

The background features a dark blue gradient with intricate, glowing light blue circuit-like patterns. These patterns consist of various geometric shapes, including lines, circles, and squares, some of which are interconnected to resemble a network or data flow. The overall aesthetic is futuristic and technological.

# AtlasXomics

Chart the unexplored depths of spatial biology

# Executive Summary - AtlasXinsights™ Service

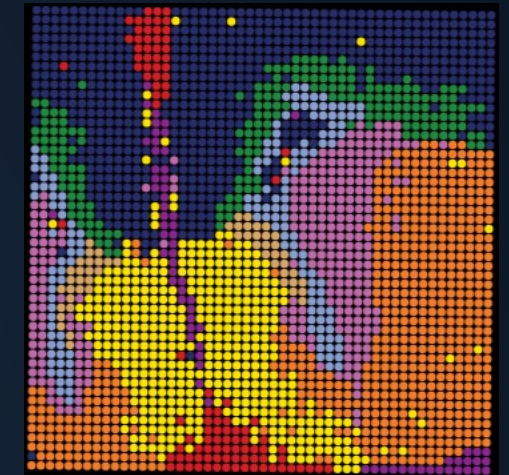
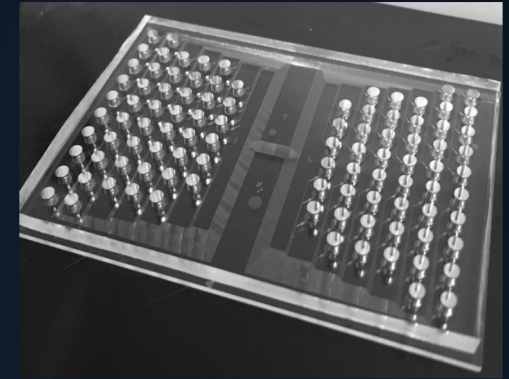
Transformative spatial maps generated by the discovery platform Deterministic Barcoding in Tissue for spatial omics sequencing (DBiT-seq)

- Enables **comprehensive, unbiased, epigenome mapping of cell states**
- Features compatibility with a wide variety of tissue types

First commercial translation of the DBiT-seq platform

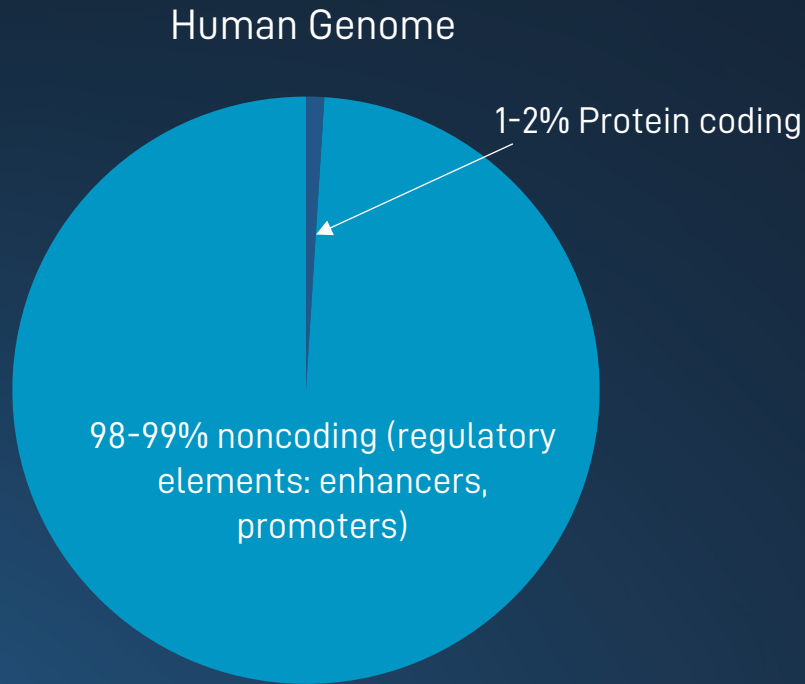
Invented by research group of **Dr. Rong Fan, Professor of Biomedical Engineering at Yale University**

- Microfluidics- and NGS-based approach
- Applications of the platform published in Cell, Science, and Nature showing epigenome, transcriptome and proteome profiling in tissue at cellular resolution

