Unil.
Faculté de biologie et de médecine

Genomic Technologies Facility
Single Cell Experiments · June 2026

Focus on Single Cell Experiments

Dear users,

Wondering **which single-cell approach is right** for your project? In this edition, we walk you through the full range of workflows we support at the Lausanne Genomic Technologies Facility — from fresh and fixed cells to combinatorial barcoding, primary analysis, and long-read isoform sequencing. Whether you're just starting to plan or ready to sequence, we're here to help.

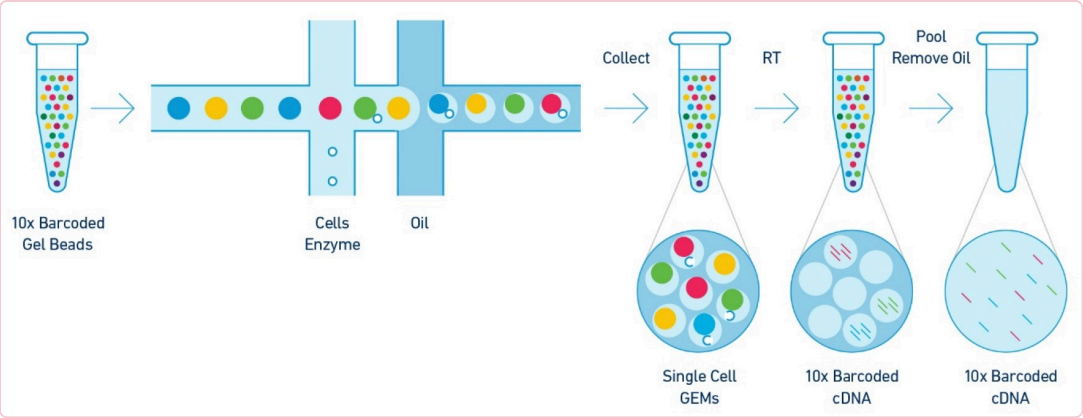
AT A GLANCE

- **Main technologies:** We run **10x Genomics** and **Parse Evercode** — covering droplet and split-pool approaches. Please enquire if you are interested in BD/Waters Rhapsody.
- **Fresh or fixed/FFPE:** Choose fresh cells/nuclei for maximum flexibility, or fixed cell/nuclei workflows for scheduling freedom and challenging sample logistics.
- **Primary analysis:** Cell Ranger and Parse Pipeline — included when libraries are prepared by GTF.
- **Long reads too:** Single-cell cDNA can go onto PacBio Kinnex for splice isoform-resolved analysis.
- **On-site option:** 10x Chromium benches at Dorigny, Agora and Biopôle SE-C, plus sample dropboxes for the UNIL/CHUV community.
- **Sequencing at any scale:** From shallow, small-scale runs for quality checks to large-scale, high-depth sequencing — open to both GTF-prepared projects and externally prepared libraries.

DROPLET-BASED

10x Genomics

Two complementary workflows are available — emulsion-based **fresh cells / nuclei**, and probe-based **fixed / FFPE** for **cells / nuclei** (Apex).



10x Chromium workflow: barcoded gel beads & cells partitioned into GEMs, then RT to pooled barcoded cDNA — **10x Genomics Chromium →**

FRESH CELLS / NUCLEI (EMULSION)

Assays: Gene Expression, V(D)J (BCR/TCR), ATAC / Multiome, cell-surface proteins and CRISPR.

Input & quality: high-viability fresh cells (>80%) or unaltered nuclei; up to 20k cells per well, recovery ≈ 70%.

Multiplexing: on-chip multiplexing (OCM, no prior cell labelling required) or antibody-based hashtags.

Sequencing: shallow-seq or full sequencing (≈ 20'000 reads per cell) requests possible with project size — adaptable prices.

FIXED CELLS / NUCLEI — APEX (PROBE-BASED)

Assays: Gene Expression and proteins (cell-surface and intracellular), human, mouse and rat only. Possibility of custom probe panel design.

Fixation & input: PFA-based, high-quality starting material (>100k cells); stable 1 week at 4°C or months at −80°C.

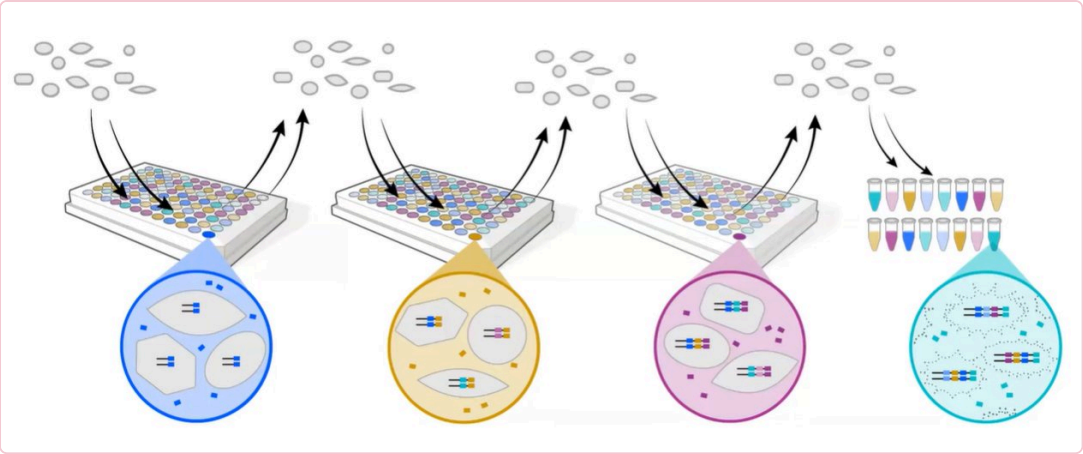
Multiplexing: by design, with 96 barcodes available at the GTF; up to 20k cells per barcode and up to 1M cells per emulsion.

