signios bio
powered by MEDGENOME

Signios Bio
bioinformatics services

Advancing omics research with comprehensive solutions and in-depth data analysis

As a leader in omics research, Signios Bio offers a comprehensive suite of bioinformatics services designed to help researchers uncover the full potential of their data. From project inception to publication, we partner closely with clients, providing not just data but deep scientific insights that are publication-ready and impactful.

Service offerings

Premade library sequencing

Ideal for clients who have already prepared libraries and need a reliable partner for high-quality sequencing.

Deliverables:

- Sequencing data in FASTQ format
- Quality control (QC) metrics and report
- Basic data summary report
- Option to add bioinformatics packages based on type of library

RNA sequencing (RNA-seq)

Uncover the complexity of the transcriptome with high-resolution gene expression profiling.

Deliverables:

Basic analysis	Standard analysis	Advanced analysis	Specialized analysis
• Data QC report • Raw data FASTQ file	• **All items in Basic Analysis +** • Alignment (BAM) file • Germline VCF • Germline variant annotation • Low frequency germline variant calling • Low frequency germline variant annotation	• **All items in Standard Analysis +** • Differential gene expression • Pathway analysis and gene ontology	• Create a custom package to fit your project • Custom analysis based on project requirements at an hourly rate • TME analysis • Fusion gene analysis

Whole genome sequencing (WGS)

Comprehensive analysis for detecting single nucleotide variants (SNVs), insertions, deletions, and structural variations across the entire genome.

Basic analysis	Standard analysis	Advanced analysis	Specialized analysis
• Data QC report • Raw data FASTQ file	• **All items in Basic Analysis +** • Alignment (BAM) file • Germline VCF • Germline variant annotation • Low frequency germline variant calling • Low frequency germline variant annotation	• **All items in Standard Analysis +** • Somatic mutation annotation • Low frequency somatic variant calling • Low frequency somatic variant annotation • Joint genotyping • Structural variant calling • Tumor/normal CNV calling • gVCF	• Create a custom package to fit your project • Custom analysis based on project requirements at an hourly rate

Whole exome sequencing (WES)

Targeted sequencing of protein-coding regions, offering a cost-effective approach for understanding coding variants linked to diseases.

Deliverables:

Basic analysis	Standard analysis	Advanced analysis	Specialized analysis
• Data QC report • Raw data FASTQ file	• **All items in Basic analysis +** • Alignment (BAM) file • Germline VCF • Germline variant annotation • Low frequency germline variant calling • Low frequency germline variant annotation	• **All items in Standard Analysis +** • Somatic mutation annotation • Low frequency somatic variant calling • Low frequency somatic variant annotation • Joint genotyping • Structural variant calling • Tumor/normal CNV calling • gVCF	• Create a custom package to fit your project • Custom analysis based on project requirements at an hourly rate

Immune profiling

Explore immune repertoire diversity and clonal expansions with specialized assays for immunology research.

Deliverables:

Basic analysis	Advanced analysis	Specialized analysis
• Data QC report • Raw data FASTQ file	• **All items in Basic analysis +** • Full-length clonotype sequences and their frequencies • Diversity scores for each sample • V & J gene usage • Phylogenetic analysis of clonotypes of interest	• Create a custom package to fit your project • Custom analysis based on project requirements at an hourly rate

Epigenetics analysis

Investigate regulatory elements, DNA methylation, histone modifications, and chromatin accessibility to understand gene regulation and epigenetic modifications.

Deliverables:

Basic analysis	Standard analysis	Advanced analysis	Specialized analysis
• Data QC report • Raw data FASTQ file	• **All items in Basic Analysis +** • Alignment (BAM) file • Bed files • Peak call files • Consensus peak calling • Hierarchical clustering analysis • Clustering, PCA, heatmap correlation	• **All items in Standard Analysis +** • Group comparison • Pathway analysis	• Create a custom package to fit your project • Custom analysis based on project requirements at an hourly rate

Cancer panel sequencing

Targeted panels for oncology research, designed to identify mutations, CNVs, and fusions relevant to cancer.

Deliverables:

TSO 500 DNA	TSO 500 DNA & RNA	TSO 500 ctDNA
• Data QC report • Raw data FASTQ file • Single nucleotide variants (SNVs) • Insertions & deletions (InDels) • Copy number variants (CNVs) • Multi-Nucleotide variants (MNVs) • Somatic variants • Structural variants • Tumor mutational burden (TMB) • Microsatellite instability (MSI)	• **All items in TSO 500 DNA +** • Gene fusions • Transcript variants • Novel transcripts • Loss of heterozygosity (LOH)	• Data QC report • Raw data FASTQ file • Single nucleotide variants (SNVs) • Insertions & deletions (InDels) • Copy number variants (CNVs)

Single-cell sequencing

Uncover cellular heterogeneity and rare cell populations with high-resolution single-cell RNA-seq and ATAC-seq.

