

Access Array EGFR / MET 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™ EGFR/MET Target-Specific Panel introduces efficient and effective primers for the analysis of these key regions of interest in cancer research. The Epidermal Growth Factor Receptor (EGFR) gene plays a critical role in the control of cell proliferation, differentiation, and survival. Abnormalities in EGFR-related pathways have been linked to a range of cancers, including lung cancer, colorectal cancer, and glioblastoma. This panel includes primers for the MET gene that encodes for the hepatocyte growth factor receptor protein. Abnormal activation has been implicated with the trigger of tumor growth, angiogenesis, and metastasis. These genes may be relevant

targets for cancer therapy and provide data needed in the development of new treatments.

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 5X coverage
- > 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 amplicons of unparalleled quality.

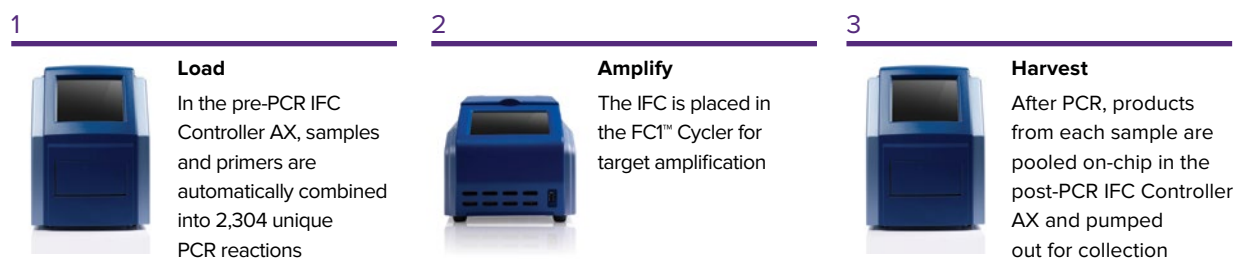


*Illumina platforms only. Ion Torrent PGM Sequencer produces data that maps to the genome at > 70%.

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.



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 EGFR/MET Target-Specific Panel across the Illumina MiSeq and HiSeq sequencers, as well as the Ion Torrent PGM sequencer.

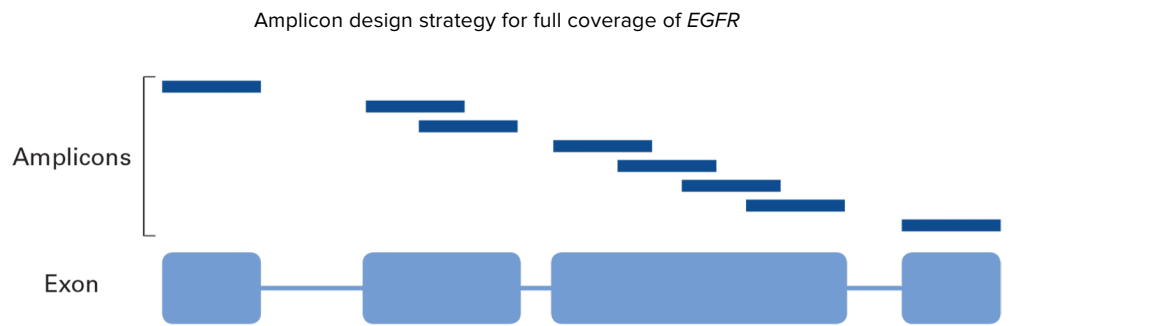


Figure 1. An illustration depicting how a tiled approach to primer design can be used to cover difficult exon regions in a gene.

