FLUIDIGM

DATA SHEET
PN 100-3489 B1

Access Array BRCA1 / BRCA2 / TP53 Target-Specific Panel

Build the highest quality amplicon libraries with qualified assays

- **Covers 100% of the exons within the genes**
- **Supported on the Illumina HiSeq and MiSeq, Ion Torrent PGM and Roche 454 sequencers**
- **Lowest cost per sample**

The Access Array™ BRCA1/ BRCA2/TP53 Target-Specific Panel introduces efficient and effective primers for analysis of the BRCA1, BRCA2, and TP53 genes. BRCA1 and BRCA2 are tumor suppressors involved in cell growth, cell division, and DNA repair. Mutations in these genes affect the DNA repair process and are associated with a higher risk of hereditary breast-ovarian cancer syndrome. TP53, which codes for the p53 tumor suppressor protein, is frequently mutated in multiple cancers. Mutations in the TP53 gene can disrupt normal cellular processes such as apoptosis, genomic DNA stability, and the inhibition of angiogenesis. Studying these genes may provide essential information about cancer progression.

The Access Array Target-Specific Panels are optimized to work with the Access Array™ System. The Access Array System builds the highest quality amplicon libraries in the least amount of hands-on time, at the lowest per sample cost for all major NGS platforms.

- > 85% uniformity of coverage at 5X from average
- > 90% mapped to the reference genome
- > 95% mapped to target
- 20 minutes hands-on time
- 50 ng input DNA

Library preparation is the foundation for a successful targeted sequencing run. However, traditional methods create bottlenecks and introduce risk to quality and reproducibility through the high number of steps and touch points in the protocols. The Access Array System eliminates these variables through its instrumentation and integrated fluidic circuits (IFCs) to provide unparalleled quality amplicons.unparalleled quality.

*Illumina platforms only. Ion Torrent PGM Sequencer produces data that maps to the genome at > 70%.

Easy Workflow

Target enrichment from DNA to a finished amplicon library can be completed in five hours in three simple steps with only 20 minutes of hands-on time.

Complete Experiments In Three Easy Steps.

1

Load

In the pre-PCR IFC Controller AX, samples and primers are automatically combined into 2,304 unique PCR reactions

2

Amplify

The IFC is placed in the FC1™ Cycler for target amplification

3

Harvest

After PCR, products from each sample are pooled on-chip in the post-PCR IFC Controller AX and pumped out for collection

DESIGNED TO COVER 100% OF EXONS

Exons are coded regions that express proteins for a particular gene. Capturing 100% of exons is a common design challenge in assay development. Fluidigm targeted oncogene assays have been designed to cover 100% of the exons contained in the respective genes increasing the probability of specific and accurate analysis.

HIGH UNIFORMITY

Coverage uniformity for a given library is defined by the percentage of amplicons that produce reads within 5X of average. This is important for planning successful sequencing runs so that minimum coverage for each amplicon can be achieved ensuring proper depth of coverage in the genomic regions of interest. Figure 2 demonstrates the coverage uniformity found in the *BRCA1/BRCA2/TP53* Target-Specific Panel across the Illumina MiSeq and HiSeq sequencers, as well as the Ion Torrent PGM sequencer.

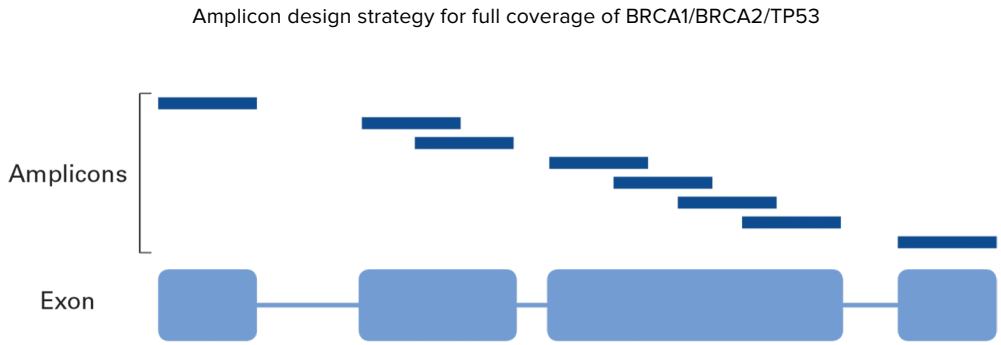

Figure 1. An illustration depicting how a tiled approach to primer design can be used to cover difficult exon regions in a gene.

