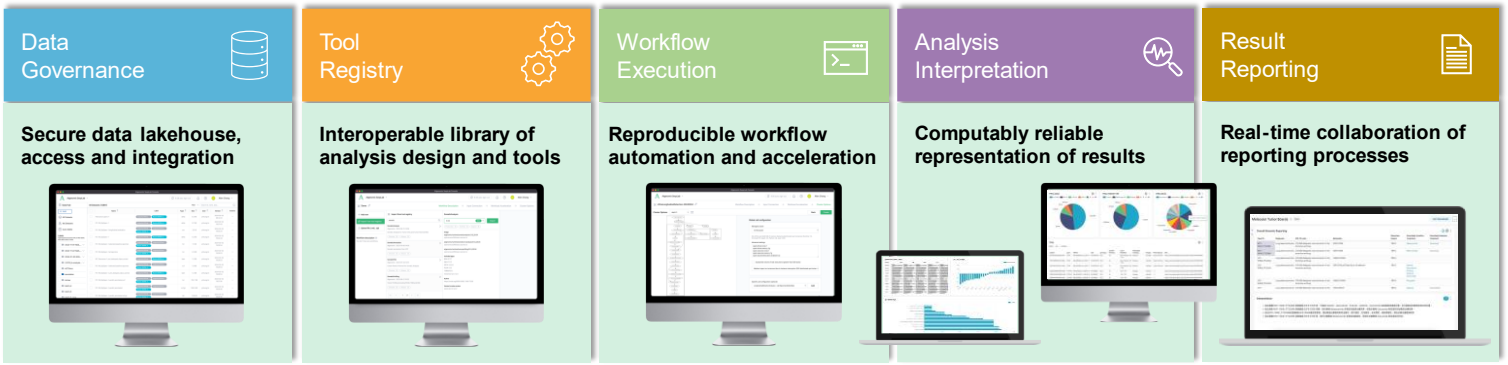
ATGENOMIX

Data and AI-driven Precision Medicine

Secure cloud-based data management and analysis workflow of genomic medicine

Atgenomix SeqsLab Platform governs the large volume of rapidly growing genomics and omics data from different layers of biological regulation and automates the diverse execution of commercially-available, open-source, and proprietary analysis workflows from sequencing to reporting at scale and speed.



Audited quality

Comply with the most relevant frameworks and rigorous compliance standards in the healthcare industry: ISO/IEC 27001, ISO/IEC 27018, ISO 13485, IEC 62304, FDA/MDCG cybersecurity guidance, FDA 21 CFR Part 11 audit trail, GA4GH, GDPR, and more.

Faster turnaround

Automate end-to-end workflows on all data with fully-managed cloud-native CPU/GPU parallel computing infrastructure, automatically scaling compute resources based on workload requirements to achieve operational efficiency.

Customizable analysis

Build scalable and reproducible workflows for a wide range of analyses by combining WDL (Workflow Description Language), SQL (Structured Query Language), AI/ML, and GraphQL (Graph Query Language) into a unified workflow.

Smarter usage

Optimize distributed workflow scheduling by partitioning datasets intelligently and leveraging in-memory processing capabilities to make efficient use of spot compute resources and to reduce the need for manual intervention.

Ready for routine clinical genomics

- Whole genome sequencing
- Whole exome sequencing
- Tumor-only and tumor-normal somatic analysis
- Longitudinal circulating tumor DNA profiling
- RNAseq, single-cell RNA analysis
- Multi-trait whole genome regression test
- SNP array analysis

