CD Genomics
The Genomics Services Company

Customized Bioinformatics Services: Empowering Your Research with Precision

In the era of rapid development in genomics and multi-omics data, standardized analysis tools often fail to meet the complex research needs—similar to a "master key" that can't open every unique scientific lock. Personalized bioinformatics analysis services are designed to overcome this challenge: we move away from one-size-fits-all workflows and tailor analysis strategies to your data type, core research questions, and research stage, maximizing the value of your data. By integrating experimental data with public database resources like TCGA and GEO, we help you precisely identify driver genes or biomarkers, construct multi-omics regulatory networks, and correlate molecular discoveries with clinical prognosis, thereby achieving three key goals: accelerating the process of data-to-mechanism analysis, enhancing the innovation and universality of research conclusions, and reducing trial-and-error costs. Whether it's overcoming publication bottlenecks, accelerating project applications, or advancing translational medicine research, we provide end-to-end, accompanying analysis with a "scientist's perspective" and "engineer's mindset," ensuring each data point becomes powerful evidence for your research story.

WHY PERFORM BIOINFORMATICS ANALYSIS?

In today's increasingly competitive research environment, bioinformatics analysis has emerged as a crucial tool for accelerating research progress, reducing costs, and enhancing the quality of outcomes. It achieves high-impact results solely through data screening and statistical analysis without the need for extensive experimental resources, thereby providing strong support for SCI publications, career evaluations, and degree applications. At the same time, bioinformatics analysis can integrate single-omics and multi-omics high-throughput sequencing data (see Figure 1) as well as resources from public databases such as TCGA and GEO to construct precise regulatory networks, uncover key driver genes and biomarkers, and guide research direction and experimental design from a big data perspective, effectively informing subsequent targeted validations. Moreover, by integrating public databases with clinical data, bioinformatics analysis can achieve precise cancer target prediction and pathway function screening, offering robust data support for clinical decision-making and translational research. Choosing bioinformatics analysis means opting for a data-driven future and seizing the forefront of research.

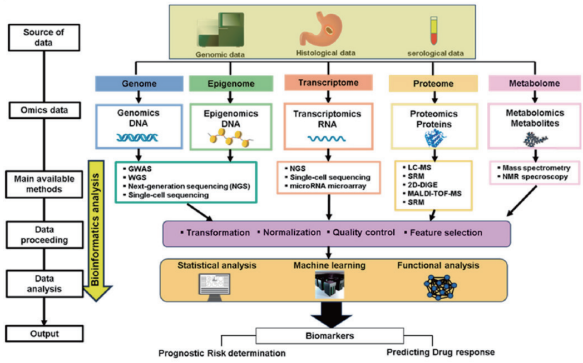


Figure1.Schematic diagram of validation of biomarker by the integration of bioinformatic analysis with multi-omics platforms. Different omics technologies analyze GC progression, from high-quality sample acquisition, data mining, and preprocessing to multidimensional data integration, ultimately identifying potential biomarkers. *Based on Matsuoka et al. (2024), Fig 1.*

The benefits of bioinformatics analysis include integrating multi-omics data and public databases to identify key biomarkers, predict therapeutic targets, and guide research, offering cost-effective, data-driven insights for clinical and translational applications.

Multi-omics Analysis Reveals IL-4 Regulation of CART Cell Exhaustion

CAR-T cell therapy has demonstrated remarkable efficacy in hematologic malignancies, yet its long-term effectiveness is limited by T cell exhaustion, characterized by dysfunctional proliferation, reduced effector cytokine production, and upregulated inhibitory receptors (e.g., PD-1, TIM-3). To elucidate the molecular mechanisms driving exhaustion, Stewart et al. 2024 employed a multi-omics approach combining CRISPR screening, RNA-seq, and ATAC-seq.

CRISPR-Cas9 genome-wide knockout screening in CAR-T19-28ζ cells identified IL-4 signaling as a critical regulator of exhaustion. **RNA-seq analysis** revealed significant upregulation of exhaustion-related genes (e.g., TOX, ENTPD1) and downregulation of effector cytokines (e.g., IL2, TNF) in IL-4-treated CD8+ CAR-T cells (FDR < 0.05, |log2FC| > 1). **ATAC-seq** further demonstrated IL-4-induced chromatin remodeling at exhaustion-associated loci (e.g., PDCD1 enhancers), corroborated in non-responders from the ZUMA-1 trial (Figure 2).

