Product note

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 Trekker Single-Cell Spatial Mapping Kit elevates single-cell research by transforming standard single-cell genomics data into spatial data. Trekker technology 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, Trekker spatial mapping integrates seamlessly with existing single-cell sequencing workflows and preserves the high molecular sensitivity of single-cell data. Moreover, Trekker technology extends beyond spatial transcriptomics to other omics assays, broadening the scope of spatial analysis.

UMAP to spatial map

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

Simplicity

Simple 1-hour workflow with no specialized instrumentation

True single-cell spatial resolution

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

Same single-cell data

Preserve the quality and sensitivity of single-cell data

Versatility

Fits into any single-cell sequencing workflow

Beyond spatial transcriptome

Venture into spatial single-cell multi-ome analysis

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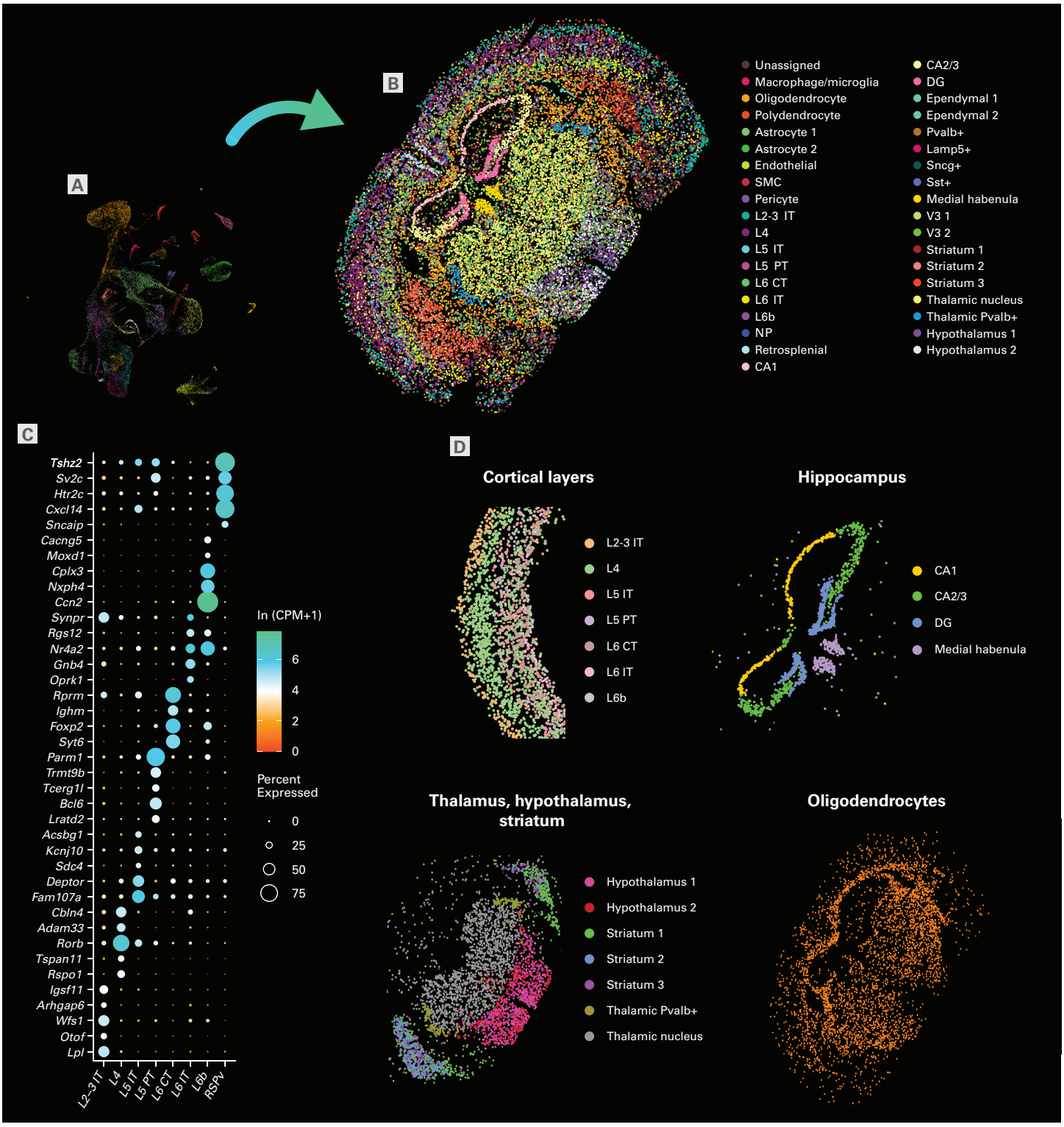
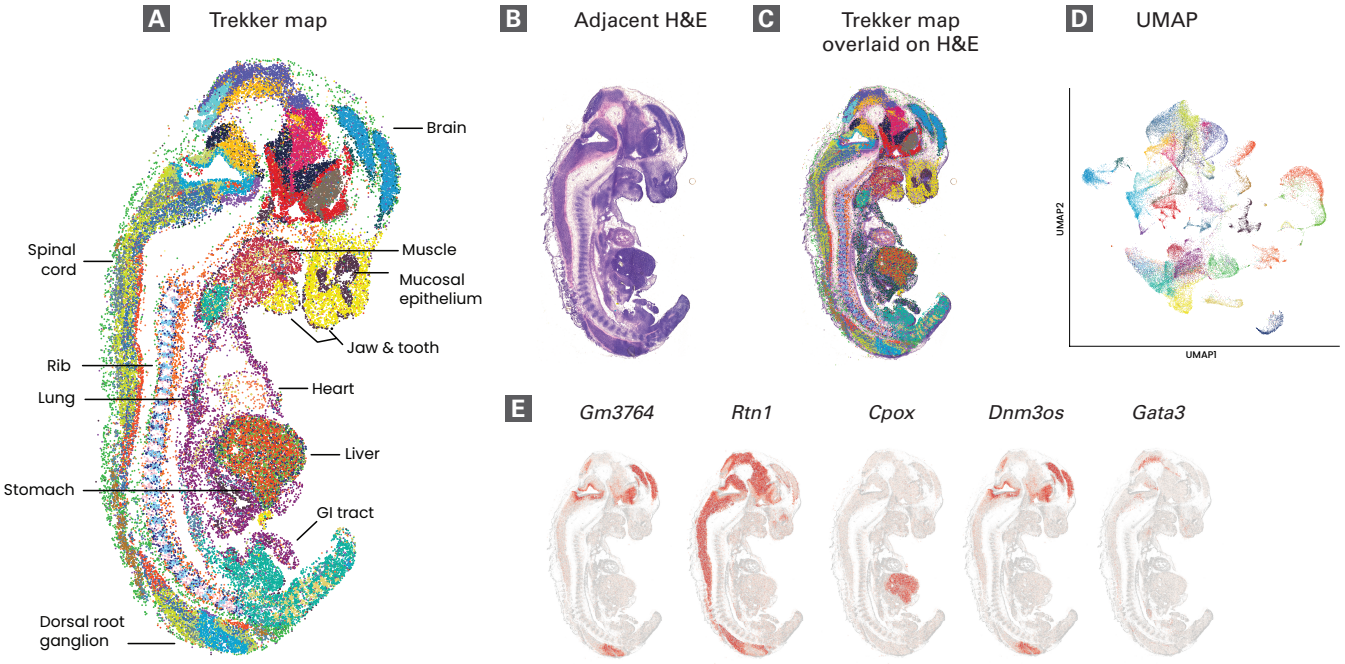


