Fast, simplified sequencing for targeted oncology research applications

Ready-to-use panels and proven Illumina sequencing deliver an efficient and accurate NGS workflow

Targeted oncology sequencing with flexibility and ease

Illumina has partnered with Pillar Biosciences® to offer a simplified, rapid next-generation sequencing (NGS) workflow for targeted oncology research applications. Pillar oncoReveal® panels for solid tumor and hematological malignancies can be run on Illumina benchtop sequencing systems, with the MiSeq™ i100 Series providing the fastest option. DRAGEN™ software and Illumina Connected Insights provide analysis and reporting.



Easy-to-implement, simplified NGS workflow



Sample to report in < 24 hours



Accurate variant detection below 5% VAF

Rapid sample-to-report NGS workflow for oncology research applications



STEP 1

Library preparation

Prepare libraries with oncoReveal panels

7-10.5 hr

STEP 2

Sequencing

Sequence on MiSeq i100 Series

7.5 hr

STEP 3

Secondary analysis

Analyze using DRAGEN Amplicon

~2 min

STEP 4

Report

Interpret variants and generate report with Connected Insights

< 10 min

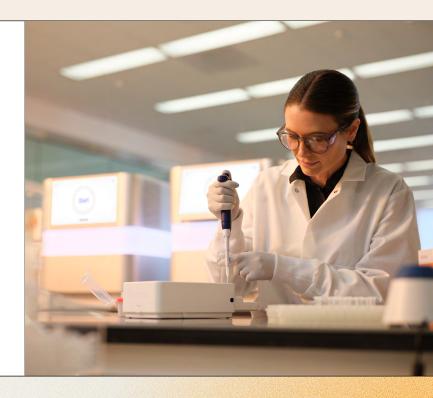


Select from a suite of targeted oncology research panels from Pillar Biosciences to run on the MiSeq i100 Series for rapid results

Pillar Biosciences targeted oncology research panel	Description	Cancer type
oncoReveal Multi-Cancer with CNV and RNA Fusion Panel	Combines DNA/RNA content across 78 genes	Solid tumor
oncoReveal Multi-Cancer RNA Fusion v2 Panel	Interrogates 18 driver genes and 83 fusion partners	
oncoReveal Solid Tumor v2 Panel	Targets 48 genes across multiple cancers	
oncoReveal BRCA1 & BRCA2 plus CNV Panel	Targets BRCA1/2 mutations and copy number variations	
oncoReveal Myeloid Panel	Interrogates 58 genes linked to hematological malignancies	Hematologic malignancy
oncoReveal Essential MPN Panel	Assays for key mutations in MPL, JAK2, and CALR genes	

Equip your research lab with targeted oncology sequencing

Pillar oncoReveal panels combined with Illumina sequencing and analysis provide accurate variant detection below 5% variant allele frequency (VAF) for single nucleotide variants (SNVs), insertions/ deletions (indels), copy number variants (CNVs), and RNA fusions, even with limited nucleic acid input or poor sample quality. These flexible solutions improve lab efficiency and reduce "no calls", repeat assays, and difficult interpretation. Go from sample to report in less than 24 hours.





Learn more



Contact your Illumina representative for more information.

