

Explore cellular diversity, cell by cell

Single Cell Gene Expression v3.1 with Feature Barcode technology

From expression profiling of genes and proteins to genome editing, Chromium Single Cell Gene Expression with Feature Barcode technology helps you address your critical research questions. Identify and characterize rare cell types and biomarkers, or examine therapeutic mechanisms of action on a cell-by-cell basis with transcriptional profiling alone or multiomic characterization. The technological advancements provided by Chromium Single Cell Gene Expression with Feature Barcode technology, along with turnkey analysis and software visualization tools, allow you to maximize insights from a wide range of sample types.

Highlights

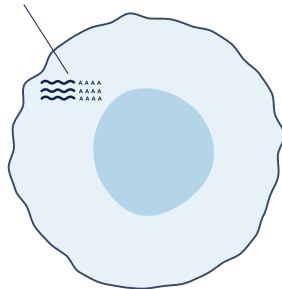
- Analyze how cellular heterogeneity contributes to your biological system with transcriptional profiling at single cell resolution across tens of thousands of cells
- Gain new insights into cell subtypes and states with multiomic readouts of gene and cell surface protein expression
- Explore cellular phenotypes with whole transcriptome analysis
- Investigate complex genetic networks and perturbed transcriptomes in normal and diseased cell types by simultaneously detecting CRISPR guides and single cell gene expression profiles

Single cell analysis capabilities

A.

Whole transcriptome gene expression

Perform whole transcriptome profiling

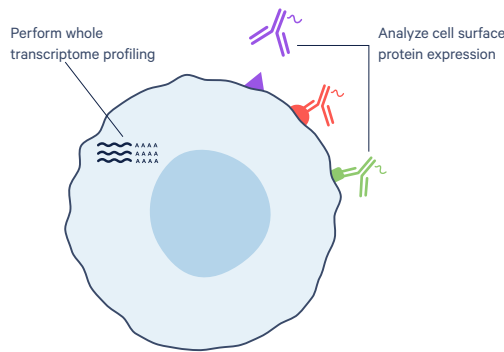


B.

Gene expression and cell surface protein expression

Perform whole transcriptome profiling

Analyze cell surface protein expression



C.

Gene expression and CRISPR perturbation screening

Perform whole transcriptome profiling

Detect sgRNA from CRISPR screen

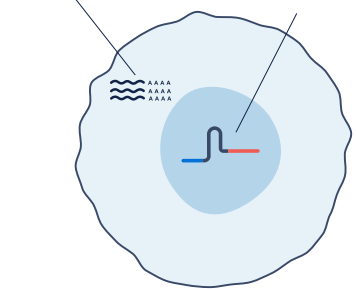


Figure 1. Resolve cellular heterogeneity with multiomic single cell profiling. **A.** Chromium Single Cell Gene Expression provides whole transcriptome 3' profiling at the single cell level for hundreds to tens of thousands of cells per sample. **B.** The addition of Feature Barcode technology enables combined gene expression profiling and cell surface protein detection with tens to hundreds of antibodies. **C.** Scale functional genomics screens with tens to thousands of perturbations in a single experiment using Feature Barcode technology, which lets you concurrently detect single guide RNA (sgRNA) and perturbed gene expression profiles in each cell.

Product features

- Profile thousands of genes at the single cell level for unbiased characterization of cell types and cell states
 - Combine gene expression analysis with detection of hundreds of cell surface proteins at high resolution for ultra-high parameter multiomic cytometry
 - Simultaneously assess CRISPR perturbation phenotypes and gene expression from the same cell to accelerate your functional genomics studies
- Leverage dual index libraries for reliable sequencing data quality
 - Combine with 3' CellPlex to multiplex up to 12 samples and recover up to 17,500 singlets* per channel, enabling larger-scale single cell studies
- * Singlets are single cells or nuclei captured after multiplet removal.

