PILLAR BIOSCIENCES

illumina®

oncoReveal™ Multi-Cancer with CNV & RNA Fusion Panel

The **oncoReveal™ Multi-Cancer with CNV & RNA Fusion Panel** is a combined DNA/RNA multi-cancer panel. The assay combines the DNA-based oncoReveal™ Multi-Cancer v4 with CNV Panel with the oncoReveal™ Multi-Cancer RNA Fusion v2 Panel allowing for joint sequencing. The assay uses proprietary Stem-Loop Inhibition-Mediated amplification (SLIMamp®) technology, a tiled amplicon-based library prep chemistry for efficient single-tube target enrichment.

Variants and CNVs detected from DNA

ABL1	CDKN2A	FBXW7	GNAS	KIT ●	NPM1	PTPN11	SRC
AKTI	CSF1R	FGFR1 ●	HNF1A	KRAS ●	NRAS	RAC1	STK11
ALK	CTNNB1	FGFR2 ●	HRAS	MAP2K1	NTRK1	RB1	TP53
APC	DDR2	FGFR3 ●	IDH1	MET ■	NTRK2	RET	VHL
ATM	EGFR ■	FLT3 ●	IDH2	MLH1	NTRK3	ROS1	
BRAF	ERBB2 ■	FOXL2	JAK2	MPL	PDGFRA ●	SMAD4	
CCNE1 ●	ERBB4	GNA11	JAK3	MYC ■	PIK3CA ●	SMARCB1	
CDH1	EZH2	GNAQ	KDR ●	NOTCH1	PTEN	SMO	

CNVs detected and verified by NIST reference standard are indicated by ■ CNVs can also be detected in genes indicated by ●

Fusions and expression insights detected from RNA

Driver gene fusions (fusion partners not listed)

ALK	EGFR	FGFR2	MET	NTRK1	NTRK3	PPARG	RAF1	ROS1
BRAF	ERG	FGFR3	NRG1	NTRK2	PBX1	PRKACA	RET	TFE3

Simple NGS library prep workflow

Maintain control of samples and results with single-tube, tiled amplification that can be performed in-house by any NGS lab

Sensitive and robust chemistry

Achieve variant detection as low as 1% VAF† without UIDs‡ even with limited DNA input or poor sample quality

Reduced fully-loaded lab costs

Improve lab efficiency and reduce “no calls”, repeat testing, and difficult interpretation decisions

‡UID, unique ID; also known as unique molecular ID (UMI); †VAF, variant allele frequency

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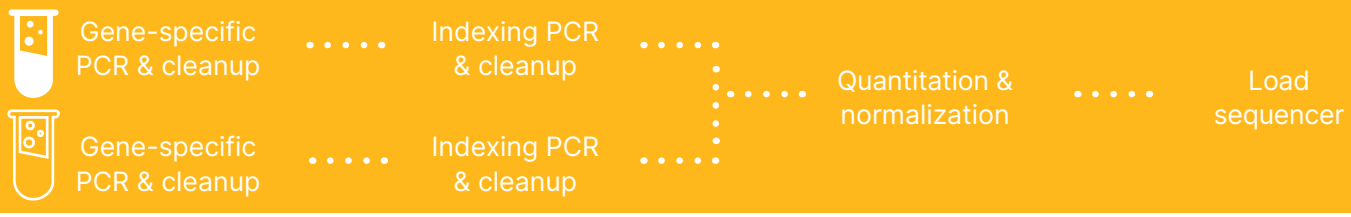
Simple, one-day workflow



Panel specifications

	oncoReveal™ Multi-Cancer v4 with CNV	oncoReveal™ Multi-Cancer RNA Fusion v2
Enrichment chemistry	Multiplex PCR using tiled amplicons	
Number of pools	2 pools	
Number of genes/amplicons	60/341	18 genes and >80 partners, plus MET 14 exon skipping
Number of targets	Hotspots in 60 genes; CNVs for 14 genes; ~33.1kb total size	Fusions in 18 driver genes; expression for 11 genes
Variant types	SNVs, small and medium indels, and CNVs	Fusion RNA transcripts
Average amplicon size	142bp (range 86bp - 185bp)	120bp
Recommended input range	5ng to 80ng DNA	10ng to 50ng RNA
Sample types	DNA from tissue or blood; FFPE	RNA from FFPE or tissue
Mapping rate	99.3% ± 0.3%	n/a
% on-target aligned reads	99.5% ± 0.1%	n/a
Coverage uniformity (% targets with >0.2x mean coverage)	98.2% ± 0.7%	n/a
Total assay time (from DNA to sequencer)	<9 hours	
Sequencing platforms	Illumina® sequencers	

For more information go to:
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