CYTOSURGE®

Live-Cell Sequencing for Same-Cell Biology

The Revolution Isn't Single-Cell - It's Same Cell

Live-seq is the world's first non-destructive single-cell sequencing workflow — and the foundation of the new paradigm of Same-Cell Biology.

Traditional sequencing kills the cell to access its RNA, giving you a terminal snapshot and forcing you to guess cellular trajectories through pseudo-time. With Live-seq you can know exactly how the same cell changes: turning snapshots into a *Movie*.

Using a FluidFM® Nanosyringe, cytoplasmic biopsies of single cells are collected while preserving cell viability, providing fundamentally novel assays for longitudinal analysis of individual cells:

- **Link phenotypical traits:** Capture the gene expression signatures behind visible traits, dynamic responses or rare cellular behaviors.
- **Temporal sequencing:** Revisit the same cell across multiple time points to uncover the gene regulatory networks driving fate decisions and plasticity.
- **Correlation to the cellular context:** decode changes in gene expression driven by cell-cell interactions and microenvironmental cues.

Live-seq reveals cellular dynamics without inferring.

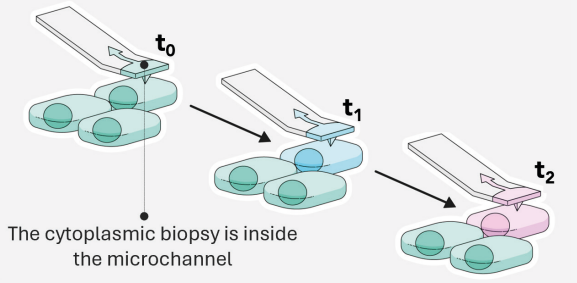

Figure 1A: Cells stay alive after collection of the cytoplasmic biopsy and remain within their cellular environment. This allows collection of different time-point samples from the same cell.

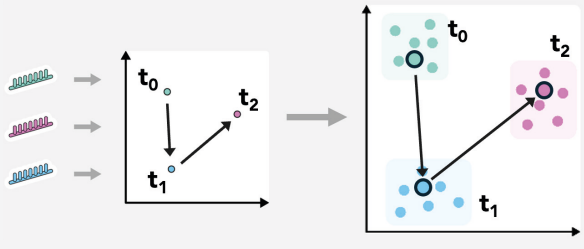

Figure 1B: Record transcriptomes from individual living cells using a low-input RNA library preparation and track the transcriptional journey of an individual cell at different time points.

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What can you do with Live-seq?

The different Live-seq assays can help to unravel the molecular drivers of cancer cell plasticity, cancer stem cell dynamics, tumor microenvironment interactions and emerging drug resistance.

Here, we use epithelial-to-mesenchymal transition (EMT) as an example to showcase the power of Live-seq in the context of cancer biology.

EMT, a key driver of cancer metastasis and therapy resistance.

Understanding transcriptional drivers at play in intermediate EMT states is critical for identification of targets for cancer therapeutics that disrupt metastatic spread and improve treatment efficacy against aggressive tumors.

EMT is a dynamic, multi-step process where epithelial cells progressively acquire mesenchymal traits. These cancer cells move, resist apoptosis, and even adapt to changing microenvironments and each intermediate state in the EMT process contributes uniquely to cancer invasiveness and metastatic potential. (Figure 2)

Understanding the transcriptional drivers in intermediate states that govern the adaptation of mesenchymal characteristics, is key to developing targeted therapies to prevent EMT and inhibit spread of primary tumors.

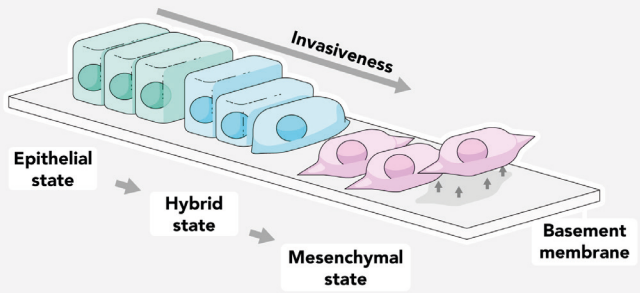

Figure 2: EMT is a dynamic process where epithelial cells acquire mesenchymal-like characteristics, which is correlated with the level of invasiveness of the cancer cell.

