

Clinicians Platform of Choice for Genomic Testing



Ensure Top Analytical Performance

Exclusively available on SOPHiA DDM, SOPHiA, the collective Artificial Intelligence (AI) for Data-Driven Medicine, detects, annotates and pre-classifies genomic variants, to help clinicians better diagnose and treat patients.

Respect Patient Privacy

SOPHiA DDM encrypts all data to the highest industry standards before storing it redundantly in secured and private data centers. The platform ensures patient privacy and respects EU Directives and National Privacy Laws.



Access to SOPHiA's Community

SOPHiA GENETICS has built the World's Largest Clinical Genomics Community with hundreds of institutions participating in the democratization of Data-Driven Medicine. Through SOPHiA DDM, thousands of experts can easily interpret the variants and flag them with the appropriate level of pathogenicity. This highly valuable information feeds the variant knowledge base and is anonymously and safely shared among the members of the community.

Benefits



Fast turnaround time:
data ready in 2 hours



Top analytical
performance



Secure data storage
and encryption

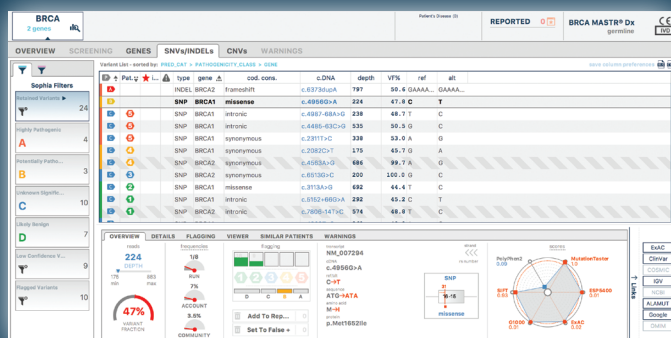
1 Login

Access the platform securely



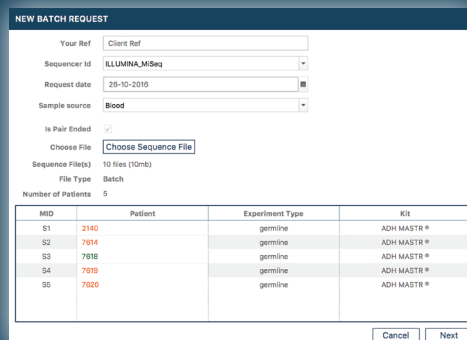
3 Data Analysis & Interpretation

- Automated quality check, alignment and variant calling
- Automatic and comprehensive variant annotation (multiple sources)
- Pre-classification of variants in different pathogenicity classes
- Variant filtering
- Facilitated interpretation through integrated databases



2 Request Creation

- Load your raw DNA sequence files
- SOPHiA DDM encrypts and processes the data



MID	Patient	Experiment Type	KIT
S1	2140	germline	ADH MASTR #
S2	7914	germline	ADH MASTR #
S3	7916	germline	ADH MASTR #
S4	7918	germline	ADH MASTR #
S5	7920	germline	ADH MASTR #

4 Variant Report

Establish your own variant report



Variant	Frequency	Pathogenicity
Selected Variants	1	
Related Variants	11	
A - Most likely pathogenic	2	Low confidence variants
B - Potentially pathogenic	2	Low coverage regions
C - Variants of unknown significance	5	No low coverage
D - Most likely benign	2	Missing/Max variant coverage

Get Actionable Information to Fight Cancer

For biologists and clinicians working on solid tumors and haematological malignancies, the OncoPortal interface provides comprehensive annotations of genome-wide associations among human gene variants, disease, and drug treatment. It is based on precision medicine intelligence with curated and reliable databases on gene biomarkers and clinical trials.

1

EGFR
Missense mutation

p.Thr790Met

VF: 50.38% depth: 2356

2

Sensitive

Osimertinib mesylate
Therapeutic agent

Carcinoma, Non-Small-Cell Lung

3

Summary:
EGFR c.2369C>T is a missense mutation in codon 790 yielding a threonine-to-methionine (T790M) amino acid change (J Thorac Oncol 2013, 8(1): 45-51). EGFR is mutated in approximately 12% of non-small cell lung ...

Clinical Trial(s): 29

Somatic classification based on variant-disease-drug association linked to the patient's tumor profile

Specific drug association with the disease and its effect in terms of sensitivity for each patient

Clinical evidence summary including known effects of each association on the disease and its treatment