HEREDITARY CANCER SOLUTION™ BY SOPHiA GENETICS

The Hereditary Cancer Solution (HCS) by SOPHiA GENETICS is a molecular diagnostic application that bundles the analytical power of SOPHiA™ AI with a capture-based target enrichment kit and full access to SOPHiA DDM® platform.

CE IVD

SOPHiA GENETICS®

Knowledge-Driven Kit Design

SOPHiA™

Collective AI for Data-Driven Medicine

SaaS Analytical Platform

The HCS panel covers the coding regions and splicing junctions (± 25 bp) of 26 most clinically relevant genes (target region of 105 kb), associated to breast and ovarian cancer, HNPCC and intestinal polyposis syndrome. It guarantees superior coverage uniformity, high on-target reads percentage and exceptional coverage in GC-rich regions, even in the first exon.

Gene panel

ATM, APC, BARD1, BRCA1, BRCA2, BRIP1, CDH1, CHEK2, EPCAM, FAM175A, MLH1, MRE11A, MSH2, MSH6, MUTYH, NBN, PALB2, PIK3CA, PMS2, PMS2CL[1]*, PTEN, RAD50, RAD51C, RAD51D, STK11, TP53, XRCC2*

Recommendations

Starting material: 200 ng
Sample source: Blood
Samples per run: Depending on sequencing platform[2]

Sequencer	Flow Cell/ Sequencing Kit	Recommended reads per sample	Samples per run
Illumina MiniSeq	High Output Kit (2x150bp)	2M	32
Illumina MiSeq	v3 (2x300bp)	1M	48
Illumina NextSeq 500/550	Mid Output Kit (2x150bp)	2M	Up to 96[3]

Wet lab

Day 1: Library Preparation
Day 2: Capture and Sequencing
Total hands-on time: 8 hours

SOPHiA analyses complex genomic NGS data by detecting, annotating and pre-classifying genomic variants to help clinicians better diagnose their patients.

- SNVs, Indels and CNVs are accurately detected in all genes of the panel
- ALU insertions are reliably recognized
- Pseudogene variants are efficiently differentiated from real ones[4]

SOPHiA leads to excellent clinical grade analytical performances[5]:

	Observed	Lower 95% CI
Sensitivity	100%	99,20%
Specificity	100%	99,99%
Accuracy	100%	99,99%
Precision	99,86%	96,42%
Repeatability	99,98%	99,98%
Reproducibility	99,93%	99,93%
Average on-target rate	79,39%	
Coverage uniformity	99,72%	
Average percentage of target region >200x	99,95%	
CNV detection	in all genes	

A total of 386 samples were processed to obtain the above-mentioned metrics

Analysis time from FASTQ files: 4 hours[6]

The results are presented in SOPHiA DDM, the platform of choice for clinicians performing routine diagnostic testing. Thanks to its intuitive user interface and integrated features, variants visualization and interpretation are facilitated, while assuring protection of clinical genomic data.

Main features

Dedicated features in SOPHiA DDM reduce the complexity of determining the pathogenicity of genomic variants.

- **Virtual Panels:** restrict the interpretation to sub-panels of genes (e.g. focus on Lynch syndrome or breast cancer)
- **Variant Filter Builder:** define and edit custom filters for efficient analysis
- **Interpretation Projects:** create interpretation projects on datasets by restricting the analysis to a specific set of genes, associated to a defined disease or reflecting patient's consent

Access to the World's Largest Clinical Genomics Community

Through SOPHiA DDM, experts from hundreds of healthcare institutions 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.

(1) The pseudogene *PMS2CL* is part of the analysis but not a gene responsible for disease
(2) Illumina®, MiSeq® and NextSeq® 500/550 are registered trademarks of Illumina, Inc., which are not affiliated with SOPHiA GENETICS®
MiniSeq™ is a trademark of Illumina, Inc., which is not affiliated with SOPHiA GENETICS®
(3) Maximum number of indices available. Sequencing recommendations for other sequencing kits and instruments available on request
(4) Due to high gene conversion rates, a definite location in *PMS2* or *PMS2CL* cannot be assigned in homologous regions of exon 12-15
(5) Performance values have been calculated on SNVs and Indels only. The detection of CNVs, Alu repeats and pseudogene variants are not part of the CE-IVD claim
(6) Analysis time may vary depending on the number of samples multiplexed and server load


SOPHiA™
The AI Democratizing Data-Driven Medicine
sophiagenetics.com | info@sophiagenetics.com | @SOPHiAGENETICS