Ion AmpliSeq Comprehensive Cancer Panel

Extensive survey of over 400 genes with just 40 ng of DNA

The Ion AmpliSeq™ Comprehensive Cancer Panel facilitates broad oncology research using as little as 40 ng of DNA, with ~16,000 primer pairs multiplexed into just 4 pools.

Working with key cancer researchers and incorporating information from literature and database searches, we designed the Ion AmpliSeq Comprehensive Cancer Panel to target the exons of tumor suppressor genes and oncogenes frequently cited and frequently mutated. The Ion AmpliSeq Comprehensive Cancer Panel is designed to simultaneously interrogate coding DNA sequences and splice variants across multiple gene families.

This pathway-based gene selection profiles the mutational spectrum in known cancer driver genes and drug targets along with signaling cascades, apoptosis genes, DNA repair genes, transcription regulators, inflammatory response genes, and growth factor genes, all in a single assay. Additionally, this panel targets the 50 genes selected in the focused Ion AmpliSeq™ Cancer Hotspot Panel v2. The Ion AmpliSeq Comprehensive Cancer Panel allows researchers to fast-track projects by minimizing time-consuming and labor-intensive primer design and target selection procedures, while targeting an extensive set of oncology research genes.

After conducting broad variant surveys, researchers may choose to conduct in-depth somatic variant analysis of a subset of genes from this panel. Using the Ion AmpliSeq™ Designer, an online tool for creating and ordering custom panels, researchers can simply enter the selected genes and create a custom cancer gene research panel in just hours.

Simplicity

- As little as 40 ng of input DNA required—enabling sequencing of formalin-fixed, paraffin-embedded (FFPE) samples

Scalability

- ~16,000 primer pairs in just 4 tubes targeting >400 genes
- Supports automation for 96-well plate–based protocols, enabling rapid processing of large projects

Speed

- DNA to variants in a single day

Dataset for this panel is available at **thermofisher.com/ioncommunity**

Ion AmpliSeq Comprehensive Cancer Panel		
Targets	Exons with >400 oncogenes and tumor suppressor genes	
Amplicon length	125–175 bp (average 155 bp)	
Primer pool size	~16,000 primers in 4 tubes	
Input DNA required	10 ng per pool, 40 ng per DNA sample	
Time to results	Single-day workflow from DNA to annotated variants (run time varies by read length and chip type)	
Sample multiplexing	Ion PI™ or Ion 540™ Chip: 4 samples, ~1,000x average coverage	
	Specification	**Observed performance**
Coverage uniformity*	>90%	94%
On-target bases**	>95%	97%
Average depth of coverage	NA	350x

* Coverage uniformity = bases covered at >20% of the mean coverage.
** On-target bases = bases mapped to target regions, out of total mapped bases per run.

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ion torrent

Simplicity: requires as little as 40 ng of DNA; FFPE-compatible

The breakthrough requirement of using as little as 10 ng of input DNA per pool, or as little as 40 ng for the entire Ion AmpliSeq Comprehensive Cancer Panel, is designed to deliver accurate sample representation even from FFPE samples, which typically yield small amounts of DNA and often exhibit low quality or degradation. Target selection is completed using basic PCR equipment.

Speed: DNA to annotated variants in a single day

The single-day workflow from DNA to annotated variants allows researchers to undertake time-sensitive assays, producing targeted libraries in about 3.5 hours using simple PCR-based technology. Transfer the libraries to the Ion Chef™ System for template preparation, and sequence them on the Ion Proton™, Ion S5™, or Ion S5™ XL Systems. Automated analysis is then performed with Torrent Suite™ Software and Ion Reporter™ Software. This software can be used to automate bioinformatics analysis including variant annotations. It is ideal for use with routine DNA research assays (Figure 1).

Scalability: superior scope for oncology research

No other oncogene panel allows surveying >400 genes using ~16,000 primer pairs in a simplified, 4-tube primer pool format. The combination of high-level multiplexing, low DNA input requirements, and genomic scope of the targets alters how researchers can approach complex oncology research.

Additionally, Ion AmpliSeq™ library construction steps are automatable using standard 96-well, plate–based protocols—further simplifying the workflow and allowing large projects to be rapidly completed without additional sample transfer steps.

Confirm variants with TaqMan Assays

Integrated with the search portal for Applied Biosystems™ TaqMan™ Assays, Torrent Suite Software enables direct submission of detected variants for orthogonal confirmation experiments. Choose either Applied Biosystems™ TaqMan™ Mutation Detection Assays powered by castPCR™ technology on Applied Biosystems™ QuantStudio™ 6, 7, or 12K Flex Real-Time PCR Systems, or TaqMan™ SNP Genotyping Assays using digital PCR on the Applied Biosystems™ QuantStudio™ 3D Digital PCR System. Accurate and reliable results are achievable in about 3 hours. Find out more at **thermofisher.com/ordertaqman**

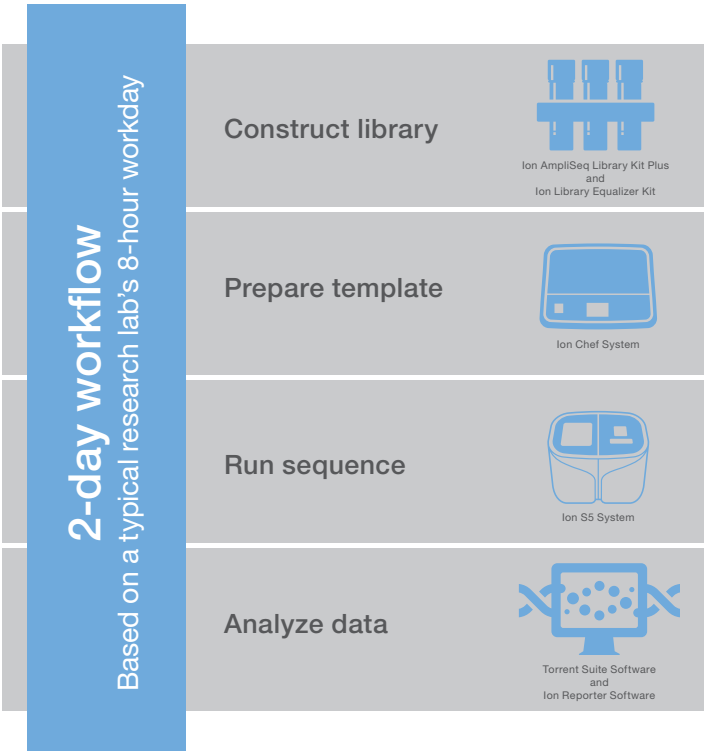

Figure 1. Ion AmpliSeq Comprehensive Cancer Panel workflow using an Ion PI or Ion 540 Chip: 4 samples, ~1,000x average coverage.

Ordering information

Product	Cat. No.
Ion AmpliSeq Comprehensive Cancer Panel (primer pool)	4477685
Ion AmpliSeq Library Kit 2.0 (8, 96, or 384 reactions for both PCR amplification and library construction)	4475345, 4480441, 4480442
Ion Xpress Barcode Adapters Kits	4471250, 4474009, 4474518, 4474519, 4474520, 4474521
Related Ion AmpliSeq products	**Cat. No.**
Ion AmpliSeq Cancer Hotspot Panel v2 (primer pool)	4475346
Ion AmpliSeq Custom Panels can be ordered via Ion AmpliSeq Designer. Find out more about custom panels at **thermofisher.com/ampliseqcustom**	

Discover how to transform your oncology research at
thermofisher.com/cancergenomics

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