comprehensive

ATAC-Seq solutions

ACTIVE MOTIF®

Enabling Epigenetics Research

ATAC-SEQ KIT

Specifications:

- ✓ Generate 16 sequencing-ready Illumina®-compatible ATAC-Seq libraries per kit
- ✓ Process 50,000-100,000 cells or 20-30 mg of tissue per sample
- ✓ Optimized protocol with all reagents and enzymes included
- ✓ Entire workflow can be completed in 4 hours

Key Highlights:

Easy to Use:

- Optimized and streamlined protocol makes ATAC-Seq assays accessible to all researchers
- Different protocols optimized for cell or tissue samples
- No specialized or expensive equipment needed

Fast Results:

- Go from samples to sequencing-ready libraries in just 4 hours

Complete Kit:

- All reagents and enzymes are included
- Kit includes assembled transposomes, containing the Tn5 transposase loaded with NGS adapters

Learn more about Active Motif's comprehensive ATAC-Seq solutions at www.activemotif.com/atac-seq

Complete kit for generating sequencing-ready ATAC-Seq libraries from cell or tissue samples

ATAC-Seq is a rapid assay that allows analysis of epigenetic profiles across the genome by identification of regions that have open or accessible chromatin states. Because of the assay's speed, simplicity, and applicability to a wide range of sample types, ATAC-Seq has become a commonly-used epigenetic assay, and it can serve as a gateway to further, more detailed epigenetic analyses.

The ATAC-Seq Kit from Active Motif provides the reagents necessary to produce 16 unique sequencing-ready Illumina®-compatible ATAC-Seq libraries from 20 – 30 mg tissue or 50,000 – 100,000 cells per reaction. The optimized protocol guides you through the steps for sample preparation, tagmentation, and library preparation, yielding next-generation sequencing-ready libraries that can be multiplexed in a single flow cell sequencing run.

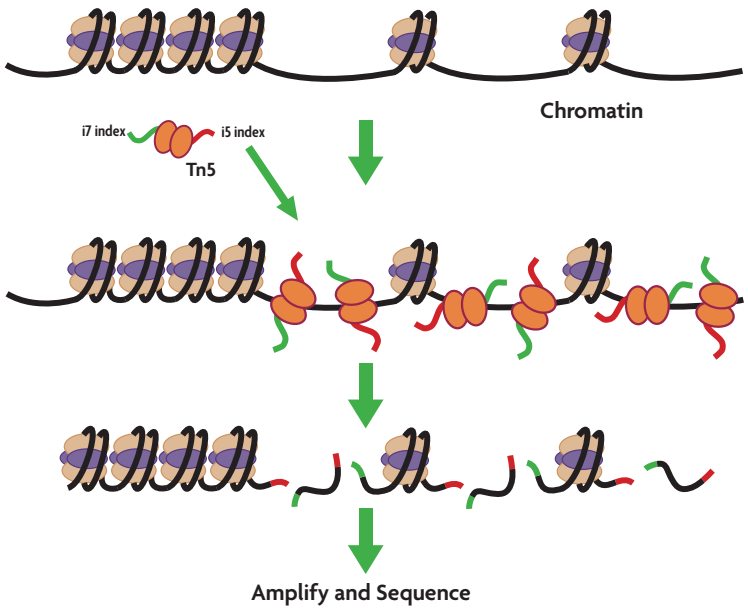


Figure 1. ATAC-Seq is based on transposase-mediated insertion of NGS adapters into open chromatin regions. This assay provides genome-wide profiles of open and accessible regions of chromatin that are indicative of transcriptionally active regions and regions of the genome containing active regulatory elements.

Generate Robust and Reproducible Data with the Active Motif ATAC-Seq Kit

The chromatin at promoters of genes that are transcriptionally active are generally open or accessible. ATAC-Seq assays result in peaks at these locations, revealing those open chromatin regions in the samples being investigated.

