

Explore Cellular Diversity at Scale

Single Cell Gene Expression v3.1 with Feature Barcode technology

Understanding complex biological systems and diseases requires in-depth knowledge of diverse cell types and critical interactions at multiple levels. 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. Explore cellular phenotypes with whole transcriptome analysis or focus on your genes of interest using targeted gene expression panels. Gain new insights into cell subtypes and states with multiomic readouts of gene and cell surface protein expression. Investigate complex genetic networks and perturbed transcriptomes in normal and diseased cell types by simultaneously detecting CRISPR guides and single cell gene expression profiles.

From assessing tumor heterogeneity, to disease pathogenesis, to immune signaling and regulation—the technological advancements provided by the Chromium Single Cell Gene Expression Solution, along with turnkey analysis and software visualization tools, allow you to maximize insight from any sample type.

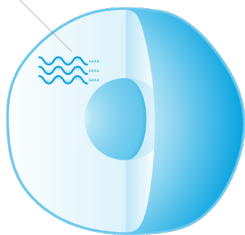
Highlights

- Identify and characterize rare cell types and biomarkers
- Analyze and understand how cellular heterogeneity contributes to your biological system
- Examine therapeutic mechanisms of action on a cell-by-cell basis
- Increase resolution of transcriptionally similar cell subtypes with protein information
- Simultaneously assess perturbation phenotypes and gene expression from the same cell with direct capture and sequencing of guide RNA and cellular transcripts
- Scale your CRISPR screens using tens to thousands of perturbations at once
- Focus on relevant genes and pathways with predesigned panels for immunology, oncology, neuroscience, and drug discovery, or design a fully custom panel

Single Cell Analysis Capabilities

A. Whole Transcriptome or Targeted Gene Expression

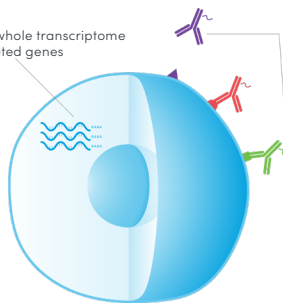
Profile whole transcriptome or targeted genes



B. Gene Expression and Cell Surface Protein Expression

Profile whole transcriptome or targeted genes

Analyze cell surface protein expression



C. Gene Expression and CRISPR Perturbation Screening

Profile whole transcriptome or targeted genes

Detect sgRNA from CRISPR screen

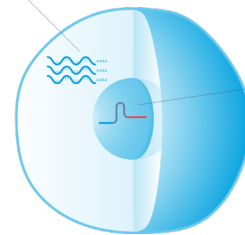


Figure 1. Single cell gene expression capabilities. Perform whole transcriptome or targeted gene expression alone or simultaneously with cell surface protein expression or CRISPR perturbation screening. **A.** Chromium Single Cell Gene Expression provides whole transcriptome 3' profiling at the single cell level for hundreds to tens of thousands of cells per sample. Narrow your focus with targeted gene expression, and use predesigned or custom panels to focus on the genes most relevant to your research. **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 target screening with tens to thousands of perturbations in a single experiment using Feature Barcode technology, which lets you concurrently detect sgRNA and perturbed gene expression profiles in each cell.

Solution Features

- Ready-to-use, robust workflow, including demonstrated protocols for diverse sample types, including cell lines, primary cells, and dissociated fresh tissue
- Compatible with whole cells and nuclei
- Compatible with Targeted Gene Expression
- Robust protocols and compatible partners for cell surface protein measurement and CRISPR guide RNA detection applications using Feature Barcode technology
- Compatible partners and support for custom CRISPR guide libraries, oligo-conjugated antibodies, and Feature Barcode oligo conjugation kits
- Easy-to-use data analysis and visualization software
- Utilizes dual index library strategy, the sequencing industry standard for maximally reliable sequencing results

System Features

- Efficiently partition 500-10,000 cells per channel, for up to 80,000 cells per run
- Scalable; run up to 8 samples in parallel
- Simple workflow
- Cell size flexibility, no lower limits
- Superior sensitivity
- High cell capture rates of up to 65%
- Low doublet rates of under 0.8% per 1000 cells
- Based on Next GEM technology

