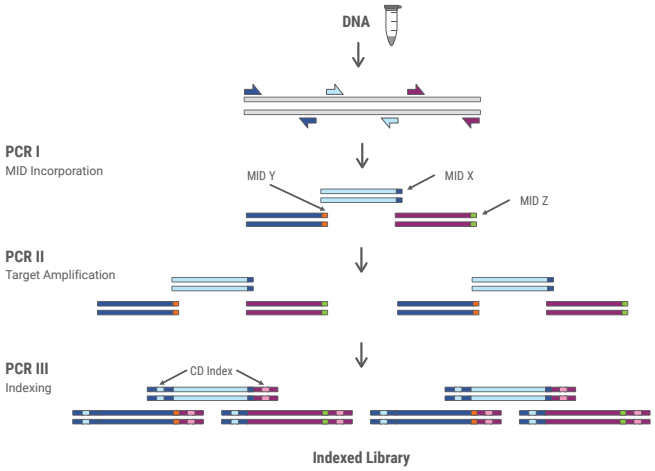
SWIFT AMPLICON HS PANELS

Confident Detection of Low Frequency Variants in Liquid Biopsy Sequencing

Highlights

- **Sensitive and Specific**
  Robustly detect SNVs and indels down to 0.25% allele frequency
- **Compatible with cfDNA and FFPE**
  Amplifies from 10-50 ng of cfDNA
- **Fast workflow, high quality data**
  From DNA to Illumina® compatible libraries within 3 hours
- **Paired Data Analysis Tools**
  Cloud-based or open source



Swift Amplicon HS Panels facilitate targeted variant calling of clinically relevant mutations at and below 1% frequency. The technology enables this by the incorporation of molecular identifiers (MIDs or UMIs), which improve sensitivity and specificity by removing false positive errors introduced during PCR and sequencing.

Supported Applications

- Oncology – liquid biopsy cfDNA and FFPE tissue
- Genome/Host Detection – Graft vs. Host Disease and Fetal in Maternal cfDNA*
- Custom targets*

** Please inquire*

High Sensitivity and Specificity for Key Mutations

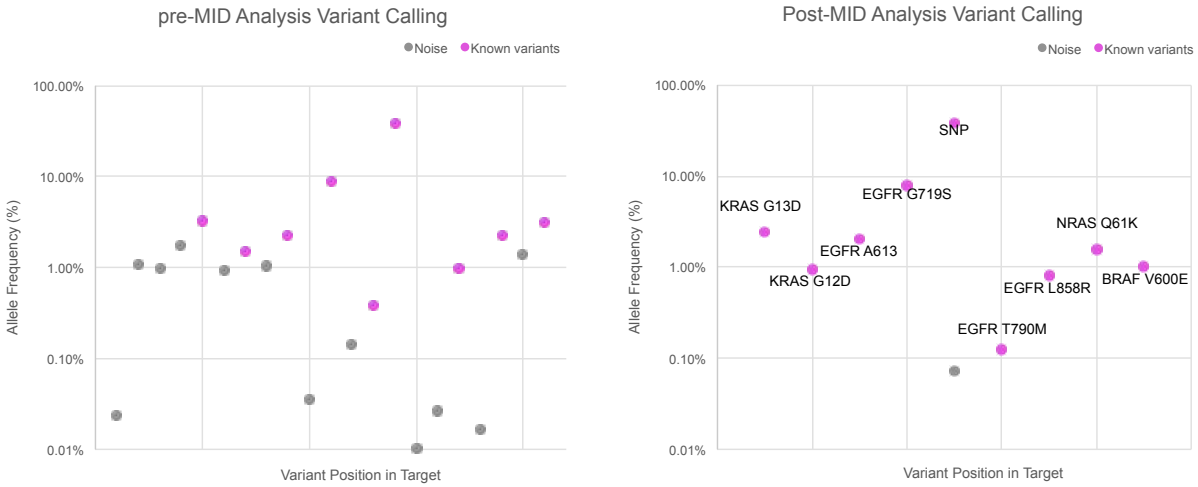


Figure 1. *Library prepared from 10 ng of Horizon™ HD701 quantitative multiplex reference standard spiked into Coriell repository DNA (NA12878) at 25% was analyzed for the presence of false positives. Variant calling before generation of a consensus sequence with MIDs (left) leads to false positive calls at and below 1%. After generation of a consensus sequence with MIDs (right), all but one false positive was eliminated while all known variants were retained.*