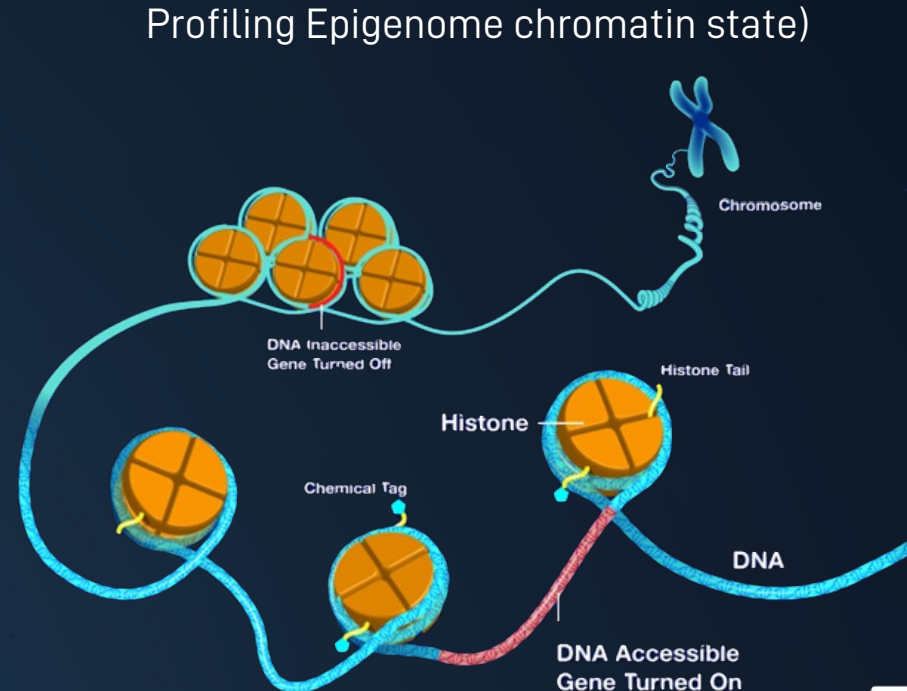


# Challenge: How does chromatin organization **modify disease** in tissue?

Many diseases are driven by alterations to regulatory sequences contained in noncoding DNA. However, these disease-causing modifications are invisible to proteomic or transcriptomic assays. Looking at the epigenome, more specifically chromatin organization, enables the study of how noncoding regulatory elements tune gene expression and dictate cell state.



**Only 1-2%** of genome is profiled by state-of-the-art transcriptome methods

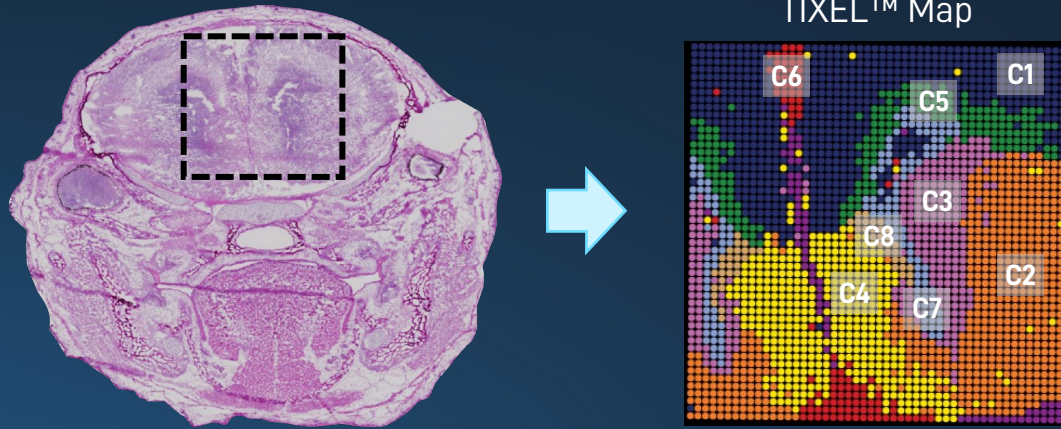


Genome.gov  
NIH National Human Genome Research Institute

**Expands the search space for therapeutics** by exploring noncoding regulatory elements that modulate gene expression

# Our solution: comprehensive spatial epigenome mapping at cellular resolution

Spatial ATAC-seq at the cellular level



Comprehensive mapping of the epigenome with next generation sequencing and microfluidics (spatial-ATAC-seq)



