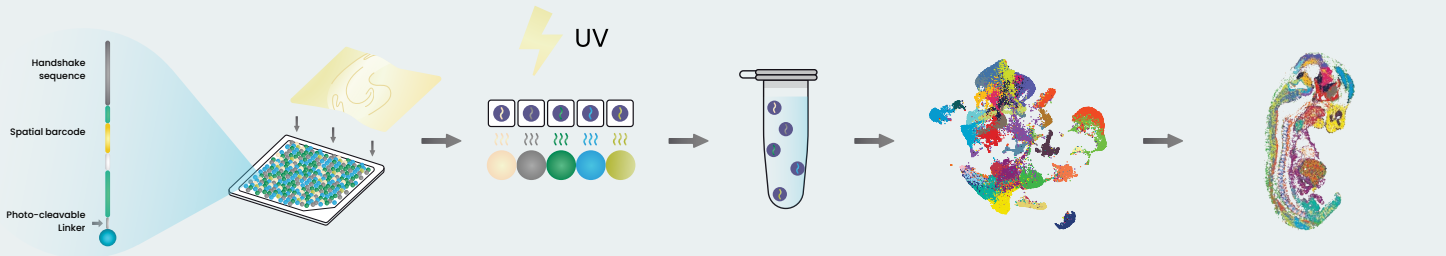
Spatial mapping of nuclei from an adult mouse brain. 27,275 nuclei from a 25 µm tissue section of an adult mouse brain were spatially positioned using a 10 mm x 10 mm Curio Trekker tile. Each dot in the UMAP (**top left**) represents a single nucleus, with a 1:1 correspondence to the spatial map (**top right**), where dots are color-coded by gene expression patterns from snRNA-seq data. Specific features of the brain section and known cell types are highlighted (**bottom right**). The top differentially expressed genes for each cortical layer, as measured by snRNA-seq, are shown (**bottom left**).

Generate high-density nuclei spatial map while preserving single-cell data quality



Spatial mapping of nuclei from an embryonic day 11 (E11) mouse embryo using the Curio Trekker workflow. 57,545 nuclei from a 25 µm tissue section of an E11 mouse embryo were spatially positioned using a 10 mm x 10 mm Curio Trekker tile. (**A**) Spatial map of the positioned nuclei. Each dot represents a single nucleus. (**B**) H&E-stained image of an adjacent tissue section demonstrates high concordance, underscoring the accuracy of spatial feature preservation by Curio Trekker (**C**) Trekker spatial data aligned with the adjacent H&E image using STalign. (**D**) UMAP with 1:1 correspondence to each dot in the spatial map. Nuclei are color-coded based on gene expression patterns derived from snRNA-seq data. (**E**) Spatial expression patterns of *Gm3764*, *Rtn1*, *Cpox*, *Ddm3os*, and *Gata3* overlaid with the H&E image in B.

Seamless integration with single-cell sequencing workflow



The core of the Trekker technology lies in its spatially barcoded surface, composed of a monolayer of 10 µm beads. A 25 µm frozen tissue section is placed onto this barcoded substrate. Upon exposure to UV light, oligonucleotides carrying spatial barcodes are cleaved from the beads and attach to the nuclei in their vicinity. The tissue is then dissociated from the substrate, and the nuclei are isolated. Single-nucleus RNA sequencing (snRNA-seq) is performed on these isolated nuclei containing spatial barcode oligos. Spatial barcode oligos are captured and amplified alongside cellular RNA. For each sample, two sequencing libraries are generated—one for gene expression data and another for spatial barcodes. A custom bioinformatics pipeline is used to map the position of each nucleus based on the spatial barcodes it contains. The Trekker protocol takes just one hour before integrating with standard snRNA-seq workflows.

Product features	
Spatial resolution	True single-cell
Sample type	Fresh frozen tissues
Tile Size	10 mm x 10 mm
Specialized capital equipment	None required
Required auxiliary equipment	Cryostat, single-cell sequencing platform, NGS sequencer
Workflow duration	1 hour upstream of single-cell workflow
Sensitivity	Same as the molecule capture sensitivity of the single-cell workflow of choice

Single-cell workflow compatibility	
Supported	**User Demonstrated**
• 10x Chromium™ 3' RNA v3.1, v4 • BD Rhapsody™ WTA	• Fluent PIPseq™ V • 10x Chromium™ Multiome ATAC + Gene Expression • ScaleBio™ Single-Cell RNA Kit

Product Name	Part Number
Trekker U 10x10 Bundle (4 Tiles)	SK017
Trekker Starter Kit (UV Lamp and Accessories)	K011
Trekker 10x10 Training Kit Bundle (2 Tiles)	SK020