

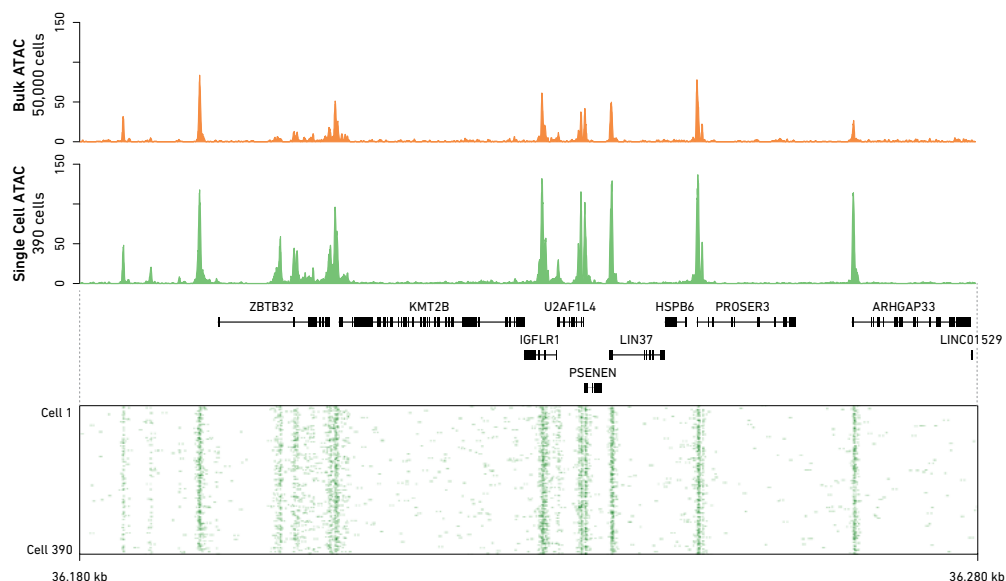
# Profiling chromatin accessibility at single cell resolution

## Chromium Single Cell ATAC

Chromatin organization compacts meters of DNA into the nucleus, making just a small fraction of DNA accessible for transcription within each cell. The Chromium Single Cell ATAC (Assay for Transposase Accessible Chromatin) solution provides a robust and scalable approach to map the epigenetic landscape at single cell resolution. Using a transposase enzyme to preferentially tag accessible DNA regions with sequencing adaptors, researchers can now generate sequencing-ready libraries and identify open chromatin regions. Our simple workflow, combined with intuitive software, enables understanding of epigenetic and regulatory variation across tens of thousands of cells.

### Highlights

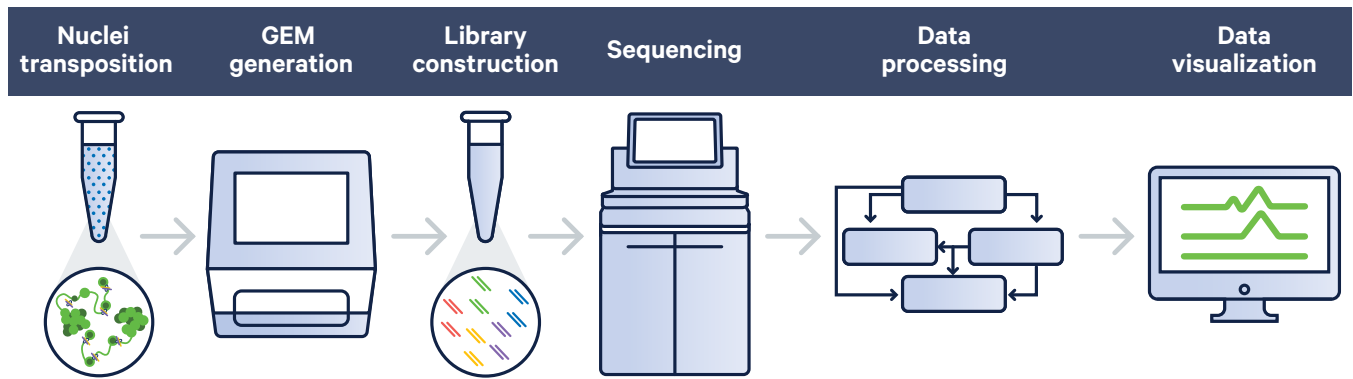
- Resolve cell types and states using genome-wide, epigenetic profiles with single cell resolution
- Discover cis-regulatory elements that drive gene expression differences between cell types and states
- Characterize cell-specific gene regulatory networks to understand the epigenetic underpinnings of disease, developmental plasticity, and cell identity
- Identify transcription factors (TFs) that determine cell identity, and perform lineage and developmental tracing



