



ACCEL-AMPLICON® PLUS LUNG CANCER PANEL

The Lung Cancer Panel offers comprehensive and exon-level hotspot coverage of 17 clinically-relevant lung genes for both small cell lung cancer (SCLC) and non-small cell lung cancer (NSCLC). The panel covers over 11,000 COSMIC and 2,500 ClinVar mutations and generates targeted libraries compatible with Illumina® sequencing platforms.

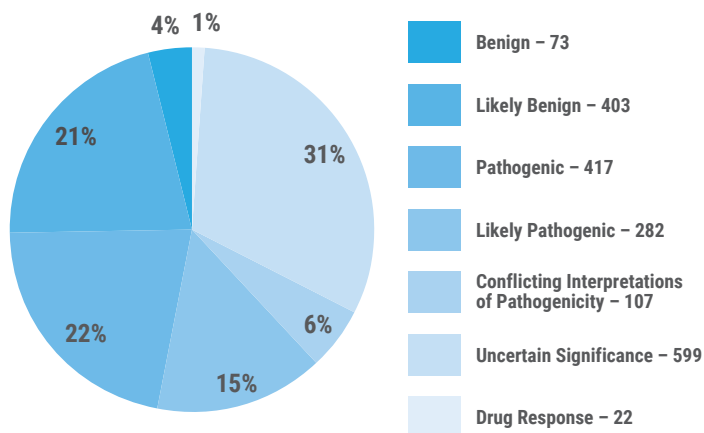


Figure 1. ACMG and AMP-classified variants of clinical significance covered by the Lung Cancer Panel

This panel enables:

- Reliable tracking of tumor/normal pairs
- Robust performance on cell-free DNA and FFPE samples
- Streamlined analysis with Primerclip or Genialis
- Easily modified to accommodate your research needs

Product Specifications

Feature	Specification
Amplicons	208
Average Amplicon Size	144 bp
Number of Genes	17
Gene List	AKT1, ALK, ARAF, BRAF, EGFR, ERBB2, ERBB4, FGFR1, FGFR2, FGFR3, KRAS, MAP2K1, MET, NRAS, PIK3CA, PTEN, TP53 (Bold indicates whole CDS coverage)
Total Target	18 kb
Input Recommended	10 ng amplifiable DNA
Assay Format	Single-tube Multiplex PCR reaction + Dual Indexed Adapters
Time Required	2 hours from DNA to library
Multiplexing on MiSeq v3 at 5000X depth (50M PE reads)	48 samples
Limit of Detection	1% SNV
Sample Compatibility	Cell line, whole blood, cell-free DNA, FFPE

Performance

Achieve Robust Sequencing Performance Over a Wide Range of Samples

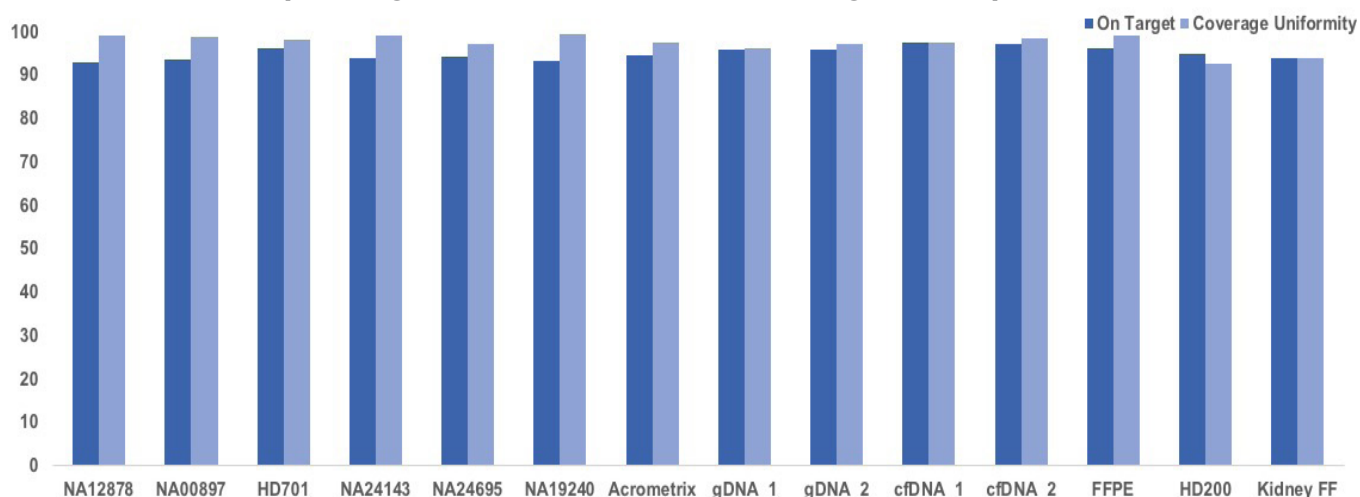


Figure 2. An array of control DNA samples (10 ng input for each) was used to generate libraries with the Accel-Amplicon Plus Lung Cancer Panel. The samples include male and female Coriell repository DNAs of different ethnicities, Horizon HD701 quantitative multiplex reference standard, the Acrometrix™ Oncology Hotspot Control, gDNA and cfDNA extracted from human blood, circulating cell-free DNA, and three formalin-compromised samples, including Horizon HD200 FFPE. Libraries were sequenced on an Illumina MiniSeq instrument and the on target aligned reads and coverage uniformity percentages were plotted.