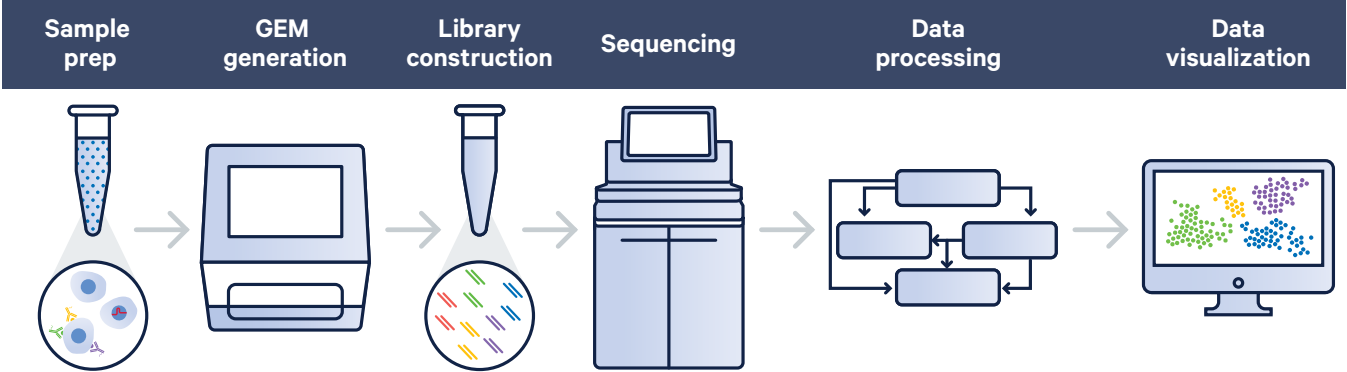


Figure 2. Efficient and streamlined workflow for multiomic profiling of biological systems. Start with a single cell suspension of unlabeled cells, oligo-conjugated antibody-labeled cells, or cells expressing compatible CRISPR guides. After GEM generation, separate libraries can be constructed from a single sample, including gene expression and cell surface protein or CRISPR guide libraries, generating multiple readouts that can be linked back to the same single cell. Process data with Cell Ranger, and visualize sample heterogeneity with Loupe Browser, our fully integrated and easy-to-use analysis and visualization software.

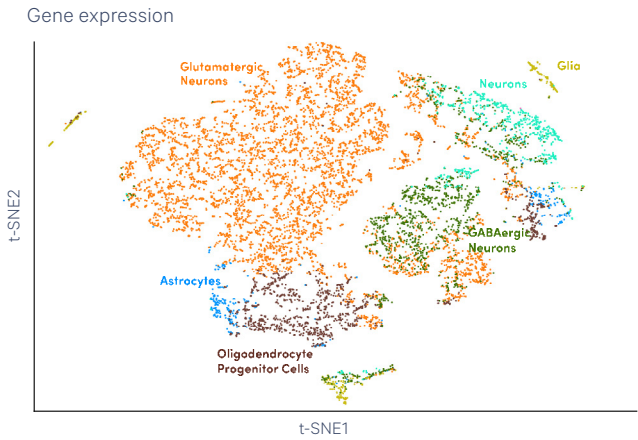
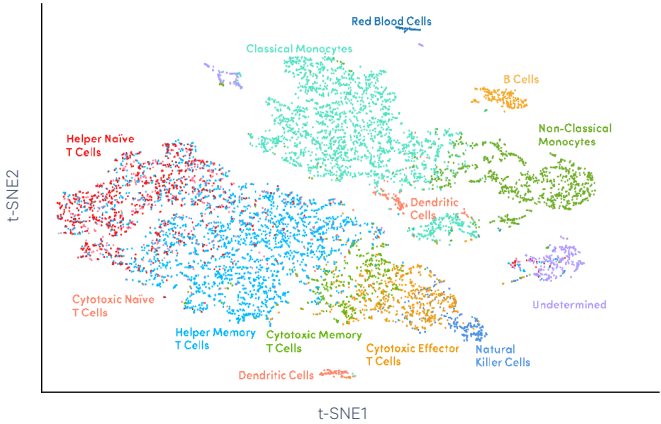