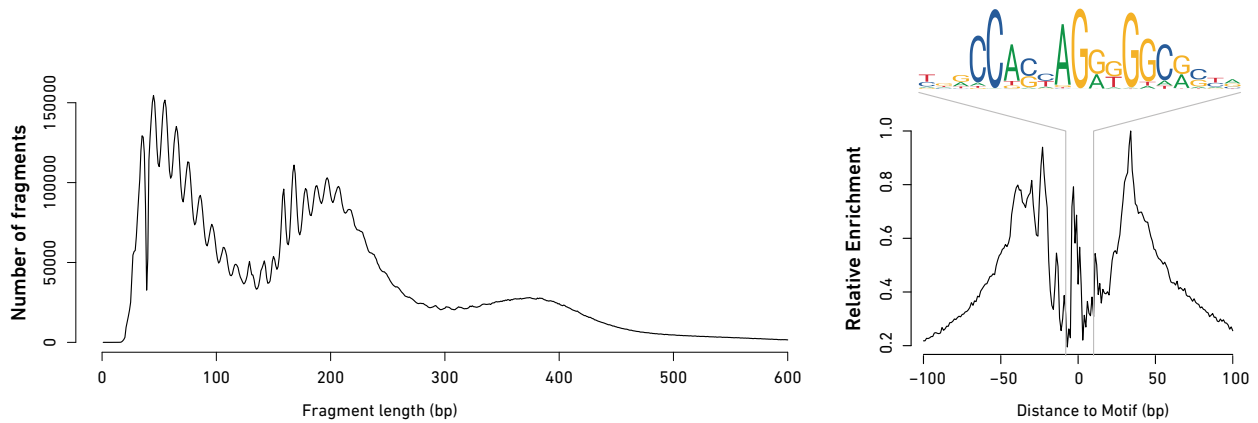
**Figure 1. Characteristic open chromatin profiles at single cell resolution.** Top: Representative tracks of open chromatin regions from GM12878 cell line. The upper track (orange) represents data gathered from 50,000 nuclei using bulk ATAC-seq, while the lower track (green) is aggregated from 390 individual nuclei run on Chromium Single Cell ATAC. Even with data from 100-fold fewer nuclei, Chromium Single Cell ATAC demonstrates a similar sensitivity to that of bulk ATAC-seq. Bottom: Transposition events detected in single cells using Chromium Single Cell ATAC from the same sample and genomic locus of GM12878 cell line.

## Product features

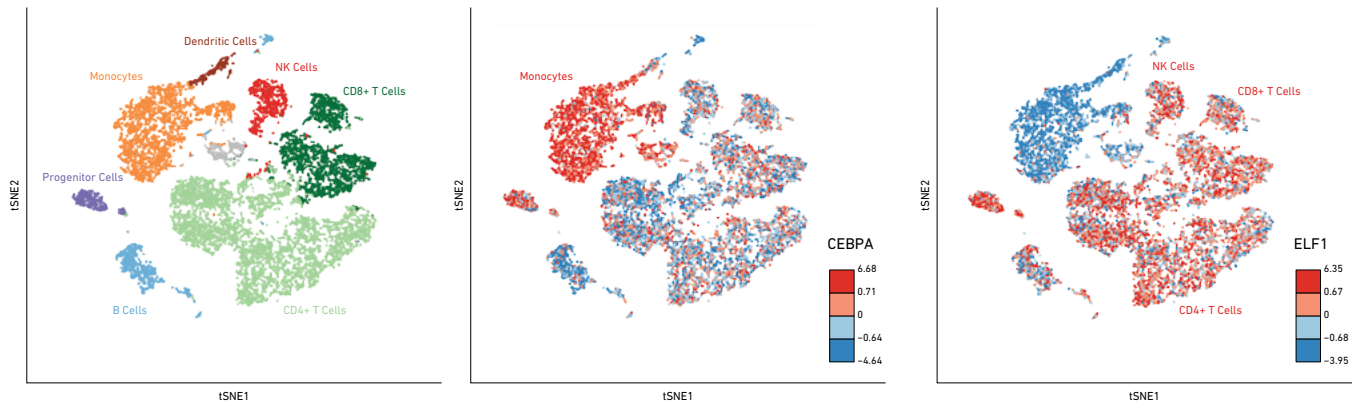
- Analyze open chromatin regions at single cell resolution, enabling deeper understanding of cellular epigenetic heterogeneity
- Perform epigenetic profiling for hundreds to tens of thousands of nuclei, enabling detection of rare cells
- Examine non-coding sequences to discover cis-regulatory elements and drivers of gene expression differences between cell types and states
- Follow a ready-to-use, robust workflow with demonstrated protocols for diverse sample types, including cell lines, primary cells, and fresh and frozen tissue
- Apply easy-to-use software and visualization tools for straightforward analysis of single cell ATAC data



