SOPHiA™

Accelerating the assessment of genomic alterations

SOPHiA PLATFORM FOR ONCOLOGY

SOPHiA Platform is the technology of choice for streamlined genomic data analysis, interpretation and reporting in the field of oncology. It enables advanced analytical performance and facilitates the visualization of genomic alterations associated with solid tumors and hematological malignancies. The platform helps experts focus on relevant and actionable genomic alterations to make more informed decisions.

HIGHLIGHTS

Achieve advanced analytical performance

SOPHiA analyzes complex NGS data by detecting, annotating and pre-classifying SNVs, Indels, and CNVs in one single experiment.

Turn data into actionable insights

The process of compiling a comprehensive list of genomic alterations, scanning all of them, and summarizing key implications is complex and time-consuming. One of the main difficulties lies in identifying the relevant genomic alterations with actionable value to support decision-making.

SOPHiA Platform offers several features for efficient and simplified variant assessment and visualization. Experts can filter down and report relevant candidates associated with a specific type of cancer.

In addition, experts can benefit from Alamut® Software Suite, a complementary solution to help handle the complex task of genomic variant annotation, filtration and exploration.

Ensure data security

Access to the SOPHiA Platform is restricted to registered users only. All data is encrypted and stored at rest with replication across geographically distinct and secure data centers.

Access to SOPHiA's Community

In the platform, experts from hundreds of healthcare institutions interpret the results and flag the pathogenicity level of variants according to their knowledge and experience. This highly valuable information feeds the variant knowledge base and is anonymously and safely shared among the members of the community.

Scalable

From targeted to comprehensive applications

Efficient

Multiple types of alterations detected in a single experiment

User friendly

No bioinformatics expertise needed

SOPHiA Platform for Oncology

Fast, easy and intuitive workflow for advanced secondary and tertiary analysis

SOPHiA Platform offers a fully integrated workflow, enabling experts to manage genomic data and efficiently explore, characterize and report relevant genomic alterations associated with solid tumors and hematological malignancies.

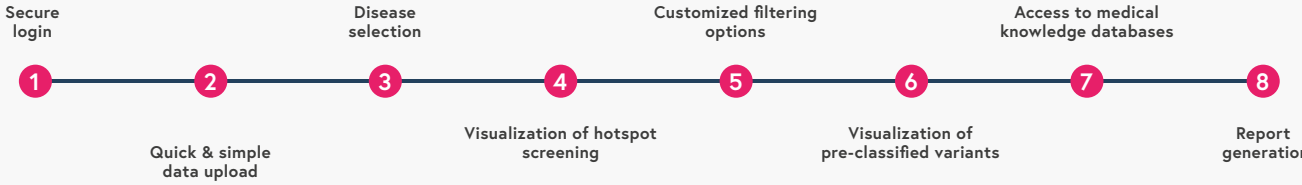
The platform offers several features that facilitate the interpretation process, such as hotspot screening which streamlines the visualization of mutated and wild type hotspot positions.

SOPHiA integrates the OncoPortal, a decision support functionality based on medicine intelligence. It enables researchers access to relevant medical knowledge databases and clinical trial registries to determine the actionability and significance of genomic alterations.

Comprehensive genomic analysis from FASTQ files

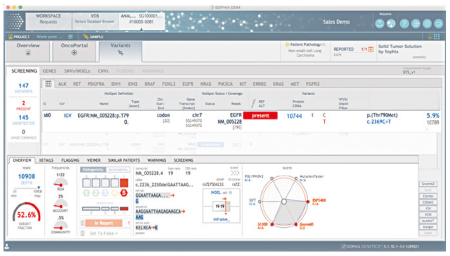
SNVs	✓
Indels	✓
CNVs	✓
Gene Fusions	✓

End-to-end workflow from raw sequencing data to actionable insights



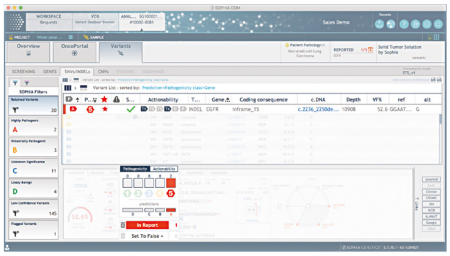
This is an example of a typical workflow. Some users may require fewer steps.

Integrated features for efficient variant interpretation and reporting



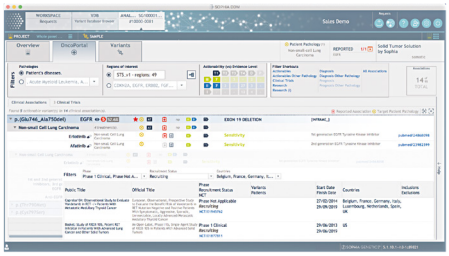
Screening

Preview the major hotspot positions present in the tumor.



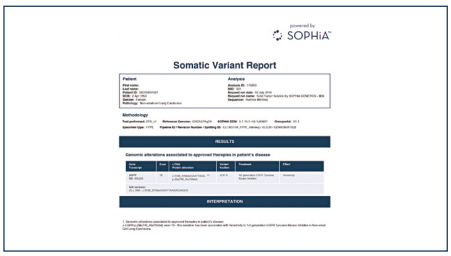
Variant pre-classification

Visualize an overview of major SNVs and Indels pre-classified by SOPHiA by level of pathogenicity.



OncoPortal

Access to relevant medical knowledge databases and clinical trial registries to determine actionability and significance of genomic alterations.



Somatic Variant Report

Generate a customizable somatic report with actionable genomic alterations.

BENEFITS

- End-to-end workflow for reduced turnaround time
- Efficient assessment of complex variants associated with solid tumors and hematological malignancies
- Focus on actionable and relevant genomic alterations

Somatic gene variant annotations and related content have been powered by, without limitation, The Jackson Laboratory Clinical Knowledgebase (JAX-CKB™).

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