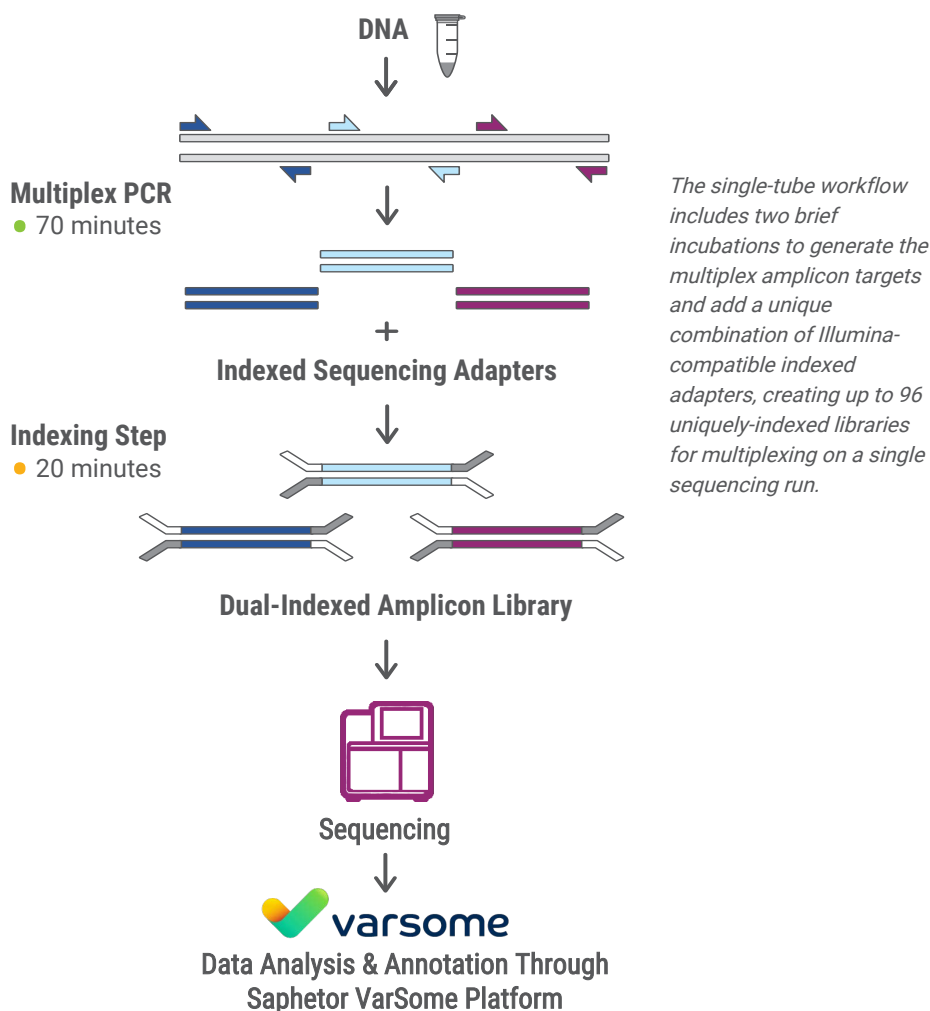
Detect Low Frequency Variants Accurately from Formalin-Compromised DNA

CHR	POS	Gene	Mutation AA	Mutation Type	Expected Frequency (%)	Average Detected Frequency (%)
7	55241707	EGFR	G719S	SNV	24.5	23.8
3	178952085	PI3KCA	H1047R	SNV	17.5	17.8
12	25398281	KRAS	G13D	SNV	15.0	14.9
1	115256530	NRAS	Q61K	SNV	12.5	11.8
7	1040453136	BRAF	V600E	SNV	10.5	11.0
3	178936091	PI3KCA	E545K	SNV	9.0	9.2
7	116339847	MET	V237fs	DEL	6.5	7.0
12	25398284	KRAS	G12D	SNV	6.0	6.6
7	55259515	EGFR	L858R	SNV	3.0	3.0
7	55242464	EGFR	ΔE746 - A750	DEL	2.0	1.4
7	55249071	EGFR	T790M	SNV	1.0	1.1

Figure 3. The Accel-Amplicon Plus Lung Cancer Panel consistently detected validated variants at the expected frequency in replicates from 10 ng of the Horizon Diagnostics Quantitative Multiplex DNA Reference Standard HD200. Variants were called by LoFreq (Genome Institute of Singapore).

Fully customizable. Rapidly create your own panel by building from our pre-designed Accel-Amplicon Plus panels. You can add any target gene including our pre-validated primers or novel targets. We will design, pool and validate your assay for you.

Single-Tube, 2-Hour Workflow



Ordering Information

Product Name	Indexing Included	Catalog No.
Accel-Amplicon Plus Lung Cancer Panel (48 rxns)	8 i5* X12 D701-712	AP-LG8048
VarSome Data Analysis Token (48 Samples)	N/A	AL-VS48

i5* Illumina Truseq CD indexes D501-D508

Visit www.swiftbiosci.com for easy ordering.



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