

Multiome insights, simplified: single-cell omics solutions for diverse sample types



Signios Bio's versatile single-cell solutions: advancing multiome analysis across diverse sample types

Traditional genomic research techniques often mask the inherent heterogeneity within complex biological systems by averaging data from millions of cells. This limitation hinders our understanding of cellular diversity and its implications for health and disease. Single-cell omics technologies have emerged as powerful tools, allowing researchers to dissect this complexity at an unprecedented resolution, analyzing the genome, transcriptome, proteome, and epigenome of individual cells.

Signios Bio is at the forefront of this revolution, offering a comprehensive suite of single-cell omics services designed to empower researchers with unparalleled insights into cellular function and heterogeneity. From sample preparation to data analysis, our expert team provides end-to-end solutions tailored to your specific research needs.

A seamless workflow for unbiased discoveries



Single-cell solutions available at Signios Bio

- Whole Transcriptome Gene Expression: Analyze the complete RNA profile of individual cells to identify novel cell types, understand cellular states and transitions, and decipher gene regulatory networks.
- Full-Length Paired TCR/BCR Sequencing: Characterize the adaptive immune repertoire by profiling paired T-cell receptors (TCRs) and B-cell receptors (BCRs) from single cells, enabling in-depth analysis of immune responses.
- Chromatin Accessibility (ATAC-seq): Investigate the accessibility of chromatin regions to regulatory proteins, providing insights into gene regulation and cellular identity.
- Cell Surface Protein Expression: Profile cell surface markers on individual cells, allowing for detailed immune phenotyping and identification of rare cell populations.
- **Multiome Sequencing:** Combine multiple omics layers, such as transcriptome and chromatin accessibility, from the same cell, providing a holistic view of cellular function.

Beyond data: insights that drive discovery

At Signios Bio, we believe in empowering our clients with more than just data. Our comprehensive bioinformatics pipelines provide actionable insights, enabling you to:

- **Uncover novel cell types and biomarkers:** Identify rare and previously unknown cell populations that play critical roles in health and disease.
- **Decipher cellular heterogeneity:** Understand the diverse functions and responses of individual cells within a population.
- **Track cellular trajectories:** Reconstruct developmental pathways and map cellular transitions during differentiation, disease progression, or treatment response
- Identify therapeutic targets: Pinpoint key genes and pathways involved in disease pathogenesis, leading to the development of novel therapeutic interventions.

Figure 2 below shows a typical specialized workflow for single-cell analysis. Our streamlined, automated analysis workflow includes deep data quality control (QC) checks that flags poor-quality data. Following this, we leverage published best-practices workflows to perform normalization, data correction, feature selection and dimensionality reduction. We perform cell- and gene-level analysis and deploy several independent analysis modules including: a) automatic and marker-based cell type annotation; b) differential gene expression analysis to identify cell-type specific, and sample specific markers; c) pathway enrichment analysis; and d) cell communication analysis on different cell types to understand how cells interact and communicate based on ligand-receptor interaction.

Figure 2. Schematics of our advanced single-cell analysis workflow.



Publication-ready figures and visualizations

At Signios Bio, we provide you with a comprehensive report which includes publication-ready tables, plots and detailed metrics to visualize and interpret the results. Our report and pipeline deliver deep insights for improved scientific outcomes by not only supplying final outputs, but also providing researchers with the raw data for further discovery using their own analysis tools.

Figure 3. Example data visualizations from our single-cell analysis report. (A) UMAP cell clustering by Seurat cluster. (B) UMAP cell clustering by annotated cell type. (C) Heat map expression of Seurat clusters. (D) Heatmap showing contribution of signals to cell groups in terms of outgoing or incoming signaling.



Signios Bio: your partner for single-cell biology

We provide you with collaboration-level support for single-cell projects – from experimental design consultation through to publication ready analysis and figures. Our extensive expertise on sample handling and deep bioinformatics analysis enable us to partner with you across:

- Single-cell 3' and 5' Gene Expression
- Single-cell Multiome: ATAC + Gene Expression
- CITE-seq: Cell Surface Protein Expression + Gene Expression
- Single-cell Immune Profiling: V(D)J expression for paired B-cell or T-cell receptors
- Visium Spatial Transcriptomics: Gene Expression analysis on sectioned tissue layer



The science of signals, the promise of cures

A MULTIOMICS RESEARCH PARTNER

Spatial transcriptomics | Single-cell | Epigenomics | WGS/WES



O Lab Location:

Signios Biosciences 348 Hatch Drive Foster City, CA 94404, USA info@signiosbio.com (888) 440-0954

Registered office & Headquarters:

Signios Biosciences 108 West 13th Street Wilmington Delaware 19801, Country of New Castle, USA