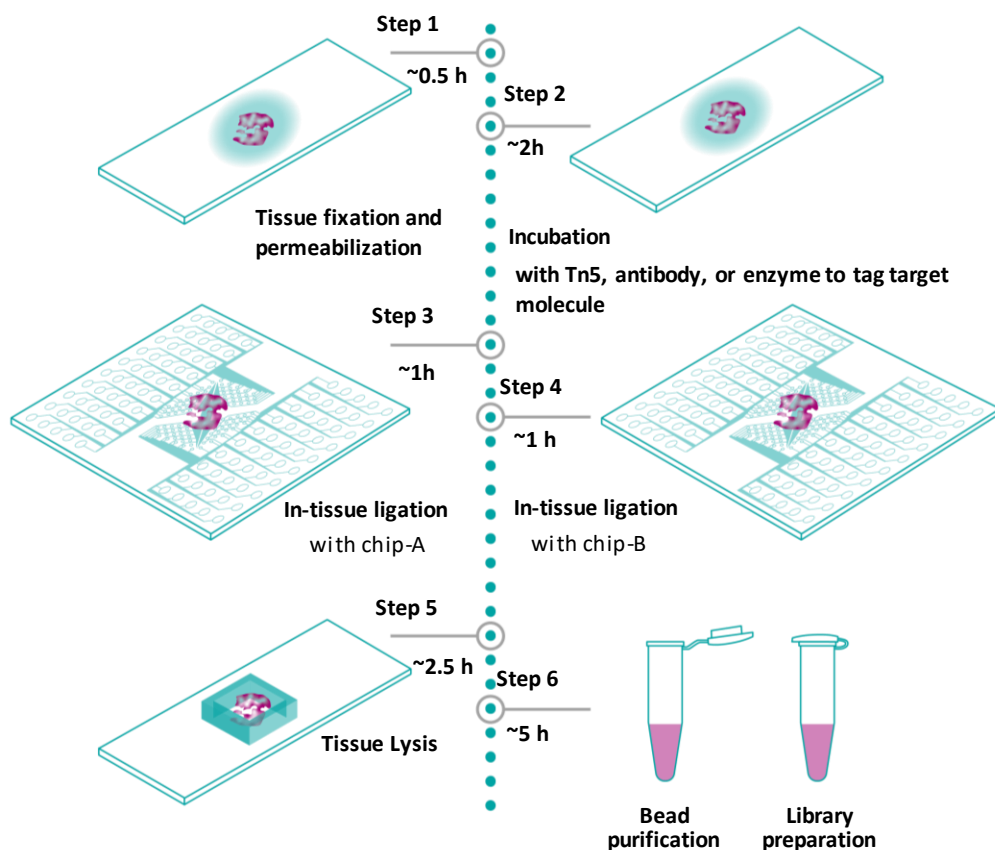## Our Platform: the first Spatial Epigenomics platform

Deterministic Barcoding in Tissue for spatial omics sequencing (DBiT-seq), invented by the research group of Professor Rong Fan of Yale University, uncovers spatial biology by combining microfluidics and next- generation sequencing (NGS). Applications of the platform published in *Nature, Nature Biotech, Science,* and *Cell*, demonstrate the platform's comprehensive, unbiased profiling of the transcriptome, proteome and, for the first time, epigenome at the cellular level.
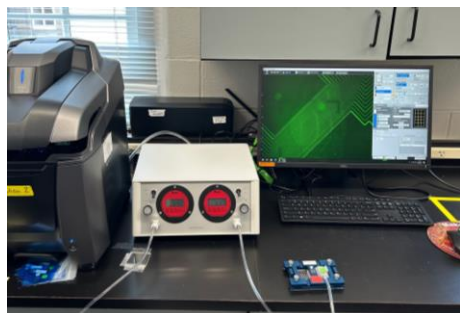

Step 1
~0.5 h
Step 2
~2h
Tissue fixation and permeabilization
Incubation with Tn5, antibody, or enzyme to tag target molecule
Step 3
~1h
Step 4
~1 h
In-tissue ligation with chip-A
In-tissue ligation with chip-B
Step 5
~2.5 h
Step 6
~5 h
Tissue Lysis
Bead purification
Library preparation
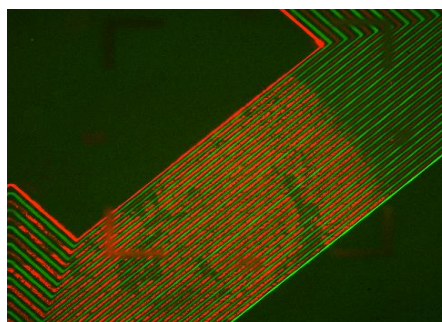
Workflow breakdown

1. **Preparation:** Tissue sections of 7-10 um, mounted on a standard 1x3 inch pathology slide, are lightly fixed and permeabilized. For spatial epigenome analysis, OCT-embedded fresh frozen tissue is utilized.