Figure 2. Reveal heterogeneous cell composition of mouse brain tissue with single cell gene expression. To visualize the global differences in gene expression signatures across different cell types, the t-SNE dimensionality reduction technique was used, which represents each cell with a single dot. Shown here is a t-SNE projection of approximately 10,000 cells isolated from embryonic mouse brain tissue (E18 mouse combined cortex, hippocampus, and ventricular zone) run in a single channel with Chromium Single Cell Gene Expression. Cells were clustered by Cell Ranger based on whole transcriptome gene expression and annotated manually in Loupe Browser. In addition to broad categories such as neurons and glia, cell subpopulations were identified through gene expression signatures, including GABAergic or glutamatergic neurons and oligodendrocyte progenitor cells.

A. Gene expression



B. Antibody

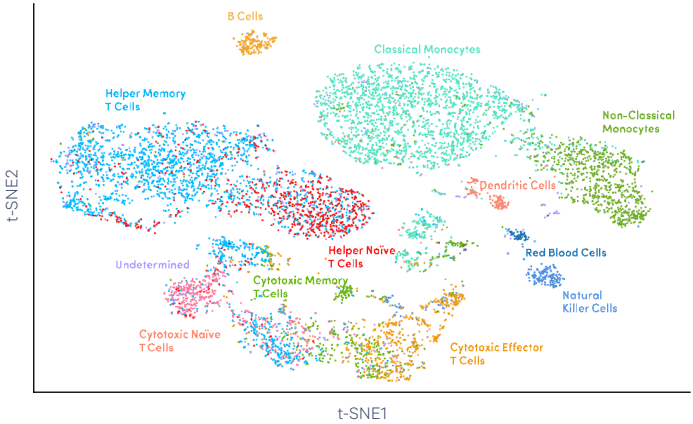
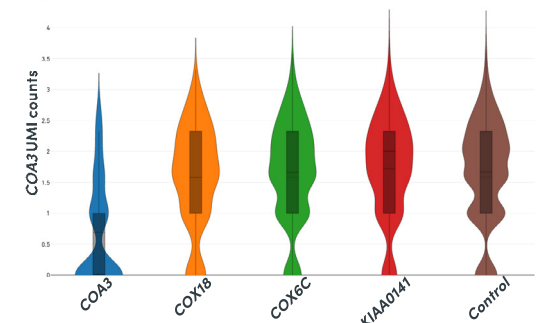
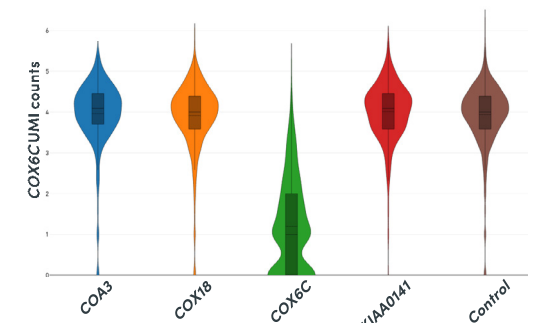


Figure 3. Multiomic data enables enhanced characterization of human immune cell subtypes. **A.** t-SNE projection of approximately 10,000 PBMCs processed with Single Cell Gene Expression and analyzed with Cell Ranger, based on whole transcriptome gene expression. **B.** Cluster analysis and t-SNE visualization of the same PBMC sample with added cell surface protein detection for 14 markers (plus 3 isotype controls). Inclusion of cell surface protein data enabled increased resolution of T-cell subpopulations, including helper, cytotoxic, and effector cells. Sequencing data for both panels was analyzed with Cell Ranger and manually annotated in Loupe Browser.

