KAPA HyperExome V2 Probes

Achieve exceptional uniformity coverage even through the extremes of the %GC regions.

Efficient whole-exome sequencing (WES) begins with expertly designed probes that effectively capture challenging genomic regions. KAPA HyperExome V2 Probes, the latest Roche WES design, delivers superior coverage of recent versions of ACMGv3.1, RefSeq, CCDS, ClinVar, Ensembl, and COSMIC genomic databases. This design also reduces sequencing requirements, with a compact capture target of 43.2 Mb covering 37.5 Mb of key content.

- **Leverage the most relevant genomic databases**
- **Unlock unique insights in clinical research** by capturing more content from key genomic databases
- **Achieve excellent coverage uniformity** across the entire range of %GC content
- **Sequence with confidence** with an improved whole-exome workflow
- **Streamline hybrid capture targeted sequencing** with KAPA HyperCap Workflow, and upfront KAPA Evo Library Prep Kits

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Leverage the most relevant databases

- Build confidence by using a design featuring updated ClinVar, RefSeq & Ensembl content*
- Achieve exceptional coverage of ACMGv3.1, CCDS, ClinVar, COSMIC, Ensembl, HGMD, & RefSeq databases
- Balance specificity & coverage with probes designed using the telomere-to-telomere genome assembly CHM13

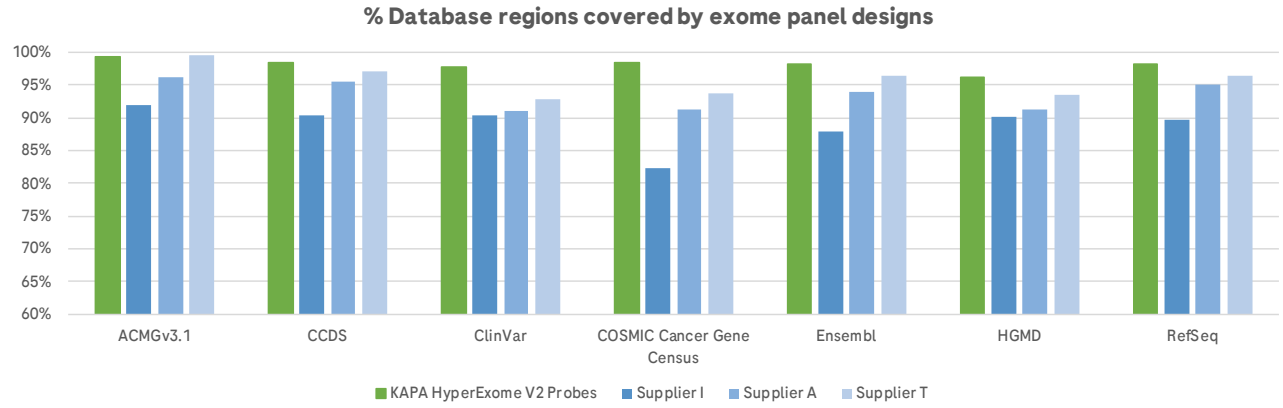

Figure 1. Superior probe database coverage by the KAPA HyperExome V2 design compared to other suppliers' designs across important genomic databases (better coverage by as much as 17%). Database data retrieved in Jan 2023, unpadded capture target used to compare across suppliers. The KAPA HyperExome V2 panel was designed to cover coding exon sequence from the following annotation sources: RefSeq (June 29, 2022), ClinVar (June 29, 2022) and Ensembl release v106.

Unlock unique insights in clinical research

- Cover more bases and reduce "blind" spots, leaving fewer unknowns
- Increase value and confidence in the results with superior coverage of database content

