

# Enhance discovery with industry-leading sensitivity at single cell resolution

## GEM-X Single Cell Gene Expression v4 with Feature Barcode technology

Critical research into questions of health and disease relies on trusted, reliable methods that support your investigations into the underlying biology. Chromium GEM-X Single Cell Gene Expression v4 was designed to meet these needs, using advanced GEM-X technology to help you uncover biological complexities with unmatched sensitivity and cell recovery efficiency for transcriptomic profiling. Characterize rare cell types, identify biomarkers, capture fragile or low-RNA-content cells, and reveal hidden heterogeneity in more samples. GEM-X technology brings improved performance and higher success rates to our end-to-end Chromium workflows, allowing you to maximize the impact of your studies and accelerate time to results.

### Highlights

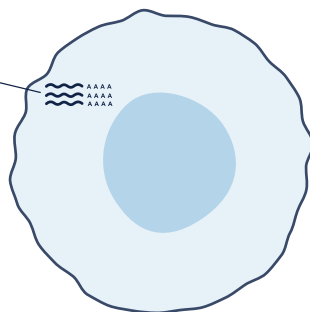
- Explore the influence of cell heterogeneity on development, disease, and more with scalable transcriptional profiling across a few hundred to tens of thousands of cells
- Further characterize cell subtypes and states with multiomic readouts of gene and cell surface protein expression for the same cell
- Uncover hidden complexity and reveal more accurate, comprehensive views of biology using technology that captures fragile cells and low-expressed transcripts
- Bring added confidence to your results by increasing sample number to improve statistical significance and accelerate time to results

