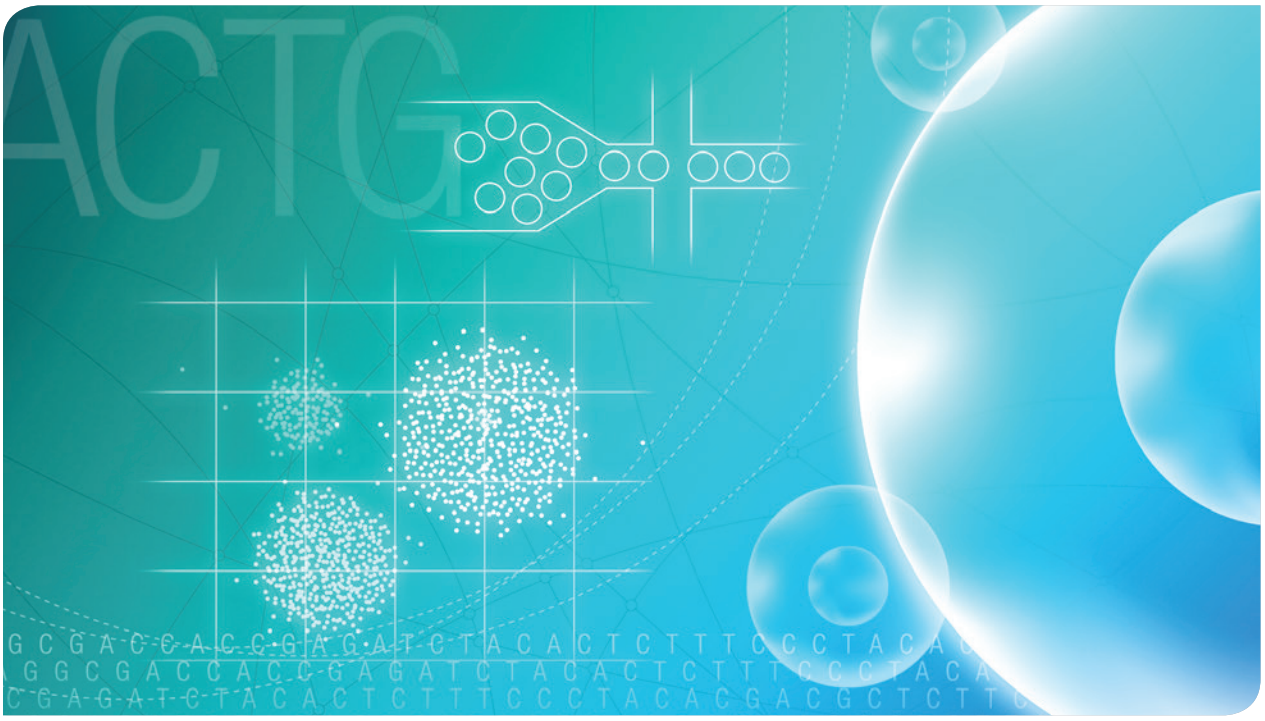


Single-Cell ATAC-Seq

The SureCell® ATAC-Seq Library Prep Kit and ATAC-Seq Analysis Toolkit enable reproducible genome-wide profiling of the epigenomic landscape at the single-cell level with a high number of unique reads per cell so you can better understand the mechanisms that drive how genes are regulated.

The Bio-Rad single-cell ATAC-Seq (scATAC-Seq) solution provides users with:

- The ability to work with both whole cells and nuclei
- A high number of unique fragments that map to the nuclear genome, ATAC peaks, and transcription start sites (TSSs)
- Up to 90% cell capture efficiency
- A fast (<8 hr) simplified workflow with minimal hands-on time and convenient start and stop points
- Adjustable cell throughput range of as few as 400 or more than 4,000 cells per sample, more than 30,000 cells/kit
- A powerful and efficient informatics tool in a flexible pipeline

