SINGLE CELL SEQUENCING

To understand gene expression at an individual cell level.

To dissect heterogeneity on tissue sample or cell populations to better predict disease

Identify new drug targets, determine rare cells types and studying immune profiling

It holds a huge potential in diseases such as cancer and neurodegeneration

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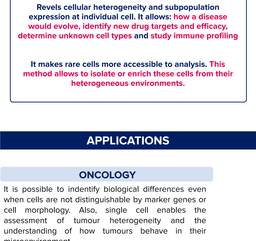
Single-Cell RNA-Seq | **Bulk RNA-Seq**



Advantage of Single-Cell RNA-Seq

Revels cellular heterogeneity and subpopulation expression at individual cell. It allows: how a disease would evolve, identify new drug targets and efficacy, determine unknown cell types and study immune profiling

It makes rare cells more accessible to analysis. This method allows to isolate or enrich these cells from their heterogeneous environments.

APPLICATIONS

ONCOLOGY

It is possible to indentify biological differences even when cells are not distinguishable by marker genes or cell morphology. Also, single cell enables the assessment of tumour heterogeneity and the understanding of how tumours behave in their microenvironment.

DEVELOPMENTAL BIOLOGY

It provides a powerful tool for studying the developmental patterns of interest at the level of individual stem or progenitor cells, enabling the determination of cell lineage. It allows the identification of the stages of differentiation and the corresponding cell types, from stem cell to mature cell, in any species and cell type.

IMMUNOLOGY

It can increase our understanding of the immune system complexity and identify and characterize immune cell on the sample, including their cell surface markers. Moreover, it can allow to identify antigen specificity for further characterization of immune cell population or antibody discovery.

NEUROSCIENCE

The central nervous system is a complex structure with many different cell types and signalling pathways. The molecular mechanisms of neuronal function, disease and injury can be better understood by comparing different states with single-cell gene expression.

LIBRARY KITS AND CRITERIA

Singleron

Input	Sample Type	Library kit
Viability 85%	Fresh Tissue *(Not frozen fresh)*	***GEXCOPE Single Cell VDJ library (TCR/BCR)***
Number of cells* > 35.000	Cell suspension	***GEXCOPE Single Cell RNA 3'***
	Organoids	

10x GENOMICS

Input	Sample Type	Library kit
Chromium Single Cell		
Viability 70%	Cell suspension	***Chromium Next GEM Single Cell 3'***
		Chromium Next GEM Single Cell 5'
Number of cells* > 5 x 10^5		***Chromium Next GEM ATAC***
		Chromium Next GEM VDJ
	Cell suspension FFPE	***Chromium Fixed RNA profiling***
PacBio ND	Single cell cDNAs generated by 10X	***SMRTbell MAS-ISO Seq (10x 3' cDNA)***
Visium Spatial		
DV200 (%)* 50%	FFPE *(Human and Mouse)*	***10X CytAssist Spatial Gene Expression FFPE***

The recommended number of cells depends on the number of cells you aim to capture.

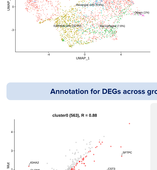
Platforms: Illumina NovoSeq 6000 | Illumina NovoSeq X | PacBio Revio

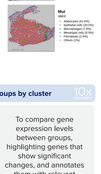
BIOINFORMATICS

Cell Type Classification

10x

To identify and categorize individual cells based on their gene expression profiles or other molecular characteristics.





Annotation for DEGs across groups by cluster

10x

To compare gene expression levels between groups, highlighting genes that show significant changes, and annotates them with relevant biological functions, pathways, or gene ontology terms.

More Services

Single Cell RNA Seq	Spatial Transcriptome Seq
Mapping GBM/PBM Generation Clustering (Cellranger count) V(D)J Assembly and profiling Cell population analysis Feature Linkage	Mapping Feature-Spot Matrices Clustering

Macrogen Europe's analysis is not limited to the services listed above. The other customized analysis are serviced upon the discussion.

THE HOUSE OF SEQUENCING — Humanizing Genomics macrogen EUROPE

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