#### Single cell analysis capabilities

##### A.

#### Whole transcriptome gene expression

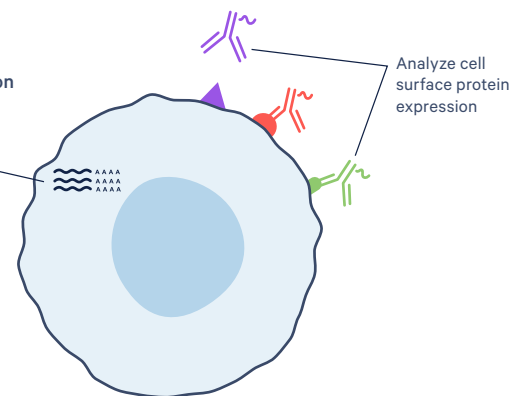
Perform whole transcriptome profiling



##### B.

#### Gene expression and cell surface protein expression

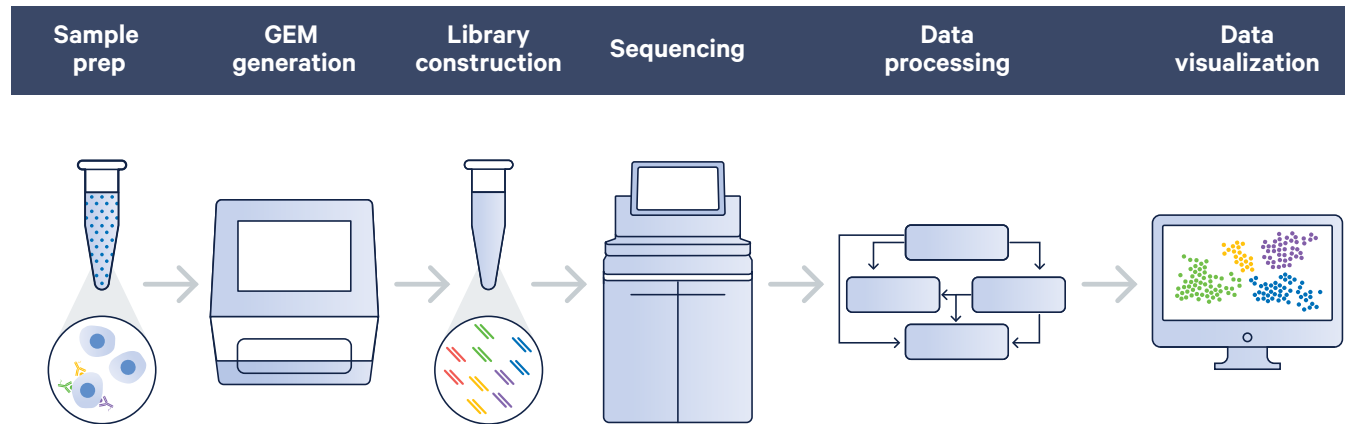
Perform whole transcriptome profiling



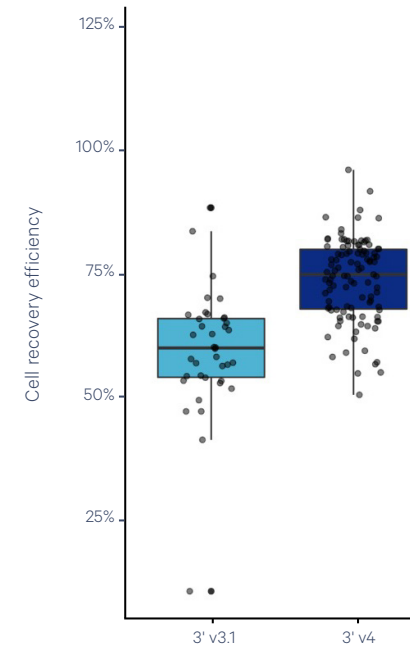
**Figure 1. Resolve cellular heterogeneity with multiomic single cell profiling.** **A.** Chromium GEM-X Single Cell Gene Expression v4 provides whole transcriptome 3' profiling at the single cell level for hundreds to tens of thousands of cells per sample. **B.** The addition of Feature Barcode technology enables combined gene expression profiling and cell surface protein detection with tens to hundreds of antibodies.

### Product features

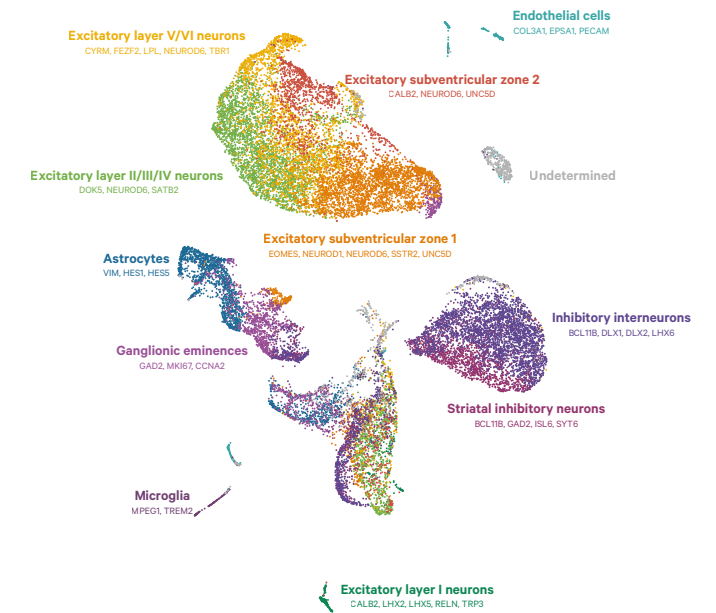
- Profile tens of thousands of genes at single cell resolution for unbiased characterization of cell types and states, even with challenging samples
- Combine gene expression analysis with detection of hundreds of cell surface proteins for ultra-high-parameter multiomic cytometry
- Leverage unmatched sensitivity to capture rare transcripts, fragile cells, and cells with low RNA content
- Lower your sequencing costs by up to 50% and reallocate resources to expand the scope of your study
- Experience improved robustness and up to 80% cell capture efficiency to make the most of precious samples and resources
- Detect more genes and UMIs per cell and increase complexity to gain a more comprehensive view of cellular heterogeneity



