KAPA HyperExome Probes

Better by Design

Combining more than a decade of probe-design experience with an improved probe-manufacturing process, the new **KAPA HyperExome** probe pools enable efficient, uniform hybridization-based capture for Whole Exome Sequencing (WES). Achieve sensitive, reliable detection of genomic alterations, including single-nucleotide variations (SNVs), indels, copy-number variations (CNVs), gene fusions, inversions, and other rearrangements within exonic regions.

- **Reduce sequencing costs and save time** through superior capture uniformity that lowers the amount of sequencing required to detect variants
- **Reliably enrich challenging, previously inaccessible exonic regions**
- **Ensure accurate sample identification** with 387 sample-tracking SNPs
- **Streamline targeted sequencing** with our HyperCap Workflow v3, driven by KAPA HyperPrep or KAPA HyperPlus Library Prep Kits

Data on file.
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Reduce sequencing costs and save time

- Optimize sequencing throughput with the compact ~43 Mb design of KAPA HyperExome
- Achieve better coverage compared to Supplier X, especially with deeper sequencing

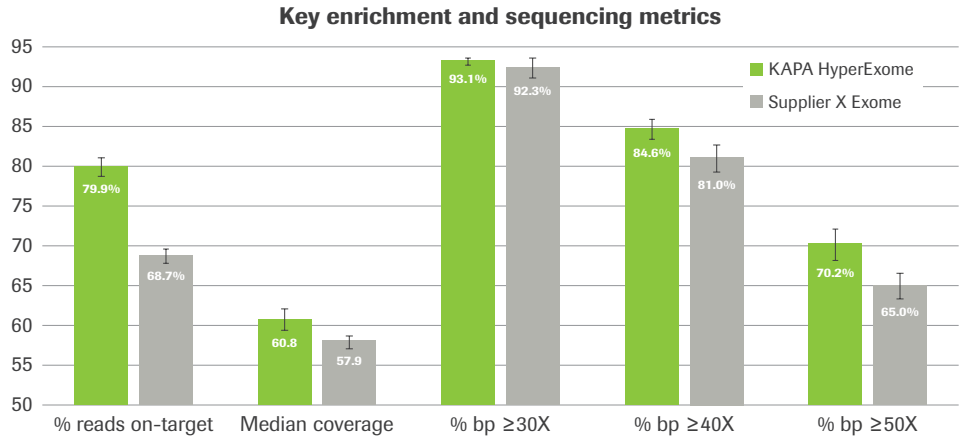

Figure 1. KAPA HyperExome yields greater % reads-on-target, deeper median coverage, and broader target coverage compared to the Supplier X Exome. Prior to capture with KAPA HyperExome probes, libraries were prepared from 100 ng of DNA with KAPA HyperPlus Kits using KAPA Universal Adapter and KAPA UDI Primer Mixes. Libraries (8) were multiplexed prior to capture, hybridized to probes for 16 hours, amplified post-capture, and sequenced on an Illumina NovaSeq sequencer (2 x 100 bp). Bars represent data from 16 different cell lines processed in triplicate.

Maximize throughput with superior capture uniformity

- Drive sequencing efficiency by leveraging design expertise and using extensively optimized panels
- Achieve best overall balance even across hard-to-capture regions

