

Simultaneous profiling of the transcriptome and epigenome from the same cell

Single Cell Multiome ATAC + Gene Expression

Transform your understanding of biology and uncover hidden insights with multiomic approaches that give you more from a single cell. Simultaneously profile gene expression and open chromatin from the same cell, across thousands of cells, with Chromium Single Cell Multiome ATAC + Gene Expression.

This product provides a unified view of a cell's gene expression profile and its epigenomic landscape. Increase the resolution of cell states, identify drivers of differential gene expression, and discover cells with similar transcriptional profiles but functionally different chromatin landscapes by leveraging two modalities at once. Chromium Single Cell Multiome ATAC + Gene Expression provides multiomic analysis for the same single cell, and has relevance for understanding drivers of tumor heterogeneity, mechanisms of therapeutic resistance, and the cell types that underlie neurodegenerative or immunological disorders.

Highlights

- Multiply your power of discovery with combined epigenomic and gene expression profiling using the assay for transposase-accessible chromatin (ATAC) to identify regions of open chromatin alongside RNA-seq
- Deepen your characterization of cell types and states with linked transcriptional and epigenomic analyses
- Discover new gene regulatory interactions
- Easily interpret epigenetic profiles with key expression markers
- Maximize insights from your precious samples with multiple readouts from the same cell

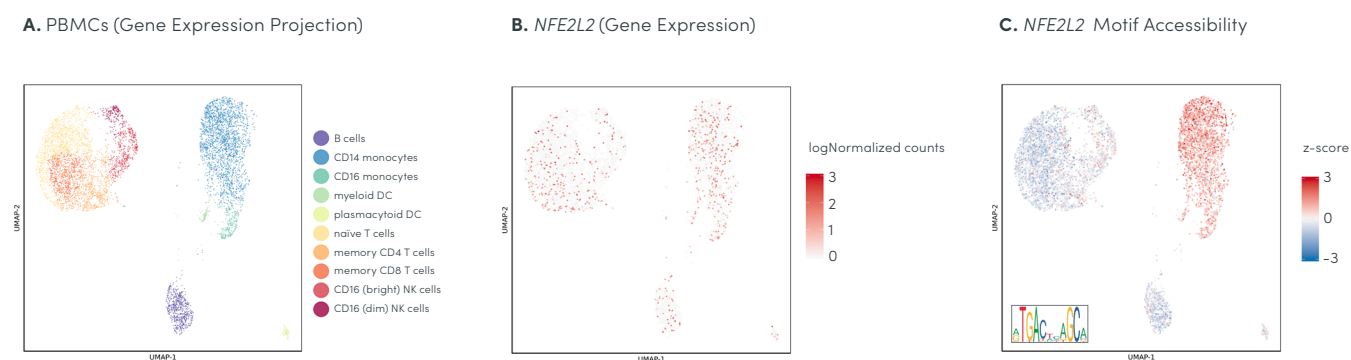


Figure 1. Simultaneous detection of gene expression and chromatin state from the same cell. Nuclei extracted from healthy peripheral blood mononuclear cells (PBMCs) were processed using Chromium Single Cell Multiome ATAC + Gene Expression. **A.** Cluster analysis was performed on 7,273 nuclei using gene expression data, and cell populations were annotated based on established marker genes. **B.** Expression of the transcription factor *NFE2L2* is observed across cell types. **C.** However, *NFE2L2* motif (inset) accessibility derived from ATAC data from the same cells is restricted to monocyte populations. The difference in *NFE2L2* expression and motif accessibility is likely a reflection of its functional status. Normally, protein produced from *NFE2L2* remains sequestered in the cytoplasm but, in response to oxidative stress, will translocate to the nucleus to regulate expression of antioxidant proteins.

Solution Features

- Integrate gene expression and epigenomic landscape through direct measurement in the same cell, eliminating the need for inferring relationships in silico
- Identify linkages between putative regulatory elements and their target genes
- Simple and robust workflow
- Easy-to-use software for data analysis and visualization

System Features

- Efficiently partition 500–10,000 nuclei per channel, for up to 80,000 nuclei per run
- Scalable; run up to 8 samples in parallel
- Recover up to 65% of loaded nuclei
- High sensitivity
- Low microfluidic multiplet rate (<1% per 1000 nuclei)
- Demonstrated with cell lines, primary cells, cryopreserved samples, and fresh and flash-frozen tissue