Cellular resolution - 25  $\mu\text{m}$  resolution, 2.5 x 2.5 **mm** ROI (region of interest) of 2500 TIXELs



Identification of unique accessible distal regions in specific clusters for cell type specific enhancer identification



Identification of differential accessible regions by condition to infer underlying epigenetic regulatory factors or mechanisms

TIXEL – 25  $\mu\text{m}$  x 25  $\mu\text{m}$  tissue element akin to picture element

# AtlasXinsights™ maps tissue microenvironment

## Spatial Epigenomics Service

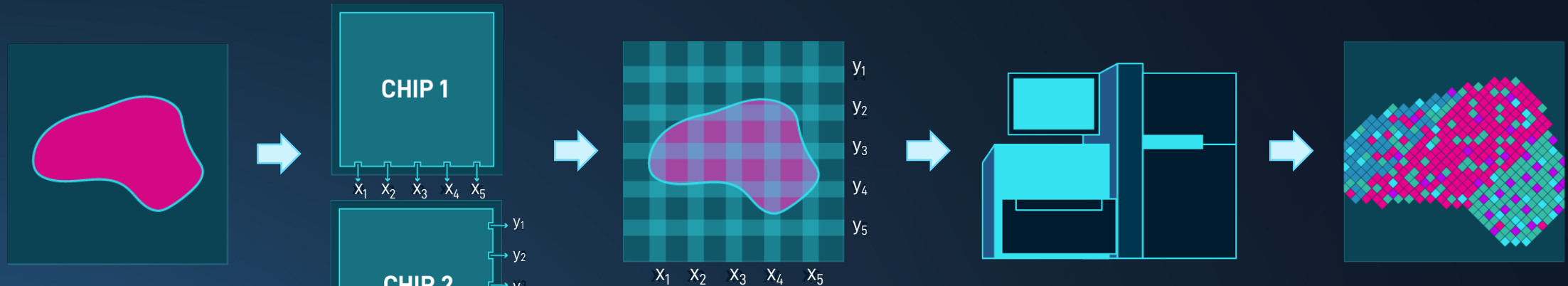
Tn5  
transposase fragments  
accessible chromatin

Microfluidics ligate x- and  
y-spatial barcodes to  
adaptors

All probes labeled with x-y  
spatial barcodes

Oligos extracted, amplified,  
and sequenced

Spatial map recreated  
at near cellular  
resolution



Inventor kits

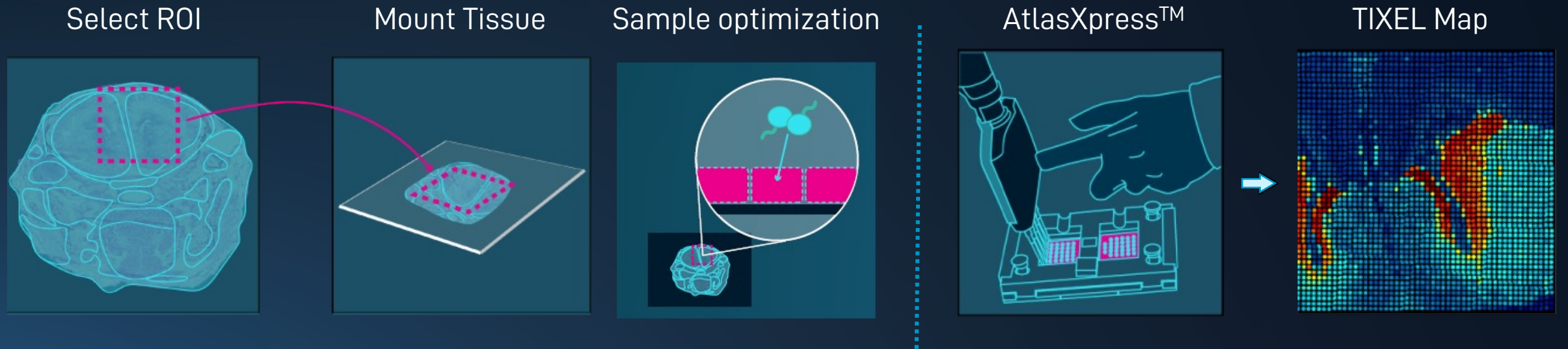
Spatial ATAC-seq reagent kit

Spatial epigenome service: Sample to data spatial epigenome analysis with spatial-ATAC-seq and early access of spatial-CUT&Tag