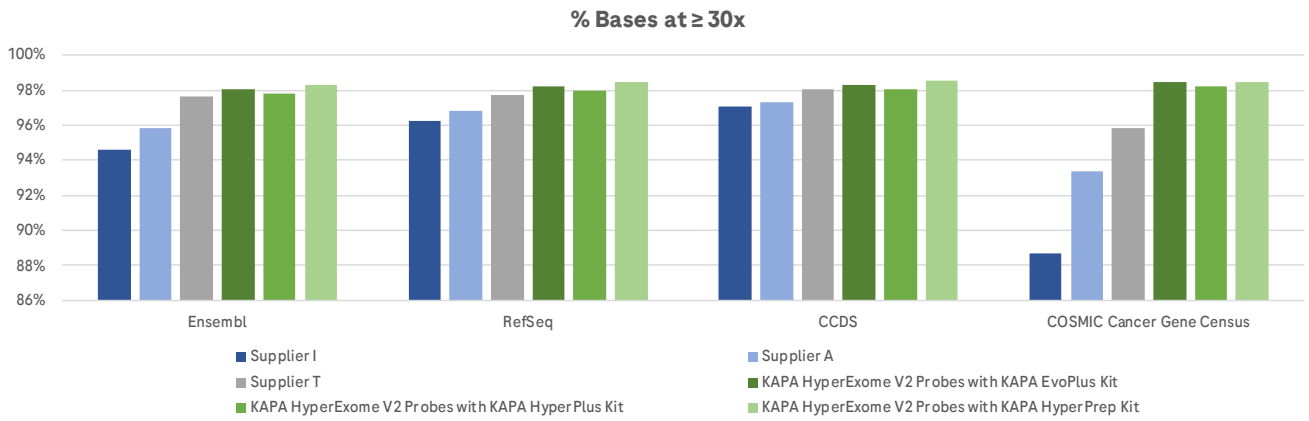

Figure 2. Percent bases covered by at least 30X across several key genomic databases. KAPA HyperExome V2 Probes deliver better database coverage compared to Suppliers I, A, and T, which leave more "blind" spots and may thus require repeated experiments and/or the addition of supplemental probes. Supplier sample prep protocols were followed with singleplex 4h hybridizations for Supplier I (3 replicates, NA12878), 8-plex O/N hybridizations for Supplier A (48 data points from 6 replicate captures of 16 coriell DNAs), 8-plex O/N hybridizations for Supplier T (72 data points from 16 coriell and 24 blood-extracted DNAs) and 16-plex O/N hybridizations for the KAPA HyperExome V2 Probes (48 data points from 16 blood-extracted DNAs in 3 captures) with the KAPA EvoPlus Kit, KAPA HyperPlus Kit, and KAPA HyperPrep Kit (48 data points from 16 coriell DNAs in 3 captures).[3]

*(end June 2022)

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Achieve higher uniformity across the entire %GC range

- Obtain exceptionally uniform coverage even through the extremes of the %GC spectrum
- Eliminate GC bias to cover low- and high-GC regions equally well, with an optimized design and uniform library amplification