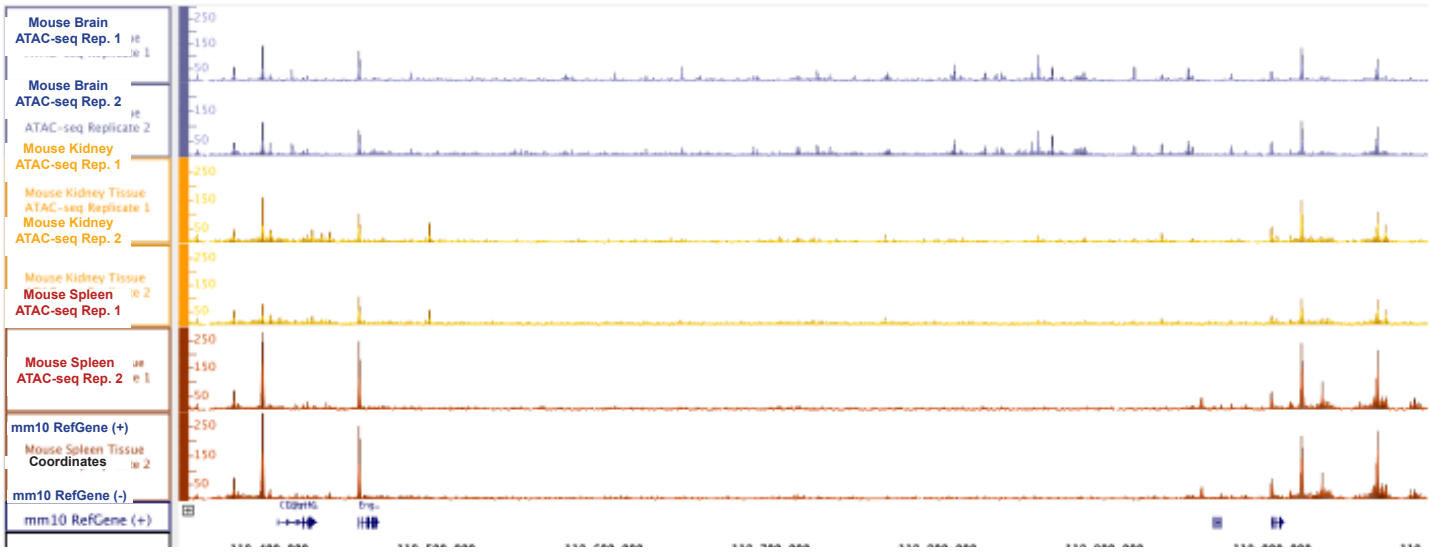


Figure 2. ATAC-Seq Kit was used to assess the genome-wide open chromatin states of several mouse tissue samples. The peaks here indicate open chromatin signal at the Rbfox3 gene, which exhibits highest expression in brain tissue.

Active Motif ATAC-Seq Kit Data Correlates Well with Illumina® Nextera™ Kit Data

The Active Motif ATAC-Seq Kit generates high-quality data. ATAC-Seq data from experiments performed with the ATAC-Seq Kit correlate very well with data generated using the Tn5 transposase from the Illumina Nextera kit.

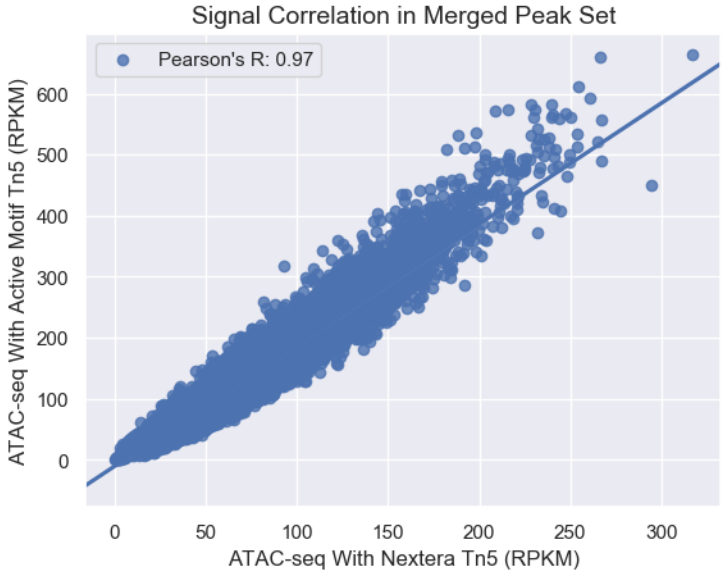


Figure 3. High correlation (Pearson correlation coefficient is 0.97) between the signal in the peaks called from ATAC-Seq datasets generated using either the Active Motif ATAC-Seq kit or the Nextera Tn5 enzyme demonstrates that the Active Motif transposase identifies the same accessible regions as the Nextera enzyme does on a genome-wide scale.

