Single-cell sequencing

- Kininogen enhances seizure susceptibility in mice possibly through bradykinin-induced modulation of calcium transients in glutamatergic and GABAergic neurons
- Lactate dehydrogenase B A Hypoxia and lactylation relative-gene as potential biomarkers for alcoholic liver disease: Integration of single-cell, bulk RNA-sequencing and experimental validation
- Interrogation of macrophage-related prognostic signatures reveals a potential immune-mediated therapy strategy by histone deacetylase inhibition in glioma
- Genetic profiling of synchronous pituitary corticotroph adenomas
- ITGA5 drives glioblastoma progression through SLK-mediated activation of the PI3K-Akt pathway
- Pro-repair macrophages driven by CGRP rescue white matter integrity following intracerebral hemorrhage
- Zileuton protects against arachidonic acid/5-lipoxygenase/leukotriene axis-mediated neuroinflammation in experimental traumatic brain injury
- Cholinergic neuron-to-glioblastoma synapses in a human iPSC-derived co-culture model

---

Single-cell sequencing technology is a powerful and rapidly advancing molecular biology technique that allows researchers to analyze the genetic and genomic information of individual cells. Unlike traditional bulk sequencing methods, which analyze a mixture of cells together, single-cell sequencing provides insights into the heterogeneity and diversity within a cell population. This technology has numerous applications in various fields, including genomics, cancer research, developmental biology, neuroscience, immunology, and more.

Key aspects

Cell Isolation: Before sequencing, individual cells need to be isolated. This can be achieved through various methods, such as flow cytometry, microfluidics, laser capture microdissection, or manual picking.

Library Preparation: After isolating single cells, researchers need to extract and amplify the genetic material, typically DNA or RNA. This is followed by library preparation, where the genetic material is converted into sequencing-ready libraries using specialized protocols.

Sequencing Platforms: Single-cell sequencing can be performed on various sequencing platforms, including next-generation sequencing (NGS) technologies like Illumina, 10x Genomics, or single-molecule sequencing platforms such as PacBio and Oxford Nanopore.

Data Analysis: The analysis of single-cell sequencing data is complex and typically involves several steps:

Quality control to filter out low-quality data.

Data normalization to correct for technical biases.

Clustering to group similar cells together.

Differential expression analysis to identify genes that are differentially expressed between cell clusters.

Trajectory analysis to infer cell development or differentiation paths.

Applications:

Cell Heterogeneity: Single-cell sequencing allows researchers to understand cellular heterogeneity within tissues and identify rare cell types or subpopulations.

Development and Differentiation: It is used to study how cells develop and differentiate into various cell types during embryogenesis or in tissue regeneration.

Cancer Research: It helps identify subclones within tumors, understand tumor evolution, and discover potential therapeutic targets.

Neuroscience: It aids in exploring the diversity of neuron types in the brain and studying neuronal development.

Immunology: Single-cell sequencing can be used to dissect immune cell populations and their responses to various stimuli.

Stem Cell Biology: It enables the characterization of pluripotent stem cells and their differentiation into specific lineages.

Challenges: Single-cell sequencing presents challenges such as high cost, technical variability, and the need for specialized bioinformatics tools to analyze the data effectively.

Overall, single-cell sequencing technology has revolutionized our understanding of cellular biology and has led to numerous breakthroughs in various scientific fields by providing a high-resolution view of individual cells' genomic and transcriptomic profiles.

Previous studies have traditionally attributed the initiation of cancer cells to genetic mutations, considering them as the fundamental drivers of carcinogenesis. However, recent research has shed light on the crucial role of epigenomic alterations in various cell types present within the tumor microenvironment, suggesting their potential contribution to tumor formation and progression. Despite these significant findings, the progress in understanding the epigenetic mechanisms regulating tumor heterogeneity has been impeded over the past few years due to the lack of appropriate technical tools and methodologies.

The emergence of single-cell sequencing has enhanced our understanding of the epigenetic mechanisms governing tumor heterogeneity by revealing the distinct epigenetic layers of individual cells (chromatin accessibility, DNA/RNA methylation, histone modifications, nucleosome localization) and the diverse omics (transcriptomics, genomics, multi-omics) at the single-cell level. These technologies provide us with new insights into the molecular basis of intratumoral heterogeneity and help uncover key molecular events and driving mechanisms in tumor development.

Hu et al. provide a comprehensive review of the emerging analytical and experimental approaches of single-cell sequencing in various omics, focusing specifically on epigenomics. These approaches have

the potential to capture and integrate multiple dimensions of individual cancer cells, thereby revealing tumor heterogeneity and epigenetic features. Additionally, this paper outlines the future trends of these technologies and their current technical limitations [1].

Single-cell RNA sequencing

Single-cell RNA sequencing

1)
Hu Y, Shen F, Yang X, Han T, Long Z, Wen J, Huang J, Shen J, Guo Q. Single-cell sequencing technology applied to epigenetics for the study of tumor heterogeneity. Clin Epigenetics. 2023 Oct 11;15(1):161. doi: 10.1186/s13148-023-01574-x. PMID: 37821906.