PARAGON GENOMICS

Excellence In- Excellence Out

CleanPlex™ OncoZoom Panel

The CleanPlex™ OncoZoom Panel is a cancer hotspot panel with 601 primer pairs in a single pool, which enables researchers to quickly survey more than 2900 commonly observed mutational positions, from 65 oncogenes and tumor suppressor genes. The panel kit contains primers, multiplex PCR reagent, digestion reagent and other reagent components necessary for constructing amplicon libraries for Next-Generation Sequencing on Illumina Sequencers.

Simplify your workflow

The entire library preparation workflow can be finished in 2.5 hours with only 30-minute hands-on time from sample DNA to sequencing-ready libraries. No need for ligation, end repair, DNA fragmentation, overnight hybridization, or microfluidic devices.

Achieve extreme uniformity

Our unique multiplex PCR buffer system and strong primer design capability ensure optimal coverage uniformity for target amplicons. For the OncoZoom panel, we have consistently observed 100% uniformity (at ≥ 0.2x mean depth) and 97% uniformity (at ≥ 0.5x mean depth).

Take on difficult samples with limited DNA input

With an average amplicon size of 146 bp, the OncoZoom panel is compatible with degraded samples such as formalin-fixed, paraffin-embedded (FFPE) tissue DNA and circulating cell-free DNA (cfDNA). You can obtain high quality sequencing data even with just 100 pg of input DNA.

Detect low-frequency alleles

Our proprietary CleanPlex™ Background Cleaning technology removes background PCR noise and enables you to reliably detect somatic mutations with a frequency as low as 0.5%.

Detect 1% of somatic mutations from Multiplex I cfDNA Reference Standard Set HD780 (N=9)

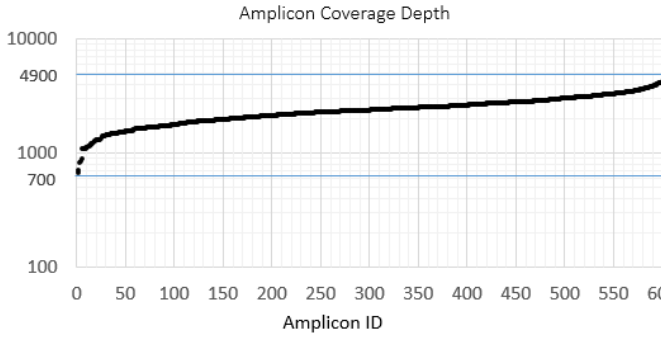
Gene	Mutation	Expected Frequency	Observed Frequency	Standard Deviation
EGFR	p.E746_A750>VP	1.0	1.3	0.4
EGFR	p.L858R	1.0	0.9	0.2
EGFR	p.T790M	1.0	1.2	0.7
EGFR	p.V769-D770insASV	1.0	0.7	0.2
KRAS	p.G12D	1.3	1.4	0.5
NRAS	p.A59T	1.3	1.4	0.5
NRAS	p.Q61K	1.3	1.4	0.5
PIK3CA	p.E545K	1.3	1.4	0.4

Detect 5% of somatic mutations from Multiplex I cfDNA Reference Standard Set HD780 (N=9)

Gene	Mutation	Expected Frequency	Observed Frequency	Standard Deviation
EGFR	p.E746_A750>VP	5.0	5.8	1.0
EGFR	p.L858R	5.0	4.4	0.7
EGFR	p.T790M	5.0	4.6	1.0
EGFR	p.V769-D770insASV	5.0	4.3	1.2
KRAS	p.G12D	6.3	7.2	1.5
NRAS	p.A59T	6.3	5.5	1.0
NRAS	p.Q61K	6.3	6.4	1.2
PIK3CA	p.E545K	6.3	6.2	1.4

*Data based on Horizon Discovery Multiplex I cfDNA Reference Standard samples with 10 ng of input DNA.

100% observed uniformity at ≥ 0.2x mean coverage



The difference between maximum amplicon coverage and minimum coverage is within 1 log.

Gene List				
ABL1	ERBB2	IDH1	NOTCH1	STK11
AKT1	ERBB3	IDH2	NPM1	TERT
ALK	ERBB4	JAK2	NRAS	TP53
APC	EZH2	JAK3	PDGFRA	TSC1
ATM	FBXW7	KDR	PIK3CA	VHL
BRAF	FGFR1	KIT	PIK3R1	
BRCA1	FGFR2	KRAS	PTCH1	
BRCA2	FGFR3	MAP2K1	PTEN	
CDH1	FLT3	MET	PTPN11	
CDKN2A	FOXL2	MLH1	RB1	
CSF1R	GNA11	MPL	RET	
CTNNB1	GNAQ	MSH6	SMAD4	
DDR2	GNAS	MTOR	SMARCB1	
DNMT3A	HNF1A	NF1	SMO	
EGFR	HRAS	NF2	SRC	

Ordering information	
Product Name	**Sku**
CleanPlex™ OncoZoom Panel (8 rxns)	916001
CleanPlex™ OncoZoom Panel (96 rxns)	916002
CleanPlex™ OncoZoom Panel (384 rxns)	916003

Specifications	
Sequencing Platform	Illumina Sequencers (MiniSeq, MiSeq, NextSeq, Hiseq)
Enrichment Method	Multiplex PCR
# of Primer Pools	1 pool
# of Primer Pairs	601 pairs
# of Target Genes	65 genes
Target Region Size	55199 bp
Amplicon Size	Average 146 bp (from 125-175 bp)
Species	Human
Recommended DNA Input (Amount)	For germline genotype calling: minimum 100 pg; For somatic mutation calling with an LOD of 1%: minimum 10 ng
Sample Type	Genomic DNA, FFPE DNA, cfDNA, and DNA from Blood, Tissue, Cell Culture, and Fine Needle Aspirate (FNA)
Sample Multiplexing (at ~2000x mean coverage)	MiSeq 2×150 read length: ~25 samples NextSeq mid output 2×150 read length: ~200 samples NextSeq high output 2×150 Read Length: ~600 samples
Coverage Uniformity (at ≥ 0.2x mean coverage)	≥95%
On-target Reads %	≥95%

PARAGON GENOMICS
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