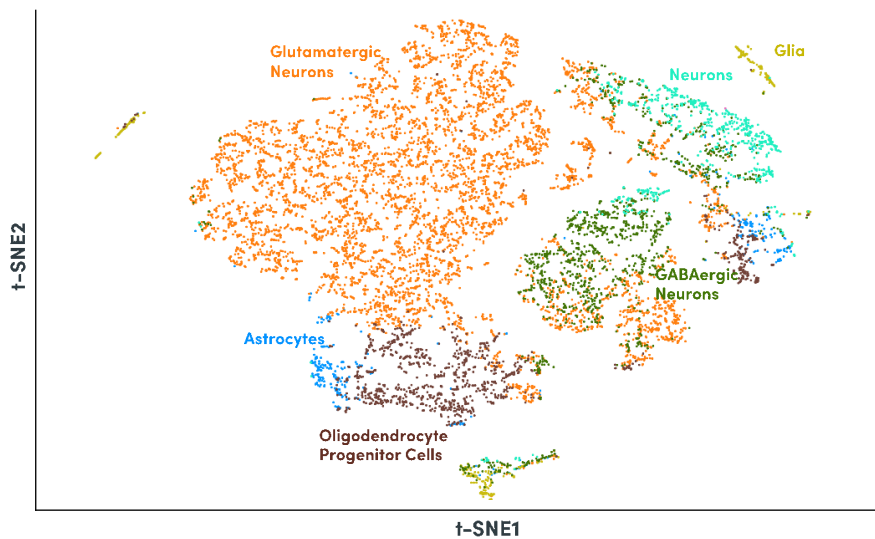
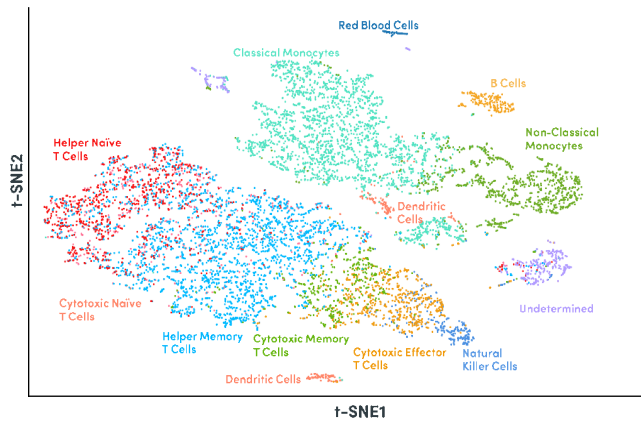


Figure 2. Heterogeneous cell composition of mouse brain tissue revealed with single cell gene expression. To visualize the global differences in gene expression signatures across different cell types, the t-SNE dimensionality reduction technique was used, which represents each cell with a single dot. 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 identifying 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

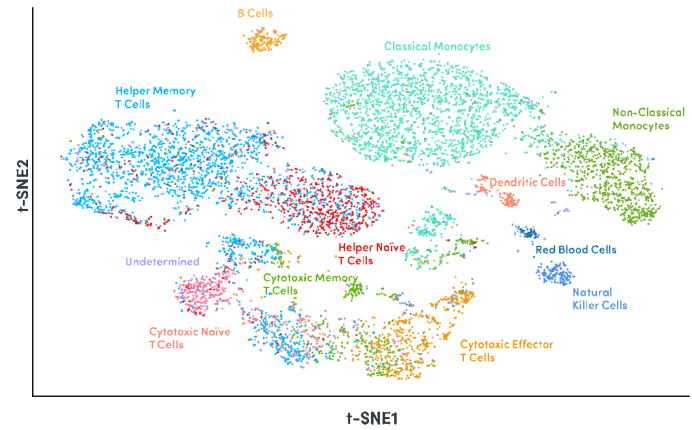


Figure 3. Enhanced characterization of human immune cell subtypes with multiomic data through cell surface protein analysis. **A.** t-SNE projection of approximately 10,000 PBMCs processed with Single Cell Gene Expression and analyzed with Cell Ranger, based on whole transcriptome gene expression. **B.** 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.