ATAC-SEQ SERVICE

Specifications:

- ✓ Submit 50,000-100,000 cells or 20-50 mg of tissue per sample
- ✓ Sequencing depth: 30 M paired-end reads per sample
- ✓ Turnaround time: 5-7 weeks
- ✓ Data deliverables include raw data along with mapping, filtering, peak calling, Excel files that provide detailed information about peaks for sample-to-sample comparisons, and other figures.

Key Highlights:

Data You Can Trust:

- We were the first ATAC-Seq service provider in the world and have successfully performed >2,000 ATAC-Seq assays
- Our clients publish ATAC-Seq data we generate in high profile journals

Easily Interpret the Results:

- Bioinformatics and support included

Fastest Path to Publish ATAC-Seq Data:

- Our end-to-end services will save you time so you can publish faster
- Dedicated protocols for different sample types
- Receive ready-to-publish figures

Learn more about Active Motif's comprehensive ATAC-Seq solutions at www.activemotif.com/atac-seq

End-to-end service for identification of open chromatin regions

Active Motif, the leading provider of ChIP-Seq and other epigenetic services, offers an end-to-end ATAC-Seq service to investigate chromatin states on a genome-wide scale. The ATAC-Seq service is designed to study open chromatin, which is known to contain active gene regulatory elements including promoters, enhancers, and insulators. The assay provides data to enable identification of accessible chromatin regions across the genome, characterization of epigenomes of disease states, and to uncover key transcriptional mechanisms controlling cell fate.

The ATAC-Seq service includes sample preparation, tagging of open chromatin regions, library generation, library QC, next-generation sequencing, and bioinformatic analysis.

Use Our ATAC-Seq Service To:

- Generate genome-wide maps of open chromatin in cell or tissue samples
- Determine if epigenetic mechanisms are at work in disease
- Gain mechanistic insight into gene regulation in response to treatment
- Uncover cell fate- or disease-related differences between samples

ATAC-Seq Services Enable Identification of Differentially Accessible Chromatin Regions

Our ATAC-Seq Service can be used to identify epigenetic changes between different samples or treatment groups by measuring chromatin accessibility on a genome-wide scale. One major advantage of this approach is that no requirement for prior knowledge of the specific epigenetic modifications that might be involved is needed, and therefore ATAC-Seq assays represent an unbiased approach.

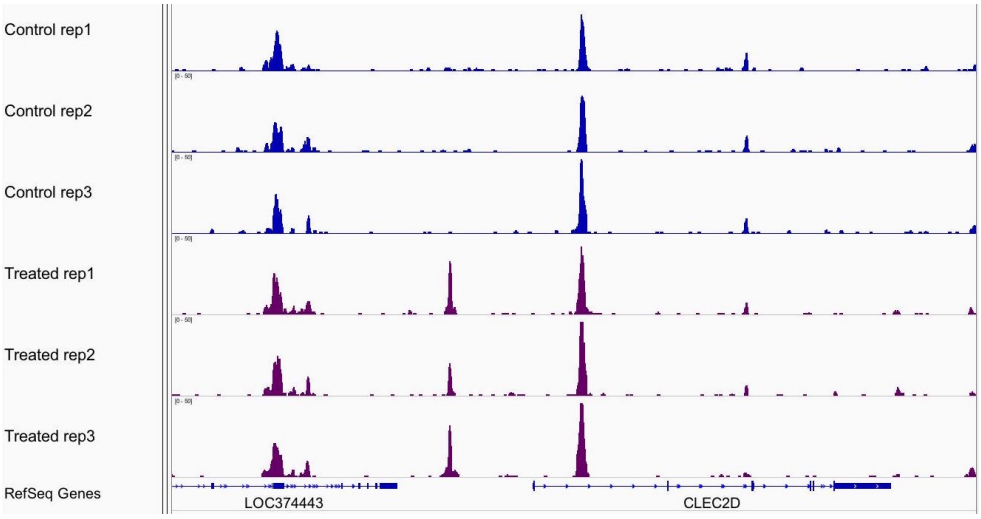


Figure 4. Active Motif's ATAC-Seq assay was performed on control and treated cells, each in triplicate. Hundreds of differential peaks were detected. The prominent differential peak depicted here is in an intergenic region.