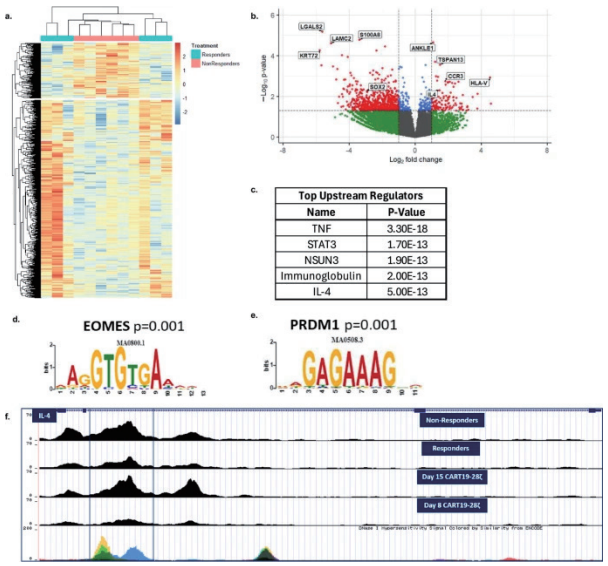


Figure 2. Transcriptomic and chromatin accessibility interrogation of pre-infusion axi-cel products. From responders and non-responders in the ZUMA-1 clinical trial identifies IL-4 as a regulator of response. *Based on Stewart et al. (2024), Fig 4.*

Whole genome sequencing and annotation of *Pseudomonas Phages*

Phage genome characterization relies on **whole genome sequencing** and annotation to determine evolutionary relationships and novel genomic features. In Kovacs et al. 2024, high-accuracy sequencing and Mummer v4.0 analysis revealed genome-wide similarity patterns,including a distinct duplicated region (Figure 3). BLASTn classification identified PaWP2 as closely related to Pseudomonas phage Chuck (98.19% identity), while PaWP1 met ICTV criteria for a novel phage (<95% similarity). Further Pharokka annotation confirmed all three phages as linear dsDNA viruses with head–tail morphology, classified under Caudoviricetes, highlighting the power of comprehensive sequencing in phage discovery.

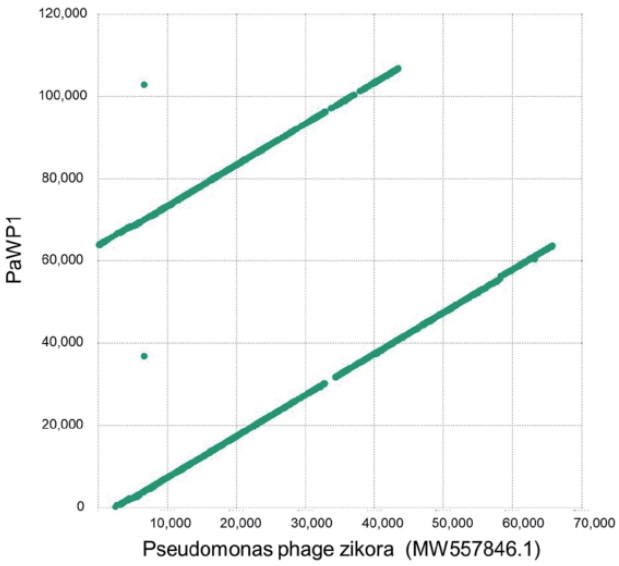


Figure3.Whole genome dot plot comparison of Pseudomonas phage zikora and PaWP1. Dot plot of Pseudomonas phage Zikora (x-axis, 65,837 bp) and PaWP1 (y-axis, 106,862 bp) genomes generated using Mummer in Galaxy. Nucleotide positions along each genome indicate synteny and structural variations.*Based on Kovacs et al. (2024), Fig S2.*

Mitochondrial genome sequencing and assembly

Mitochondrial genome characterization requires high-accuracy sequencing and assembly to generate complete mitogenomes and analyze genetic variation.In Omar et al. 2025, total genomic DNA was extracted using the DNeasy tissue kit, followed by short-insert library preparation and sequencing on an Illumina NovaSeq 6000 platform. Quality filtering with Trimmomatic ensured high-confidence reads for assembly. MitoZ identified mitochondrial contigs, which were aligned against the NCBI mitogenome database for validation. Genome circularity was confirmed using MUMmer, and final visualization in Geneious provided a comprehensive mitogenome map (Figure 4), demonstrating the effectiveness of advanced sequencing in mitochondrial genome analysis.

