SOPHiA GENETICS™

SOPHiA DDM™ Enhanced Clinical Exome Solution

The genomic application that integrates a capture-based target enrichment kit with the advanced analytics of the SOPHiA DDM™ Platform. The SOPHiA DDM™ Enhanced Clinical Exome Solution builds on the trusted SOPHiA DDM™ Clinical Exome Solution v3, adding targeted probe enhancements for hereditary cancer and carrier screening indications* to boost coverage in critical regions, alongside robust analytical modules designed to reliably detect difficult-to-call variants.

*A pharmacogenomics enhancement will be available later this year.

Main Features

The SOPHiA DDM™ Enhanced Clinical Exome Solution covers the coding regions (±5bp of intronic regions) of 6,380 genes, the entire mitochondrial genome, and non-coding variants known to be associated with rare and inherited disorders. The hereditary cancer and carrier screening enhancements boost coverage of 94 and 155 genes, respectively.

Gene Panel

- 6,380 genes
- Entire mitochondrial genome
- ~ 200 non-coding variants with known pathogenicity in deep introns/enhancer/promoter genes

Variants Called

General variant types:
SNVs, Indels, CNVs, mitochondrial variants, *Alu* insertions

Specific variants:
Large deletions in *HBA1* and *HBA2*, Gene/pseudogene analysis for *PMS2*, *SMN1*, *CYP21A2*, and *TNXB*, *MSH2* Boland inversions, *CFTR* polyTGT tract

Recommendations

Starting material
50 ng

Sample type
Blood

Samples per run for > 50x coverage depth
24 for NextSeq® 550, high-output kit
8 for NextSeq® 550, mid-output kit
24 for NextSeq® 1000/2000, P2 XLEAP reagents
120 for NextSeq® 1000/2000, P4 XLEAP reagents
120 NovaSeq™ S2 flow cell (1 lane)
144 NovaSeq™ S4 flow cell (1 lane)

Wet Lab

Day 1:
Library Preparation

Day 2:
Capture and Sequencing

Hands-on library preparation time:
2.5 hours

Analytical Performance

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

Analysis time from FASTQ: 3.5 hours[1]

	Observed
Sensitivity for SNVs/Indels[2]	99.8%
Precision for SNVs/Indels[2]	99.0%
Sensitivity for CNVs 2-4 exons (1-2 exons) in exome backbone[3]	98.2% (83.0%)
Sensitivity for CNVs (1-2 exons) in enhanced regions[4]	98.0%
Average on target region >25x (>50x)	99.3% (99.0%)
Spike-in / exome coverage ratio	3.5-4

1. For 8 samples of >50M reads. Analysis time may vary depending on the number of samples multiplexed and server load.
2. SNV and Indel performance metrics are based on six well characterised reference samples with more than 7,300 confirmed variants each. For each sample, 50M reads were sequenced on an Illumina NextSeq® instrument.
3. Analytical performance for CNVs has been calculated on 80 CNVs, sequenced on NextSeq® instrument.
4. Analytical performance for CNVs has been calculated on more than 50 confirmed CNVs, of which 15 were single exon CNVs and 5 CNVs affecting two exons, sequenced on an Illumina NextSeq® instrument.

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 turn-around time:

- **GRCh38/hg38 based analytics** – Select your transcript of choice and leverage insights from frequently updated variant annotation catalogs and zygosity annotation
- **Variant pathogenicity prediction** – Prioritize variants for further analysis with point-based ACMG classification and SOPHiA DDM™ machine learning-based ABCD prediction
- **Virtual Panels** – Restrict interpretation to sub-panels of genes of interest using the HPO or OMIM®
- **Cascading Filters** – Apply custom filtering options and save strategies for future analyses
- **Familial Variant Analysis (trio-analysis)** – Identify pathogenic variants considering different modes of inheritance, through a family-based approach
- **Alamut™ Visual Plus** – Streamline your interpretation with enhanced genomic visualization and comprehensive variant annotation
- **Reporting** – Generate customized CAP- and CLIA-compliant reports

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, the SOPHiA DDM™ MaxCare Program provides assistance with assay set up for a fast and worry-free transition to routine testing.

Secure and unlimited data storage

Access to the SOPHiA DDM™ Platform is restricted to registered users only. The Platform provides unlimited and unrestricted storage, while keeping data safe by applying the highest industrial standards of encryption in compliance with your local data security policies.

The SOPHiA GENETICS Community

Join one of the largest global networks of healthcare institutions to securely and anonymously share knowledge with your peers and confidently assess even challenging variants.

Product code: **BS0130ILLRGLY10**

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