SOPHiA GENETICS™

Clinical Exome Solution v3

The genomic application that combines a capture-based target enrichment kit with the analytical capabilities and advanced features of the SOPHiA DDM™ platform. SOPHiA Clinical Exome Solution v3 offers enhanced probe design and increased detection capabilities for a deeper investigation of Mendelian diseases.

Main Features

SOPHiA Clinical Exome Solution v3 covers the coding regions (±5bp of intronic regions) of 4,728 genes, the entire mitochondrial genome and non-coding variants known to be associated with rare and inherited disorders (probe footprint of ~16 Mb). Probe design is highly optimized to guarantee high on-target reads percentage and coverage uniformity even in GC-rich regions, including the first exon.

Gene Panel	Variants Called	Recommendations	Wet Lab
• 4,728 genes • Entire mitochondrial genome • ~ 200 non-coding variants with known pathogenicity in deep introns/enhancer/ promoter genes	SNVs Indels CNVs (97% genes)	**Starting material** 200 ng DNA **Sample type** Blood **Samples per run for > 50x coverage depth / Sequencer (Flow Cell)** 16 for Illumina NextSeq® 500/550 Mid Output v2 (2x150bp) 48 for Illumina NextSeq® 500/550 High Output v2 (2x150bp) 48 (per lane) for Illumina NovaSeq® 6000 (SP) 96 (per lane) for Illumina NovaSeq® 6000 (S1)	**Day 1:** Library Preparation **Day 2:** Capture and Sequencing **Total library preparation time: 1.5 days**

Analytical Performance*

The SOPHiA DDM™ platform analyzes complex NGS data by detecting, annotating and pre-classifying multiple types of genomic variants in all the genes of the panel.

Analysis time[1] from FASTQ: 6 hours

	Observed (%)	Lower 95% CI
Sensitivity for SNVs/Indels[2]	99.46	99.34
Precision for SNVs/Indels[2]	99.62	99.51
Sensitivity for CNVs 2-4 exons (1-2 exons)[3]	98.2 (83.0)	
Sensitivity for mitochondrial SNVs/Indels detection[4]	>99.9	
Coverage uniformity	99.4	
Average on target region >20x (>50x)	99.3 (84.3)	

One Simple Intuitive Platform: Beyond Analytics

Accelerated assessment and reporting of genomic variants

Dedicated features in SOPHiA DDM™ reduce the complexity of determining the significance of genomic variants and facilitate the interpretation process, thus reducing turnaround time:

- **GRCh38/hg38 based analytics -** Annotate variants accurately
- **Dual-Variant Pre-classification –** Improve assessment of variants pathogenicity with both ACMG scores and SOPHiA GENETICS machine learning –based predictions
- **Virtual Panels -** Restrict the interpretation to sub-panels of genes of interest using the HPO or OMIM browser
- **Cascading Filters -** Apply custom filtering options for quicker screening of relevant variants and save strategies for future analyses
- **Familial Variant Analysis (trio-analysis) -** Identify disease causing variants considering different modes of inheritance, through a family-based approach

After the interpretation, you can generate a customizable variant report, including valuable information to support decision making.

Global support at every step

We offer local support anywhere in the world. Our dedicated bioinformaticians help save time and resources, ensuring fast resolution of workflow disruptions. In addition, our Set Up Program provides assistance with assay set up for fast and worry-free transition to routine testing.

Secure and unlimited data storage

The SOPHiA DDM™ platform provides unlimited and unrestricted storage, while keeping data safe by applying the highest industrial standards of encryption in compliance with local data security policies.

Access to the SOPHiA GENETICS community

Through the SOPHiA DDM™ platform genomics experts from >1000 healthcare institutions interpret their findings and flag the pathogenicity level of variants. This highly valuable information enriches the variant knowledge base and is safely shared among the members of the community, supporting their decision-making process for research purposes.

1. Analysis time may vary depending on the number of samples multiplexed and server load.
2. SNV and Indel performance metrics are based on more than 6'100 variants. For each sample, 16.25M reads per sample were used. Sequencing was performed using an Illumina NextSeq® instrument.
3. Analytical performance for CNVs has been calculated on 80 CNVs, sequenced on NextSeq® instrument.
4. Sensitivity for mitochondrial SNVs/Indels has been calculated on 96 variants (93 SNPs and 3 Indels), sequenced on NextSeq® instrument.

***For Research Use Only. Not for Use in Diagnostic Procedures.**