Enrich INSIGHTS

KAPA HyperExome V2 Probes

The art of efficient Whole-Exome Sequencing (WES) begins with probe-design expertise that can shed light to challenging genomic regions. KAPA HyperExome V2 Probes are the latest Whole-Exome Sequencing solution from Roche, delivering superior coverage of the recent versions of ACMGv3.1, RefSeq, CCDS, ClinVar, Ensembl, and COSMIC genomic databases within a compact capture target of 43.2 Mb with low sequencing requirements. This novel solution enables users to:

Unlock previously inaccessible genomic regions	with the renowned design expertise and extensive panel optimization from Roche
Stay up-to-date	using a high-performing exome efficiently covering recent database versions such as the ACMGv3.1
Improve whole-exome sequencing	with the KAPA HyperCap Workflow now also supporting the KAPA EvoPlus Kit for higher quality sequencing data
Experience consistent performance	by NGS-based probe QC and functional QC (capture and sequencing) for every KAPA HyperExome V2 lot
Streamline the entire whole-exome sequencing solution	leveraging the AVENIO Edge true walk-away automation

Better by design

Leverage more than 15 years of probe-design experience and a design that is optimized by using the T2T (telomere-to-telomere) genome assembly to properly address potentially problematic regions not apparent in the GRCh38 genome assembly.

- Maximize sequencing coverage starting from a better exome design
- Achieve more with less by covering 37.5 Mb of key content with only 43.2 Mb of capture space
- Deliver higher quality results by covering more regions from the key genomic databases

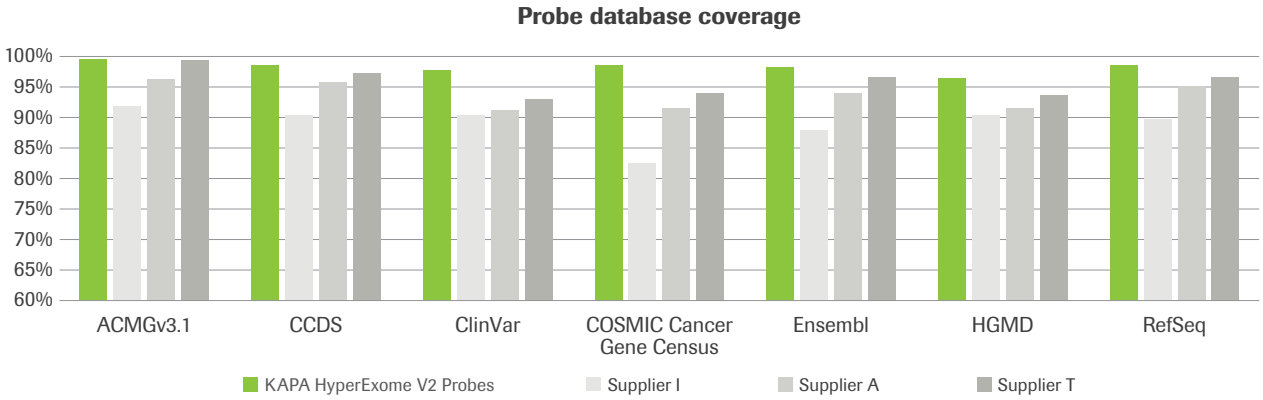


Figure 1. Superior probe database coverage by the KAPA HyperExome V2 design compared to other suppliers' designs across important genomic databases (even up to 17% better). Database data retrieved in Jan 2023, unpadded capture target used to compare across suppliers. The KAPA HyperExome V2 panel was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

Sequencing efficiency

The KAPA HyperExome V2 Probes are extensively optimized for sequencing efficiency using real world samples in the streamlined KAPA HyperCap Workflow leveraging the KAPA EvoPlus, KAPA HyperPlus, and KAPA HyperPrep Kits to efficiently cover hard-to-capture regions.

