# Single cell profiling on more samples with no time constraints

## Fixed RNA Profiling

Single cell RNA sequencing is increasingly being used to profile larger numbers of samples, corresponding to cohorts of patients or different perturbations, making an efficient and scalable workflow of paramount importance. PFA fixation allows samples to be collected, shipped to a central location, and analyzed without sacrificing integrity or data quality, creating new possibilities for sample accessibility, throughput, and batched analysis. Profile hundreds of thousands of fixed single cells at once, unlocking a massive number of opportunities to bring single cell biology into the future, particularly in translational and clinical labs where fragile samples or time constraints would otherwise preclude analysis.

## Highlights

- Fix human or mouse samples at the point of collection to lock in their biological states and preserve fragile cells
- Improve sample collection, preparation, and processing steps to streamline single cell workflows
- Reduce experimental variability and increase efficiency by batching and multiplexing samples
- Generate highly sensitive measurements of gene expression and cell surface proteins simultaneously


**Figure 1. Gene expression profiling on your schedule.** Chromium Single Cell Fixed RNA Profiling enables single cell gene expression studies on precious samples that were previously inaccessible because of logistical challenges in sample handling. Fixation at the point of sample collection preserves fragile biology and greatly streamlines workflows to provide critical insights on more samples.

## Product features

- Profile gene expression for thousands to hundreds of thousands of cells or nuclei with a sensitive probe-based method that captures the whole human or mouse transcriptome to detect even low-expressing genes
- Store samples without losing data quality, allowing you to batch samples in the same run and minimize experimental variability
- Multiplex up to 16 samples per channel to enable increased throughput, expanding your capabilities to profile large numbers of samples while reducing cost per sample
- Lock in cell state and then combine gene expression analysis with detection of hundreds of cell surface proteins at high resolution for ultra-high parameter multiomic cytometry
- Follow a ready-to-use, robust workflow with optimized, demonstrated protocols for diverse sample types, including cell lines, primary cells, and dissociated tissue containing fragile cells

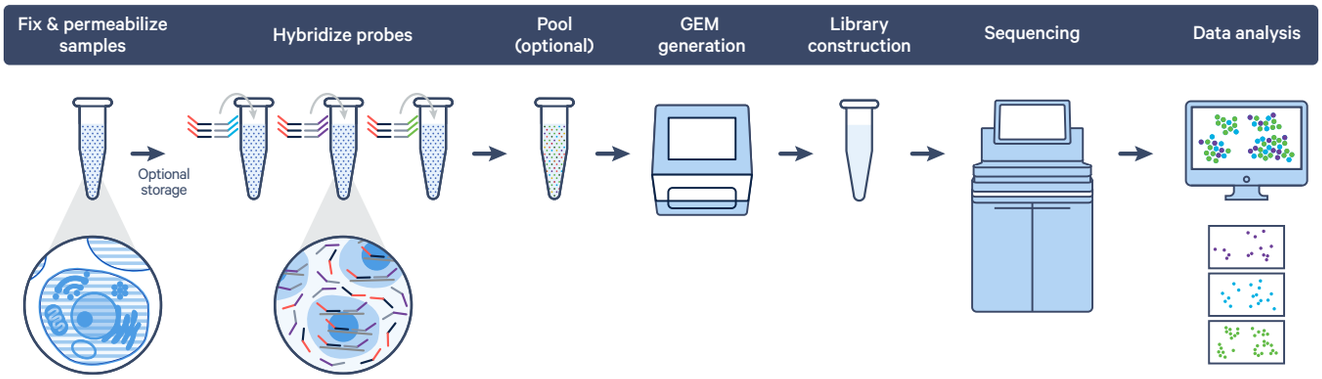


**Figure 2. Chromium Single Cell Fixed RNA Profiling enables an efficient and streamlined workflow for sample management and processing.** Cells are fixed and permeabilized and can be safely stored or transported without compromising data quality. Once ready to proceed, samples are hybridized to probe sets and may be processed individually (single sample workflow) or pooled with up to 16 samples in a single lane of a Chromium chip (multiplex workflow). During GEM generation the probe sets are ligated and extended to incorporate unique barcodes. Next sequencing libraries are prepared, sequenced and analyzed using 10x Genomics Cell Ranger and Loupe Browser software tools.