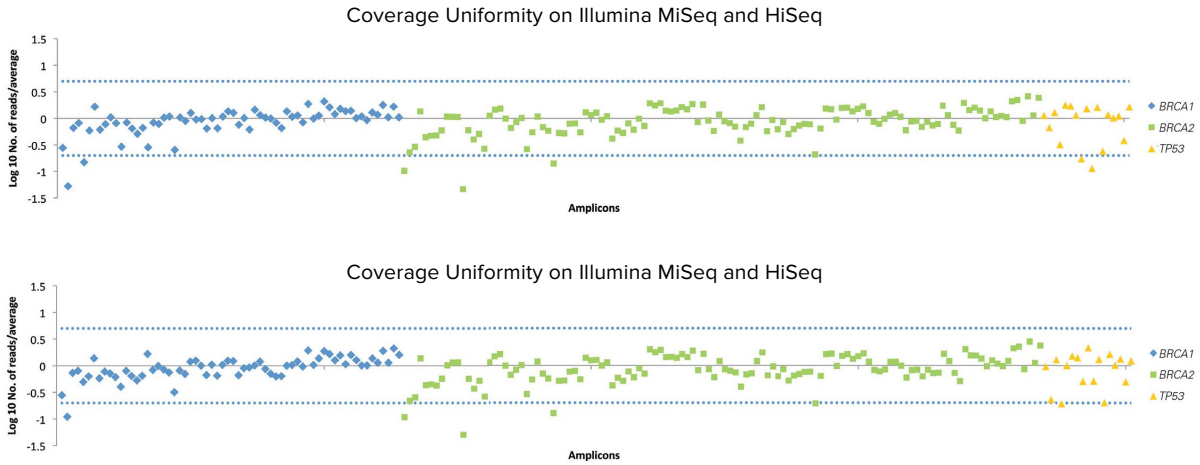

Figure 2. The coverage uniformity for the Ion Torrent PGM, Illumina MiSeq, and HiSeq sequencers is > 95%.

HIGH SPECIFICITY

Mapping to the target region of interest is an indication of specificity. The Access Array Target-Specific Panel mapped to their targets at 99%, exceeding the specification.

The Access Array *BRCA1/BRCA2/TP53* Target-Specific Panel, when combined with the Access Array System, is the fastest, simplest, and most accurate approach to generating libraries for assaying these critical oncogenes. The specificity and sensitivity of PCR makes it the ideal amplicon library creation strategy. The Access Array System is the only high-throughput target enrichment system designed to work with all major next-generation sequencing instruments. The system combines the cost and throughput benefits of microfluidics with the proven performance and flexibility of PCR while reducing hands-on time to produce superb accuracy in the library construct.

The era of next-generation sequencing arrived with a great deal of promise, and much of that promise depends on reliable, accurate, and specific sample preparation. There are other methods for sample preparation, but only one is considered the most straightforward and least error-prone. Unlock the promise of NGS, and easily move from sample to sequence ready with the Access Array System today.

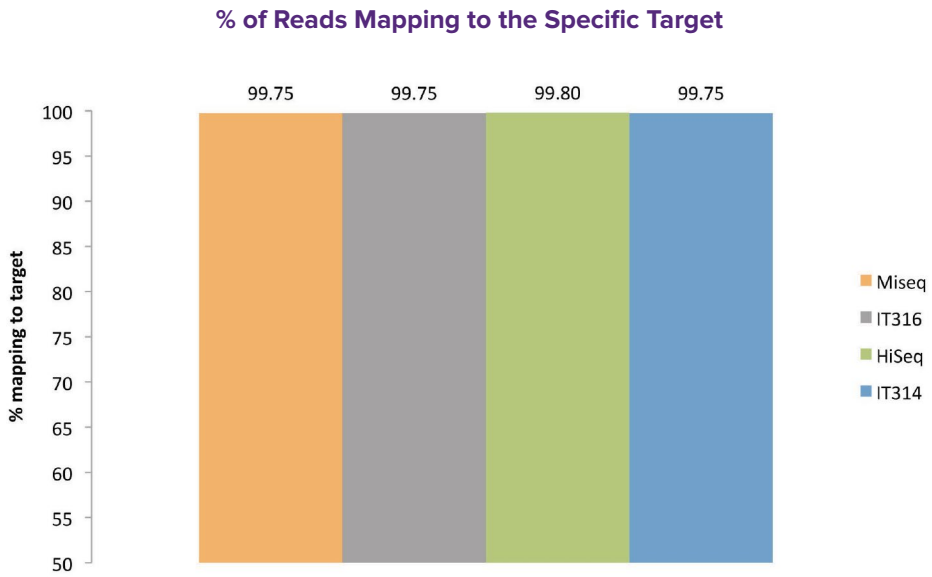

Figure 3. The Access Array Oncogene Target-Specific Panels mapped to their targets at 99% in validation.

FLUIDIGM SOLUTIONS
Fluidigm Access Array™ System for Next-Generation Sequencing

- **High Throughput**
  Simultaneously enrich targets of interest from 48 samples at a time. When used with the Access Array Barcode Library, each library is uniquely tagged allowing upto 384 samples to be pooled and sequenced in a single multiplex sequencing run with no additional library preparation
- **Ease of Use**
  Produce 48 sequencer-ready libraries from genomic DNA in three steps
- **Open Platform**
  Works across all next-generation sequencing platforms, including all Illumina systems, the Ion Torrent PGM, and 454, as well as upcoming third-generation sequencers
- **High Quality**
  Perform powerful data analysis with excellent amplicon uniformity

SPECIFICATIONS 210 bp Primer Set

Gene	# of Primers	Amplicon Length (Average)
BRCA1	64	190 bp
BRCA2	120	184 bp
TP53	16	197 bp

ORDERING INFORMATION

Product	P/N
Access Array BRCA1/BRCA2/TP53 Target-Specific Panel	100-5451

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