Sequencing: probe sequencing, standard ≈ 10'000 reads per cell — a flexible and cost-effective design.

🧪 SPLIT / POOL

Parse Evercode

A combinatorial split-pool barcoding approach — no instrument required, and highly scalable across many samples.



Split-pool combinatorial barcoding: cells pass through successive barcoding plates to give each cell a unique barcode combination — **Parse Biosciences Evercode →**

Highly Multiplexed

1–384 samples by design, any species, from 10k up to 5M cells.

Whole Transcriptome

Not probe-based — enables velocity, variant, non-coding RNA and transgene analysis.

WORKFLOW & SPECIFICATIONS

Assays: Gene Expression, V(D)J and CRISPR.

Fixation & input: methanol-based fixation, high-quality starting material, stored <6 months at −80°C; as low as 10k cells, with bead-based capture for low input.

Input/output: fixed kit formats (10k / 100k / 1M / 5M cells), with ≈ 70% recovery using v4 kits and a derisking pilot option from Parse.

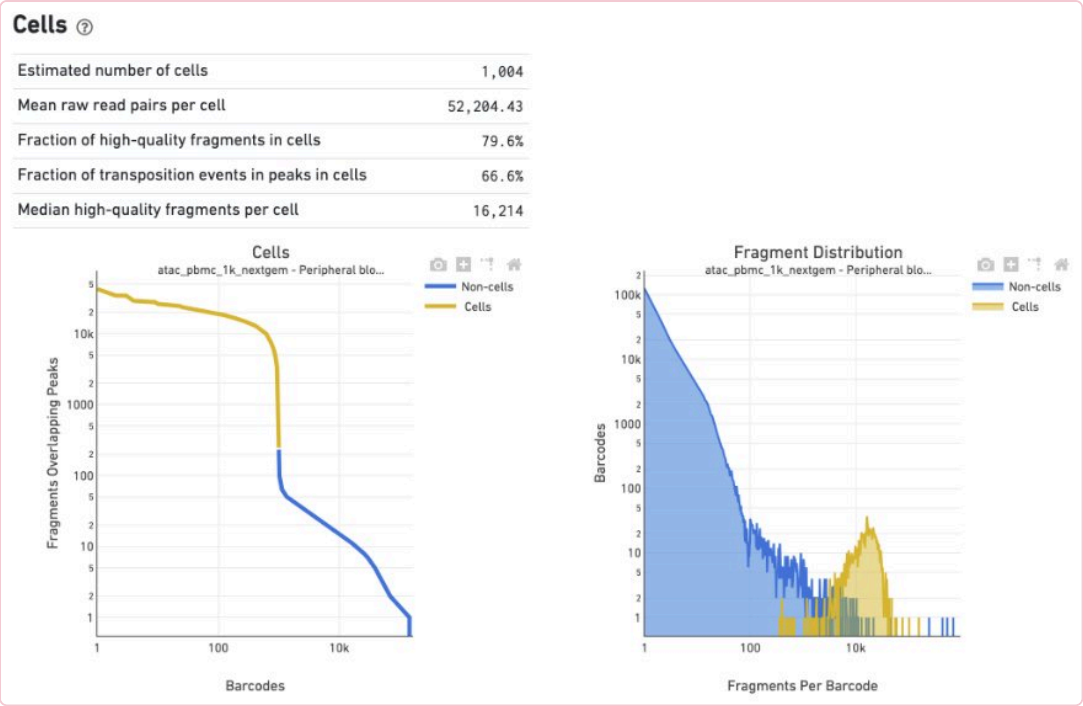
Sequencing: whole-transcript (polyA + hexamers), standard ≈ 5'000 reads per cell (v4).

Parse × GTF offer: Parse sponsors GTF-prepared libraries through a special deal — discounts on kits or on part of the sequencing.