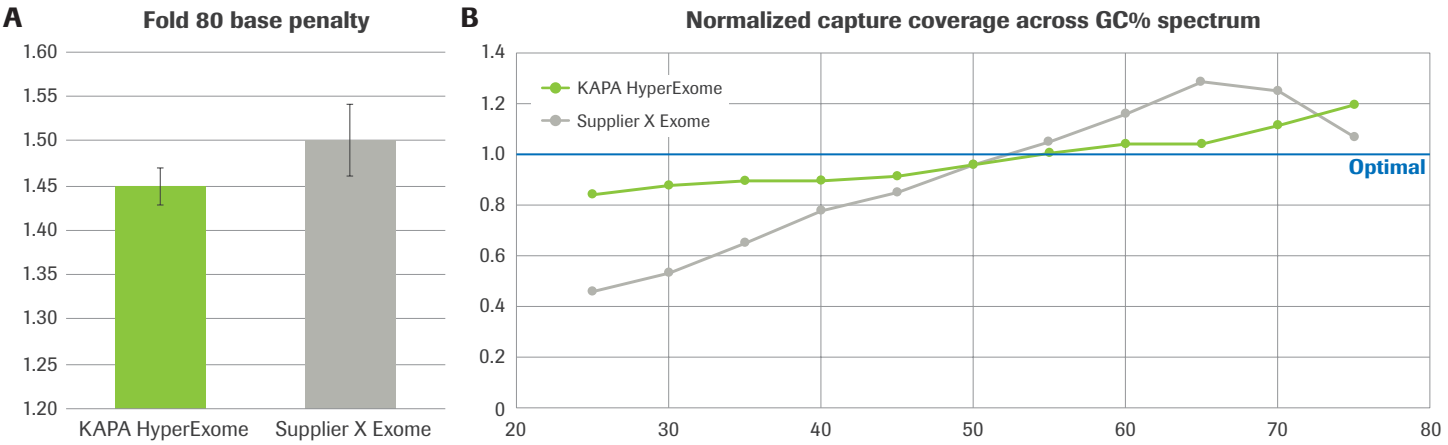

Figure 2. KAPA HyperExome achieves highly uniform coverage—even across regions with high or low %GC. Prior to capture with KAPA HyperExome probes, libraries were prepared from 100 ng of DNA with KAPA HyperPlus Kits using KAPA Universal Adapter and KAPA UDI Primer Mixes. Libraries (8) were multiplexed prior to capture, hybridized to probes for 16 hours, amplified post-capture, and sequenced on an Illumina NovaSeq sequencer (2 x 100 bp). Bars represent data from 16 different cell lines processed in triplicate. Each dataset in Panel B is derived from a different cell line.

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Reliably enrich challenging, previously inaccessible exonic regions

- Improve coverage of key research genes in important genomic databases including ACMG59, CCDS, and ClinVar
- Discover more variants with the comprehensive-yet-compact KAPA HyperExome panel

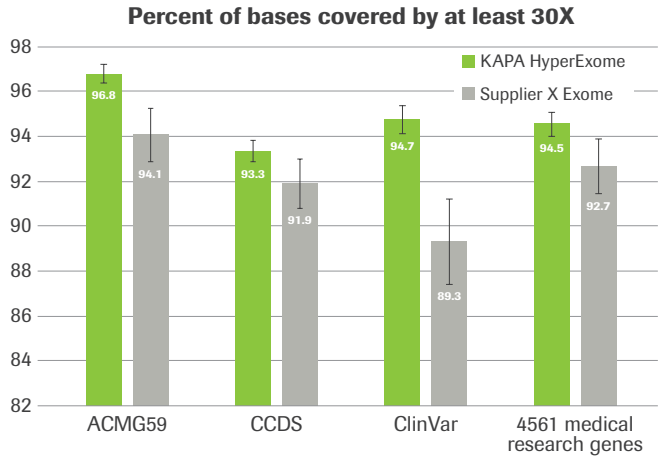


Figure 3. KAPA HyperExome provides better coverage of important genomic databases compared to the Supplier X Exome. Prior to capture with KAPA HyperExome probes, libraries were prepared from 100 ng of DNA with KAPA HyperPlus Kits using KAPA Universal Adapter and KAPA UDI Primer Mixes. Libraries (8) were multiplexed prior to capture, hybridized to probes for 16 hours, amplified post-capture, and sequenced on an Illumina NovaSeq sequencer (2 x 100 bp). Bars represent data from 16 different cell lines processed in triplicate.

Ensure accurate sample identification

Researchers often use control spike-ins to track samples throughout NGS workflows. However, sample-handling errors can still lead to incorrect sample identification. HyperExome targets 387 selected SNP positions to serve as intrinsic sample identifiers that are independent of sample handling, enabling researchers to:

- Eliminate errors associated with manual addition of sample-tracking spike-ins
- Increase the reliability of NGS results with greater confidence in sample identity
- Reduce costly sample misidentification

