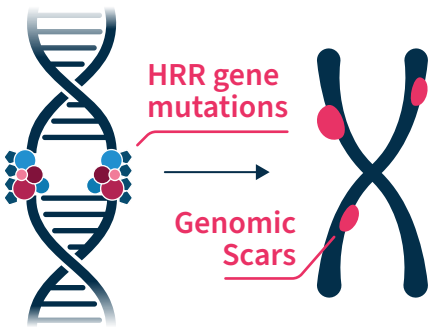
SOPHiA GENETICS™

SOPHiA DDM™ Extended Homologous Recombination Solution (ExtHRS)

Go beyond *BRCA* analysis and broaden your detection capabilities

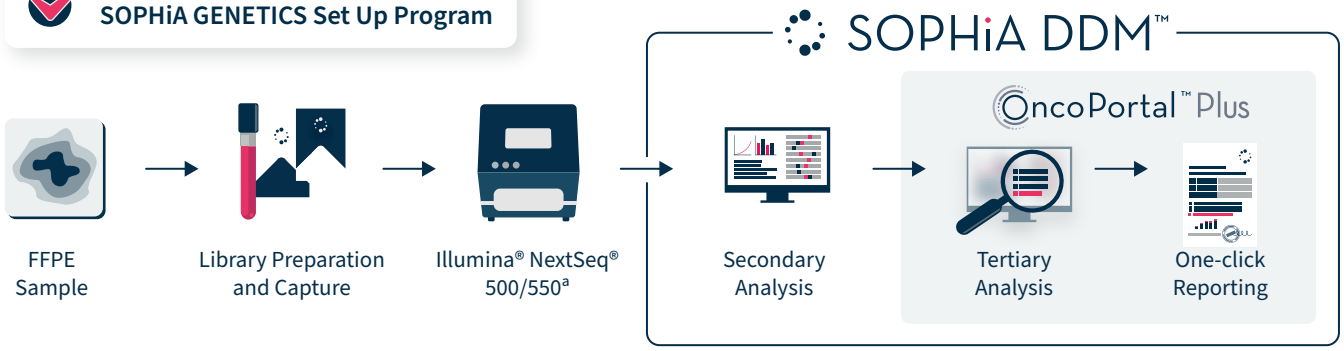
Genetic abnormalities in **homologous recombination repair (HRR) genes**, beyond ***BRCA1*** and ***BRCA2***, can lead to **homologous recombination deficiency (HRD)** in several cancer types, including ovarian, breast, prostate, colon, lung, and pancreatic[1].



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 GENETICS Set Up Program



Read-to-sequence libraries in only 1.5 days • **High sample multiplexing capability** • **User-friendly interpretation and reporting**

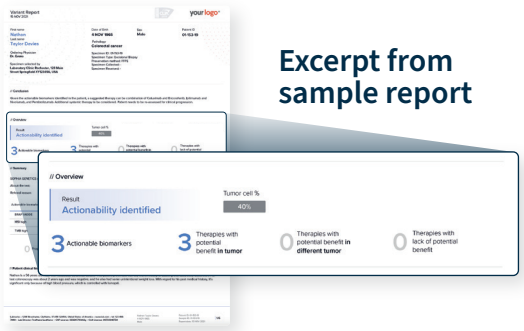
Benefits of SOPHiA DDM™ ExtHRS

- 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 JAX-CKB™.

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



Advanced analytical performance[2]

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: *BRCA1, BRCA2, RAD51B, TP53*	16 genes: *ATM, BARD1, BRCA1, BRCA2, BRIP1, CDK12, CHEK1, CHEK2, FANCL, PALB2, PPP2R2A, RAD51B, RAD51C, RAD51D, RAD54L, TP53*	28 genes: *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.* *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	5.9 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™: BS0108TFSRSML03-016; BS0108TFSRSML03-032	BS0124ILLRSMY08-32

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

[a]Also compatible with NovaSeq® sequencers. FFPE, formalin-fixed, paraffin-embedded; Indels, insertions and deletions; NGS, next generation sequencing; SNV, single nucleotide variant.

1. Mekonnen N, et al. Front Oncol. 2022;12:880643. 2. Data on File.