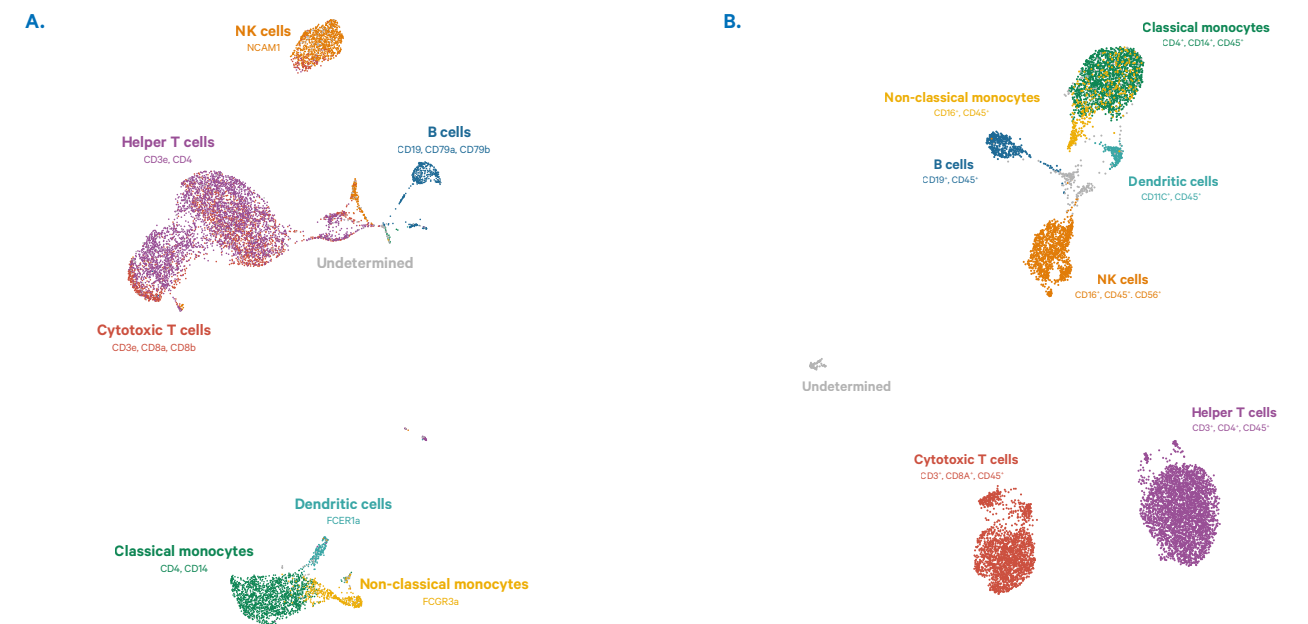
**Figure 2. Efficient and streamlined workflow for multiomic profiling of biological systems.** Start with a single cell suspension of unlabeled cells or oligo-conjugated antibody-labeled cells. After GEM generation, separate libraries can be constructed from a single sample, including gene expression and cell surface protein 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 intuitive analysis and visualization software.