DATA

Primary Analysis

Primary-analysis pipelines are available, matched to each technology:



*Example primary-analysis QC output: a Cell Ranger web-summary report (Cells dashboard, showing the barcode rank/knee plot and fragment distribution used to assess cell calling and library quality) — **10x Cell Ranger →***

✓ **10x Cell Ranger**

✓ **Parse Pipeline**

✓ **Included** when libraries are prepared at the GTF — otherwise a flat fee plus a per-sample fee applies for user libraries

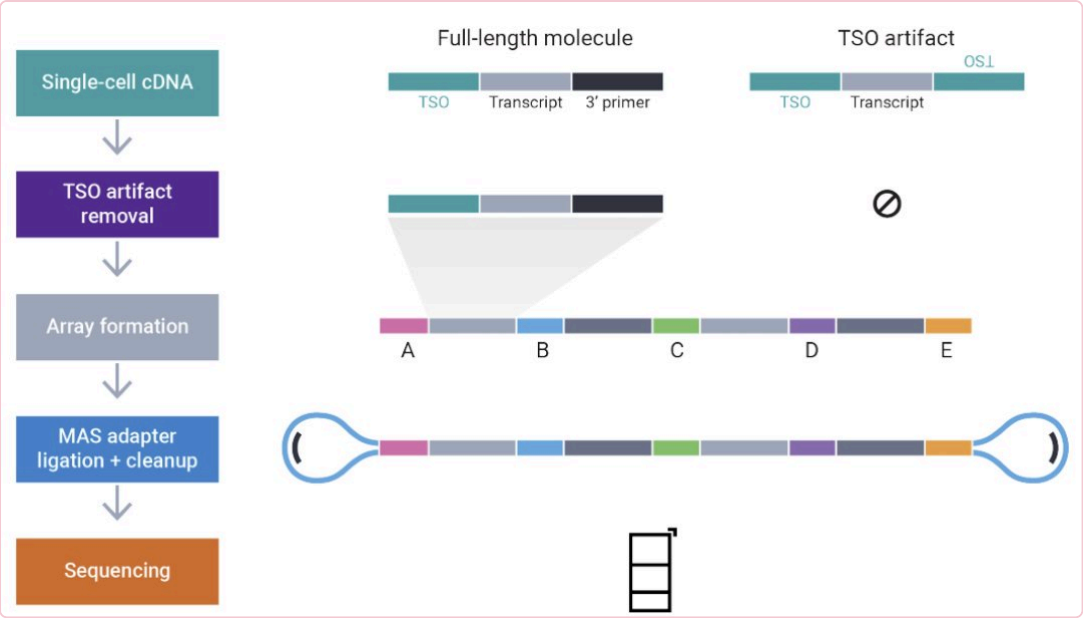
✓ **Custom genomes** prepared by the GTF to fit your project's reference and annotation needs

Please note: secondary analysis is not a standard service.

🧬 ISOFORMS

Long Read Single Cell — PacBio Kinnex

Single-cell cDNA — generated from 10x fresh and Parse workflows — can be taken onto **PacBio Kinnex** for splice isoform-resolved, single-cell analysis.



Kinnex (MAS-Seq) workflow: TSO-artifact removal, concatenation of full-length cDNA into arrays, MAS adapter ligation and long-read sequencing — PacBio Kinnex single-cell →

Isoform Resolution

Resolve **different splicing isoforms** across cell types with single-cell isoform analysis.

~100M Reads

Kinnex library prep + PacBio sequencing delivers **≈ 100M reads** per run.

WORKFLOW & PRICING

HiFi: up to 20kb Illumina-quality reads.

Input: cDNA from 10x fresh or Parse single-cell workflow.

Steps: single-cell cDNA generation → Kinnex library preparation → PacBio sequencing → read segmentation + single-cell isoform analysis.

Pricing: highly competitive — the GTF is a well-renowned PacBio service provider.

📍 ON LOCATION

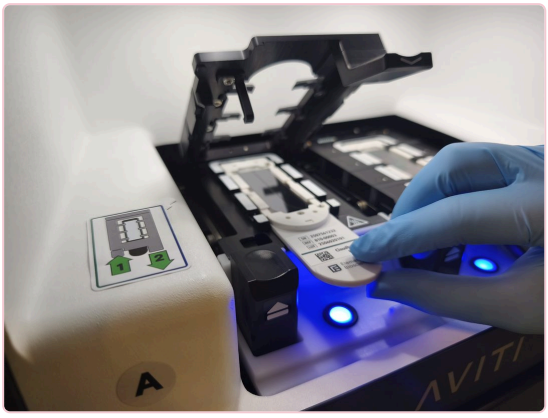
We come to your samples

Run your single-cell experiment **directly at the GTF** — bring us your cells or your finished libraries. Or leave your samples where they are: with a **10x Chromium and benches at Agora and Biopôle**, we come to your precious samples, so they never have to travel. Finished libraries can simply be left in the **dropbox** in the Agora and Biopôle labs.

SEQUENCING

Sequencing at any scale

From low throughput quality-check shallow sequencing to deep large-scale runs, we sequence your libraries — or ours — at exactly the scale your science needs.



Loading of a flow cell on the AVITI instrument

Planning a single-cell experiment?

Fill in the **Single Cell Form** before our first meeting so we can focus the discussion — we are happy to help from experimental design to data delivery.

Contact us: contactGTF@unil.ch

For more information, visit our website: **https://wp.unil.ch/gtf**

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