KAPA HyperCap Oncology Panel

Better by Design

Leveraging more than a decade of probe design experience with an improved probe manufacturing process, the **KAPA HyperCap Oncology Panel** combines targeted interrogation of genes associated with somatic oncology with greater sequencing efficiency. Order this 214 Kb hybrid capture panel today and start investigating genes associated with oncology tomorrow.

- **Capture 13 genes strongly associated with somatic oncology**, along with additional hotspot variants commonly included in commercial FFPET and cfDNA controls
- **Access valuable, often elusive information** from low-quality FFPET samples
- **Achieve >97.5% of target coverage at 1000X** from as little as 10 ng cfDNA with (10 M high-quality clusters)
- **Streamline targeted sequencing with our HyperCap Workflow v3**, driven by KAPA HyperPrep or KAPA HyperPlus Library Prep Kits

Gene List, Full	CDS Coverage
ATM	KRAS
BRCA1	MET
BRCA2	MYCN
BRIP1	RAD51C
CHEK2	RAD51D
EGFR	TP53
ERBB2	

Project: KAPA HyperCap Fixed Panels, Pleasanton, CA 2021
For Research Use Only. Not for use in diagnostic procedures.

Access valuable, often elusive information from low-quality FFPET samples

- Improve sequencing accuracy with low-quantity and low-quality FFPET DNA samples by achieving a high percentage of error-free positions across your target (>94%) **(Figure 1)**
- Achieve uniform and deep sequencing coverage with >92% of bases covered within 0.5X–2X of the median and >88% of exon bases covered at >300X **(Figure 1)**

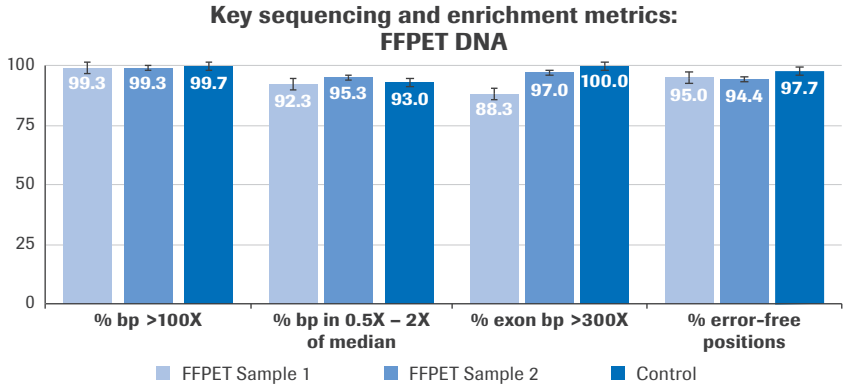

Figure 1. Key sequencing metrics from the KAPA HyperCap Oncology Panel with real-world, low-quality FFPET DNA and a control FFPET DNA sample, using KAPA Universal UMI Adapters. Sample libraries were prepared in duplicate from real-world samples and Horizon™ HD789 FFPET DNA following the KAPA HyperCap FFPET DNA workflow (10 ng FFPET DNA) using the KAPA HyperPlus Kit. Following single-plex probe hybridization, capture, and cleanup, final libraries were sequenced on a NextSeq™ 550 system (2 x 150 bp) and downsampled to 10 M high-quality filtered clusters prior to analysis. Error bars represent standard deviation.

Achieve >97.5% of target coverage at 1000X from as little as 10 ng cfDNA

- Attain high genome equivalent recovery rates and cover >97.5% of your target bases at ≥1000X from just 10 ng of cfDNA with the KAPA HyperCap cfDNA Workflow **(Figure 2)**
- Detect unique input molecules and recover a high percentage of duplex molecules by leveraging the ultra-high sensitivity provided by KAPA Universal UMI Adapters

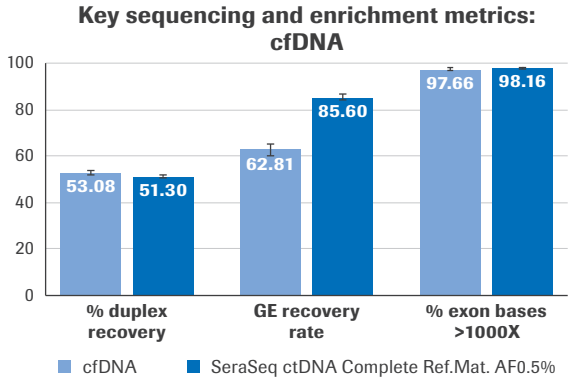

Figure 2. Key sequencing metrics for real-world and control cfDNA samples using the KAPA HyperCap Oncology Panel. Libraries were prepared from five cfDNA samples from healthy donors in parallel with SeraSeq® ctDNA Complete™ Reference Material AF0.5%; libraries were prepared in duplicate from 10 ng of DNA. The KAPA HyperCap cfDNA workflow was followed using the KAPA HyperPrep Kit, KAPA Universal UMI Adapters, and single-plex probe hybridization and capture. Final libraries were sequenced on a NovaSeq™ 6000 system (2 x 150 bp). Reads were downsampled to 50 M high-quality filtered clusters per sample. Light blue bars represent the average of all cfDNA samples. Error bars represent standard deviation.

Ordering information

Product Name	Capture Reactions	Catalog No.
KAPA HyperCap Oncology Panel	12	09462473001
	24	09462481001
	48	09462490001

Learn more at:
https://go.roche.com/HyperCapHP

Request an evaluation of the KAPA HyperCap Oncology Panel at:
https://go.roche.com/HyperCapEval

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