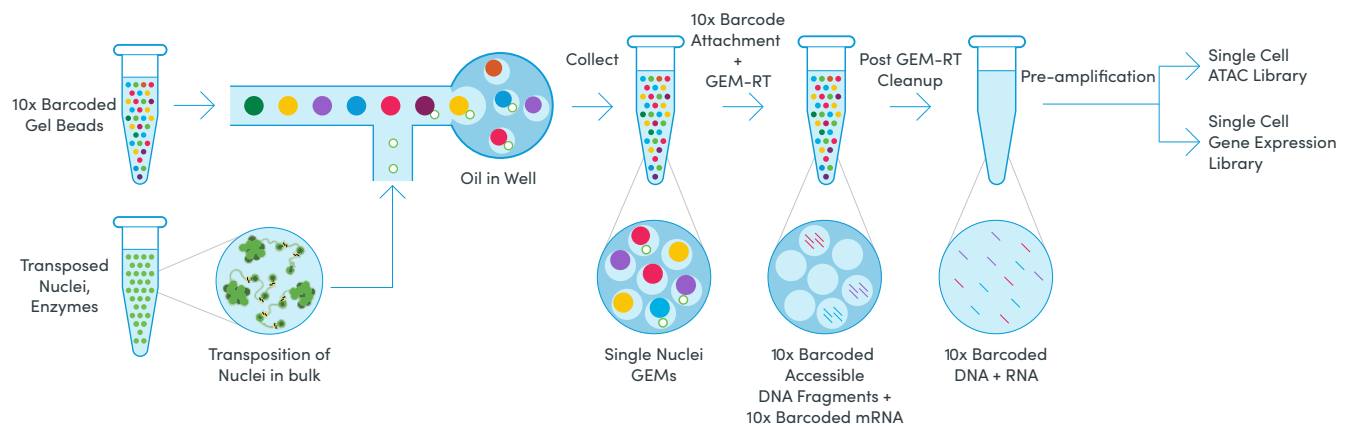


Figure 2. Efficient and robust workflow. Access a unified view of transcription and the chromatin landscape by combining gene expression and ATAC-seq data from the same single cell with a simple, streamlined workflow. Starting with a single nuclei suspension, transposition is performed in bulk before individual nuclei are captured in GEMs (Gel Bead-in-emulsion), where DNA fragments and the 3' ends of mRNA are barcoded. Generate two complementary libraries from each sample, and link gene expression and open chromatin profiles back to the same cell with certainty.

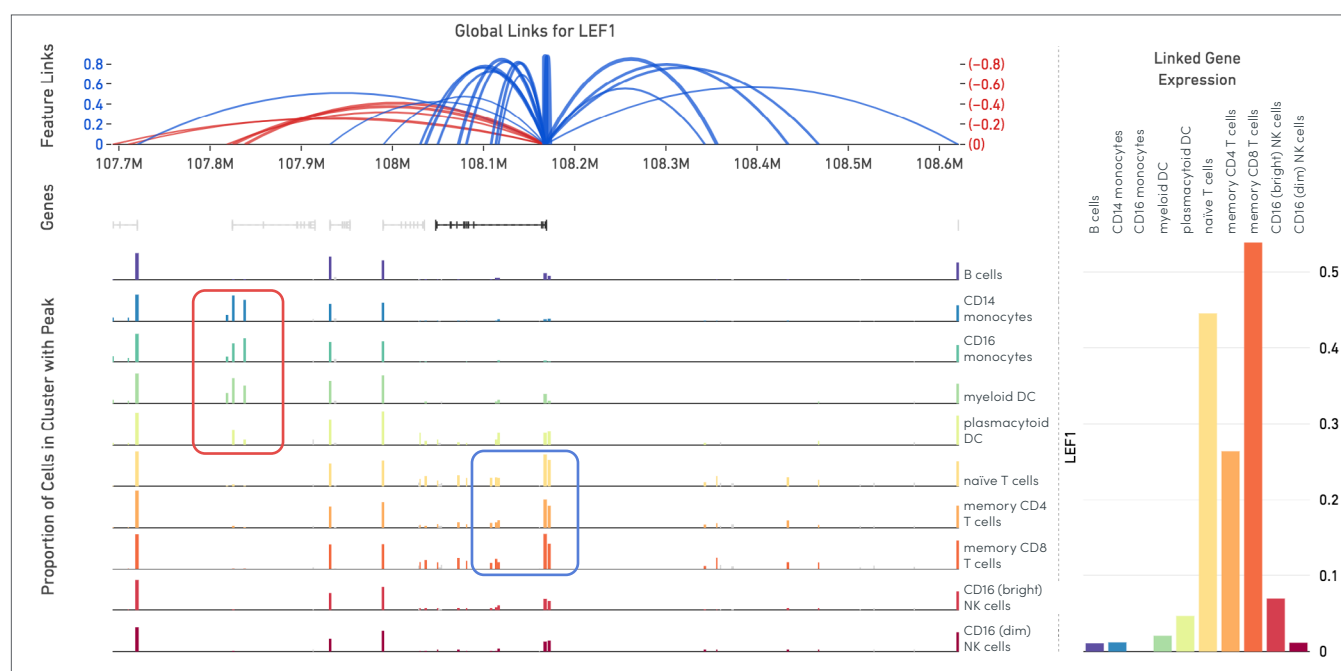
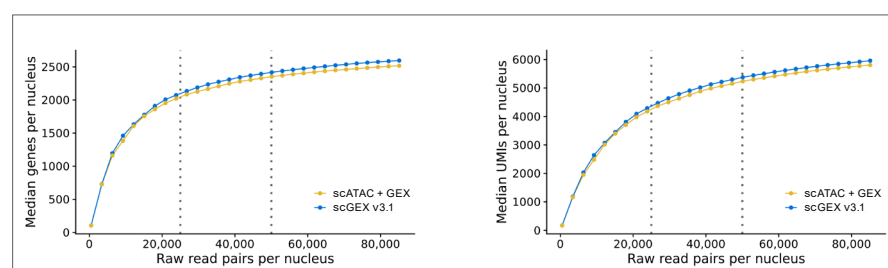