2. **Incubation:** Reagents for omics of interest are introduced and incubated within the tissue, facilitating targeted interaction with specific biomolecules.

3. **Barcode Ligation:** Utilizing microfluidic channels, DNA barcodes are delivered to the tissue via two separate chip-mediated ligations. This generates a 2D grid of unique barcodes, turning the tissue section into a spatially-resolved matrix.

4. **Tissue Lysis:** The tissue is lysed, releasing the tagged biomolecules for subsequent analysis.

5. **Purification and Library Preparation:** Bead purification is conducted followed by library preparation, ensuring a high-quality input for next-stage sequencing.

Easily Integrated Platform

Easy to adopt platform leverages existing workflows

Liquid delivery with microfluidics to map omics readouts in tissue

Adopting DBiT-seq in your laboratory is a straightforward process. Designed to seamlessly integrate with pre-existing molecular biology workflows, the technology enhances your investigative toolkit without disrupting your established operations. This easy-to-adopt platform leverages standard lab equipment . The platform enables you to create high-resolution spatial maps of tissue samples using familiar workflows and existing infrastructure.

Hardware requirements

The DBiT-seq leverages instruments from standard molecular biology workflows to allow an easy adoption. DBiT-seq requires two custom tools: the AtlasXpress, which aids in the application of its microfluidics chips to a tissue sample and a vacuum regulator, which enables the precise delivery of reagents to the tissue.
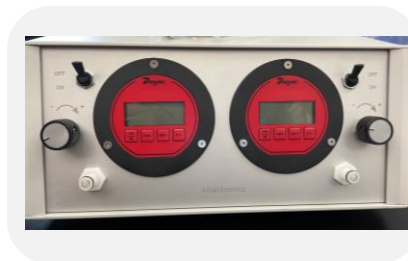
Custom Hardware

Leveraging standard workflows

AtlasXpress

Seals our microfluidic chips to tissue mounted slide

### Vacuum regulator

Precise regulation of flow in the chip

1. Epifluorescence scanning microscope with tiling capacity (e.g. Keyence BZ-X, EVOS M7000)

2. Access to Next Generation Sequencer (NGS): spatial ATAC-seq requires 200-300M reads 150 Paired-end (60-90 Gb/sample)

3. Vacuum source or standard house vacuum

4. Standard PCR/NGS library preparation materials and equipment

5. Positive pressure source (optional): Facilitates slide/tissue drying

Consumable kits

Our Spatial ATAC-seq kit offers a comprehensive solution, equipping you with all the essential reagents and microfluidic chips required for efficient tagmentation and spatial barcoding. Designed for easy adoption, our microfluidic chips are dust resistant and compatible with multi-channel pipettes, ensuring a hassle-free integration of our platform.

Microfluidic Chips

Reagent/Sample optimization kits
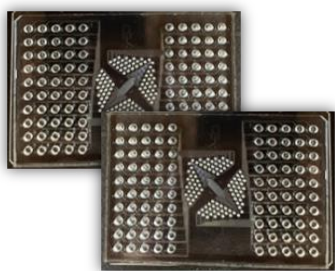
X and Y Chip Pair (50 inlets/outlets)
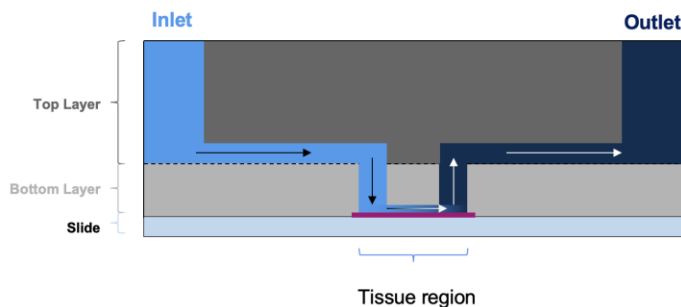
Multilayer PDMS protects channels from dust
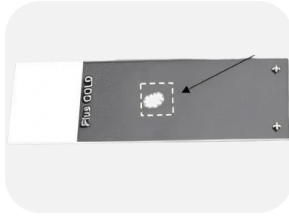

