# *Enrich*
# CONFIDENCE

## KAPA HyperExome Probes

A targeted DNA enrichment strategy such as whole exome sequencing (WES) can improve variant detection capabilities, reduce sequencing costs and increase sample throughput. It is becoming one of the most powerful tools of modern genomics as an invaluable asset for the detection of disease-associated mutations. Excellence in probe design, manufacturing technology and workflow optimisation are all critical requirements for WES to enable confident detection of single nucleotide variations, insertions, deletions, copy-number variations, gene fusions, inversions and other rearrangements. The KAPA HyperExome Probes incorporate proven and innovative probe design approaches with the high-fidelity KAPA Target Enrichment Probes.

- **Maximise sequencing efficiency**
- **Access the genomic regions that really matter**
- **Call variants with confidence**
- **Experience reproducible quality**

## KAPA HyperExome Probes—Access the content that matters

Reduce sequencing costs with the high-performing KAPA HyperExome Probes that have been extensively optimised and validated with the streamlined KAPA HyperCap Workflow and get:

- Superior uniformity with high on-target and low duplication rates to achieve better target coverage and minimise re-testing (Figures 1-4)
- Enhanced multiplexing capabilities with validated pre- and post-capture pooling and unique dual indexing
- Increased throughput and cost savings with reaction pack sizes that exceed 4000 reactions
- Broad database coverage for RefSeq, CCDS, Ensembl, GENCODE and ClinVar with an efficient compact design of only 43 Mb (capture target)

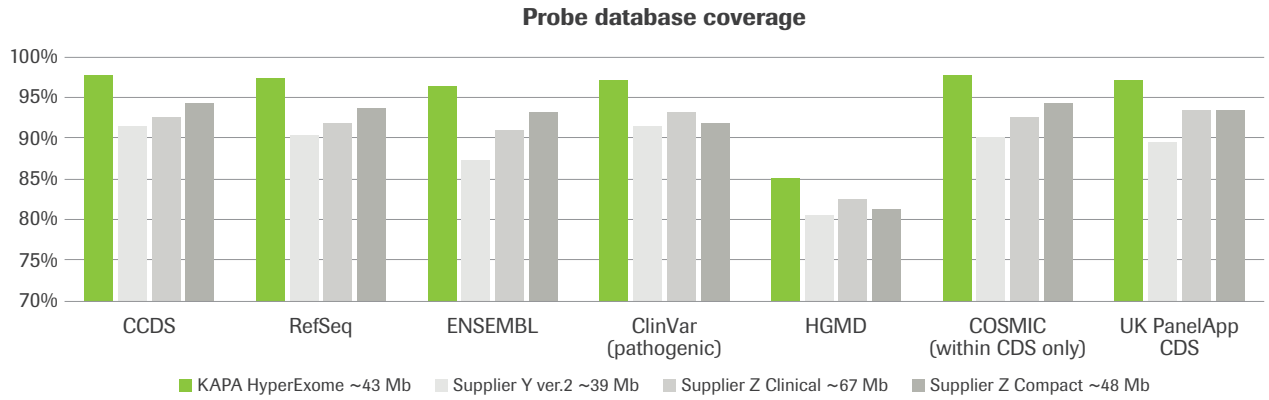



**Figure 1. KAPA HyperExome Probes cover significantly higher percentage of the gene databases than other suppliers' exomes.** (Database data retrieved Feb 2020, except HGMD which is HGMD_professional_2018.2.)

## Better target coverage to call variants with confidence

Utilise a fully validated and optimised KAPA HyperCap Workflow to ensure result confidence and reproducibility

- Combine higher on-target rate and superior uniformity to achieve broader target coverage at relevant depths and better coverage of the medical research databases (Figures 1-4)
- Detect SNPs with 98.7% sensitivity and 99.7% specificity and save sequencing costs with superior uniformity (Figures 4A - 4B)
- Intrinsically target 387 sample-tracking SNPs so that you can safely track the sample's identity throughout the workflow with ease

