Innomics

Empowering Research with High-Quality Multi-Omics

Innovation Omics

VERSION: 202410

CONTENTS

About Innomics

Innomics Inc. boasts nearly two decades of profound expertise in Multi-Omics (Genomics, Transcriptomics, Spatial Omics, Epigenomics, Proteomics and Metabolomics), offering end-to-end next-generation sequencing (NGS) and Mass Spectrometry (MS) solutions to researchers and healthcare professionals. Through the utilization of advanced technologies, a steadfast commitment to continuous innovation, spanning almost 20 years, of delivering exceptional US local lab services, Innomics ensures cost-effective, high-quality solutions. Our aim is to assist clients in swiftly and effectively achieving their research objectives.

1. Vision:

Driving Innovation in Multi-Omics

2. Mission:

Empowering Research with High-Quality Multi-Omics

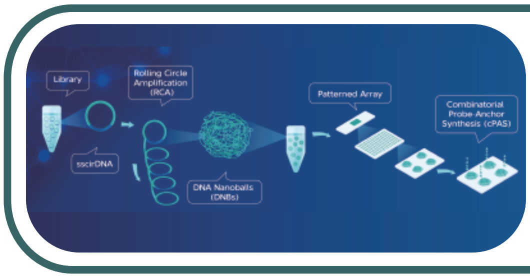
3. Core Values:

Quality | Security | Affordability | Professionalism

Innomics History and Highlights

2010

Innomics Inc. was founded in Cambridge, Massachusetts, to provide comprehensive next-generation sequencing (NGS) services in the US.



2017

Innomics introduced a $600 **Whole Genome Sequencing (WGS)** service to the US market, utilizing its first **DNBSEQ™** platform.

2018

Innomics established a **Mass Spectrometry (MS) Services Lab** in San Jose, California, to expand its expertise in Multi-Omics.

2023

Innomics launched Spatial Transcriptomics sequencing technology, **Stereo-seq**, to empower research customers.

2024

Innomics MS lab relocated to Sunnyvale, California, to better accommodate growth and enhance services.

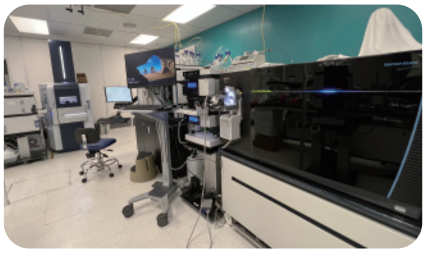
📍 Innomics US Main Office (Cambridge, Massachusetts)

📍 Innomics Local Services Lab (Sunnyvale, California)

Innomics Lab, based in Sunnyvale, California

Aims to provide high-quality Multi-Omics services while ensuring efficient and cost-effective workflow

Multi-Omics Analysis Platform	Integrated NGS & MS Omics Solution
DNBSEQ™ Service Provider	Comprehensive & Validated Portfolio
Premium Local Lab Services	Leading Experts & Rapid Turnaround



Research Areas

- Cancer Research
- Genetic and Rare Disease
- Human Microbiome
- Environmental Science
- Immunology Research
- Agriculture Science
- Drug Discovery
- Food Science