Spatial barcoding reagents for Spatial ATAC-seq

Our **spatial ATAC-seq kit** includes: our microfluidic chips, spatial barcodes, **Tn5 Transposase loaded with our custom adaptors, sequencing adapters, buffers and enzymes.**

We also recommend using our **Sample Optimization Kit** to optimize the Tn5 reaction in different tissue types and ensure high quality reagent delivery with our microfluidics:. This kit includes flow QC chips and bulk ATAC-seq reagents.

Process Overview: From Tissue Preparation to Sequencing Library

Explore a streamlined step-by-step overview of the AtlasXomics process, covering crucial stages and paving the way for valuable data analysis and research discoveries.
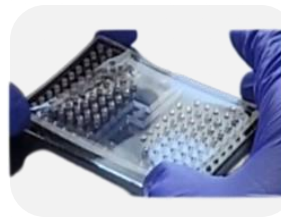
Tissue prep/ bulk chemistry

1. Mount tissue on 1x3 in slide

2. Run reaction in tissue

3. Affix chip to tissue mounted slide

Spatial Barcoding (Repeated for XY)

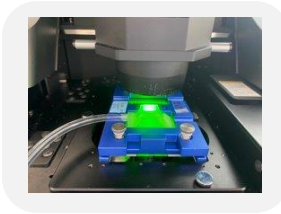4. Pipette reagents into chip
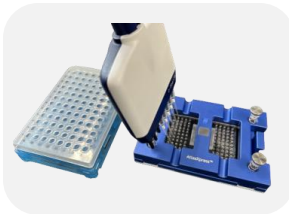
5. Apply vacuum

6. Image in microscope

7. Lyse the tissue and prepare the library
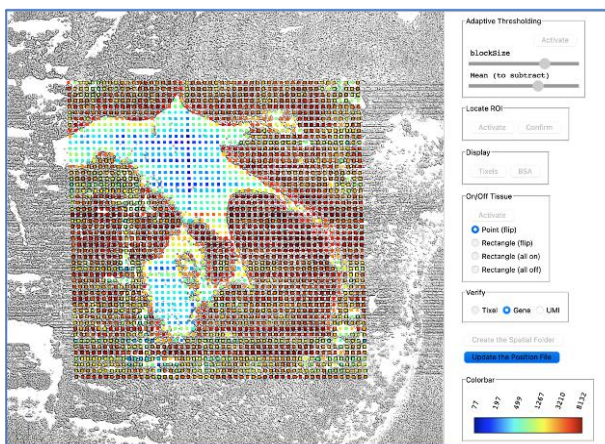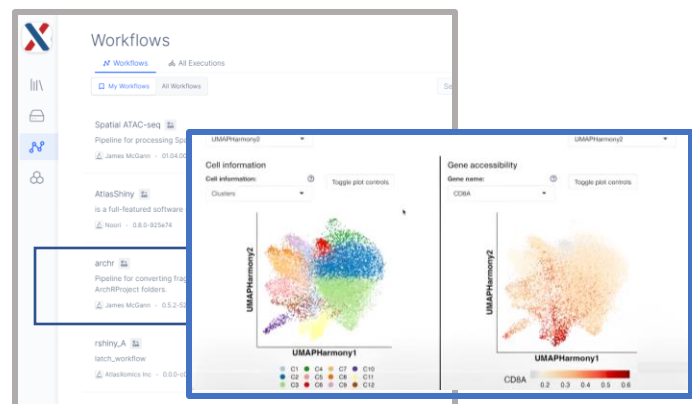

AtlasXomics Software Suite

AtlasXomics simplifies data analysis with our robust software suite of products. Easily align your spatial genomics data, process FastQ files, and delve deeper with integrated tools like Seurat and ArchR. From data generation to visualization, our kits accelerate your path to research insights.

AtlasXbrowser

Identify on/off tissues, align with NGS data with BF image.

Atlas data analysis products

Data analysis can be completed with established tools (Seurat, ArchR). Process FastQ files and visualize.

AtlasXomics