**Inventor kit:** Microfluidics chips and hardware required to deliver your reagents to tissue

**Spatial ATAC-seq kit:** All custom reagents (enzymes and barcodes) to run spatial ATAC-seq

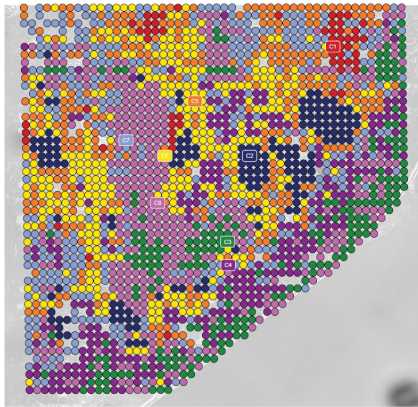
# Customer interactions guide our process at each step of analysis



Our team works closely with the investigator to identify and interrogate a 2.5 x 2.5 mm region of interest (ROI) that best addresses their biological question.

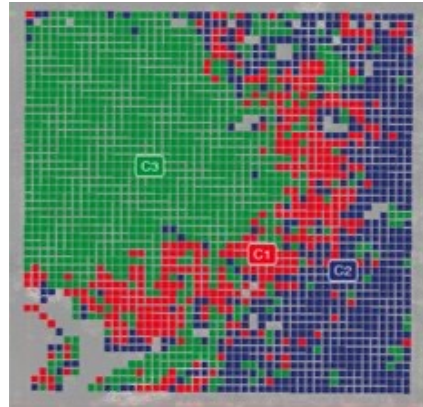
- Investigators mount ~10um thick fresh frozen OCT embedded tissue sections onto custom 2 x 3 inch slides and then ship their samples to our lab.
- AtlasXinsights™ runs optimization experiments to find the best permeabilization conditions to extract the maximum accessible DNA, connects with the investigator to locate the ROI, runs DBiT-seq, and provides QC and detailed data reports with analyses that the investigator can iterate with our software tools.