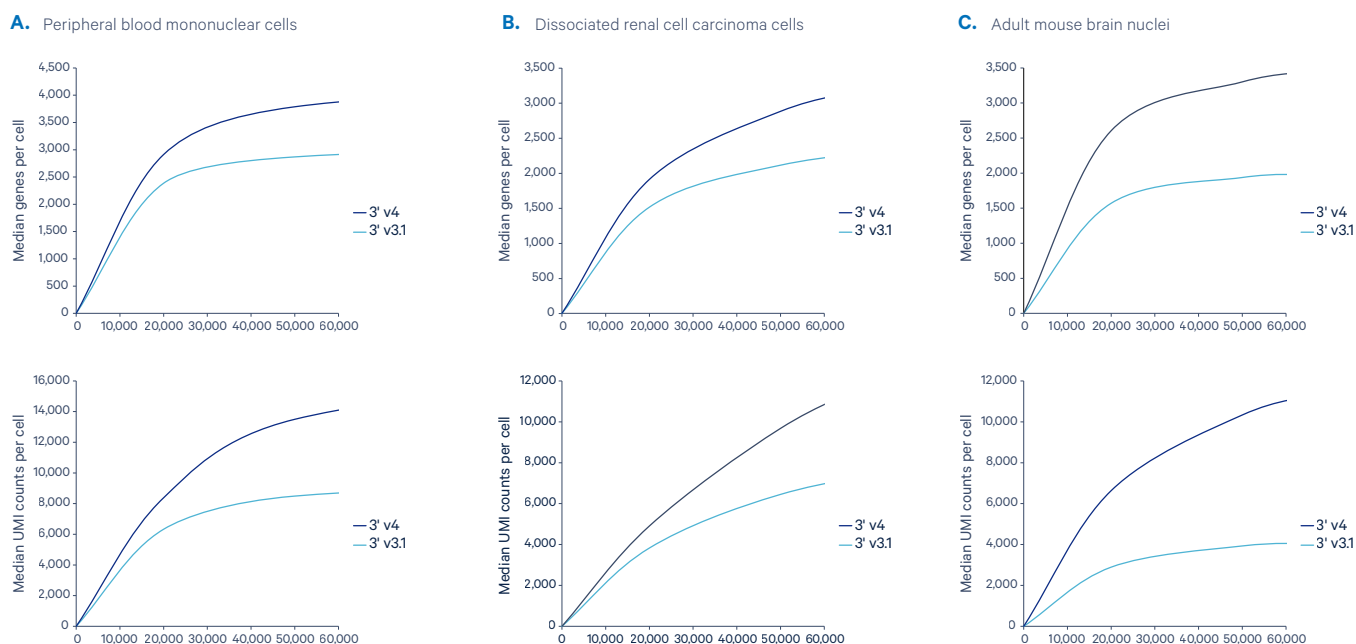
**Figure 3. Improved cell recovery efficiency with GEM-X.** Cell recovery efficiency was assessed with 318 independent single cell runs. Targeted cell loads ranged between 1,000–10,000 cells. Median cell recovery efficiency for GEM-X (3' v4) was 15% higher, compared to Next GEM (3' v3.1).



**Figure 4. Reveal heterogeneous cell composition of complex tissue with single cell gene expression, powered by GEM-X.** Aggregated UMAP projection of 21,331 cells from eight technical replicates profiled with the GEM-X Single Cell Gene Expression v4 solution. Cells were isolated from dissociated embryonic mouse brain tissue (E18 mouse combined cortex, hippocampus, and ventricular zone). Each cell is represented by a single dot. Broad categories of neuronal populations were identified through canonical gene expression markers.



**Figure 5. Multiomic data generated with GEM-X Single Cell v4 provided complementary insights into immune cell subtypes in human primary cells. A.** UMAP projection of 9,372 PBMCs. Each cell is represented by a single dot. Broad categories of immune cell populations were identified through canonical gene expression signatures. **B.** UMAP projection of the same sample clustered based on cell surface protein expression using a panel of nine markers.



**Figure 6. Substantial increase in library complexity with GEM-X Single Cell Gene Expression v4 across three complex sample types.** Sample types tested are as follows: PBMCs (A), dissociated cells obtained from renal cell carcinoma tissue (B), and nuclei obtained from an adult mouse brain (C). Each sample type was run in duplicate.

Gene expression profiling products	Product code
Chromium GEM-X Single Cell 3' Kit v4, 4 rxns	1000686
Chromium GEM-X Single Cell 3' Kit v4, 16 rxns	1000691
Chromium GEM-X Single Cell 3' Chip Kit v4, 4 chips	1000690
Dual Index Kit TT Set A, 96 rxns	1000215
Library Construction Kit C, 16 rxns	1000694
Feature Barcode technology products	Product code
Chromium GEM-X Single Cell 3' Feature Barcode Kit v4, 16 rxns	1000702
Dual Index Kit NT Set A, 96 rxns	1000242
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	<a href="#">Download Cloud Analysis</a>
Loupe Browser	<a href="#">Download</a>
Compatible partner products	
Biogen TotalSeq™-B <a href="http://biogen.com/totalseq">biogen.com/totalseq</a>	<a href="#">Learn more</a>

## Product specifications

- Efficiently partition 500–20,000 cells per channel, for up to 160,000 cells per run
- Scalable; run up to 8 samples in parallel
- Cell size flexibility with no lower limits
- High cell capture rates of up to 80%
- Low doublet rates of 0.4% per 1,000 cells

## Contact us

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LIT000220 - Rev A - Product Sheet - GEM-X Single Cell Gene Expression

