FEATURE BARCODING TECHNOLOGY FOR CELL SURFACE PROTEIN

The Chromium Single Cell Gene Expression Solution with Feature Barcoding technology (with Next GEM technology) combines cell surface protein detection with an unbiased readout of each single cell transcriptome. Cell surface proteins serve as biomarkers to help distinguish individual cells. As an alternative to the fluorescent tags used in flow cytometry, Feature Barcoding technology leverages antibodies conjugated to DNA barcodes for single cell sequencing. Barcode diversity vastly expands the number of markers you can analyze per assay and improves cell type resolution.

This robust solution allows you to gather highly multiplexed surface marker information in hundreds to tens of thousands of cells. Layer cell surface protein expression data over digital gene expression data, on a cell-by-cell basis, to measure cell surface protein markers and protein isoforms that are difficult to differentiate at the transcript level. These capabilities expand your ability to identify cell types and states, as well as detect rare cell types, all in a single assay at single cell resolution.

Improved Resolution of Cell Types with the Addition of Cell Surface Protein Detection

tSNE projections of ~5,500 peripheral blood mononuclear cells (PBMCs) output by Cell Ranger. A. PBMCs are grouped together based on digital gene expression information. B. PBMCs were then grouped by cell surface protein expression profiles. The additional information from antibody UMI counts better resolved many canonical cell types compared to gene expression data alone—naïve and experienced T cells, CD4+ and CD8+ T cells (populations denoted with asterisk*), for example.

Learn More at 10xgenomics.com/single-cell
Single Cell Gene Expression with Cell Surface Protein

**HIGHLIGHTS**

- Perform cellular phenotyping to identify novel targets, biomarkers, and cell types and states without the need for pre-selected gene expression targets
- Simultaneously examine gene expression and protein abundance in the same cell
- Detect under-represented transcripts of key protein markers
- Detect protein isoforms
- Evaluate differences between mRNA and cell surface protein expression profiles
- Obtain similar protein expression performance as gold-standard flow cytometry
- Better implement published methods like CITE-Seq/REAP-Seq using our new and improved workflow

**SOLUTION FEATURES**

- Ready-to-use, robust protocols including applications using Feature Barcoding technology
- Compatible partners for oligo conjugated antibodies
- Documentation for custom conjugations for use with Feature Barcoding technology
- Easy to use and convenient software with Cell Ranger Analysis Pipelines and Loupe Cell Browser visualization tool
- Based on Next GEM technology

**SYSTEM FEATURES**

- Partition 100 – 80,000+ cells efficiently
- Scalable; run up to 8 samples in parallel
- Superior sensitivity
- Simple workflow
- Cell size flexibility, no lower limits
- High cell capture rates of up to 65%
- Low doublet rates of under 0.9% per 1000 cells

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**Differentiation of PTPRC Expressing PBMCs via Detection of CD45RA and CD45RO Isoforms**

*TSNE feature plots depicting PTPRC mRNA (coding for CD45 protein), and CD45RA and CD45RO protein expression. Oligo-conjugated antibodies against CD45RA (HI100) and CD45RO (UCHL1) were used to identify CD45 isoforms which are difficult to differentiate at the transcript level. Color gradient represents UMI counts where dark blue associates with higher UMI counts (higher gene or protein expression levels). While PTPRC is expressed across most cells in the sample and is detected at the mRNA level, the additional information from the isoform-specific antibodies allows differentiation of naive and memory populations.*

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In PBMCs, flow cytometry and Feature Barcoding technology reveal similar cell populations when fluorescence intensity is compared with UMI counts per cell.