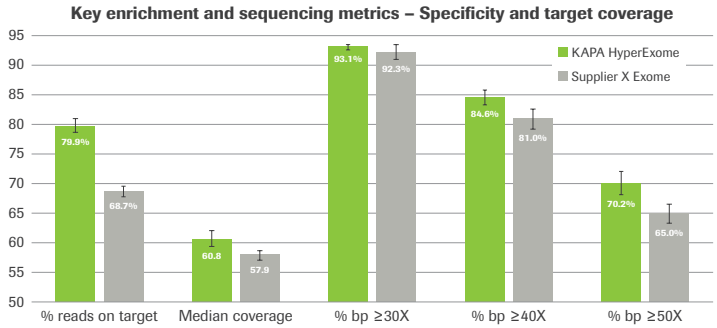



**Figure 2*. KAPA HyperExome Probes deliver higher % of reads on-target (specificity), deeper median coverage and broader target coverage at the depths of ≥30, 40 or 50 unique reads than Supplier X.**

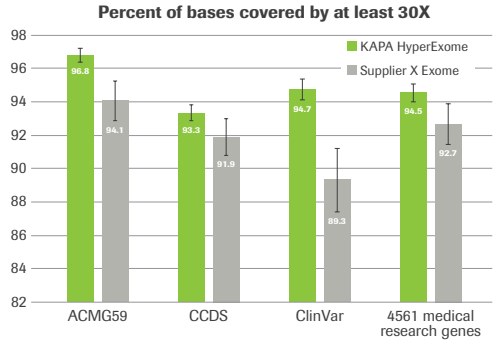
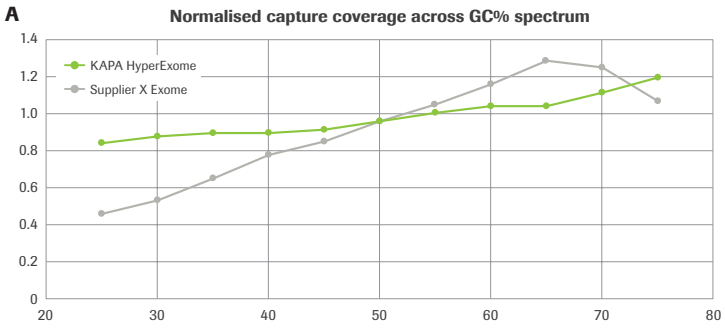



**Figure 3*. KAPA HyperExome Probes covers higher percentage of important genomic databases by the minimum of 30 unique reads, compared to Supplier X's exome.**



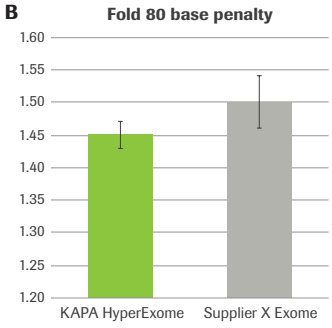




**Figure 4A*. KAPA HyperExome shows higher uniformity across the GC% spectrum, with less GC bias compared to Supplier X's exome.**

**Figure 4B*. KAPA HyperExome Probes shows better uniformity by a lower Fold 80 base penalty than Supplier X's Exome.** (Fold 80 shows the fold amount of additional sequencing to bring 80% of the target to the current mean coverage, lower is better).

## Experience reproducible quality

The KAPA Target Enrichment Probes are manufactured with a new state-of-the-art process that offers high performance and high reproducibility

- NGS-based probe pool QC confirms presence and concentration of each probe in every probe pool that is manufactured
- Manufactured with KAPA HiFi DNA Polymerase, the KAPA Target Enrichment Probes demonstrate extremely high sequence fidelity that enables high on-target rates
- Single production lots of up to 100k reactions ensure the highest reproducibility for your routine testing workflows

*For both suppliers, the respective protocol was followed, starting from 16 cell line reference DNAs split in two 8-plex pre-capture hybridisations in triplicate, to a total of 48 data points. Starting DNA amount was 100 ng for KAPA HyperExome and 50 ng for Supplier X. Both exomes were subsampled to numbers of high-quality reads proportional to each exome's capture target size (60 million reads for KAPA HyperExome, 51 million reads for Supplier X exome) sequenced on a NovaSeq6000 system 2 x 100 bp run, in each case.

**For more information, please contact your local Roche representative.**
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