Key publications

NEW: Fluidic force microscopy, Zambelli, *et al.*, Nature Reviews Methods Primers (2026)

Live-seq enables temporal transcriptomic recordings of single cells, Chen *et al.*, Nature (2022)

Tunable Single-Cell Extraction for Molecular Analysis, Guillaume-Gentil *et al.*, Cell (2016)

Live-seq can support the identification of transcriptional targets that drive invasive EMT states in cancer as they unfold.

An epithelial cell undergoes a dynamic transition to acquire more mesenchymal-like characteristics. Multiple cytoplasmic biopsies can be taken from the same cell going through EMT. From each of the cytoplasmic biopsies a transcriptome can be recorded. (Figure 3A)

The heatmap visualizes the temporal mRNA expression changes of key genes, and highlights the molecular shifts that accommodate the cellular plasticity during EMT. (Figure 3A)

The use of cytoplasmic biopsies for single-cell RNA sequencing transforms the readout from static snapshots into a dynamic timeline of different EMT cell states and transitions. (Figure 3B)

Integrated time-lapse imaging can further enhance the dataset by correlating transcriptomic data with the cellular morphology and behavior of the same living cell.

This new workflow can capture gene expression patterns driving EMT and its intermediate states.

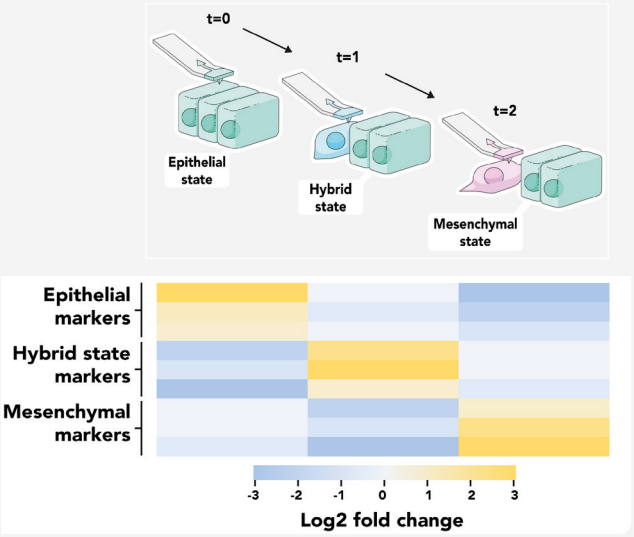

Figure 3A: A FluidFM Nanosyringe is used to collect cytoplasmic biopsies at different timepoints during EMT. The corresponding heatmap of the recorded transcriptomes shows differential gene expression between different EMT states.

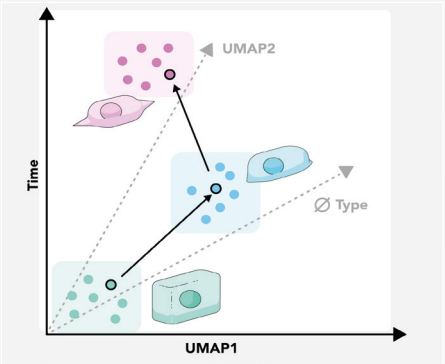

Figure 3B: Sampling different timepoints throughout EMT allows correlation of cell state transitions of individual cells.

These new insights can accelerate target discovery and offer promising new therapeutic strategies that disrupt EMT-driven mechanisms in cancer.

Check out use cases and customer stories on our blog.

How do cytoplasmic biopsies work?

Live-seq is powered by the FluidFM® OMNIUM platform and offers a streamlined workflow for cytoplasmic biopsy collection.

The FluidFM® Nanosyringe, gently pierces the cell with minimal cell perturbation resulting in high viability after collection. Integrated cell tracking enables to follow a cell's downstream behavior, phenotype or sample it again.

About the FluidFM® OMNIUM platform

Semi-automated point-and-click workflows offer ease-of-use for implementation of Live-seq in your lab:

- High cell viability after sampling.
- Integrated measurement tool to determine precise extraction volume per cell.
- Integrated microscope and software for optical cell tracking between biopsies.
- Cells can remain in optimal cell culturing conditions within the incubator for the entire duration of the experiment.

Interested to learn more?

available from:

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Live-seq in practice.
Webinar replay & slides:
"Cellular Time Travel: Determine Today's Transcriptome, Study Tomorrow's Response."

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