

## Overview

The 10x Genomics Chromium System, powered by GemCode Technology, provides a precisely engineered reagent delivery method that enables thousands of micro-reactions in parallel. Samples are encapsulated into hundreds to tens of thousands of uniquely addressable partitions each containing an identifying barcode for downstream analysis.

Each Gel Bead, infused with millions of unique oligonucleotide sequences, is mixed with a sample, which can be high molecular weight (HMW) DNA, individual cells, cells labeled using Feature Barcoding technology, nuclei, nuclei treated with transposase, or Cell Beads. Gel Beads and samples are then added to an oil-surfactant solution to create Gel Beads-in-emulsion (GEMs), which act as individual reaction vesicles in which the Gel Beads are dissolved, and the sample is barcoded.

Barcoded products are pooled for downstream reactions to create short-read sequencer compatible libraries. After sequencing, the resulting barcoded short read sequences are fed into turnkey analysis pipelines that use the identifying barcodes to map reads back to their original HMW DNA, single cell, or single nucleus of origin.

## Available Protocols

### Single Cell Gene Expression

The Chromium Single Cell Gene Expression Solution provides a comprehensive, scalable solution for cell characterization and gene expression profiling of hundreds to tens of thousands of cells. It can help to uncover gene expression variability and identify rare cell types in heterogeneous samples to better characterize cellular contributions during development and disease. Feature barcoding technology such as CRISPR screening and cell surface protein barcoding may also be available

## Single Cell ATAC

Single Cell ATAC accelerates the understanding of the regulatory landscape of the genome, thereby providing insights into cell variability. The chromatin profiling of tens of thousands of single cells in parallel allows researchers to see how chromatin compaction and DNA-binding proteins regulate gene expression at high resolution.

## How to Submit

Before beginning any submission for 10x genomics, a consult with the HTSF lab director, Piotr Mieczkowski is required. Please contact our customer service team to set up a meeting. Contact information can be found on the HTSF website. For detailed instructions on 10x genomics please refer to the *How to Submit Guide, Alternative Technologies* for sample requirements. There is a different set of instructions on *Forms and Guides, Alternative Technologies* for:

- Study Made libraries (HTSF-10x Submission Instructions for STUDY MADE libraries)
- Studies submitting for HTSF to make 10x libraries (HTSF-10x Manifest HTSF Made Libraries)

In addition to a TracSeq manifest, a special study made 10x manifest will also need to be filled out and sent to the HTSF when submitting samples. This manifest will be used for the TracSeq.