Infographic

Single-cell RNA Sequencing:
Reading the transcriptome one cell at a time

Bulk RNA-seq measures the average signal of millions of cells. Single-cell RNA-seq (scRNA-seq) keeps the identity of each cell, revealing the cell types, states and rare populations that averaging erases.

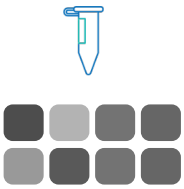
Averaging hides the biology

A tissue sample is a mixture of many cell types and states.

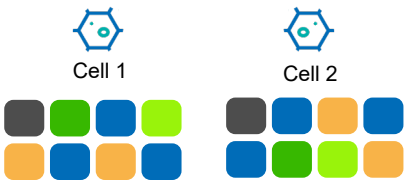
Bulk sequencing reports one blended profile.

Single-cell sequencing keeps every cell's transcriptome separate.

Tissue



Bulk sequencing reports one blended expression profile. One averaged expression value per gene across the whole population. Rare or minority cell-state signals are diluted within the majority cell population and are difficult to assign to specific cell types.



Single-cell sequencing keeps every cell's transcriptome separate.
One independent expression profile per cell. Distinct cell types, transitional states and rare populations can be resolved, subject to sample quality, cell throughput and sequencing depth.

scRNA-seq workflow explained

Droplet- and well-based microfluidic platforms isolate individual cells and tag their RNA with a unique molecular identifier before sequencing.

1 Tissue dissociation

Tissue is enzymatically and mechanically dissociated into a suspension of intact, viable single cells (or nuclei, for frozen or fragile samples).

2 Single cell encapsulation

A microfluidic chip partitions cells into thousands of nanoliter droplets, or individual microwells, so that each compartment ideally holds exactly one cell plus one barcoded bead.

3 Barcoding and reverse transcription

Each bead carries a unique cell barcode plus random unique molecular identifiers (UMIs). Inside the droplet, mRNA is captured and reverse-transcribed into barcoded cDNA, tagging every transcript with its cell of origin.

4 Library construction and sequencing

Barcoded cDNA from all cells is pooled, amplified and converted into a sequencing library, then sequenced at high throughput, to generate millions of short reads.

5 Computational analysis

Reads are demultiplexed by cell barcode, aligned, and counted into a cell-by-gene expression matrix. Dimensionality reduction (PCA, UMAP) and clustering then reveal distinct cell populations and trajectories.

What single-cell resolution adds

Unbiased cell-type discovery
Identifies known and novel cell types and subtypes directly from expression profiles, without relying on pre-selected markers.

Rare population detection
Enables detection of low-frequency cell populations (e.g. stem cells, circulating tumour cells) that are masked by bulk averaging.

Cellular heterogeneity mapping
Captures the full spread of states within a nominally "single" cell type, rather than one averaged expression value.

Trajectory & lineage inference
Orders cells along differentiation or activation paths, reconstructing dynamic biological processes from a static snapshot.

Cell–cell interaction analysis
Reveals ligand–receptor signaling relationships between specific cell populations within the same sample.

Multi-omic extension
Barcode-based capture generalizes to chromatin accessibility, protein epitopes and spatial coordinates alongside RNA.

@: info@mgi-tech.eu