Active Motif's ATAC-Seq Service is Highly Reproducible

For some experiments it is beneficial to perform replicates to be able to identify differences between samples that are statistically significant. The ATAC-Seq service offered by Active Motif is highly reproducible, meaning that any differences seen between replicates or experimental groups are likely to be real biological differences rather than technical artifacts.

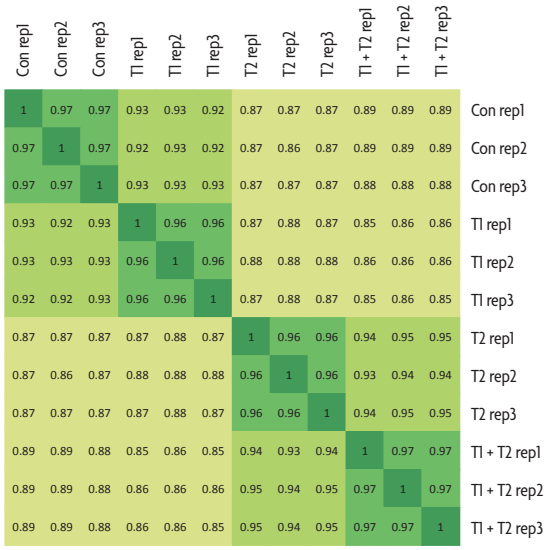


Figure 5. Active Motif's ATAC-Seq assay was performed under four different cellular conditions, each condition in triplicate. The Pearson correlation coefficients were generated and graphed for each pair-wise comparison. The data demonstrate the assay is highly repro-ducible with correlation coefficients near >0.95 for replicates. Four separate groups are clearly visible in the heat map, showing that triplicates are more similar to each other than to other samples and indicating that there are differences between sample types.

SINGLE-CELL ATAC-SEQ SERVICE

Specifications:

- ✓ Submit 100,000-2M cells or 20-50 mg of tissue per sample
- ✓ Sequencing depth: 250 M paired-end reads per sample
- ✓ Turnaround time: 6-8 weeks
- ✓ Data deliverables include raw data along with mapping, filtering, peak calling, Excel files that provide detailed information about peaks for sample-to-sample comparisons, files for visualization on the 10x Genomics Loupe Cell Browser, and other figures.

Key Highlights:

Single-Cell ATAC-Seq Data You Can Trust:

- Our end-to-end service saves you time so you can publish faster
- Dedicated team of expert scientists handles every step

Sample-Specific Protocols:

- We have already optimized conditions for many sample types so you don't have to

Easily Interpret the Results:

- Identify subpopulations of cells within complex populations
- Bioinformatics and support included

Learn more about Active Motif's comprehensive ATAC-Seq solutions at www.activemotif.com/atac-seq

End-to-end service to identify open chromatin regions at single-cell resolution

Single-cell ATAC-Seq (scATAC) is based on transposase-mediated insertion of sequencing adapters into open chromatin regions followed by microfluidic single-cell sorting and labeling. This assay, like traditional ("bulk") ATAC-Seq, provides profiles of open and accessible regions of chromatin that are indicative of active regulatory regions, but at single cell resolution.

Our scATAC-Seq service enables examination of genome-wide chromatin accessibility of thousands of cells in parallel, allowing examination of subpopulations of cells within a heterogenous population that would otherwise be lost in standard ATAC-Seq assays.

Use Our Single-Cell ATAC-Seq Service To:

- Identify cancer stem cells or infiltrating macrophages within tumor samples
- Identify novel cell subpopulations that are responsible for response to drug treatments (i.e. responders vs. resistant cells)
- Identify subpopulations of cells with variations in chromatin accessibility that can provide insight into developmental trajectories (i.e. brain development, T-helper cell development, B-cell differentiation)

Identify Variations in Chromatin Accessibility Across Different Cell Populations Within a Single Sample

scATAC-Seq can be used to identify cell subpopulations with different chromatin accessibility profiles within complex samples, eliminating the need for isolation strategies like FACS or magnetic sorting that could alter the biology due to sample manipulation.

