iGeneTech
艾吉泰康

MultipSeq® BRCA1/2 Research Assay V2

iGeneTech Bioscience Co., Ltd.

PRODUCT OVERVIEW

- Target Size: 19.5 kb
- Detection range: SNV、InDel
- Coverage: Covering all exons of *BRCA1* and *BRCA2*, including at least 10 bp up- and downstream of each exon and the entire UTR regions, plus 228 ClinVar non-exon positions classified as pathogenic, likely pathogenic, or of uncertain significance.
- Recommend Sequencing Data: 0.2 Gb/5000×
- Applications: Health screening, risk assessment

ADVANTAGES

Sensitive and precise

Probes are designed against all transcripts in the target region for hybrid-capture enrichment, enabling low-cost, ultra-deep and highly sensitive detection.

Comprehensive coverage

Fully covers the target regions.

Excellent performance

Stable and superior metrics in coverage, capture efficiency, and uniformity

Convenient and efficient

Short experimental time (3-4 hours) and simple operation.

PERFORMANCE

High sensitivity and accuracy in mutation detection

Gene	Variant	Expected Allelic Frequency	Observed by ddPCR	NGS Allelic Frequency
BRCAI	p.S1634G	5.0%	4.6%	4.5±0.4%
BRCA1	p.K1183R	5.0%	4.7%	4.8±0.4%
BRCAI	p.P871Q	45.0%	46.8%	48.3±2.7%
BRCAI	p.K820E	5.0%	4.9%	5.1±0.1%
BRCAI	p.S694S	5.0%	4.5%	4.7±0.3%
BRCAI	p.D435Y	5.0%	4.2%	4.9±0.4%
BRCA2	p.N289D	5.0%	5.2%	5.3±0.3%
BRCA2	p.H743H	5.0%	4.9%	4.5±0.4%
BRCA2	p.N991D	5.0%	4.7%	5.2±0.9%
BRCA2	p.S1172S	5.0%	5.1%	5.2±0.5%
BRCA2	p.V1269V	5.0%	5.9%	5.3±0.3%
BRCA2	p.L1521L	100.0%	100.0%	100.0±0.0%
BRCA2	p.N1784fs	10.0%	10.4%	11.3±0.9%
BRCA2	p.V2171V	100.0%	100.0%	100.0±0.0%1
BRCA2	p.V2466A	100.0%	100.0%	00.0±0.0%
BRCAI	p.R1443*	1.0%	1.0%	0.74±0.0%
BRCA2	p.K1132K	45.0%	47.2%	44.1±2.0%
BRCA2	p.D1420Y	5.0%	4.8%	5.1±0.4%
BRCA2	p.K1691fs	5.0%	4.7%	7.6±0.9%
BRCA2	p.S455S	5.0%	5.6%	5.6±0.7%

Note: iGeneTech MultipSeq® BRCA1/2 Research Assay V2 (for Illumina) was used to test Cobio BRCA reference standard：100% detection rate for 21 mutants,and the detected frequencies were essentially consistent with the theoretical mutation frequencies.

Stable and superior capture performance across multiple sample types

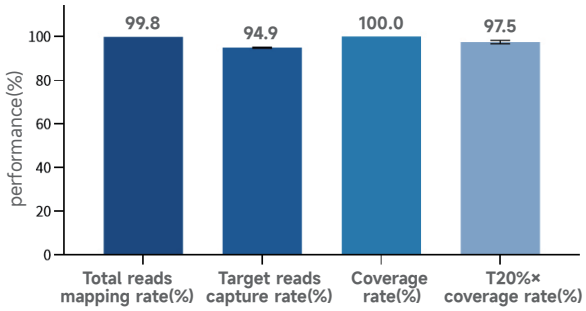

Figure 1. Performance in different sample types.

Genomic DNA was extracted from blood, female saliva, and male saliva samples. Libraries were prepared with 40 ng input gDNA each and sequenced on the Illumina NovaSeq 6000 platform (2 × 150 bp paired-end) to an approximate depth of 120 Mb per sample.

PRODUCT INFORMATION

Product Name	Spec.	Cat.
MultipSeq® BRCA1/2 Research Assay V2* 96 rxn	96 rxn	M62232
IGT® UDI Primer 1-96 (10 μM each, for Illumi	96* 1 rxn	C80202

**IGT® can provide kits compatible with Illumina, MGI etc., as well as universal reagents corresponding to each platform.*

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