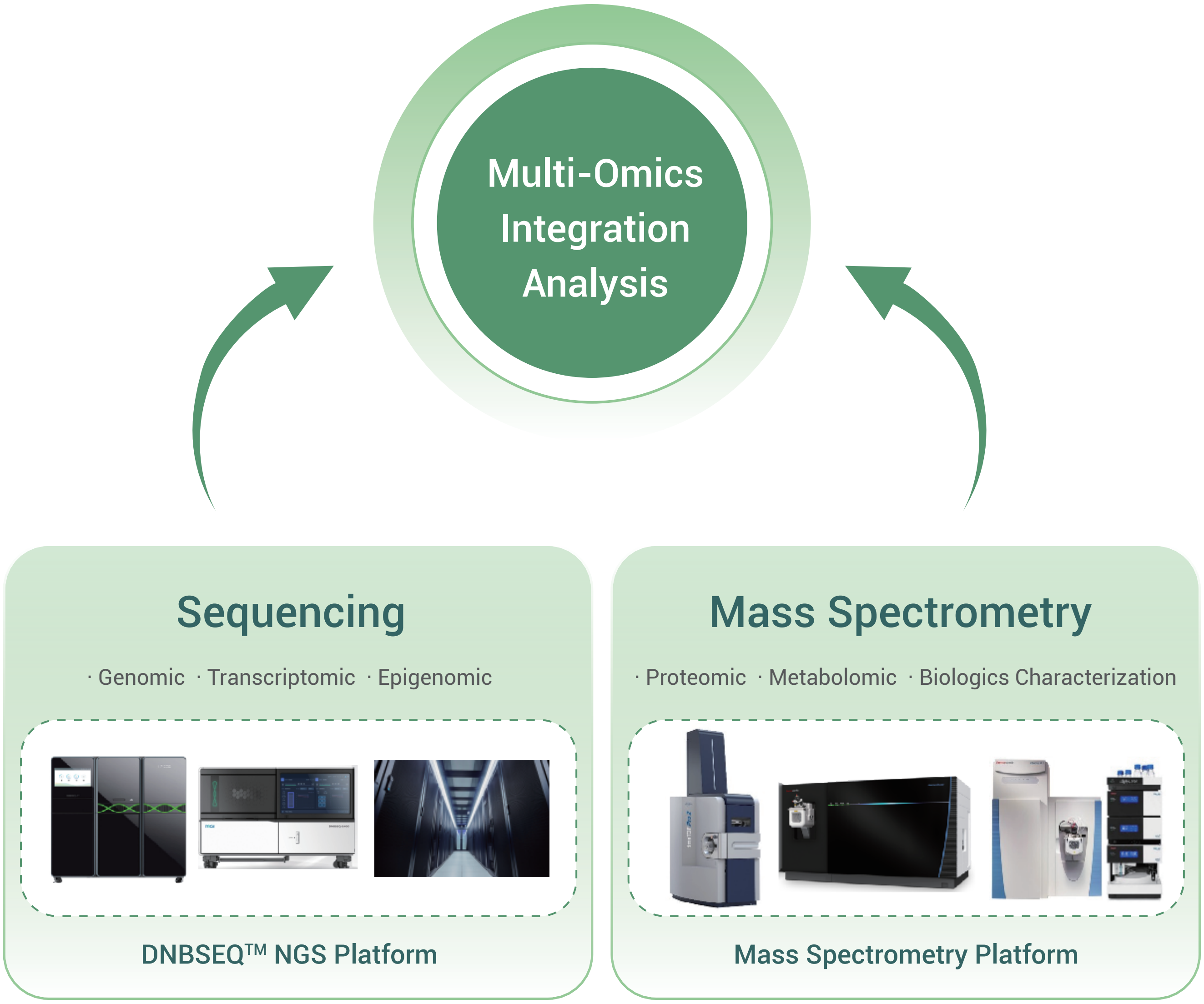
Delivering Excellence

- Quality Data
- Rapid Turnaround
- Competitive Pricing
- Custom Solutions

Innomics Multi-Omics Technologies

Multi-Omics is the integrative biological analysis of different data sets from single omics areas for new insight. An integrated Multi-Omics approach to research enables a more comprehensive understanding of genotypic, phenotypic and environmental relationships and their association to disease and health of an organism.

Innomics offers Multi-Omics services to look across Genomics, Transcriptomics, Spatial Omics, Epigenomics, Proteomics and Metabolomics, with the flexibility to customize solutions that meet your specific needs.



Multi-Omics Integration Analysis

Sequencing

· Genomic · Transcriptomic · Epigenomic

DNBSEQ™ NGS Platform

Mass Spectrometry

· Proteomic · Metabolomic · Biologics Characterization

Mass Spectrometry Platform

Overview of Innomics Premium Multi-Omics Technologies

List of Innomics Sequencing Services

Human Whole Genome Sequencing

· Experience of processing more than 1,000,000 samples
· Superior SNP/InDel Detection
· 10 working days rapid service available
· gDNA input as low as 50 ng

Whole Exome Sequencing

· Experience of processing more than 100,000 samples
· 10 working days rapid service available
· FFPE, low input DNA, saliva samples accepted

Plant & Animal Whole Genome Re-Sequencing

· Even coverage of reads and lower GC content bias
· Experience sequencing over 150 different species
· Higher data utilization

De Novo Sequencing

· Multiple Platforms: DNBSEQ™, PacBio Revio/Sequel II
· Hi-C technology: Auxiliary Assembly
· T2T genome assembling accepted
· Assembled more than 250 species so far and published 200 species in top tier journals
· Professional, highly experienced team to help with project evaluation

Metagenomic Sequencing

· Exploring microbial diversity and functional genomics free of pure culture
· Experience of processing 100,000 samples from a variety of environments
· Experience of mGWAS associated with chronic disease