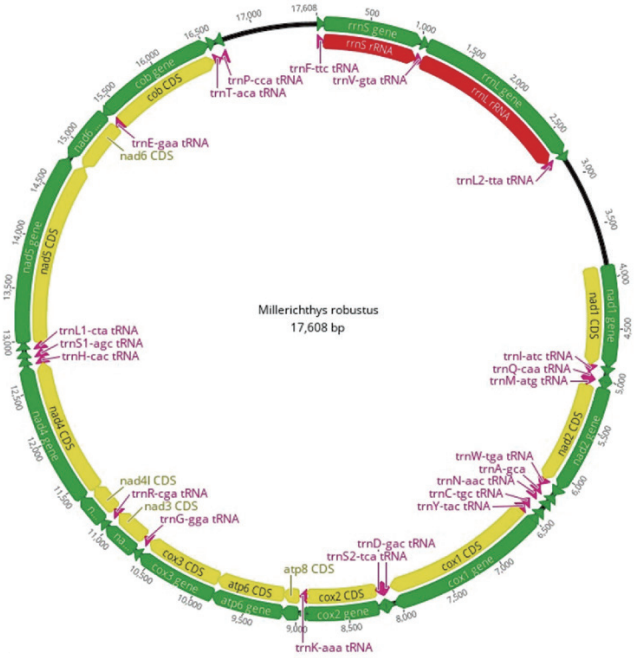


Figure4.The mitochondrial genome of Millerichthys robustus, visualized with Geneious v.2022.2 (Biomaters). *Based on Omar et al.(2025), Fig 1.*

Mouse RNA-seq Analysis for Gene Expression Profiling

RNA-seq analysis offers powerful insights into gene expression and regulation. In Sze et al 2023, total RNA was extracted from mouse skin tissues and analyzed. After rRNA depletion and library preparation, high-quality paired-end reads were generated on the NovaSeq 6000 platform. The reads were aligned to the GRCm39 reference genome for accurate quantification. Differentially expressed genes (DEGs) were identified using DESeq2, with a significance threshold of $|\log2FC| > 0.5$ and $p < 0.01$. Further annotation through eggNOG, COG, Pfam, Swiss-Prot, and KEGG databases, along with GO enrichment and KEGG pathway analysis, enabled a comprehensive understanding of the biological processes involved, highlighting the utility of RNA-seq for gene expression analysis (Figure 5).

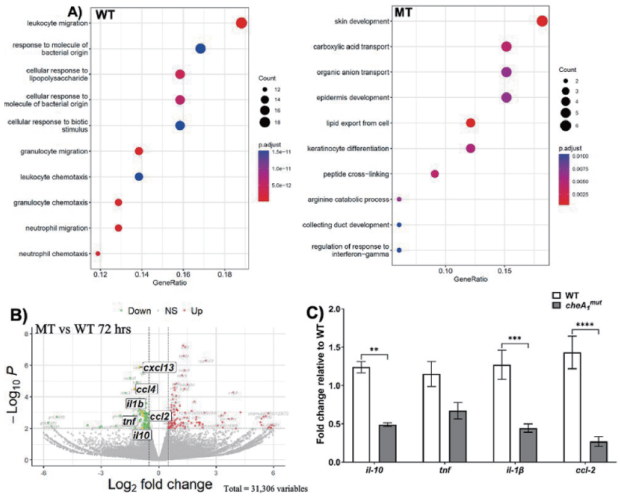


Figure5.RNA-seq analysis of BALB/c mouse skin tissues infected by WT and cheA1^{mut}. (A) Scatter plot of enriched KEGG pathways for DEGs between Sham and infected samples.(B) Volcano plot of DEGs between MT (cheA1 mut) and WT at 72hr p.i.(C) qRT-PCR analysis of il-10, tnf, il-1β, and ccl-2 in WT and cheA1 mut samples. *Based on Sze et al.(2023), Fig 11.*