# Spatial ATAC-seq service has been validated across a wide range of tissue types



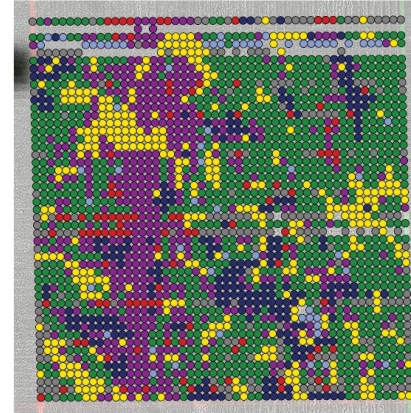
**Mouse Spleen**

TSS: 18,108  
Peaks: 114,777



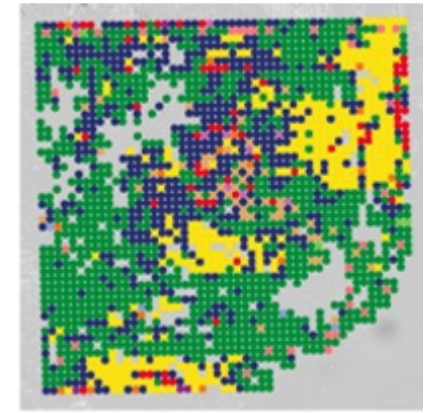
**Mouse Kidney**

TSS: 7,318  
Peaks: 87,544



**Mouse Melanoma**

TSS: 5,426  
Peaks: 60,006



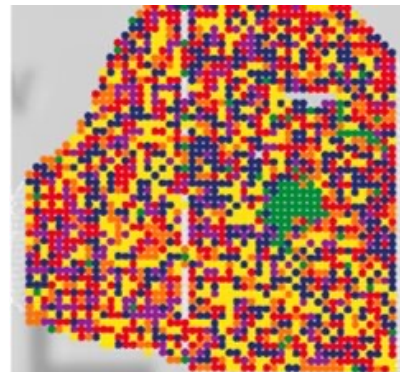
**Human Melanoma**

TSS: 4,826  
Peaks: 123,391



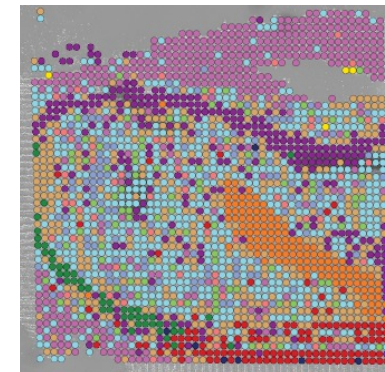
**Germline PDX**

TSS: 5,66  
Peaks: 150,394



