



HRDTrack Test

Homologous Recombination Deficiency (HRD) status in tumor

Features

Comprehensive Content	 Statistically infer Genome Aberration Score from high quality genome-wide SNP markers representative of multiple ethnicities Identifies variants from complete coding regions & splice boundaries of BRCA1 & 2 genes & 13 HRR genes CCNE1 amplification status
Technologically advanced	 UMI-enabled library preparation to minimize errors Automated analysis & reporting Supports low input material
Clinically Validated & Accurate	 Validated across ~200 samples including reference standards, normal ovarian cancer samples and known clinical samples Sensitivity - 96.3%, Specificity - 98.3%, Accuracy - 97.05% Validated across FFPE tumor specimens with varied tumor content (10-90%); >20% tumor content is required Validated using different DNA input concentrations (10-200ng); ~30 ng of DNA input is required 100% concordance achieved with Myriad MyChoice HRD test

Validation

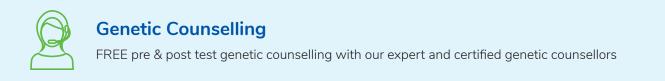
Samples	Concordance	Overall Percent Agreement 97.38% (n=191)
Reference Standards (10)	100%	100 98.3% 96.3%
Healthy Ovarian Tissue (21)	100%	ment (NPA) ment (PPA) 08
HRD Positive Clinical Samples (111)	96.39%	Agreer — 09
HRD Negative Clinical Samples (59)	98.3%	e Bercent 05
Myriad My Choice HRD (5)	100%	0 Lositive 0

Test Details

Test Code	Test Name	Sample type	ТАТ
MGM1892	HRDTrack Test	Tumor tissue (>20% Tumour Content)	21 days



Science is our DNA • Innovation is our Focus • Precision is our Expertise • Human Impact is our Vision





Talk to the Experts:

1800 103 3691
 diagnostics@medgenome.com
 www.medgenome.com



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