SOPHiA GENETICS™

SOPHiA DDM™ Homologous Recombination Deficiency (HRD) Solution

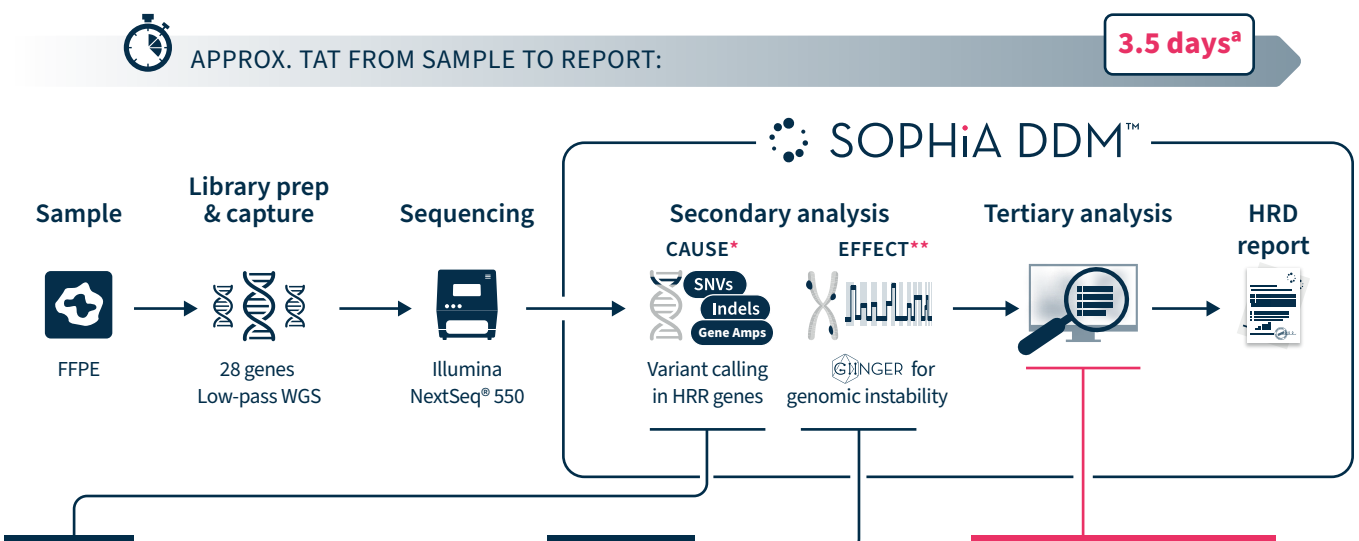
Go beyond homologous recombination repair (HRR) mutation detection

SOPHiA DDM™ HRD Solution is a **decentralized** next generation sequencing (NGS) application for HRD detection in **ovarian cancer** samples, combining:

- Targeted sequencing of germline and somatic mutations in **28 HRR genes** (including *BRCA1* & *BRCA2*)
- A **deep learning algorithm**, GIInger™, that utilizes **low-pass whole genome sequencing (WGS)** data to recognize patterns of **genomic instability**

SOPHiA DDM™ HRD Solution accelerates and empowers your clinical research decisions by offering **affordable, reliable** and **timely** in-house results.

Streamlined sample-to-report workflow



*CAUSE

- Detection of SNVs and Indels in 28 HRR genes (incl. *BRCA1/2*), powered by **PEPPER™** algorithm.
- Gene amplification analysis, including *CCNE1*, powered by **MUSKAT™** algorithm.

**EFFECT

Assessment of genomic instability by leveraging data from low-pass WGS coverage profiles (1x), powered by deep learning **GIInger™** algorithm.

TERTIARY ANALYSIS

- Variant annotation with *BRCA* Exchange (*BRCA1/2* only)
- Evidence-based decision-making support with OncoPortal™ Plus

Reduced hands-on time

with **single capture** wet lab workflow, high **multiplexing** capabilities, and **automation options**

Rapid adoption in-house

with customized support and analytical performance verification from the **SOPHiA DDM™ MaxCare Program**

No extra servers

required for data analysis, due to the **speed and responsiveness** of the cloud-based SOPHiA DDM™ Platform

Empowering clinical cancer research decisions

PARTNER SPOTLIGHT

Diagnosticos da America (Dasa), Brazil

- Dasa, the largest integrated health network in Brazil, introduced SOPHiA GENETICS approach to HRD detection as the **first decentralized solution in Latin America.**
- Dasa needed an **affordable** HRD solution that helped **improve workflow efficiency.**
- With SOPHiA DDM™, Dasa were able to assess the HRD status of over **2,000 samples in less than 2 years.**

> *"The decentralized approach of SOPHiA GENETICS has enabled us to increase our **scalability and output** – in less than two years, we've tested the HRD status of over **2,000 in-house samples**. The powerful analytics of SOPHiA DDM™ have helped us to **maximize genomic insights** from these samples and advanced our clinical research capabilities."*

Ana Gabriela
Genomic Business Unit, Sr. Manager | Dasa, Brazil

Specifications

Sample type	FFPE ovarian cancer tissue
Input	Minimum of 50 ng DNA per sample
Gene content	**28 HRR genes covered:** *AKT1*, ATM, BARD1, BRCA1, BRCA2, BRIP1, CCNE1, CDK12, CHEK1, CHEK2, ESR1*, FANCA, FANCD2, FANCL, FGFR1*, FGFR2*, FGFR3*, MRE11, NBN, PALB2, PIK3CA*, PPP2R2A, PTEN, RAD51B, RAD51C, RAD51D, RAD54L, TP53.* **Genes with hotspot/select exon coverage only.*
Variant called	SNVs, Indels, gene amplifications
Instrument type	Illumina NextSeq® 550
Max. sample plexity	• Illumina NextSeq® 550 Mid Output Kit: 8 samples • Illumina NextSeq® 550 High Output Kit: 24 samples
Approx. TAT	3.5 days • Library prep. – 1.5 days • Sequencing & data upload – 1.5 days • Data analysis – 12 hours[a]
Automation	Please contact info@sophiagenetics.com or your local sales representative to learn more about users' experience with automation
Product code	BS0121ILLRSMY08-32

Want to learn more? Contact us at: **info@sophiagenetics.com**

[a] Analysis time may vary depending on the number of samples multiplexed and server load.
Amps., amplifications; FFPE, formalin-fixed paraffin-embedded tissue; HRD, homologous recombination deficiency; HRR, homologous recombination repair; PARPi, poly(ADP)-ribose protein inhibitor; SNV, single nucleotide variant; TAT, turnaround time; WGS, whole genome sequencing.