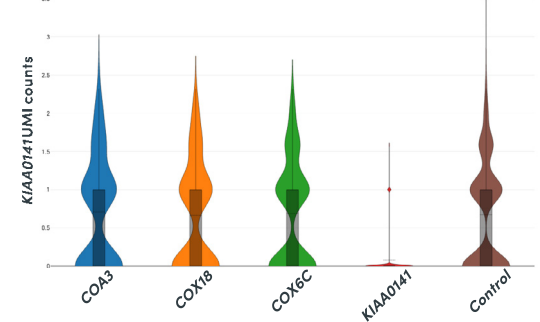
A.



B.



C.



D.

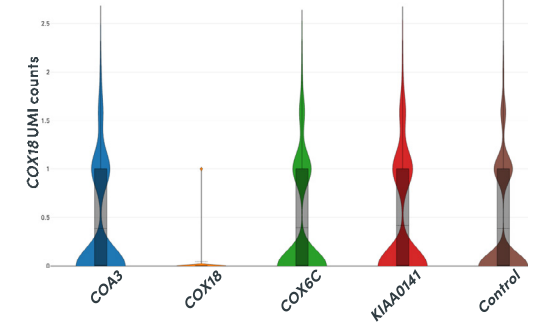


Figure 4. Accelerate functional genomics studies with simultaneous capture of CRISPR guides and gene expression profiles at single cell resolution. **A-D.** Violin plots demonstrate knockdown efficiency across multiple gene targets in a pooled CRISPR screen using a human cell line (K562) constitutively expressing dCas9-KRAB. Shown are UMI counts of four target genes from cells containing experimental or control sgRNA, as output by Loupe Browser. The sgRNA target genes (Guide Assignments) are listed on the x-axis. The y-axis indicates median UMI counts for COA3 (**A**), COX6C (**B**), KIAA0141 (**C**), and COX18 (**D**).

Product specifications

- Efficiently partition 500–10,000 cells per channel, for up to 80,000 cells per run
- Scalable; run up to 8 samples in parallel
- Cell size flexibility, no lower limits
- High cell capture rates of up to 65%
- Low doublet rates of 0.8% per 1,000 cells

High-throughput option

- For high-throughput (HT) single cell gene expression experiments (2,000–320,000 cells or up to 730,000 singlets,* with 3' CellPlex sample multiplexing), see the Product Sheet for [Chromium Single Cell Gene Expression HT](#)

* Singlets are single cells or nuclei captured after multiplet removal.

Gene expression profiling products	Product code
Chromium Next GEM Single Cell 3' Kit v3.1, 4 rxns	1000269
Chromium Next GEM Single Cell 3' Kit v3.1, 16 rxns	1000268
Dual Index Kit TT Set A, 96 rxns	1000215
Chromium Next GEM Chip G Single Cell Kit, 16 rxns	1000127
Chromium Next GEM Chip G Single Cell Kit, 48 rxns	1000120
Feature Barcode technology & sample multiplexing products	Product code
3' Feature Barcode Kit, 16 rxns	3' Feature Barcode Kit, 16 rxns
3' CellPlex Kit Set A, 48 rxns	3' CellPlex Kit Set A, 48 rxns
Dual Index Kit NT Set A, 96 rxns	Dual Index Kit NT Set A, 96 rxns
Dual Index Kit NN Set A, 96 rxns	Dual Index Kit NN Set A, 96 rxns

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
Software	
Cell Ranger	Download Cloud Analysis
Loupe Browser	Download
Compatible partner products	
Biolegend TotalSeq™-B www.biolegend.com/totalseq	Learn More
SigmaAldrich*+ 10x Genomics Custom CRISPR Lentiviral Products www.SigmaAldrich.com/10xCRISPRpools	Learn More

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LIT000093 - Rev E - Product Sheet - Explore cellular diversity, cell by cell

