Arima Multi-Omics

Flexible, end-to-end multi-omics services for Hi-C, RNA-Seq, ATAC-Seq - coupled with appropriate Illumina or PacBio sequencing

Combine Hi-C, RNA-seq, and ATAC-seq for a Complete Regulatory Picture

Gene expression data alone reveals what is changing in your biology, but not why. By integrating Arima Hi-C – which enables chromosome-scale genome assembly and maps 3D chromatin architecture – with RNA-Seq for gene expression profiling and ATAC-Seq for chromatin accessibility, you gain a complete view of gene regulation. Whether you need one assay or all three (sequenced on either Illumina or PacBio platform), Arima's flexible multi-omics services delivers structure, mechanism, and function from a single trusted partner.

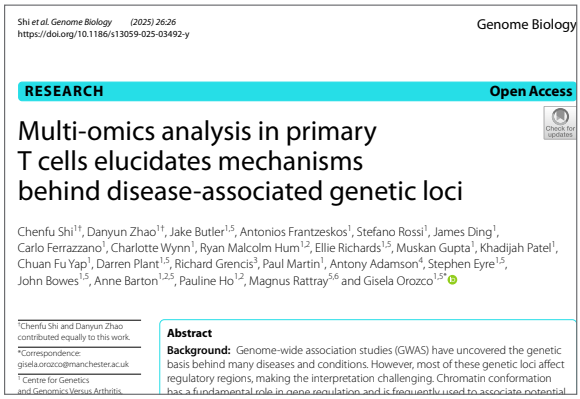
Benefits

One partner, complete data – integrate 3D genome structure, chromatin accessibility, and gene expression without coordinating across multiple providers

Flexible sample compatibility – work with fresh frozen tissue, cell pellets, FFPE, and low-input samples across mammalian, plant, and other organisms

Built-in quality assurance – integrated QC checkpoints at every stage deliver reliable, reproducible, publication-quality results

End-to-end support – from multi-omics library prep through sequencing and bioinformatics, all from a single team



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Genome Biology

RESEARCH Open Access

Multi-omics analysis in primary T cells elucidates mechanisms behind disease-associated genetic loci

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1 Centre for Genetics and Genomics Versus Arthritis

Abstract

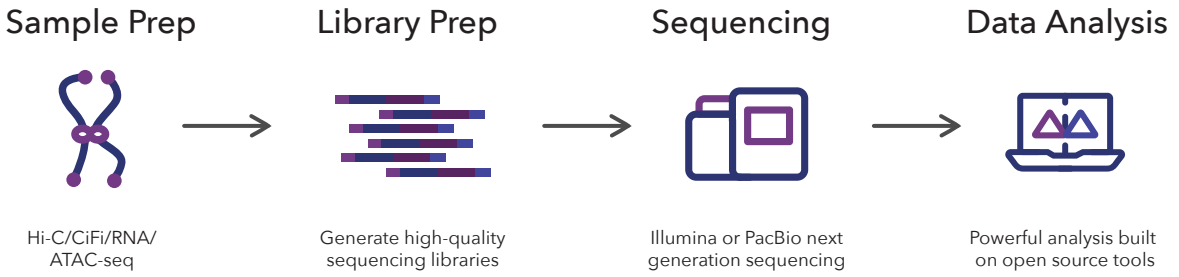
Background: Genome-wide association studies (GWAS) have uncovered the genetic basis behind many diseases and conditions. However, most of these genetic loci affect regulatory regions, making the interpretation challenging. Chromatin conformation has a fundamental role in gene regulation and is frequently used to associate potential

Shi, C., Zhao, D., Butler, J. et al. Multi-omics analysis in primary T cells elucidates mechanisms behind disease-associated genetic loci. Genome Biol 26, 26 (2025).

Multi-Omics and 3D Genomics Decode Arthritis Disease Mechanisms

Researchers at the University of Manchester combined Hi-C, RNA-Seq, and ATAC-Seq data from primary T cells isolated from psoriatic arthritis patients to decode how disease-associated genetic variants influence gene regulation. By integrating 3D chromatin architecture (Hi-C), gene expression (RNA-Seq), and chromatin accessibility (ATAC-Seq), the team identified specific enhancer-gene connections and TAD boundary disruptions that explain how distant non-coding variants drive autoimmune disease risk.

Workflow



Product List

Product	Description	Size	SKU
Arima Hi-C Service	Sample processing through library preparation	Per sample	A201010
Arima ATAC-Seq Service	Sample processing through library preparation (15 Gb/sample)	Per sample	A201097
RNA Sequencing (Poly-A)	Standard RNA-seq with PolyA selection (30M reads/sample)	Per sample	A201096
RNA-Seq Analysis	QC report and FASTQ files	Project based	A201101
ATAC-Seq Analysis	QC report and BAM files	Project based	A201102
Multi-Omic Data Analysis	QC report and FASTQ/BAM files as appropriate	Project based	A201104
PacBio Sequencing	DNA extraction, library preparation and PacBio sequencing	Project based	A201095

Specifications

Category	Specification (minimum)	
Sample Input	• Fresh frozen tissue: 50 mg • Whole blood: 1mL • Plant tissue: 2.5g	• Cells: >1 million cells • FFPE – 4 slides • Cell Pellet (RNA-seq) >1x10^4 cells
Sequencing Requirements	• Illumina or PacBio Sequencing • Coverage varies based on # of samples pooled, genome size and application	
Analysis Pipeline	• Primary data: FASTQ or BAM file • Downstream analysis: Varies by application	

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