Validated Detection of Sub 1% Variants from cfDNA Reference Standard

Gene	Mutation	Chr	Position	10 ng SeraSeq ctDNA AF 0.5%			20 ng SeraSeq ctDNA AF 0.25%		
				Expected AF	Observed AF Rep 1	Observed AF Rep 2	Expected AF	Observed AF Rep 1	Observed AF Rep 2
BRAF	p.V600E	7	140453136	0.5%	0.19%	0.45%	0.25%	0.18%	0.18%
EGFR	p.T790M	7	55249071	0.5%	0.43%	0.57%	0.25%	0.33%	0.36%
EGFR	p.L858R	7	55259515	0.5%	0.86%	0.43%	0.25%	0.26%	0.25%
KRAS	p.G12D	12	25398284	0.5%	0.59%	0.47%	0.25%	0.20%	0.48%
NRAS	p.Q61R	1	115256529	0.5%	0.91%	0.56%	0.25%	0.30%	ND
EGFR	p.E746_A750delELREA	7	55242465	0.5%	0.24%	0.61%	0.25%	0.11%	0.07%
EGFR	p.D770_N771ins	7	55249012	0.5%	0.43%	0.57%	0.25%	0.32%	0.36%

Table 1. *The Swift Amplicon HS EGFR Panel consistently detected known variants in replicates from 10 ng SeraSeq™ ctDNA Reference Material v2 AF0.5% and 20 ng SeraSeq ctDNA Reference Material v2 AF0.25%. Variants were called from an MID based consensus sequence by LoFreq.*

Achieve Robust Sequencing Performance with cfDNA and High Molecular Weight DNA

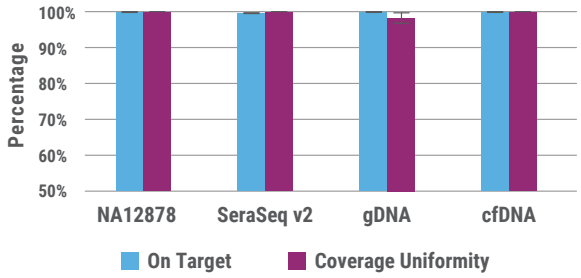


Figure 2. *Different sample types (10 ng input for each) were used to generate libraries with the Swift Amplicon HS EGFR Panel. The samples include Coriell repository DNA (NA12878), SeraSeq ctDNA Reference Material v2, genomic DNA (gDNA) isolated from whole blood from three different individuals, and matched cfDNA extracted from plasma from the same individuals. Libraries were sequenced on an Illumina MiniSeq® or MiSeq® and the target aligned reads and coverage uniformity (>20% of the mean) percentages were plotted.*

Specifications

Feature	Swift Amplicon HS EGFR Panel
Input DNA Required and Limit of Detection	10 ng for 0.5% detection; 20 ng for 0.25% detection
Unique Molecular ID	10 bp inline for > 1M molecular identifiers
Amplicons	17
Amplicon Size	134 bp (min 106 bp, max 149 bp)
Genes Covered	Hotspots in *EGFR, BRAF, KRAS, NRAS*
Assay Format	Single tube multiplex PCR; 3 hours DNA-to-Library
Components Provided	Target specific primer pool, PCR and library preparation reagents including indexing primers
Depth Recommendations	1M reads (0.5% from 10ng), 1.5M reads (0.25% from 20ng)
Multiplexing Capability	30 libraries on Illumina® MiSeq® v2
Sequencing Performance	> 95% On-Target and Coverage Uniformity
Compatible Platforms	Illumina

Ordering Information

Product Name	Reactions	Catalog No.
Swift Amplicon HS EGFR Panel	24	HS-51024

Visit **www.swiftbiosci.com** for easy ordering.

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