



# Single-Cell Flex RNA Sequencing

## Product Overview

The **10x Single Cell Flex** assay provides probe-based transcriptional profiling of formaldehyde fixed samples at the single-cell level across thousands of cells per sample, allowing to detect several thousand transcripts per cell. Barcoded probes enable sample multiplexing for up to 384 samples. 10x's Flex kits are based on the generation of nanoliter-scale droplets in which a single cell/nucleus will bind to a gel bead coated with oligos containing a unique barcode, UMIs and sequences to capture the hybridized probes. Captured products will undergo a reverse transcription step allowing for the generation of cDNA, then of libraries. Sequencing will be performed on the NovaSeq X Plus platform (Illumina) with tailored sequencing settings based on the project design and the user's needs.

## What is Included

- Cell sorting using FACS (optional)
- Probe hybridization and GEM generation
- Single Cell library preparation
- Quality control of cDNA and library
- Library pooling and sequencing on Illumina NovaSeq X Plus
- FASTQ files
- Standard data processing, QC, and basic bioinformatics analysis including cell annotation and differential gene expression (optional).

## Input and quality requirements

### Isolation of cells or nuclei

Isolation, fixation and counting of cells or nuclei is the responsibility of the user. Contact [SCOP](#) to consult.

### Quality

The quality of the cells/nuclei will reflect the downstream process – poor quality leads to poor data.

SCOP strongly recommends performing a pilot experiment to assess both sample and data quality.

### Sample drop-off

The hybridization step requires 25,000-500,000 fixed cells/nuclei per sample/probe barcode. Fixed samples should be delivered at a specific concentration which depends on the desired number of cells/nuclei. Please contact [SCOP](#) for more information.

## Data Deliverables

The data will be processed through CellRanger. The data will be transferred to the shared folder including:

- FASTQ files
- Preprocessed data stored in Seurat objects
- HTML file with key stats and figures.