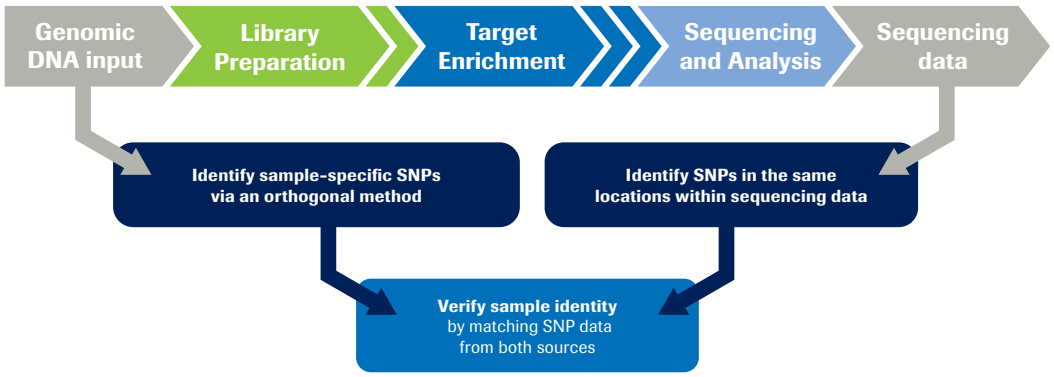
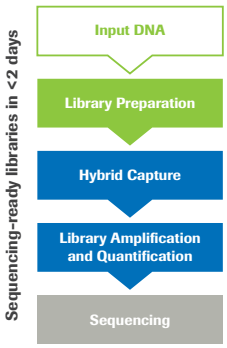


Figure 4. Overview of sample tracking with the 387 tracking SNPs captured by KAPA HyperExome probes. In order to confirm sample identification after sequencing, the unique identity of each sample is first established by using an independent, orthogonal method (e.g., qPCR, SNP array, Sanger sequencing) to classify ~60 – 100 sample-specific SNPs; it is important to select SNPs that correspond to those captured by the KAPA HyperExome panel. The sample identities are then confirmed by matching the SNP data from both sources.

Streamline target enrichment with the KAPA HyperCap Workflow v3

KAPA HyperCap Workflow v3 delivers complex libraries by combining the high conversion rate of KAPA HyperPrep or KAPA HyperPlus Kits with KAPA Target Enrichment, creating a streamlined, single-vendor supported workflow.

- Multiplex up to 16 samples in the same capture, and potentially post-capture multiplex more samples in the same sequencing lane with KAPA UDI Primer Mixes; 97-384 Primer Mixes will be available soon
- Reduce workflow complexity and hands-on time with KAPA Universal Enhancing Oligos, eliminating the need for adapter-matched blocking oligos
- Automate the entire KAPA HyperCap Workflow v3 without the need for a SpeedVac—now with all hybridization and bead wash steps at 55ºC



Explore KAPA Target Enrichment Probes: Better by Design

- KAPA Target Enrichment Probes are manufactured with KAPA HiFi DNA Polymerase and demonstrate extremely high sequence fidelity, high on-target rates, and high accuracy and reproducibility
- The concentration and presence of each probe in every probe pool is confirmed by NGS-based QC
- Production lots of up to 100,000 capture reactions ensure the highest reproducibility for your routine testing workflows

Ordering information

Product name	Capture reactions	Catalog No.
KAPA HyperExome Prep Kit Complete KAPA HyperCap Workflow v3 NGS sample prep kit for 192 8-plex reaction samples *Includes: KAPA HyperPrep Kit, Universal Adapters, HyperBeads, Probes Resuspension Buffer, HyperExome, HyperCapture Reagent Kit, and HyperCapture Bead Kit*	192 8-plex rxns	09107592001
KAPA HyperExome Plus Kit Complete KAPA HyperCap Workflow v3 NGS sample prep kit for 192 8-plex reaction samples *Includes: KAPA HyperPlus Kit, Universal Adapters, HyperBeads, Probes Resuspension Buffer, HyperExome, HyperCapture Reagent Kit, and HyperCapture Bead Kit*	192 8-plex rxns	09107606001
KAPA HyperExome Probes	12	09062548001
	24	09062556001
	48	09062564001
	96	09062572001
	192	09062599001
	384	09062602001
	768	09062629001
	1152	09062637001
	1536	09062645001
	Inquire for larger pack sizes	

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KAPA HyperExome is part of Roche Sequencing Solutions' new KAPA Target Enrichment Portfolio. Learn more at **go.roche.com/HyperExome**.

KAPA HyperCap Workflow v3 is an integrated, <2-day sample preparation workflow for target-enriched NGS that combines KAPA Library Preparation and KAPA Target Enrichment probes. Learn more at **go.roche.com/HyperCap**.

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