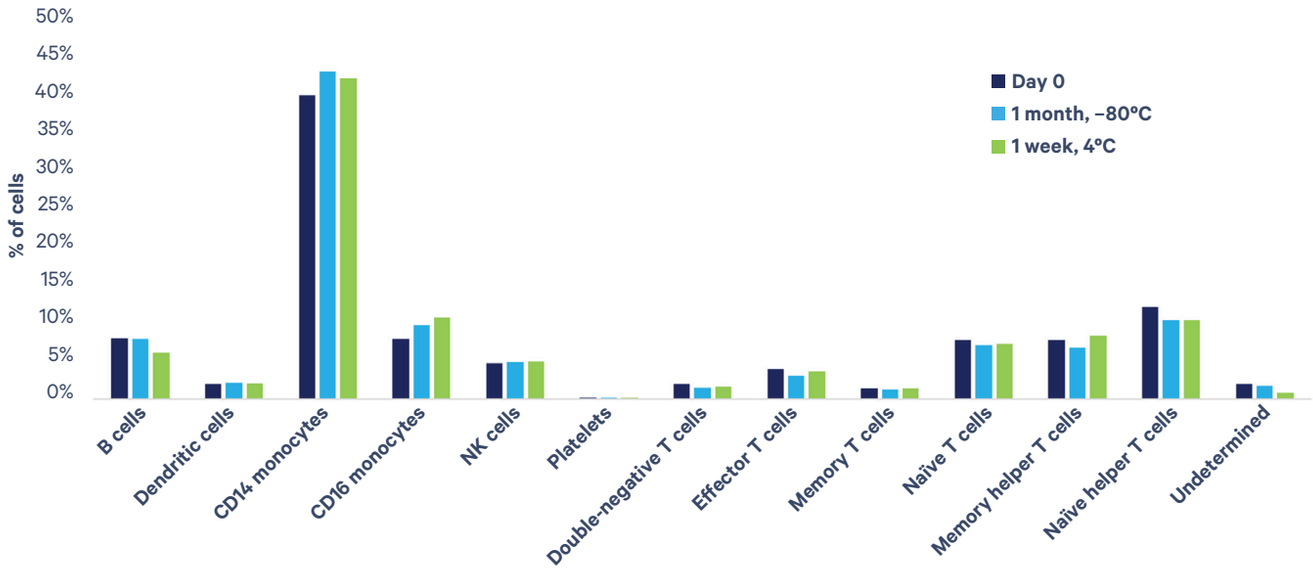


**Figure 3. Storage stability of fixed samples.** Single cell gene expression profiling of human PBMCs, fixed and run immediately (Day 0), after storage at 4°C for one week, or after storage at -80°C for one month. Key populations of cell types are stable over time, demonstrating that the biology can be locked in with PFA fixation to enable transportation and storage, relieving constraints of running single cell experiments.

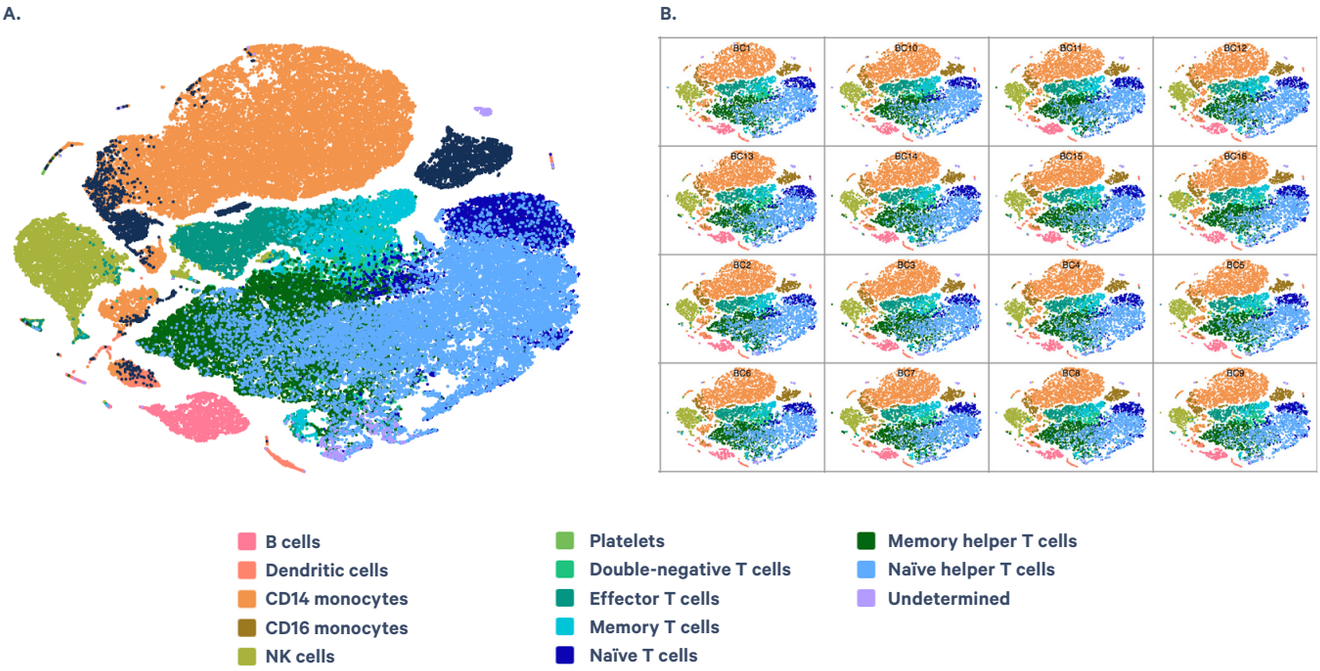


**Figure 4. Cell clustering of gene expression data from fixed samples.** Human PBMCs were fixed and split into 16 samples, each hybridized with a barcoded set of probes. Samples were pooled together and run on a single lane of a Chromium X chip. **A.** t-SNE plot showing 80,000 cells from all pools, overlaid together, with distinct clusters representing each cell type. **B.** t-SNE plots showing the same data split by barcode to demonstrate that there are no batch effects and that multiplexing is an effective strategy for reducing experimental variability while vastly increasing sample throughput for single cell experiments.

**Contact us**
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