Deliverables:

Basic analysis	Standard analysis	Advanced analysis	Specialized analysis
• Data QC report • Raw data FASTQ file	• **All items in Basic analysis +** • CellRanger outputs of sequencing QC metrics • CellRanger outputs of gene expression and heatmap visualization • CLOUPE file for use in LOUPE browser • Advanced QC via Seurat	• **All items in Standard Analysis +** • Advanced filtering of low-quality cells, contamination, multiplets etc. • Dimensionality reduction and clustering analysis on filtered data • Interactive t-SNE plot with cluster information • General cell type annotation • Differential gene expression analysis for clusters and annotated cell types • Pathway enrichment analysis • Group comparison	• Create a custom package to fit your project • Custom analysis based on project requirements at an hourly rate • Differential accessibility peak analysis for clusters and cell type in multiome projects • Differential protein analysis for clusters and cell type in CITE-seq projects

Spatial transcriptomics

Spatially resolve gene expression within tissue architecture, enabling deeper understanding of tissue heterogeneity.

Deliverables:

Basic analysis	Standard analysis	Advanced analysis	Specialized analysis
• Data QC report • Raw data FASTQ file	• **All items in Basic Analysis +** • SpaceRanger generated key sequencing and gene expression metrics • SpaceRanger generated tissue plot colored by cluster • SpaceRanger generated t-DNA projected spot clusters • CLOUPE file for use in LOUPE browser	• **All items in Standard Analysis +** • Advanced filtering of low-quality spots, rRNA, mitoRNA, and hemoglobin contamination • PCA and optimized clustering of high-quality spots • Spatial dimensional plots with filtered spots and heatmap of gene expression across clusters • Spatial localization of individual clusters • Cell type annotation from public databases and associated spatial plots by cell type	• Create a custom package to fit your project • Custom analysis based on project requirements at an hourly rate • Cell type annotation with custom markers and associated spatial plots by cell type • Interactome spatial visualization including number and strength of interactions

Long-read sequencing

Ideal for resolving complex genomic regions, structural variations, and isoform-specific expression analysis.

Deliverables:

Variant detection	*de novo* assembly	Isoform discovery
• Run folder with HiFi reads as aligned (BAM) file • VCF	• Run folder with HiFi reads as aligned (BAM) file • Report of assembly metrics • Transgene identification (if applicable) • FASTA file of primary contigs • FASTA file of haplotigs • Genome annotation (add on)	• Report containing summary metrics for primers, reads, transcripts, transcript classifications, and more • Full-length non-concatemer (FLNC) reads as BAM file • FASTQ files of both low and high-quality isoforms • Mapped high-quality isoforms as BAM file • Collapsed filtered isoforms as GFF
Metagenomics	**Targeted sequencing**	**Methylation (5mC) profiling**
Full-length 16S: • Run folder with HiFi reads • ASV classification at genus and species level **Shotgun Metagenomics:** • Run folder with HiFi reads • Genome-resolved taxonomic matches • LCA taxonomic profiles	**Pure-target, AAV, amplicon:** • Run folder with HiFi reads as aligned (BAM) file • Variant VCF files • All target plots • QC – Target Genotype Table	• Run folder with HiFi reads as aligned (BAM) file • 5mC CpG report • HiFi reads with 5mC calls in BAM format

Why partner with Signios Bio?

- **Scientific collaboration:** Our team of experienced bioinformaticians and scientists are more than just service providers; we become collaborators in your research. We offer deep data analysis and work closely with you to interpret results.
- **Data-driven insights:** We don't just provide data; we deliver insights. Our customized analysis and visualizations make it easier for you to extract meaningful conclusions and advance your research.
- **Publication-ready results:** All our deliverables are designed to be ready for publication, saving you time and ensuring you have high-quality figures and tables to support your research story.
- **Comprehensive support:** From experimental design to data interpretation, we provide end-to-end support tailored to your specific research needs.

With Signios Bio, researchers gain a trusted partner committed to unlocking the full potential of their omic data and achieving breakthroughs in scientific discovery. Let us help you make the leap from data generation to impactful, data-driven science.

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The science of signals, the promise of cures

A MULTIOMICS RESEARCH PARTNER

Transcriptomics I Spatial | Single-cell | Immune profiling | Epigenomics | WGS/WES

Contact

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