Figure 3. Identification of putative regulatory elements directly linked to a gene of interest. Global links for *LEF1* indicate open chromatin peaks that are either correlated (blue arcs) or anti-correlated (red arcs) with *LEF1* gene expression across a 1 Mb window for the same 7,273 PBMC nuclei seen in Figure 1. *LEF1* expression levels and open chromatin peaks are color coded by cell type. Cell-type specific expression of *LEF1* is correlated with linked open chromatin regions near the *LEF1* promoter that are enriched specifically in naive and memory T cells (blue box). Cells with low *LEF1* expression, such as monocytes and myeloid dendritic cells, each have an open chromatin region several hundred kilobases away that may be repressive (red box).

A. Gene Expression



B. ATAC

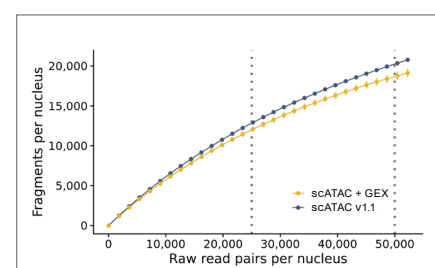


Figure 4. Generate high quality single cell gene expression and ATAC libraries. Mouse embryonic E18 brain samples were processed using Chromium Single Cell Gene Expression, Chromium Single Cell ATAC, and Chromium Single Cell Multiome ATAC + Gene Expression. Analysis of gene expression data included sequencing reads mapping to introns. Sensitivity of gene expression or ATAC signals was determined across a range of read depths using in silico downsampling. **A.** Gene expression sensitivity, as measured by median genes per nucleus or median UMIs per nucleus, is comparable between Single Cell Gene Expression v3.1 and Single Cell Multiome ATAC + Gene Expression. **B.** Similarly, ATAC sensitivity, as measured by high-quality unique fragments per nucleus, is comparable between Single Cell ATAC v1.1 and Single Cell Multiome ATAC + Gene Expression.

Research areas

- Cancer Biology
- Immunology
- Immuno-oncology
- Neuroscience
- Stem Cell & Developmental Biology

Applications

- Biomarker Discovery
- Cell Lineage & Developmental Program Tracing
- Cellular Heterogeneity & Rare Cell Population Detection
- Gene Regulatory Networks
- Response to Therapeutic Interventions

Products	Product Code
Chromium Next GEM Single Cell Multiome ATAC + Gene Expression Reagent Bundle, 16 rxns	1000283
Chromium Next GEM Single Cell Multiome ATAC + Gene Expression Reagent Bundle, 4 rxns	1000285
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Chromium Next GEM Chip J Single Cell, 16 rxns	1000230
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