In Kakiyama et al 2024, The high-quality RNA was processed and sequenced using the Illumina HiSeq 50 platform at CD Genomics. After filtering raw reads through a series of quality control steps, clean reads were mapped to the reference genome using HISAT2. Differential gene expression analysis was carried out with DESeq2, setting fold change ≥2 and FDR <0.05 as thresholds. The results revealed significant alterations in gene expression related to lipid metabolism in the livers of WT and StarD5-/- mice. A heatmap of these differentially expressed genes was generated, further emphasizing the role of RNA-Seq and advanced bioinformatics in uncovering molecular insights in biomedical research (Figure 6).

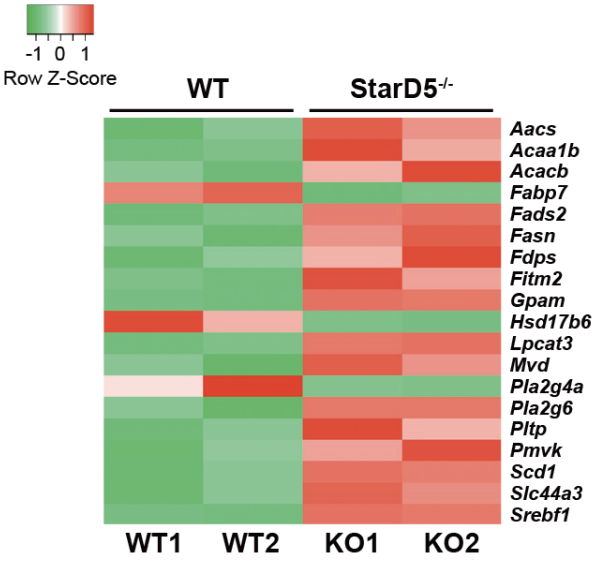


Figure6.heatmap of differentially expressed genes in lipid metabolism in the livers of WT and StarD5-/- mice. *Based on Kakiyama et al.(2024), Fig 1(E).*

Reduced representation bisulfite sequencing (RRBS) analysis

Reduced representation bisulfite sequencing (RRBS) enables in-depth analysis of DNA methylation patterns across specific genomic regions. In this study, high-accuracy sequencing and Trim Galore data processing revealed a detailed methylation landscape after bisulfite conversion. Raw sequencing data were filtered for quality, ensuring high-confidence results, and FastQC analysis provided essential quality statistics. Methylation sites were mapped to the reference genome to identify differential methylation patterns. This approach highlighted key epigenetic markers, emphasizing the role of RRBS in understanding DNA methylation regulation and its applications in gene expression and disease research.