**Mouse Muscle**

TSS: 5,14  
Peaks: 44,614

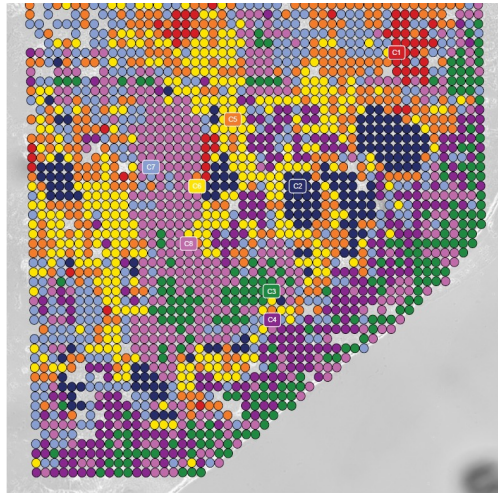


**Mouse Hippocampus**

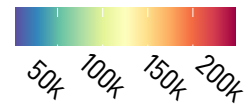
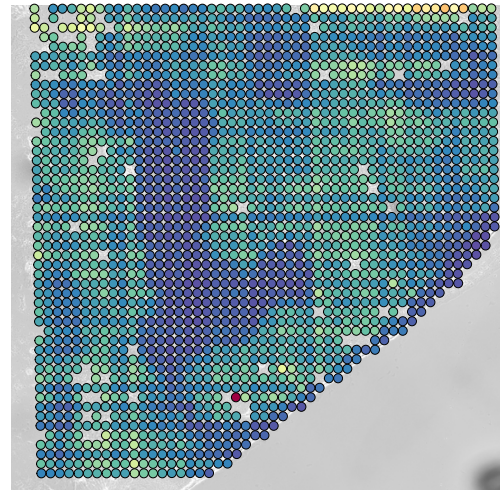
TSS: 7,16  
Peaks: 74,186

Tissue quality is evaluated by gold standard quality metrics to ensure performance

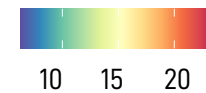
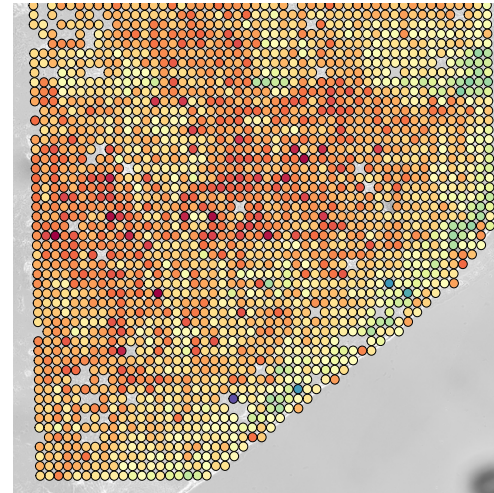
Spatial UMAP



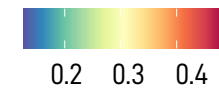
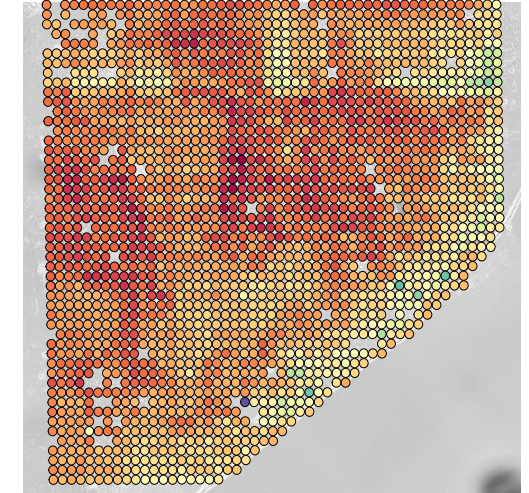
Fragment distribution