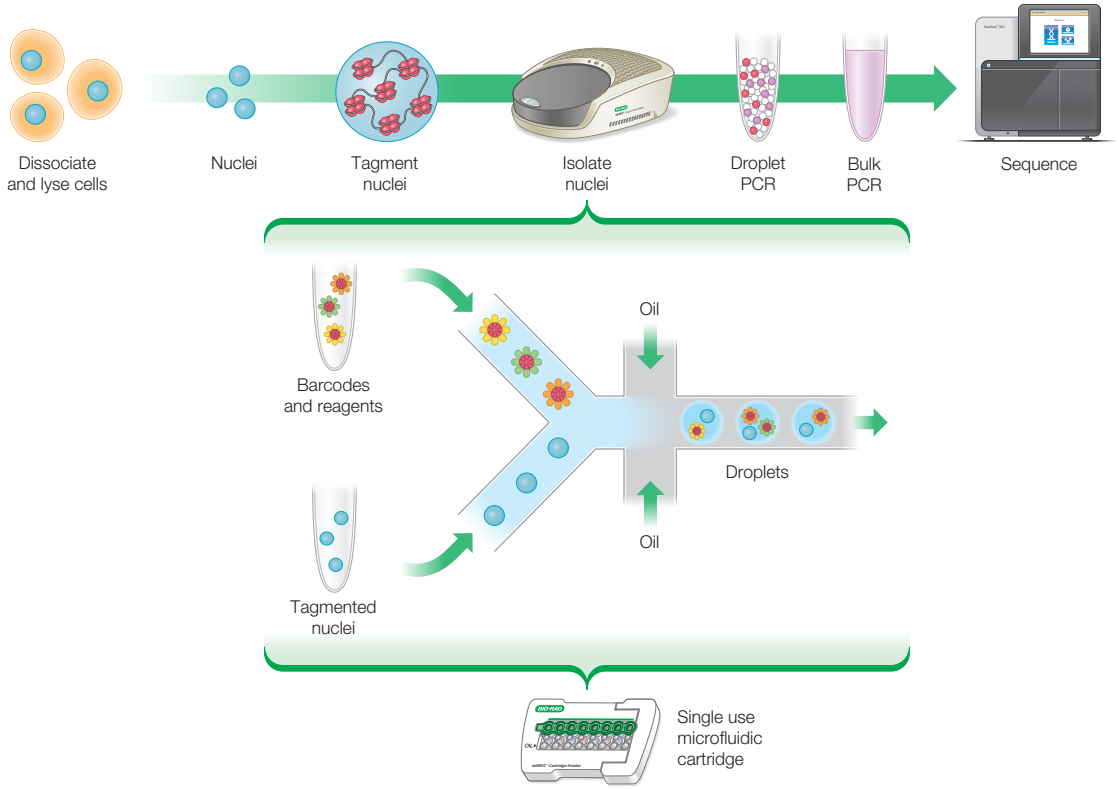
Visit **bio-rad.com/scATACSeqKit** for more information.

BIO-RAD

High-Resolution Mapping of Open Chromatin with scATAC-Seq

Single-cell ATAC-Seq (assay for transposase-accessible chromatin using sequencing) with high cell throughput provides a novel method with which to map genome-wide chromatin accessibility for thousands of individual single cells. The simple one-day workflow provides easy access to epigenetic information, including transcriptional dynamics from cell to cell.

Single cells or their isolated nuclei are tagged at regions of open chromatin using hyperactive Tn5 transposase in a bulk reaction. Barcoding and amplification of tagged sites within individual droplets generate a library of fragments representative of the original open chromatin profile of each cell.



scATAC-Seq Workflow

Bio-Rad's scATAC-Seq workflow is streamlined and offers users:

- Less than 8 hours of cell and library prep time
- Sample-to-sample reproducibility
- Flexible control over workflow with multiple safe stop points
- Minimum hands-on time

1	Tagment isolated nuclei or whole cells	
2	Encapsulate tagmented nuclei/cells and barcode beads in droplets	
3	Barcode fragments	Safe Stop
4	Break emulsion and purify barcoded product	Safe Stop
5	Amplify barcoded fragments to generate libraries	

scATAC-Seq Applications

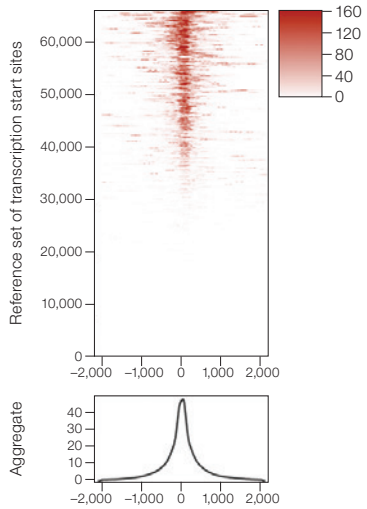
Single-cell ATAC-Seq allows you to take your studies to the next level.