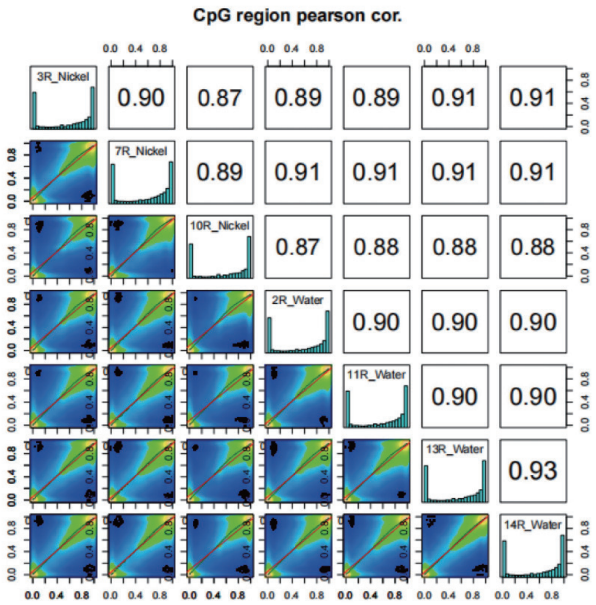
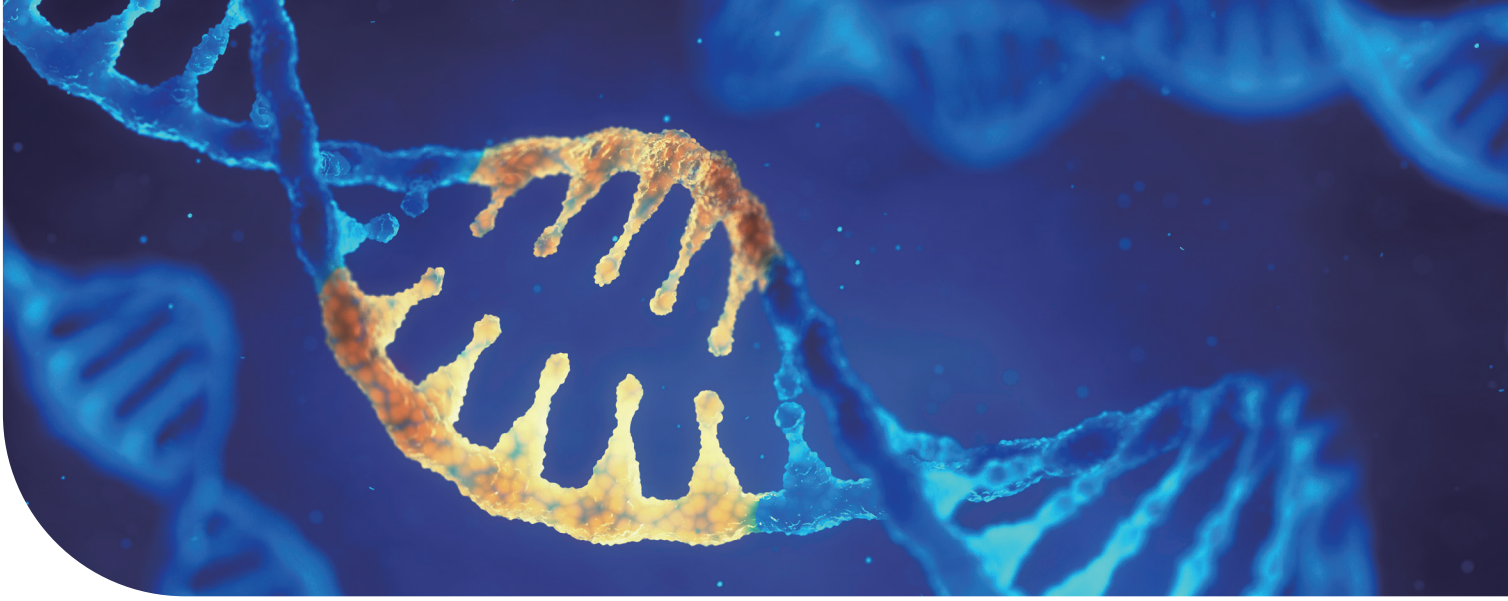


Figure7.Sample correlation analysis (nickel nitrate vs. water). The figure illustrates the Pearson correlation coefficients of CpG regions under different treatment conditions. It includes multiple samples treated with nickel nitrate and water, with the Pearson correlation coefficients displayed numerically above the corresponding scatter plots. The scatter plots depict the distribution of data points within each sample, with colors ranging from blue to yellow indicating the density of data points, where the yellow areas represent higher data point density. *Based on Nkongolo et al.(2024), Fig 4.*



WHY CHOOSE US

• Professional Technical Team

We have a highly skilled team of experts covering multiple fields, including oncology, epidemiology, statistics, and computer science. Our team members participate in various research projects and possess extensive experience in clinical research, bioinformatics analysis, and fundamental research, providing professional support from multiple perspectives.

• Comprehensive Sequencing and Analysis Services

We offer not only high-quality sequencing services but also in-depth bioinformatics analysis. Our services include single-omics and multi-omics high-throughput data analysis, advanced analysis based on public databases, and customized analysis solutions. We cover nearly all bioinformatics analysis needs, delivering precise and professional data interpretation for researchers.

• Comprehensive Research Support

While adhering to academic integrity, we provide end-to-end support, from data analysis to scientific writing, including manuscript writing guidance, journal submission recommendations, and assistance in responding to peer review comments. Additionally, we offer systematic research training to help researchers master the essential skills for SCI paper publication, accelerating the translation of research findings.

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