Whole Genome Bisulfite Sequencing

· Even coverage of reads and reliable methylation profiling
· Lower duplication and higher data-use efficiency
· Accurate localization of methylation sites at single-base resolution

Spatial Transcriptomics

· Single cell resolution
· Centimeter-level field of view
· Compatible with multiple species and sample types

Transcriptome Sequencing

· Multiple Platforms:
DNBSEQ™, PacBio Revio/Sequel ll
· Multiple protocols to fulfill different sample types
· Experience of processing more than 120,000 samples
· Total RNA input as low as 200 pg

Small RNA Sequencing

· Precise quantification by UMI technology
· Experience of processing more than 60,000 samples
· Total RNA input as low as 5 ng, exosome RNA also included

Single Cell Sequencing

· Abondance single cell service experience
· Various sample types handling experience
· Multi-platform's services available
· Both low and high throughput

Premade Library Sequencing

· 10 working days rapid service available
· Compatible with most library construction kits on the market
· FASTQ files are delivered and suitable for most bioinformatics analysis processes

Proteomics and Metabolomics

· A rich variety of mass spectrometers to satisfy different needs
· Providing gene-expression validating correlation analysis
· More than 10 years of MS experience in the fields of medical, agricultural and microbial research

List of Innomics Mass Spectrometry Services

Proteomics

Service Name		Application
Untargeted Quantitative Proteomics	Isobaric Labeling TMT Quantitative Proteomics	Investigating changes in protein expression. Simultaneous testing in 2-18 samples at once.
	Label-Free Data-Independent Acquisition (DIA) Quantitation	Investigating changes in protein expression. Suitable for large cohort studies.
Post-Translational Modification (PTM) Proteomics	Protein Phosphorylation Analysis	Identification and quantitation analysis of various protein modifications in the proteome, screening for potentially phenotype-altering modified proteins.
Protein Identification and Profiling	Gel Spot Identification Gel Band Identification Proteome Profiling Analysis	Protein Identification in various types of samples.

Biologics Characterization

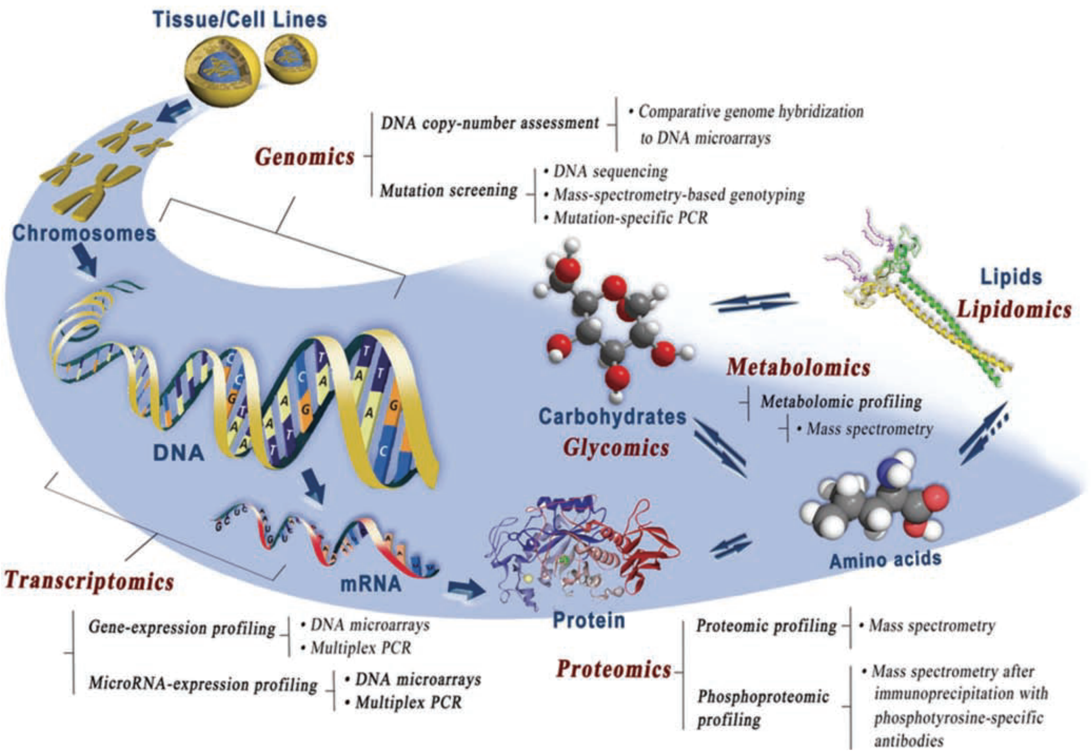
Service Name		Application
Biologics Characterization	Intact Mass	Determine the whole intact mass of the recombinant protein or biological sample.
	Native Mass	
	Peptide Mapping	Characterize and monitor the molecular details of a therapeutic protein drug at each position in the amino acid sequence.