**Figure 2. The Chromium Next GEM Single Cell ATAC workflow.** Nuclei are transposed in bulk, followed by partitioning on a microfluidic chip into nanoliter-scale GEMs in the Chromium instrument. The transposed DNA of individual nuclei are identified with a unique 10x Barcode. Libraries are generated and sequenced, and 10x Barcodes are used to associate individual reads back to individual partitions and, thereby, each individual cell.



**Figure 3. High-quality single cell ATAC-seq libraries.** Left: Insert size distribution of Single Cell ATAC fragments from GM12878 cells reveals protection of DNA by individual nucleosomes and nucleosome multimers, along with a nucleosome periodicity of 184 base pairs. Right: Cumulative footprinting signal at predicted transcription factor (CTCF)-binding sites in GM12878 cell line generated by aggregating Chromium Single Cell ATAC data. The dotted lines indicate the location of the known CTCF motif (pictogram above the plot; JASPAR CTCF motif MA0139.1).



**Figure 4. Single nuclei epigenetic profiling of peripheral blood mononuclear cells (PBMCs).** Left: t-SNE projection of ~10,000 PBMCs from a healthy donor. Each cell is plotted in t-SNE coordinates, colored by their annotated cell types. Major subpopulations were identified based on enrichment scores of well characterized TF motifs and cell type-specific peaks. Clustering patterns suggest that there is extensive substructure within each major classification. Middle, Right: Single nuclei epigenetic profiles overlaid on t-SNE projections for CEBPA (marker of monocytes) and ELF1 (marker of T cells and natural killer (NK) cells). The PBMC population comprises 20% of monocytes and 66% of T and NK cells—consistent with FACS analysis of the cells.

## Product specifications

- Efficiently partition 500–10,000 nuclei per channel, for up to 80,000 nuclei per run
- Scalable; run up to 8 samples in parallel
- High nuclei capture rates of up to 65%
- Low doublet rates of 0.8% per 1,000 cells

Chromatin accessibility profiling products	Product code
Chromium Next GEM Single Cell ATAC Kit v2, 16 rxns	1000390
Chromium Next GEM Single Cell ATAC Kit v2, 4 rxns	1000406
Chromium Next GEM Single Cell ATAC Library and Gel Bead Kit v1.1, 16 rxns	1000175
Chromium Next GEM Single Cell ATAC Library and Gel Bead Kit v1.1, 4 rxns	1000176
Chromium Next GEM Chip H Single Cell Kit, 48 rxns	1000161
Chromium Next GEM Chip H Single Cell Kit, 16 rxns	1000162
Single Index Kit N Set A, 96 rxns	1000212
Sample preparation products	
Chromium Nuclei Isolation Kit	Expected mid-2022
Instrument compatibility	Product code
Chromium iX & Accessory Kit, 12 Mo. Warranty	1000328
Chromium iX & Accessory Kit, 24 Mo. Warranty	1000329
Chromium X & Accessory Kit, 12 Mo. Warranty	1000331
Chromium X & Accessory Kit, 24 Mo. Warranty	1000332
Chromium X Upgrade Package	1000330
Chromium Controller & Next GEM Accessory Kit, 12 Mo. Warranty	1000202
Chromium Controller & Next GEM Accessory Kit, 24 Mo. Warranty	1000204
Software	
Cell Ranger ATAC Pipeline <a href="https://go.10xgenomics.com/scATAC/">go.10xgenomics.com/scATAC/</a>	<a href="#">Download</a>
Loupe Browser <a href="https://go.10xgenomics.com/scATAC/loupe-cell">go.10xgenomics.com/scATAC/loupe-cell</a>	<a href="#">Download</a>

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