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

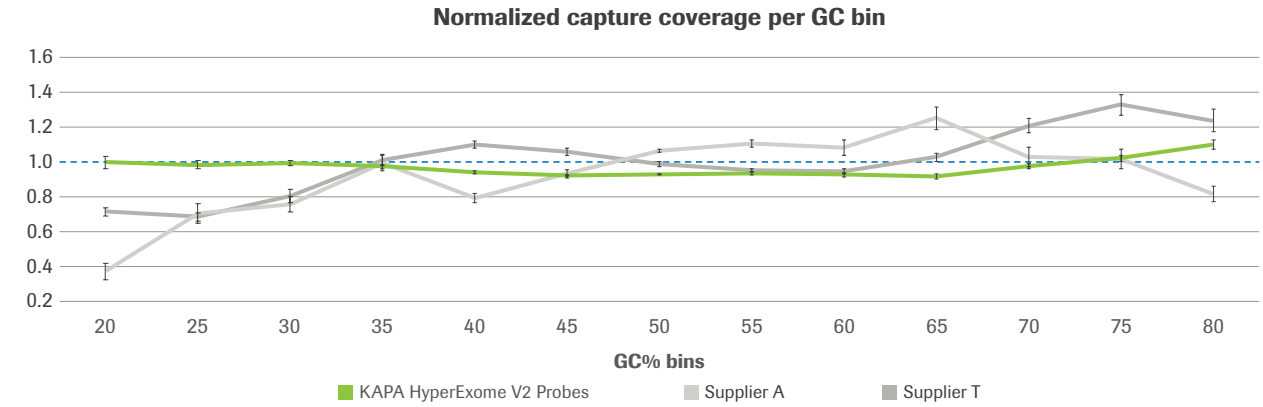


Figure 2. Exceptional uniformity of normalized capture coverage across the extremes of the GC% spectrum. The blue dashed line represents the optimal uniformity in the ideal state that all regions—regardless of their GC content—would be equally covered. Supplier sample prep protocols were followed with 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). For KAPA HyperExome V2 Probes the KAPA HyperCap Workflow v3.4 was followed for a total of 54 libraries multiplexed into the hybridization by 16 (3 replicate captures) or by 1 (6 singleplex captures). Final libraries were sequenced on a NovaSeq™ 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 suppliers' exomes.

Data on file with Roche.
For Research Use Only. Not for use in diagnostic procedures.

Exceptional content coverage

Lead in whole-exome sequencing by confidently covering more content from the key genomic databases. Unlock unique insights in clinical research with the KAPA HyperExome V2 Probes.

- Cover more bases, see what others may find difficult to see
- Add more value and confidence in the results with superior database regions' coverage
- Eliminate "blind" spots—leave fewer unknowns

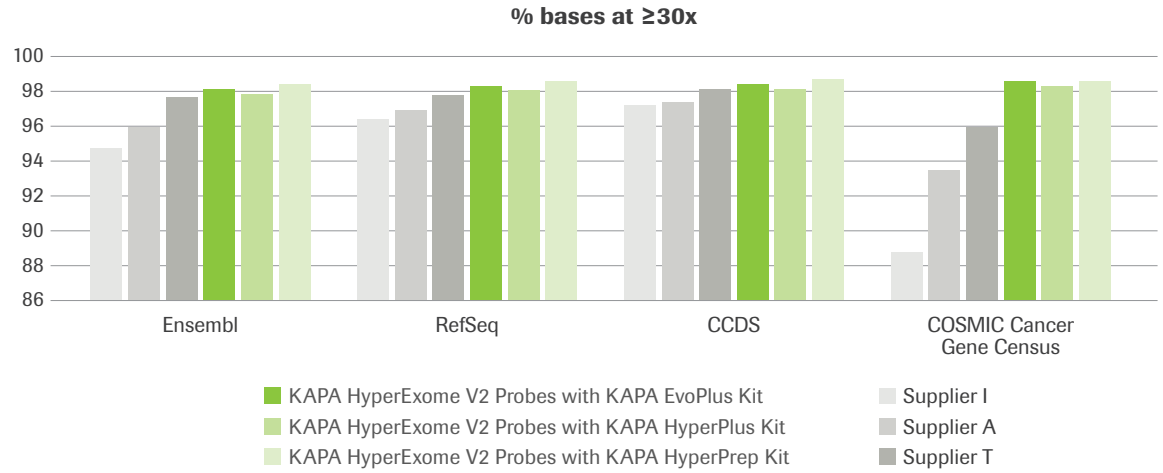


Figure 3. Percent bases covered by at least 30x across some of the key genomic databases such as Ensembl, RefSeq, CCDS, and COSMIC Cancer Gene Census, based on a January 2023 snapshot. KAPA HyperExome V2 Probes deliver better database coverage compared to Suppliers I, A, and T that are leaving more "blind" spots, which may lead to repeats or need for spike-in 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 and KAPA HyperPlus Kit and with the KAPA HyperPrep Kit (48 data points from 16 coriell DNAs in 3 captures). KAPA HyperExome V2 Probes enriched libraries were sequenced on a NovaSeq™ 6000 System at 2 x 100 bp and 60 M high-quality reads were analyzed per library. Supplier-enriched libraries were sequenced proportionally to their capture target size.