Metabolomics

Service Name		Application
Untargeted Metabolomics	Untargeted Metabolomics	Relative quantification. Comprehensive profiling of metabolites. Exploratory research, wide search for key metabolites.
Lipidomics	Quantitative Lipidomics	Absolute quantification of over 4,000 lipids in 51 lipid subclasses.
	Quantitative Lipidomics for Plants	Semi-quantitative analysis of approximately 1,700 lipids using internal standards.
High-throughput Targeted Metabolomics	HM Pro2300	Absolute quantification of over 2,000 metabolites, including 700 small molecules and 1,600+ lipids, covering various important metabolites and core metabolic pathways.
	HM700	Absolute quantification of 700 small molecules, including 400+ metabolites related to gut microbiota.
	HML1600	Absolute quantification of over 1,600 lipids in 12 lipid subclasses.
Targeted Metabolomics	Anthocyanin, Phytohormone, Carotenoids, Energy Metabolism, Bile Acid, Tryptophan Metabolism, Amino Acid etc.	Absolute quantification of target metabolites. Validation of untargeted metabolomics and lipidomics results.
Widely-targeted Metabolomics	Widely-targeted Plant Metabolomics	Relative quantification of a large number of target metabolites.
	TM Widely-Targeted Metabolomics	

List of Multi-Omics Correlation Analysis Services

Service Name	Application
Proteomics + Transcriptomics Correlation Analysis	Gain a panoramic view of gene expression by studying its multi-level regulation.
Quantitative Proteomics + Phosphoproteomics Correlation Analysis	Analyze biological response mechanisms from multiple dimensions and draw a panoramic view of protein expression.
Metabolomics + Metagenomics/16S Correlation Analysis	Comprehensive analysis of the interaction mechanism among microorganisms, metabolites, and hosts.
Metabolomics + Transcriptomics/Proteomics Correlation Analysis	Comprehensive analysis of biological expression regulation, investigating the mechanism from cause to effect in two dimensions.
Metabolome + Genome Re-sequencing Correlation Analysis	Comprehensive analysis of genotypic, phenotypic, and environmental relationships and their association to disease and health of an organism.



Schema of omics technologies, their corresponding analysis targets, and assessment methods. DNA (genomics) is first transcribed to mRNA (transcriptomics) and translated into protein (proteomics) which can catalyze reactions that act on and give rise to metabolites (metabolomics), glycoproteins and carbohydrates (glycomics), and various lipids (lipidomics). The assessment methods for genomics include DNA copy-number assessment with comparative genome hybridization to DNA microarrays, together with mutation screening with DNA sequencing, mass-spectrometry-based genotyping, and mutation-specific PCR. The assessment methods for transcriptomics include gene-expression profiling with DNA microarrays and multiplex PCR, together with microRNA-expression profiling with DNA microarrays and multiplex PCR. The assessment methods for proteomics include proteomic profiling with mass spectrometry, together with phosphoproteomic profiling with mass spectrometry after immunoprecipitation with phosphotyrosine-specific antibodies. The assessment method for metabolomics includes metabolomic profiling with mass spectrometry (based on Sawyers, 2008)

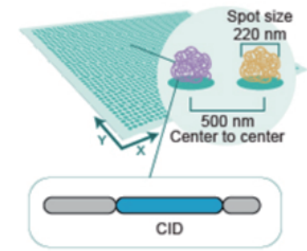
Innomics Spatial Transcriptome Service — Stereo-Seq

Built on DNA Nanoball (DNB) technology, Innomics' proprietary Stereo-Seq technology offers researchers a novel tool to explore spatial biology with unprecedented field-of-view and resolution.

- Engaged in nanoball technology for over 10 years.
- Enables spatial transcriptome studies and analyses at tissue, cellular, subcellular, and molecular levels using fresh or frozen tissues.
- Offers spatial transcriptomics, spatial proteomics, and spatial metabolomics from a single sample.
- Provides centimeter-level panoramic field-of-view, with customized chips up to 13 cm × 13 cm, suitable for various tissue types.
- Independently Developed Customized Interactive Bioinformatics Tools.