Spatial TSS Score



Spatial FRIP



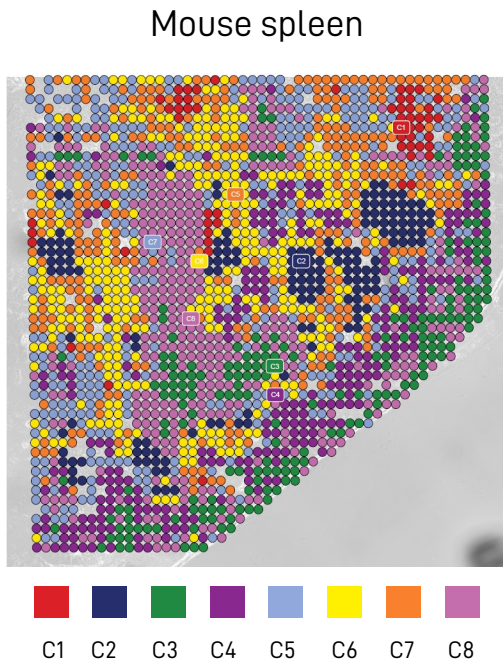
Mouse spleen  
(200M reads)

Low quality regions will be filtered out of analysis for better performance

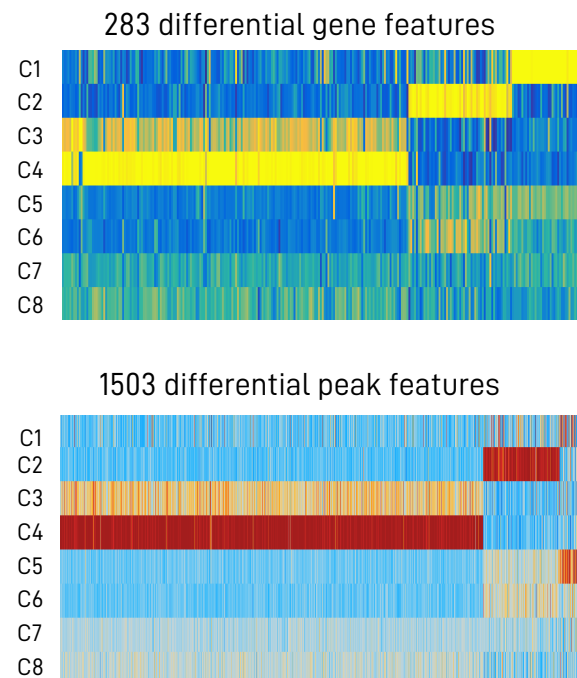


# Standard data report provides comprehensive look at spatial chromatin accessibility

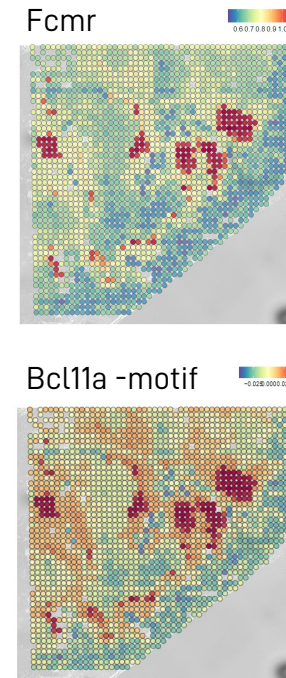
## Spatial UMAP



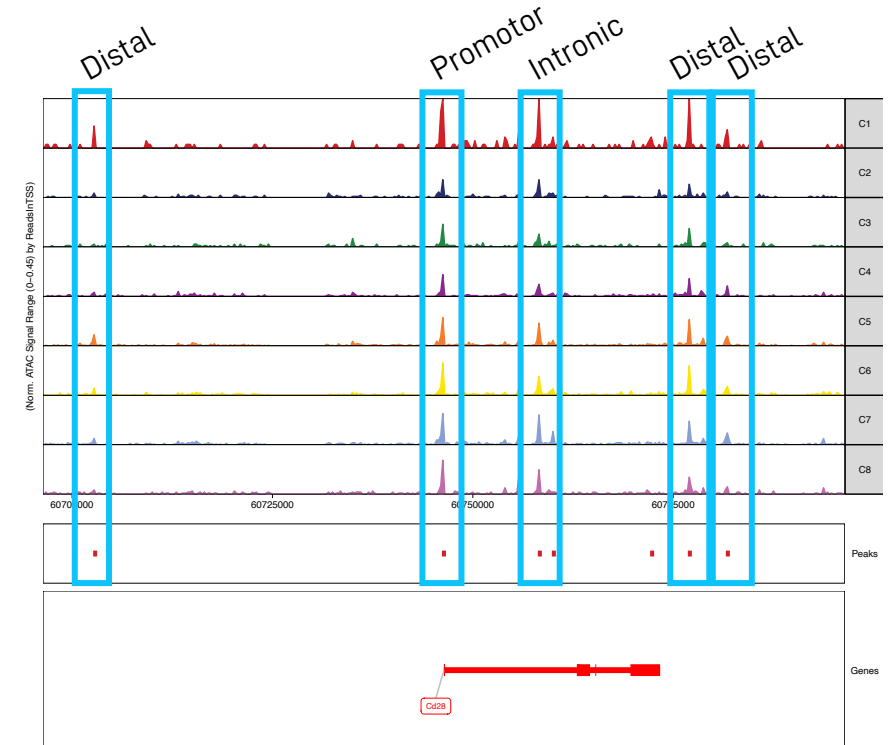
## Differential features



## Gene / motif maps



## Spatial chromatin accessibility

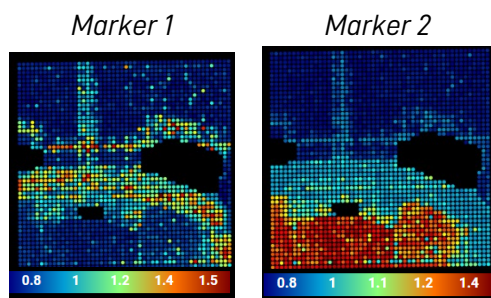


AtlasXomics will provide list of top peaks (distal, intronic, promotor), accessible genes, and raw data