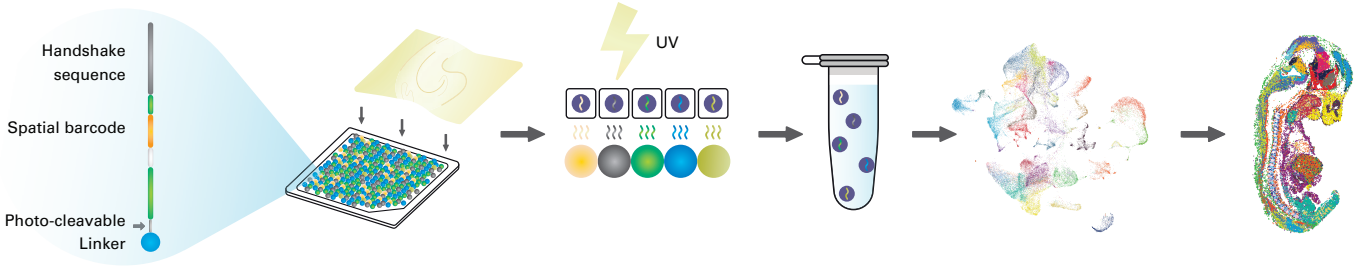
Spatial mapping of nuclei from an adult mouse brain. 27,275 nuclei from a 25 µm tissue section of an adult mouse brain were spatially positioned using a 10 mm x 10 mm Trekker tile. Each dot in the UMAP (**Panel A**) represents a single nucleus, with a 1:1 correspondence to the spatial map (**Panel B**),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

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 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 Trekker tile. **Panel A**. Spatial map of the positioned nuclei. Each dot represents a single nucleus. **Panel B**. H&E-stained image of an adjacent tissue section demonstrates high concordance, underscoring the accuracy of spatial feature preservation by the Trekker kit. **Panel C**. Trekker spatial data aligned with the adjacent H&E image using STalign. **Panel 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. **Panel E**. Spatial expression patterns of *Gm3764*, *Rtn1*, *Cpox*, *Ddm3os*, and *Gata3* overlaid with the H&E image in **Panel B**.

Seamless integration with single-cell sequencing workflow



Bead with spatial barcode | Melt tissue on Trekker tile | Tag nuclei with photocleaved spatial barcode | Isolate nuclei | Single nucleus RNA-seq | Trekker bioinformatics analysis places nuclei in space based on spatial barcodes associated with each nucleus

The core of the Trekker technology lies in its spatially barcoded surface, composed of a bead monolayer. 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. Integrating the Trekker protocol adds just one hour upstream of standard snRNA-seq workflows.

Product note

Trekker Single-Cell Spatial Mapping Kit

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, next-generation sequencer
Workflow duration	1 hr upstream of single-cell workflow
Sensitivity	Same as the molecule capture sensitivity of the single-cell workflow of choice

Single-cell workflow compatibility

Supported

- 10x Chromium Single Cell 3' RNA v3.1, v4
- BD Rhapsody WTA

User-demonstrated protocols

- BD Rhapsody Single-Cell ATAC-Seq and mRNA WTA
- BD Rhapsody Single-Cell TCR/BCR Next and mRNA WTA

PRODUCTS

Cat. #	Product
SK017	Trekker U 10x10 Bundle (4 Tiles)
K011	Trekker Starter Kit (UV Lamp and Accessories)
SK020	Trekker 10x10 Training Kit Bundle (2 Tiles)

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