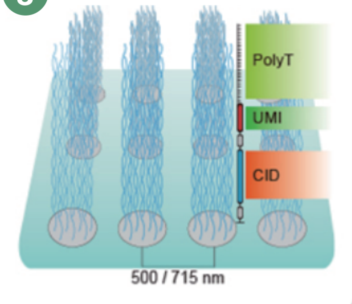
Project Workflow

1 DNB pattemed chip

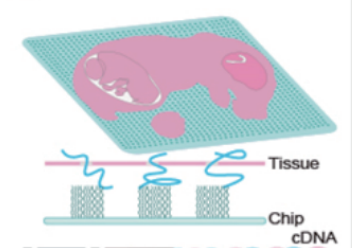


2 CID sequencing

3 Stereo-seq chip

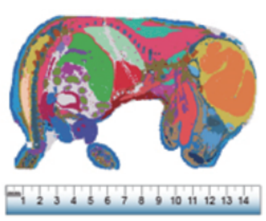


4 *In situ* RNA capture



5 Library construction & sequencing

6 Spatially resolved transcriptomic profiling



Stereo-seq Transcriptomics enables a "tissue-to-data" solution through the spatial barcode (Coordinate ID, CID) with centimeter-scale panoramic field of view and a maximum field of view of 13 cm x 13 cm, enabling the rendering of a panoramic molecular cell map of organs and life.

Innomics Dr. Tom Data Visualization Solution

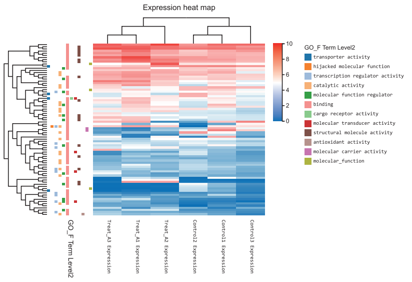
Innovation Omics

Innomics Dr. Tom's Multi-Omics Data Mining System is designed for researchers who need powerful, yet user-friendly bioinformatics tools. whether you're new to bioinformatics, short on time, or looking to delve deeper into your data, Dr. Tom is here to help.

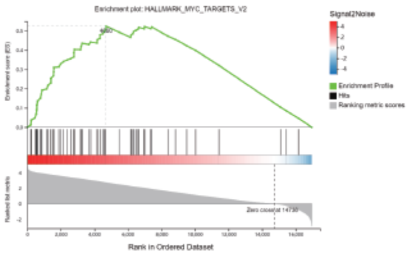
Dr. Tom Offers

- Interactive data visualization tools for intuitive analysis.
- Seamless integration from data tables to visual figures with just one click.
- Comprehensive Multi-Omics database support, including mRNA, lncRNA, small RNA, and protein.
- Customized data analysis capabilities right from your gene expression data.
- Trusted by thousands of researchers worldwide and cited in over 300 publications.

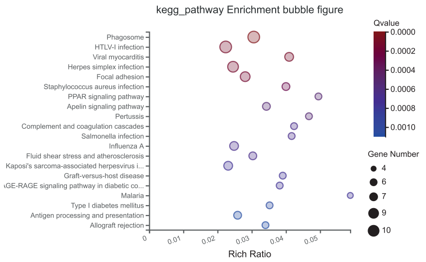
Core Capabilities



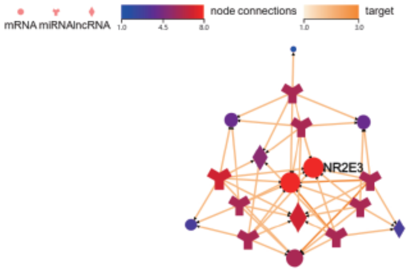
Expression Analysis



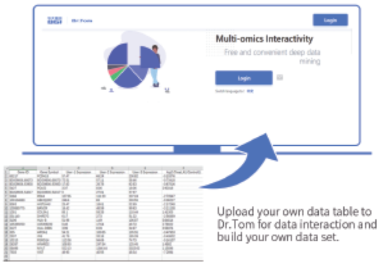
GSEA analysis



Enrichment Analysis



Association Analysis



Upload your own data table to Dr.Tom for data interaction and build your own data set.

Custom Datasets Uploading

To get an account for your in-depth RNA-Seq data interpretation, please click and register at:
https://biosys.innomics.com

If you have any questions or would like to discuss how our services can help you with your research, please don't hesitate to contact us at P_contact@innomics.com. We look forward to hearing from you!

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