Sequence with confidence

Increase result confidence by following sample identities throughout the workflow with sample-tracking SNPs that the KAPA HyperExome V2 Probes are covering. Explore new potential capabilities with a unique set of 96 probes, composed of non-naturally occurring sequences that are included in the panel.

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

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 SNP 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.

Data on file with Roche.

Order with ease

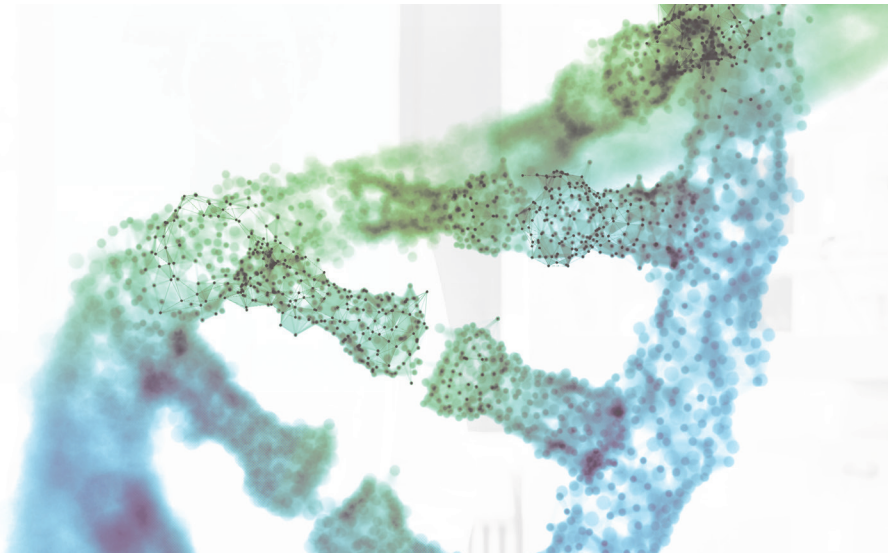
The KAPA HyperExome V2 Probes are available from 12 to 1536 reactions. For increased ordering convenience, three KAPA HyperExome V2 Kits including all the Roche kits that you need for your WES workflow are available, depending on the KAPA Library Preparation Kit of choice. Order your KAPA HyperExome V2 Kit of choice and complement it with the KAPA UDI Primer Mixes of choice for a seamless WES experience by a single trusted vendor.

Ordering information

Roche cat. no.	Description	Kit size
9718630001	KAPA HyperExome V2 Probes, 12 rxn	12 reactions
9718648001	KAPA HyperExome V2 Probes, 24 rxn	24 reactions
9718656001	KAPA HyperExome V2 Probes, 48 rxn	48 reactions
9718664001	KAPA HyperExome V2 Probes, 96 rxn	96 reactions
9718672001	KAPA HyperExome V2 Probes, 192 rxn	192 reactions
9718699001	KAPA HyperExome V2 Probes, 384 rxn	384 reactions
9718702001	KAPA HyperExome V2 Probes, 768 rxn	768 reactions
9718729001	KAPA HyperExome V2 Probes, 1152 rxn	1152 reactions
9718737001	KAPA HyperExome V2 Probes, 1536 rxn	1536 reactions
9983759001	KAPA HyperExome V2 Prep Kit – 192 samples	Convenient all-in-one package for 192 samples – All kits provided except the KAPA UDI Primer Mixes – For Covaris sonicated DNA input - Talk to a Roche representative today
9983775001	KAPA HyperExome V2 Plus Kit – 192 samples	Convenient all-in-one package for 192 samples – All kits provided except the KAPA UDI Primer Mixes – Integrated enzymatic DNA shearing – Talk to a Roche representative today
9983783001	KAPA HyperExome V2 Evo Kit – 192 samples	Convenient all-in-one package for 192 samples – All kits provided except the KAPA UDI Primer Mixes – Next-Gen Integrated enzymatic DNA shearing – Talk to a Roche representative today

Demo data

Demo data is available for evaluation.
Please contact a local Roche representative.



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