scATAC-seq service

Beyond the Transcript: Single-Cell Epigenetics Reveals Hidden Cellular Regulation

The scATAC-seq service offered by Singleron utilizes our SCOPE-chip technology to enable precise and sensitive genome-wide mapping of chromatin accessibility. This service enables the assessment of the open chromatin landscape and its impact on gene regulation.

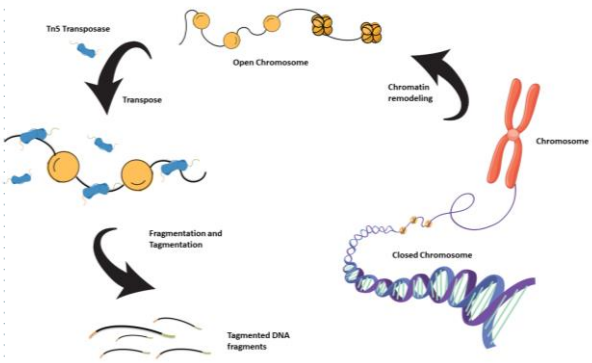


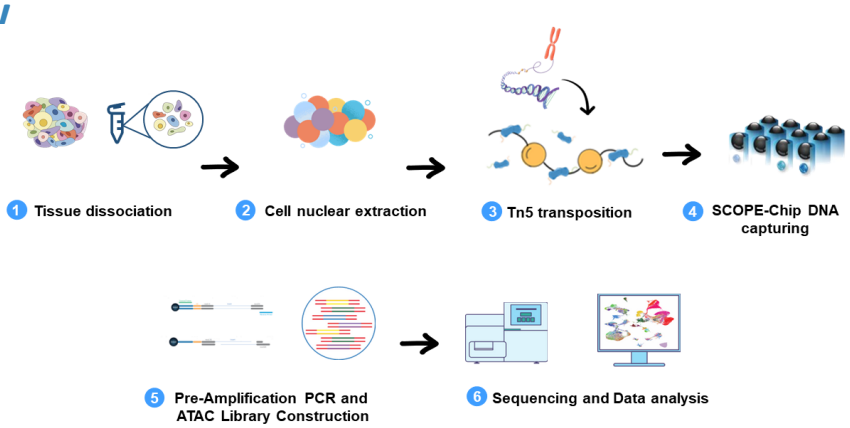
Figure 1. Chromatin Remodeling and Tagmentation in Open Chromatin Regions by Tn5 Transposase

Highlights

- **End-to-end service** from tissue dissociation to BI analysis
- **7 weeks Turnaround Time**
- **Tailored bioinformatic analysis**
- **Compatible with different tissue type**

scATAC seq workflow

Figure 2. The process starts with tissue dissociation and nuclei extraction. Following nuclei isolation, tagmentation occurs: Tn5 enzyme, pre-loaded with sequencing indexes, fragments DNA in open chromatin regions and attaches indexing adapters. The tagmented nuclei are loaded onto the SCOPE-chip, lysed, and the DNA is captured by beads with unique barcodes. These barcodes allow for library amplification via PCR, preparing the DNA for sequencing.



Our scATAC seq principle

- Our **instrument-free** SCOPE-chip technology, combined with our scATAC beads, specifically captures tagmented DNA.

Figure 3. Schematic diagram of our SCOPE-chip and bead

Demo Results

Highly efficient nucleus capture and high-quality clustering in scATAC-seq analysis of mouse embryos

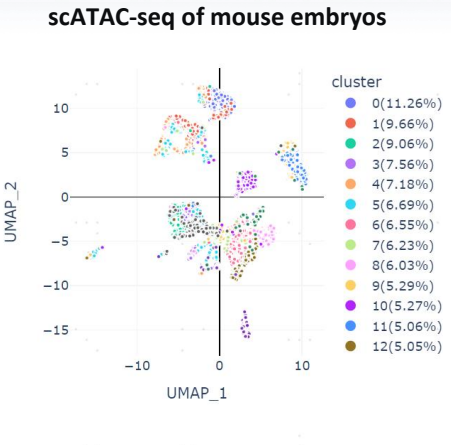


Figure 4. scATAC-seq of mouse embryos yielded 7,880 nuclei from 15,000 cells. Each cell produced ~30,741 reads (58.5% high-quality), with 55.42% overlapping chromatin accessibility peaks, potentially linked to gene regulation.

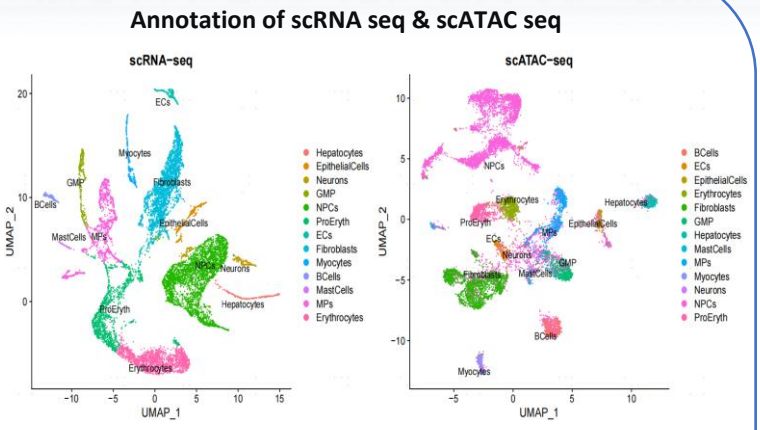


Figure 5. Precise annotation of single-cell transcriptome is achieved through marker genes in mouse embryo, followed by accurate annotation of single-cell ATAC cell atlas using the "label transferring" method.

scATAC-seq reveals depth-independent clustering and peak consistency.

The scATAC data from mouse embryos was employed to evaluate consistency across different scATAC library sets.

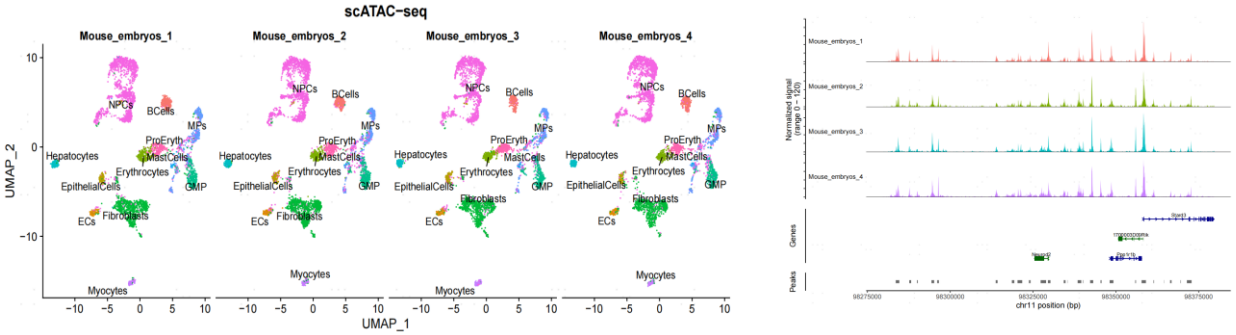


Figure 6. No significant difference was observed in the cell cluster and peak distribution of scATAC-seq among parallel groups.

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