# Customer feedback drives deeper analysis of underlying biology

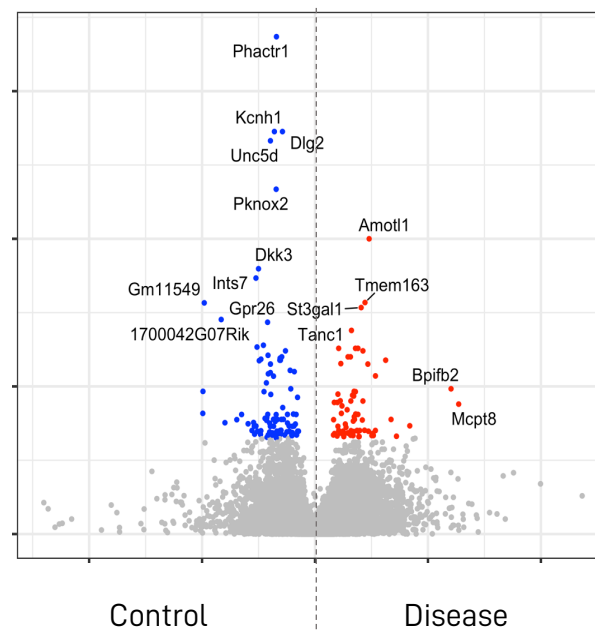
## Cluster annotation

Manual annotation with known cell markers



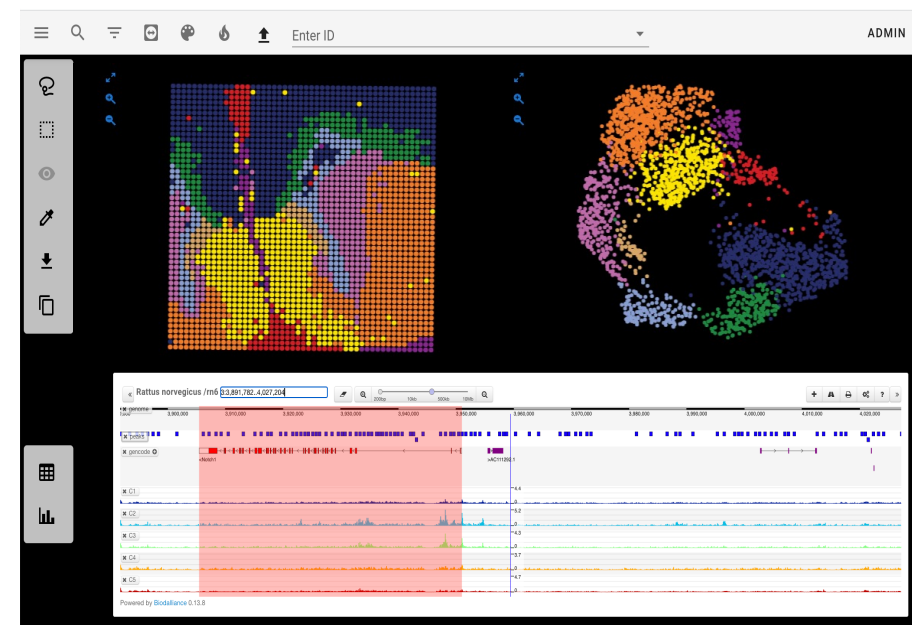
## Differential analysis by condition

Compare overall differences by cluster or sample

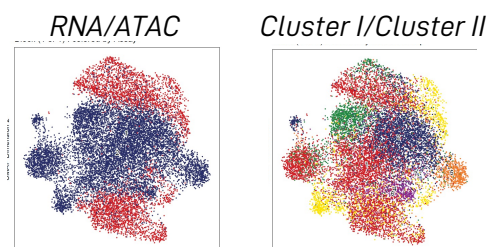


## Interactive browser exploration

Explore the data independently (in development)



Integration with annotated single cell data



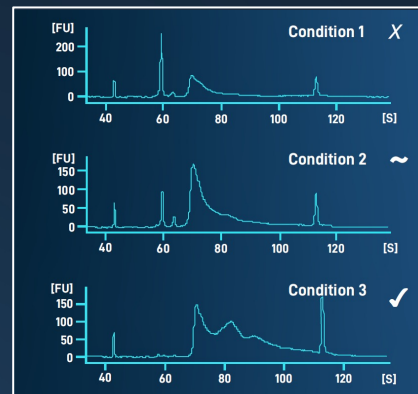
# AtlasXomics Service: Complete question-to-answer solution to explore the epigenome

1



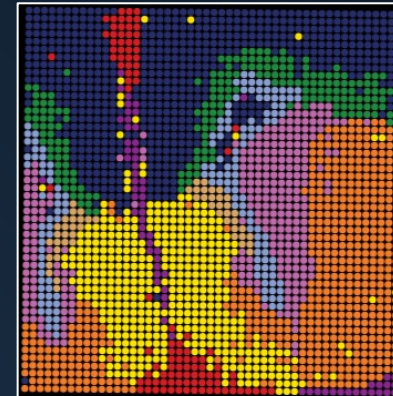
Meet with our service lead to determine your biological question and region of interest

2



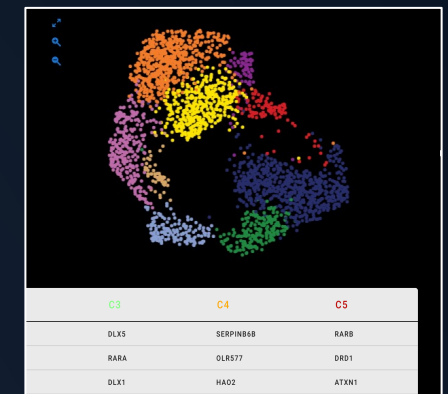
Sample optimization summary to determine the best conditions for your tissue type

3



Specialized data report of spatial epigenomic results with detailed quality summary

4



Follow-up analysis based on your initial feedback (complimentary to first time users)

How we can help answer your biological questions:

- Map the diverse **epigenomic landscape** in tissue microenvironment
- Determine changes in **chromatin accessibility between treatment groups** for specific cellular neighborhoods
- Localize **differential promotor accessibility** changes to specific tissue regions
- Identification of **unique accessible distal regions** in specific clusters for cell type specific enhancer targets
- Connecting H&E **morphology to chromatin accessibility** variations



Contact us at [info@atlasxomics.com](mailto:info@atlasxomics.com)

Find us on [LinkedIn](#) or [Twitter](#)