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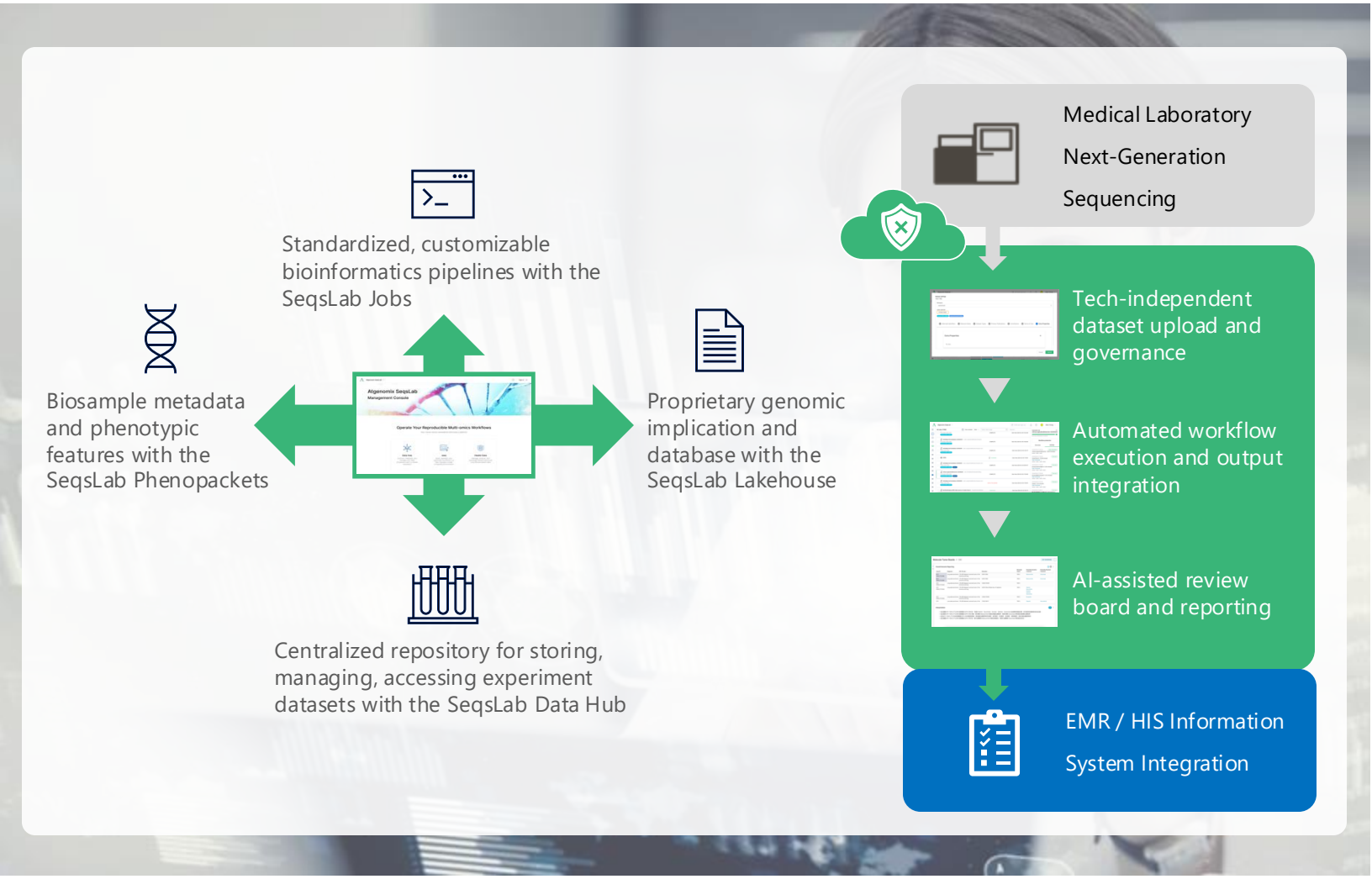
Integrating Atgenomix SeqsLab in your routine clinical genomics



Exceptional Workflow Scalability

Cluster computes

WORKFLOW AUTOMATION EXECUTION METHOD APPLIED IN **CLOUD-NATIVE BIOMEDICAL INFORMATICS** PLATFORM

FAIR data & tools

WORKFLOW AUTOMATION AND **DECENTRALIZED NAMING METHOD** WITH RUN SHEET FOR SEQUENCING EXPERIMENTS

Dataflow of Inputs & Outputs

OPTIMIZATION OF A CLUSTER COMPUTING NETWORK FOR SEQUENCING DATA ANALYSIS USING **ADAPTIVE DATA PARALLELIZATION**

Task Commands

AUTOMATING **MULTIMODAL** COMPUTATIONAL WORKFLOWS

Workflow	Before	Increased throughput performance	Reduced compute cost [4]	Result consistency
Whole genome sequencing secondary and tertiary analysis [1]	> 25 hours	+10X (2.8 hours)	70%	99.9%
Joint genotyping of whole genome for 2,500 samples [2]	> 1 month	+16X (40 hours)	60%	100%
Whole genome regression of 10 traits for 100,000 samples [3]	> 90 hours	+20X (4.5 hours)	90%	100%

(1). Broad institute BWA-MEM/GATK4 best practice, including QC.
(2). Broad institute GATK v4.2 workflow.
(3). Regenie pipeline developed by Regeneron Genetics Center.
(4). The cost for the community workflows is based on the cost of running the workflows in a typical 64-core, 512GiB RAM Linux virtual machine (Azure E64d_v5).

