



PARAGON GENOMICS
Excellence In- Excellence Out

CleanPlex™ BRCA1 & BRCA2 Panel

The CleanPlex™ BRCA1 & BRCA2 Panel contains 218 pairs of PCR primers targeting the full exon of the BRCA1 and BRCA2 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.

100% coverage of BRCA1 and BRCA2 with superior uniformity

The panel covers 100% of the coding regions and 10 bases beyond the exon-intron boundaries of the BRCA1 and BRCA2 genes. The observed uniformity of this panel (at $\geq 0.2x$ mean coverage) is over 99%.

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.

Take on difficult samples with limited input DNA

With an average amplicon size of 158 bp, this panel is compatible with degraded samples such as formalin-fixed, paraffin-embedded (FFPE) tissue DNA and circulating cell-free DNA (cfDNA). Obtain high quality sequencing data for germline genotype calling with just 200 pg of input DNA.

Ordering information

Product Name	SKU
CleanPlex™BRCA1 & BRCA2 (8 rxns)	916005
CleanPlex™BRCA1 & BRCA2 (96 rxns)	916006
CleanPlex™BRCA1 & BRCA2 (384 rxns)	916007

Specifications

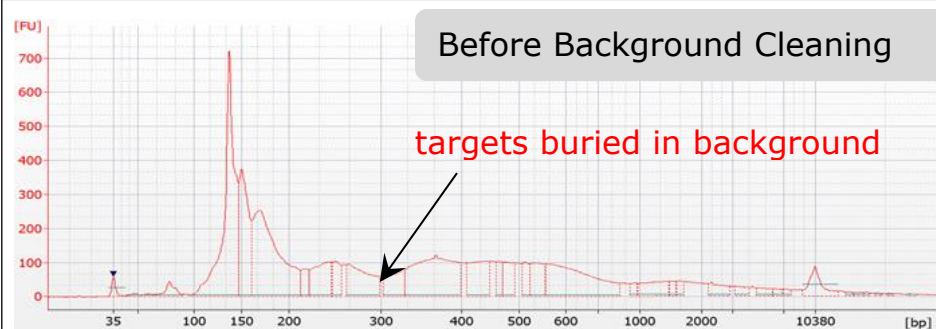
Sequencing Platform	Illumina Sequencers (MiniSeq, MiSeq, NextSeq, HiSeq)
Enrichment Method	Multiplex PCR
# of Primer Pools	2 pools
# of Primer Pairs	218 pairs
# of Target Genes	2 genes
Target Region Size	19268 bp
Amplicon Size	Average 158 bp (from 125-180 bp)
Species	Human
Recommended Input DNA (Amount)	For germline genotype calling: minimum 200 pg For somatic mutation calling with an LOD of 1%: minimum 20 ng (10 ng /pool)
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: ~55 samples NextSeq mid output 2×150 read length: ~425 samples NextSeq high output 2×150 Read Length: ~1300 samples

Looking to simplify NGS target enrichment



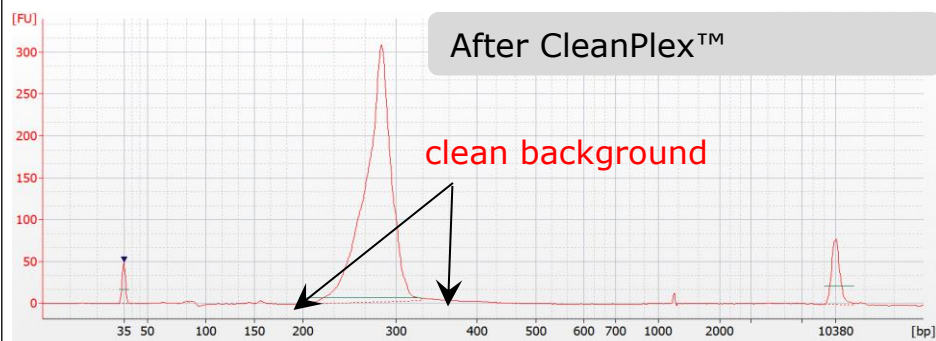
Before Background Cleaning

targets buried in background



After CleanPlex™

clean background



Most target enrichment kits do not provide effective background cleaning, resulting in sequencing of non-specific PCR products post amplification, which translates into the generation of excess reads.

By using CleanPlex™ technology, background noise is greatly reduced and only the targets of interest are sequenced. This proprietary multiplex PCR technology eliminates DNA fragmentation, hybridization and ligation steps, resulting in higher target coverage, on-target rates and lower

Important advantages to NGS lab operations and data quality

	Competitor X	Paragon Genomics CleanPlex™ Solution
Uniformity	87 - 97%	>98%
Specificity	87 - 97% on-target bases	>97% on-target bases
Time	6 hours	2.5 hours
Minimum Sample input	20 - 40 ng	0.1 ng
Workflow	5 steps	3 steps

Comparison of Paragon Genomics CleanPlex™ solution multiplex PCR method with a competitor