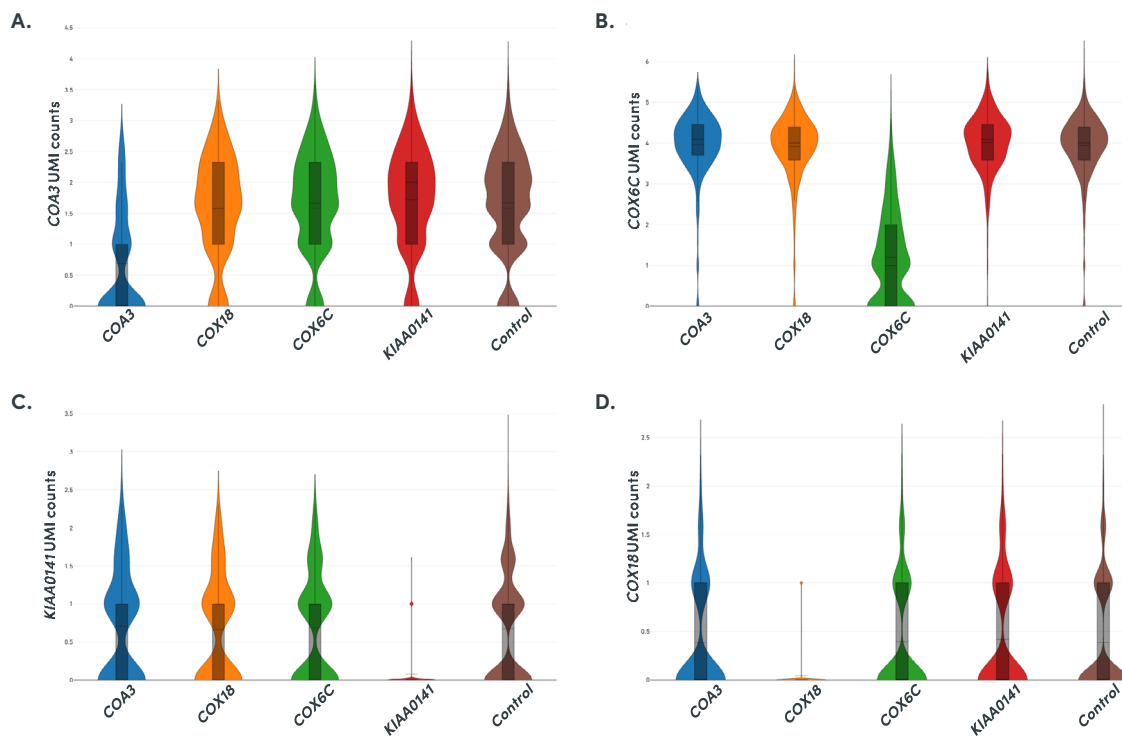


Figure 4. Simultaneous capture of CRISPR guides and gene expression profiles, at single cell resolution, using Feature Barcode technology. **A-D.** Violin plots demonstrating knockdown efficiency across multiple gene targets in a pooled CRISPR screen using a human cell line (K562) constitutively expressing dCas9-KRAB. Shown are UMI counts of four target genes from cells containing experimental or control single guide RNA (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**).

Research areas

- Cancer Biology
- Neuroscience
- Immunology
- Stem Cell Biology
- Translational Research

Applications

- Tumor Heterogeneity
- Cell Differentiation & Lineage Tracing
- Therapeutic Response and Resistance
- Biomarker Discovery
- Target Validation
- Single Cell CRISPR Screens

Additional resources

Datasets	go.10xgenomics.com/scRNA-3/datasets
Seminars	go.10xgenomics.com/scRNA-3/seminars
Application Notes	go.10xgenomics.com/scRNA-3/app-notes
Technical Support	go.10xgenomics.com/scRNA-3/support
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For more locations in US, EU and Asia visit:

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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
3' Feature Barcode Kit, 16 rxns	1000276
Dual Index Kit TT Set A, 96 rxn	1000215
Dual Index Kit NT Set A, 96 rxn	1000242
Chromium Next GEM Chip G Single Cell Kit, 16 rxns	1000127
Chromium Next GEM Chip G Single Cell Kit, 48 rxns	1000120
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Chromium Controller & Accessory Kit, 24 Mo. Warranty	120246
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