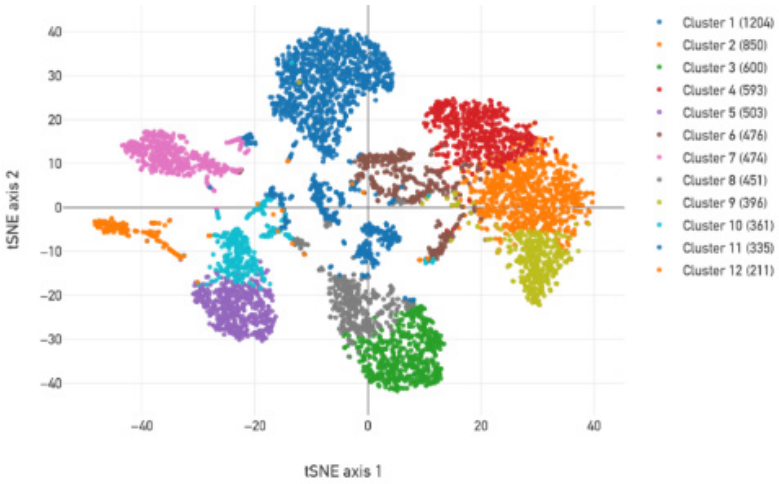


Figure 6. Single-Cell ATAC-Seq data generated from mouse kidney tissue. Each color-coded cluster on the tSNE plot represents populations of cells that had the same open chromatin profile. Using this approach, 12 cell populations were identified from a single sample.

scATAC-Seq Reveals Cell Subpopulation-Specific Data that Would Not be Captured by "Bulk" ATAC-Seq

scATAC-Seq enables mapping the open chromatin profiles of cell subpopulations within complex or heterogeneous samples. This approach allows researchers to uncover mechanisms driving disease phenotypes or other biological processes by individual cell populations.

