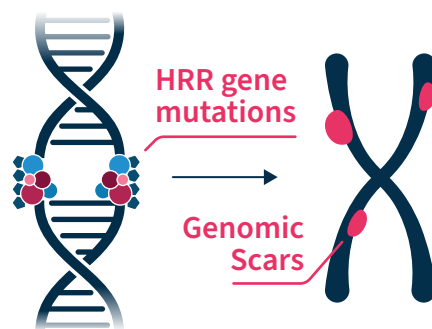


SOPHiA DDM™ Extended Homologous Recombination Solution (ExtHRS)

Go beyond *BRCA* analysis and broaden your detection capabilities

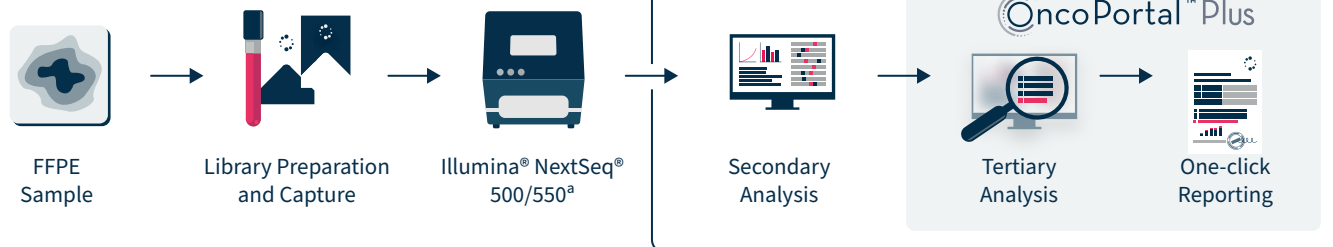
Genetic abnormalities in **homologous recombination repair (HRR) genes**, beyond *BRCA1* and *BRCA2*, can lead to **homologous recombination deficiency (HRD)** in several cancer types, including ovarian, breast, prostate, colon, lung, and pancreatic¹.

SOPHiA DDM™ ExtHRS is a **sample-to-report NGS application** that allows researchers to go further with their HRR mutation sequencing and identify the cause of HRD across cancer types.



Streamline your workflow with SOPHiA DDM™ ExtHRS

 Rapid adoption in-house with SOPHiA DDM™ MaxCare Program



Read-to-sequence libraries in **only 1.5 days**

High sample **multiplexing capability**

User-friendly interpretation and reporting

Benefits of SOPHiA DDM™ ExtHRS



Empower in-house expertise on HRR sequencing with a **sample-to-report NGS workflow**



Detect, annotate and pre-classify **SNVs, Indels, and gene amplifications** in 28 HRR-associated genes

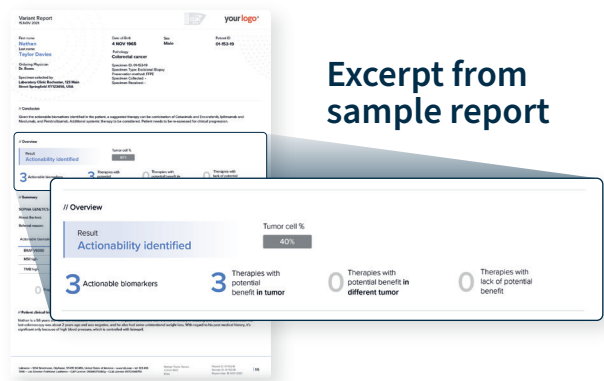


Accelerate your research with our powerful proprietary algorithms and versatile **SOPHiA DDM™ Platform**

Confident decision-making and one-click reporting

OncoPortal™ Plus matches **tumor molecular profiles** with **clinical associations** and available **clinical trials**, leveraging expertly curated evidence powered by Genomenon Clinical Knowledgebase (CKB).

After interpretation, the **flexible reporting tools** enable users to prepare **push-button**, comprehensive reports that are **customizable** to their needs.



Advanced analytical performance²

100% sensitivity^a

99.99% specificity^a

High coverage uniformity

Accurate gene amplification detection with MUSKAT™ technology

^a Based on internal verification of 51 FFPE ovarian cancer samples. Specificity analysis characterized samples only.

Our comprehensive Homologous Recombination Solutions portfolio

	SOPHiA DDM™ mini HRS	SOPHiA DDM™ HRS	SOPHiA DDM™ ExtHRS
Genes	4 genes: <i>BRCA1</i> , <i>BRCA2</i> , <i>RAD51B</i> , <i>TP53</i>	16 genes: <i>ATM</i> , <i>BARD1</i> , <i>BRCA1</i> , <i>BRCA2</i> , <i>BRIP1</i> , <i>CDK12</i> , <i>CHEK1</i> , <i>CHEK2</i> , <i>FANCL</i> , <i>PALB2</i> , <i>PPP2R2A</i> , <i>RAD51B</i> , <i>RAD51C</i> , <i>RAD51D</i> , <i>RAD54L</i> , <i>TP53</i>	28 genes: <i>AKT1*</i> , <i>ATM</i> , <i>BARD1</i> , <i>BRCA1</i> , <i>BRCA2</i> , <i>BRIP1</i> , <i>CCNE1</i> , <i>CDK12</i> , <i>CHEK1</i> , <i>CHEK2</i> , <i>ESR1*</i> , <i>FANCA</i> , <i>FANCD2</i> , <i>FANCL</i> , <i>FGFR1*</i> , <i>FGFR2*</i> , <i>FGFR3*</i> , <i>MRE11</i> , <i>NBN</i> , <i>PALB2</i> , <i>PIK3CA*</i> , <i>PPP2R2A</i> , <i>PTEN</i> , <i>RAD51B</i> , <i>RAD51C</i> , <i>RAD51D</i> , <i>RAD54L</i> , <i>TP53</i> . *Hotspots
Sample type	FFPE, fresh-frozen tissue	FFPE, fresh-frozen tissue	FFPE, fresh-frozen tissue
Starting material	50 ng DNA	50 ng DNA	50 ng DNA
Reads per sample (2x150bp)	1.6 million	4.7 million	8 million
Samples/run for 1000x coverage depth (2x150bp)	- Up to 24 samples for Illumina MiniSeq™ kit - Up to 32 samples for Illumina MiSeq® kit v3 - Up to 24 samples for Illumina MiSeq® kit v2	- Up to 8 samples for Illumina MiSeq® kit v3 - Up to 4 samples for Illumina MiSeq® kit v2 - Up to 16 samples for on Torrent™ Ion S5™ System	Up to 32 samples for Illumina® NextSeq® 500/550 Mid Output Kit^a
Product codes	BS0111ILLRSMY05-16; BS0111ILLRSMY05-32; BS0111ILLRSMY05-48	MiSeq®: BS0108ILLRSMY05-16; BS0108ILLRSMY05-32; BS0108ILLRSMY05-48 IonTorrent™: BS0108TFSRSMY03-016; BS0108TFSRSMY03-032	BS0124ILLRSMY08-32

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

^aAlso compatible with NovaSeq® sequencers. FFPE, formalin-fixed, paraffin-embedded; Indels, insertions and deletions; NGS, next generation sequencing; SNV, single nucleotide variant.
All product and company names are trademarks™ or registered® trademarks of their respective holders. Use of them does not imply any affiliation with or endorsement by them. SOPHiA GENETICS™ Homologous Recombination Applications are for research use only - not for use in diagnostic procedures
1. Mekonnen N, et al. Front Oncol. 2022;12:880643. 2. Data on File.