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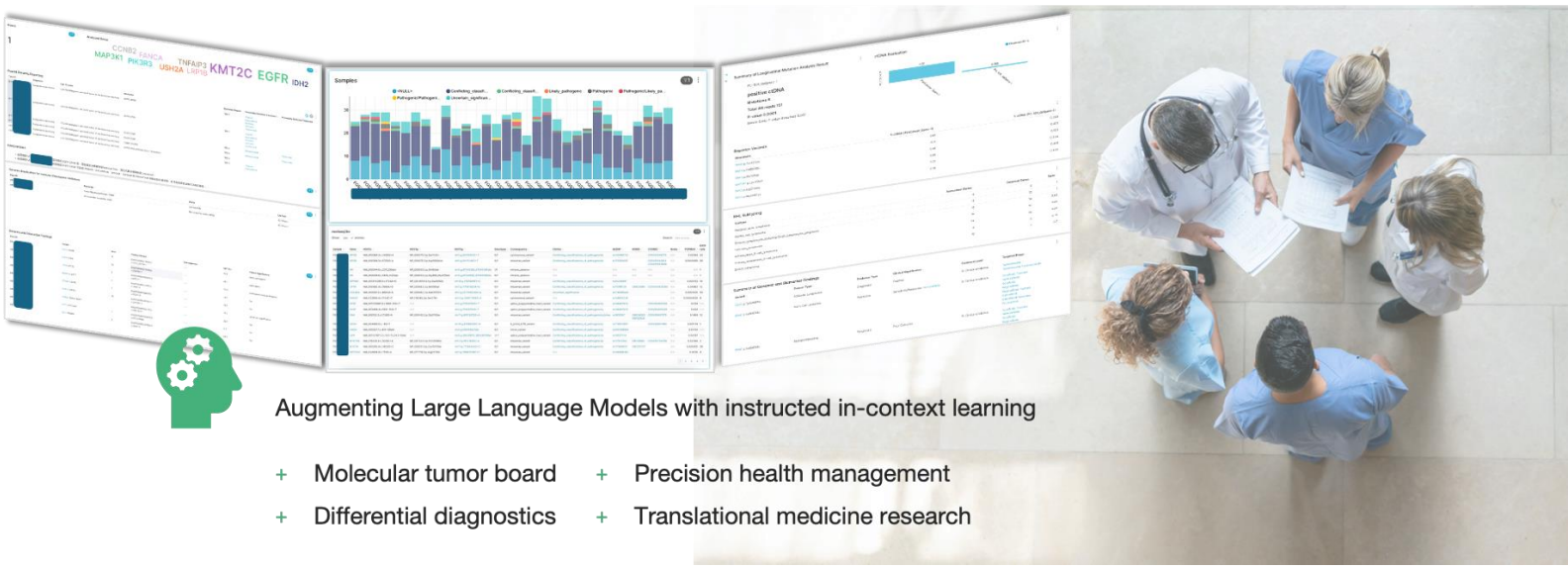
Democratizing Access to Make Discoveries that Improve Healthcare Outcomes

Dedicated omics data lakehouse combined with Generative AI to identifying and prioritizing diagnostic targets in real-time and unleashing the power of the world's best scientific minds.



Robust Body of Evidence

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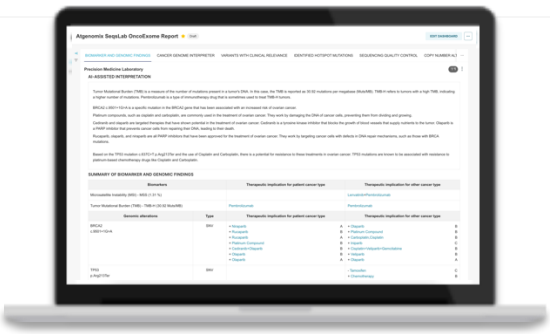
Atgenomix SeqsLab OncoExome

Whole Exome Analytical Solution for Cancer



The genomic profiling application that integrates capture-based target enrichment kits with the data analytics capabilities and accelerated computing features of Atgenomix SeqsLab Platform.

Atgenomix SeqsLab OncoExome provides standardized detection workflow and enhanced analytical capabilities for the comprehensive cancer genomic profiling.

Main Features

Comprehensive coverage of multiple types of variants, and actionable genomic biomarkers in up to 1,275 genes, enabling data-guided decision making.

Exome Library	Variants Called	Biomarkers Analyzed	QC Metrics
• Capture-based target enrichment • Sequencing with Unique Molecular Identifier (UMI)	SNVs Indels CNVs *	MSI TMB LOH * HRD * Splicing prediction Therapy implications	Total bases Q ≥ 30 Duplicate reads Mapping rate On-target reads Coverage of targeted regions Coverage uniformity

* An intended Panel of Normals (PON) with similar technical properties of the tumor is required for the analyses. Atgenomix provides additional workflows for generating PON.

Analytical Capabilities

SeqsLab OncoExome analyzes complex WES data by calling, annotating and classifying genomic variants in all the targeted regions.

Turnaround time from FASTQ	~3 hours
Tumor-only analysis	Available
Genome Reference	GRCh38

Optimized table output for easy interpretation to genes, alterations, and biomarkers of interest.

Integrated Workflow for Genomic Analysis, Interpretation and Reporting

Sequencing → Data upload & governance → Calling, Annotation & QC → Classification & Profiling → Visualized Interpretation → Collaborative Reporting

Automated with sequencing sample sheet

Tech-independent secure data transmission and governance in your dedicated data repository.

Audited bioinformatics workflow quality

Analysis application certified to ISO 13485 and in accordance with IEC 62304.

Faster access to results

Automatic database classification and layered biomarker profiling as well as integration of proprietary database.

Streamlined case and cohort discussions

Real-time query, identification and prioritization of test targets for your tumor board.

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Not for use in diagnostic procedures.