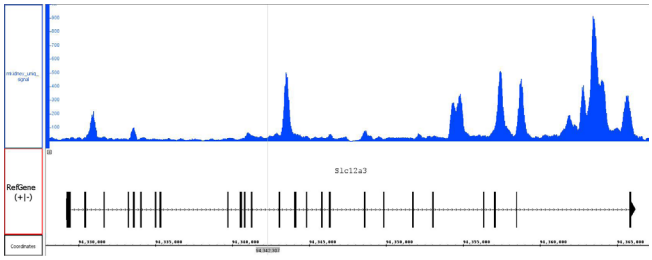
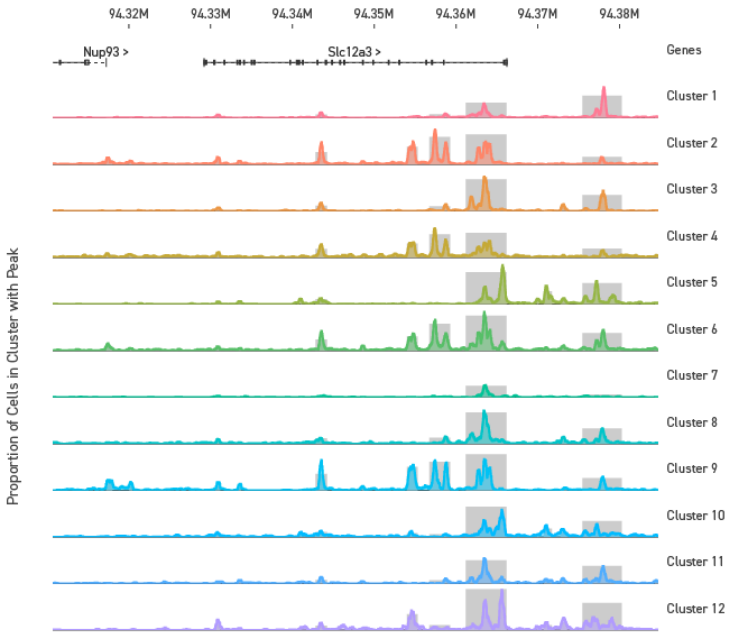
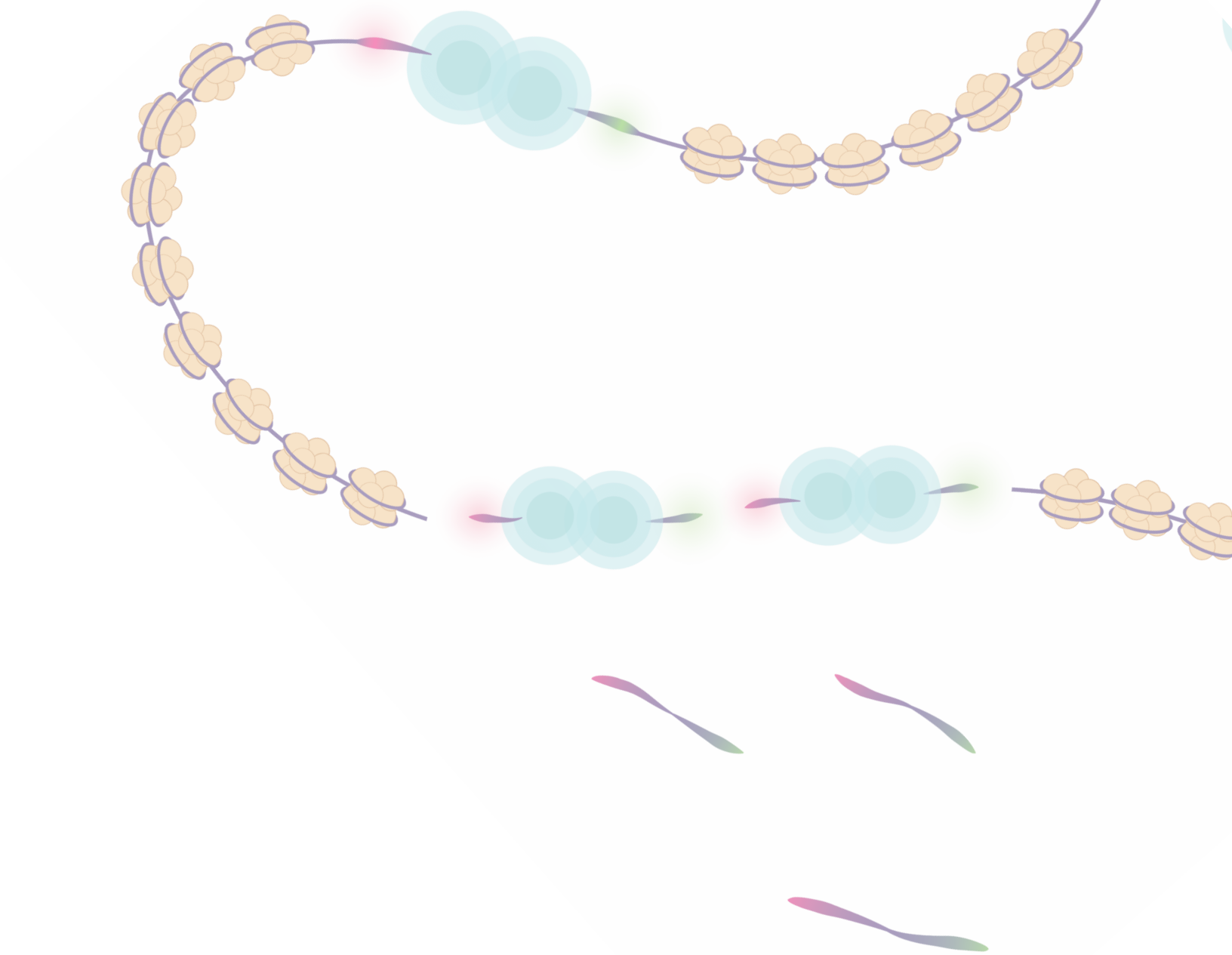


Figure 7. *Above panel*: Representative region from genome-wide "bulk" ATAC-Seq using mouse kidney tissue.

Right panel: Same representative region as "bulk" ATAC-Seq from genome-wide scATAC-Seq data. Each cell cluster is displayed as a unique peak track and represented in a different color. scATAC-Seq provides the resolution to identify unique open chromatin peak profiles for each cell population, allowing for the identification of cells that are driving a specific phenotype.





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