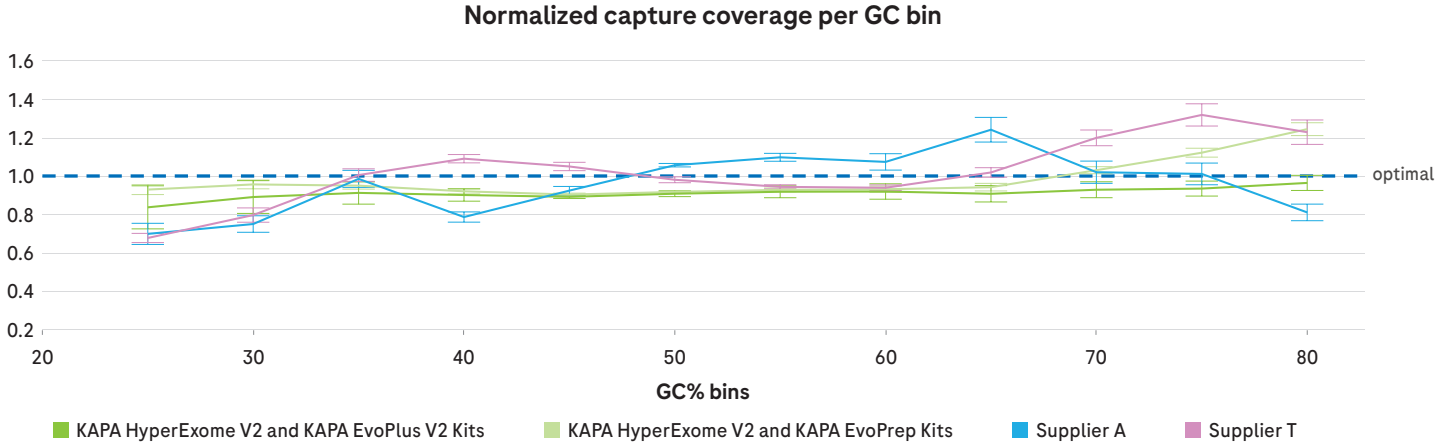


Figure 3. Exceptional uniformity of normalized capture coverage across the extremes of the GC% spectrum. Vendor sample prep protocols were followed with 8-plex o/n hybridizations for vendor A (48 data points from 6 replicate captures of 16 coriell DNAs), 8-plex o/n hybridizations for vendor T (72 data points from 16 coriell and 24 blood extracted DNAs). For KAPA HyperExome V2 Probes the KAPA HyperCap Evolved Workflow v4 was followed. A total of 32 libraries were prepared with the KAPA EvoPrep Kit or the KAPA EvoPlus V2 Kit starting from 100 ng of blood extracted DNA samples and were hybridized by 2 x 16-plex captures for each kit workflow. Final libraries were sequenced on a NovaSeqTM 6000 System at 2 x 100 bp and 60 M high-quality reads were analyzed per library and proportionally to the capture target for the other vendor exomes.

Sequence with confidence

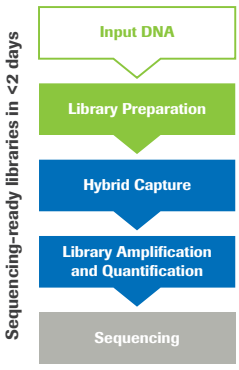
Increase result confidence by following sample identities throughout the workflow with sample-tracking endogenous SNPs covered by the KAPA HyperExome V2 Probes. Or, explore new potential capabilities with a unique set of 96 probes that are included in the panel and designed to capture non-naturally occurring sequences that can be spiked into samples.

- Select from an extensive list of 529 sample-tracking SNPs that includes the Pengelly[1] and Yousefi[2] sets
- Rely on high precision (99.49%) and recall (98.95%) for SNP detection
- Explore new possibilities with 96 utility probes embedded in the design, which may be used to capture exogenous synthetic DNA fragments, potentially used as process controls

Streamline targeted sequencing with the KAPA HyperCap Workflow

KAPA HyperCap Workflow delivers complex libraries by combining the high conversion rate of KAPA EvoPrep, and KAPA EvoPlus V2 Kits with KAPA HyperExome V2 Probes, 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,1-384
- 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 without the need for a SpeedVac—now with all hybridization and bead wash steps at 55°C



1. A SNP profiling panel for sample tracking in whole-exome sequencing studies. Pengelly RJ, et al. Genome Med. 2013 Sep 27;5(9):89. doi: 10.1186/gm492. eCollection 2013
2. A åSNP panel for identification of DNA and RNA specimens. Yousefi S, et al. BMC Genomics. 2018 Jan 25;19(1):90. doi: 10.1186/s12864-018-4482-7.
3. Project: Roche KAPA HyperExome V2 Launch Data, Pleasanton, CA, Mar. 2023

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Fully automated whole-exome sequencing (WES) on the AVENIO Edge Liquid Handling System

- No prior NGS and/or automation experience required
- As little as 20 minutes of deck setup time for the entire WES workflow
- Automated quantification, normalization and pooling
- Complementary support team to help you along the way

Ordering Information

Product name	Capture reactions	Catalog No.
KAPA HyperExome V2 Probes	12	9718630001
	24	9718648001
	48	9718656001
	96	9718664001
	192	9718672001
	384	9718699001
	768	9718702001
	1152	9718729001
	1536	9718737001

Demo data
Demo data files are available for evaluation. Please contact your local Roche Genomics Sales Specialist.

KAPA HyperExome V2 Probes
Learn more at **go.roche.com/HyperExomeV2**

KAPA HyperCap Workflow
Learn more at **go.roche.com/HyperCap**

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