Use scATAC-Seq to:

- Answer deep questions about regulation of gene expression through interrogation of promoters, enhancers, or other regulatory elements
- Validate single-cell RNA-Seq studies as an orthogonal approach
- Identify cell-specific regulatory signatures that are phenotypic of diseased cell variants and mechanisms of cell fate

Gene-Specific Data

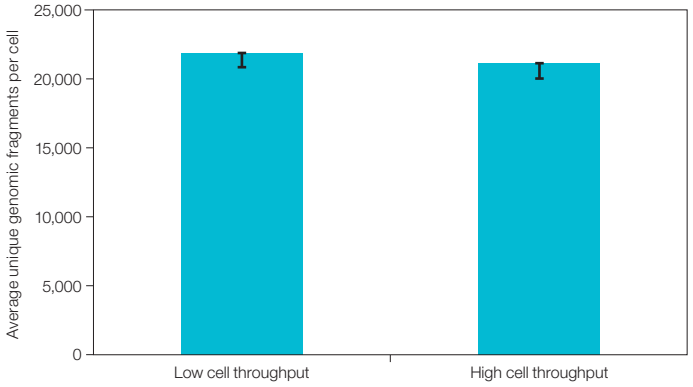
High signal/noise with more than 40 times better alignment to TSSs



Bio-Rad's scATAC-Seq solution detects TSSs with high signal to noise. Reads are mapped to a reference set of TSSs to form an aggregate distribution aligned to TSSs and extended 2,000 bp in both directions. The value at the center of the distribution represents the TSS score.

Highly Sensitive and Reproducible Results

Achieve >20,000 unique fragments at 50,000 reads/cell for a wide dynamic range of cell throughput



	Mixed NIH 3T3 and K562 Cells	
	Low–Cell Throughput Samples	High–Cell Throughput Samples
Average unique genomic fragments per cell	21,828	21,176
Lower 95% confidence interval	20,761	19,956
	N = 42	*N = 28*

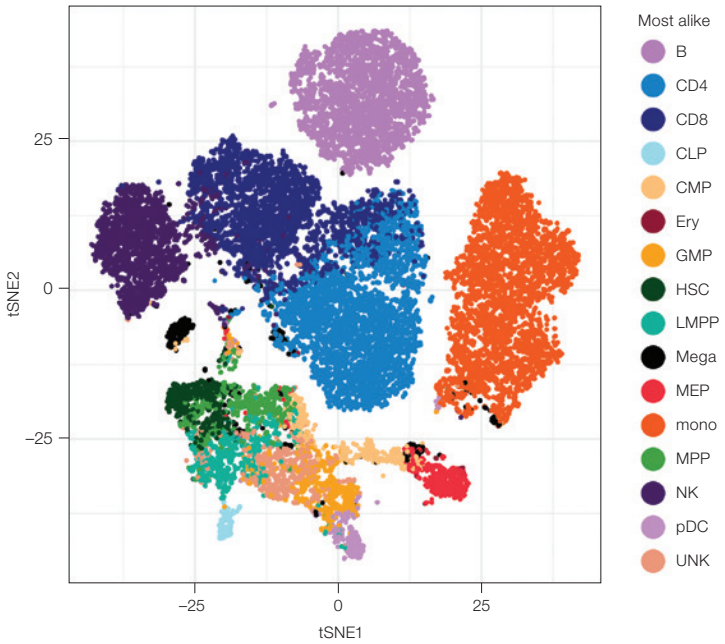
In a mixed-species experiment with an equal input of mouse NIH 3T3 and human K562 cells, greater than 20,000 unique genomic fragments per cell are detected at 50,000 reads/cell. Low–cell throughput samples had an average of 397 cells per sample, while high–cell throughput samples had an average of 4,408 cells per sample.

Capture Efficiency

Highly reproducible cell utilization can be obtained across multiple samples, experiments, or users.

Cell Input	Cell Output	Cell Utilization, %
7,392	4,644	63
7,840	5,073	65
7,488	4,621	62
7,648	4,443	58
6,848	4,340	63
6,656	4,649	70
6,976	5,044	72
6,400	3,720	58
6,976	4,351	62
7,456	3,735	50
3,184	3,159	99
6,380	4,477	70
6,022	3,777	63
7,424	5,116	69
6,976	4,331	62
7,424	4,786	64
7,193	4,240	59
8,128	6,130	75
8,384	6,506	78