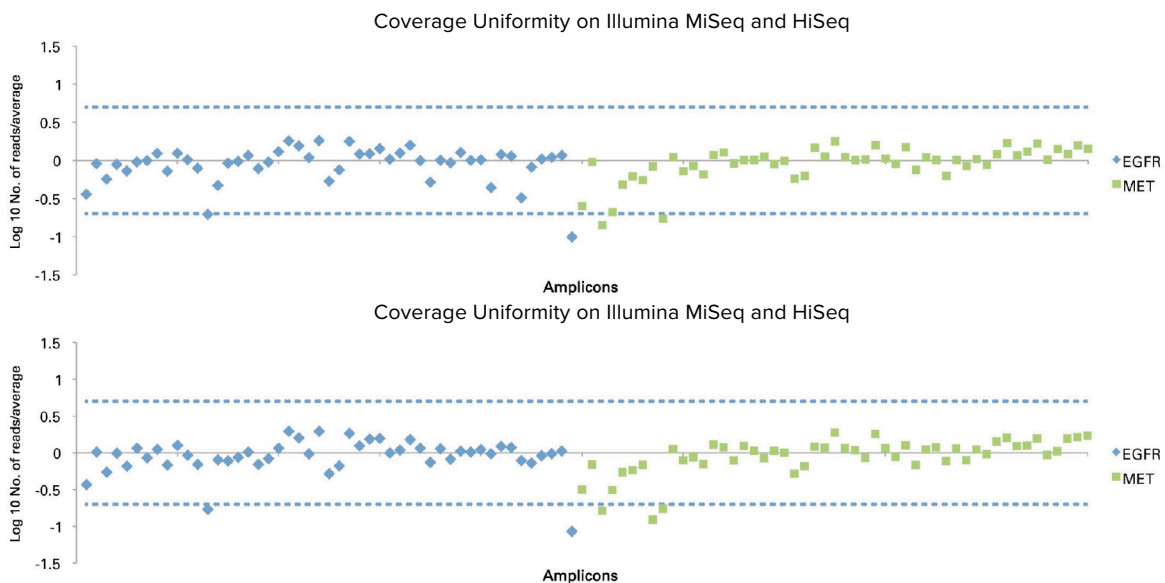


Figure 2. The coverage uniformity for the Ion Torrent PGM, Illumina MiSeq, and HiSeq sequencers is > 95%.

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 EGFR/MET 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.

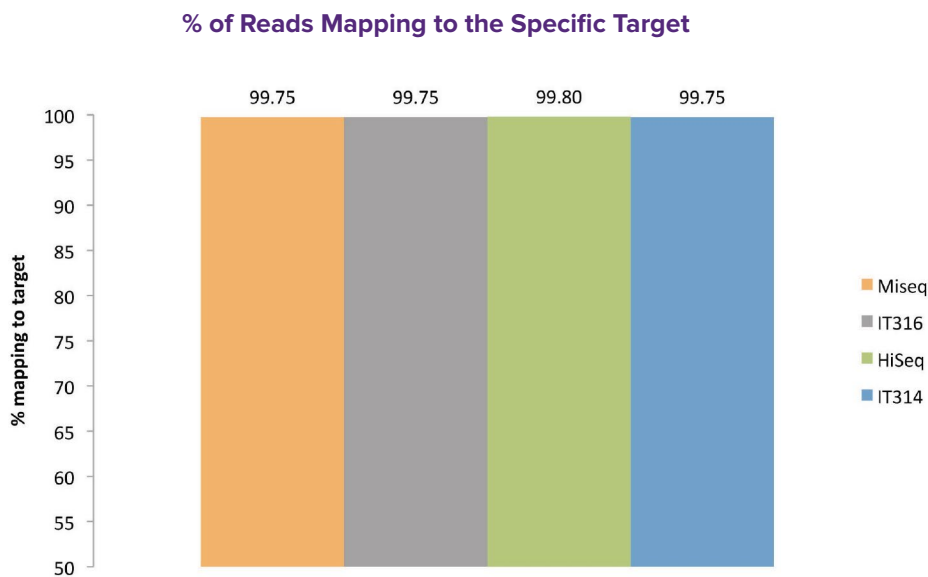


Figure 3. The Access Array Oncogene Target-Specific Panels mapped to their targets at 99% in validation.

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)
EGFR	49	180 bp
MET	50	180 bp

ORDERING INFORMATION

Product	P/N
Access Array EGFR/MET Target-Specific Panel	100-6060

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