Cell Classification

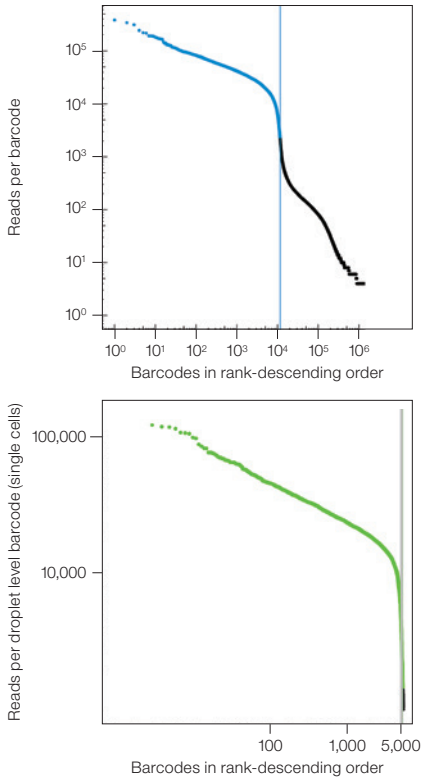


scATAC-Seq data can deconvolute highly complex cellular populations into their constitutive subsets. Using chromatin accessibility data, scATAC-Seq facilitates identifying and enumerating cell types within existing epigenomic data from complex cellular mixes. Analysis in collaboration with F. Duarte, C. Lareau, V. Kartha, Buenrostro Lab, Broad Institute of MIT and Harvard.

Simple, Yet Powerful, Data Analysis Options

Bio-Rad's bioinformatic pipeline enables rich data analytics in a transparent and flexible software pipeline of industry-standard tools. Secondary analysis starts with your FASTQ files and outputs biologically interpretable data that can be loaded into popular tertiary analysis tools like Seurat and ChromVAR.

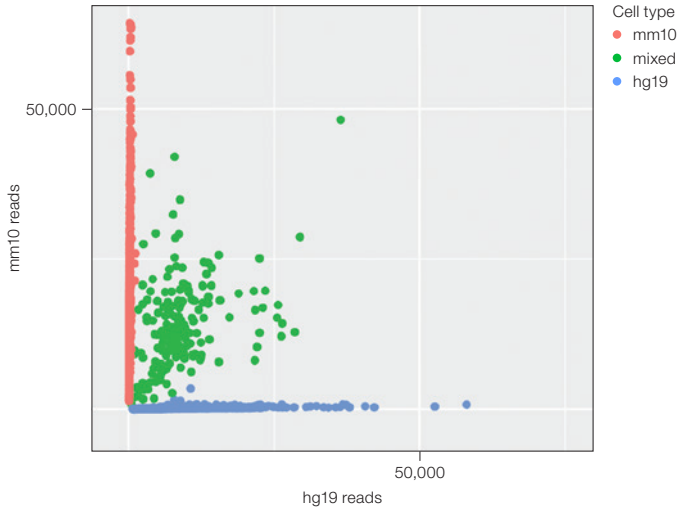
- Estimates gain and loss of chromatin accessibility within peaks
- Enables accurate and robust clustering of scATAC-Seq profiles and characterization of sequence motifs associated with gene expression
- Identifies cis- and trans-acting elements that are the source of diverse cellular phenotypes



Knee plots. Top, barcodes are sorted in descending order according to the number of unique reads per barcode. The data shown to the left of the vertical blue line represent barcodes that tag single cells. Pairwise comparisons are performed across these barcodes to identify those with a high percentage of shared fragments. These are merged bioinformatically to create droplet-level barcodes, which define single-cell data. Bottom, single cells sorted in descending order according to the number of unique reads per cell (green line).

Confident Single-Cell Transcript Identification

Minimum crosstalk (<5%) with more than 5,000 cells of mixed species



An equal number of mouse NIH 3T3 and human K562 cells were mixed and processed with the SureCell ATAC-Seq Library Prep Kit and ATAC-Seq Analysis Toolkit. These data show a sample with 5,024 cells. Droplets containing both human and mouse cells are shown in green and droplets with only human or mouse cells are shown in blue and red, respectively. Based on these data, cross talk, or the percentage of cell doublets, is calculated as 3.76%.

Ordering Information

Catalog #	Description
17004620	**SureCell ATAC-Seq Library Prep Kit**, includes SureCell ATAC-Seq Reagent Box A, SureCell ATAC-Seq Reagent Box B, and ddSEQ M Cartridges
12009359	**ddSEQ M Cartridges**
12009358	**SureCell ATAC-Seq Reagent Box A**
12009357	**SureCell ATAC-Seq Reagent Box B**
12009360	**SureCell ATAC-Seq Index Kit**
12004336	**ddSEQ Single-Cell Isolator**, includes instrument and associated component consumables

Visit bio-rad.com/scATACSeqKit for more information about single-cell ATAC-Seq and for additional application data.

BIO-RAD

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Life Science Group

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