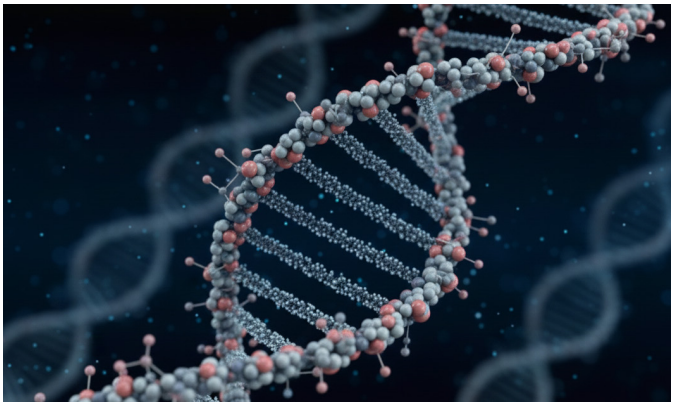
Tech Spotlight
WES on AVITI™ sequencer

KAPA HyperExome V2 Probes for Element Biosciences™ Trinity™ Workflow

Ultra-streamlined, high-efficiency whole exome sequencing

Whole exome sequencing (WES) is a well-established next-generation sequencing (NGS) method for interrogating the coding regions of the genome with high sensitivity and cost efficiency.[1] Nevertheless, traditional hybridization-based WES protocols remain time-consuming, laborious, and error-prone.

KAPA HyperExome V2 Probes offer a highly optimized WES panel, designed to cover even the most challenging regions with high uniformity. Combined with the **KAPA EvoPlus V2** or **KAPA EvoPrep Kits** and the **Element Biosciences Trinity Workflow on AVITI™ sequencers**, high-performance exome sequencing has never been easier.



On-sequencer target enrichment significantly reduces the time to result, without compromising exome sequencing performance

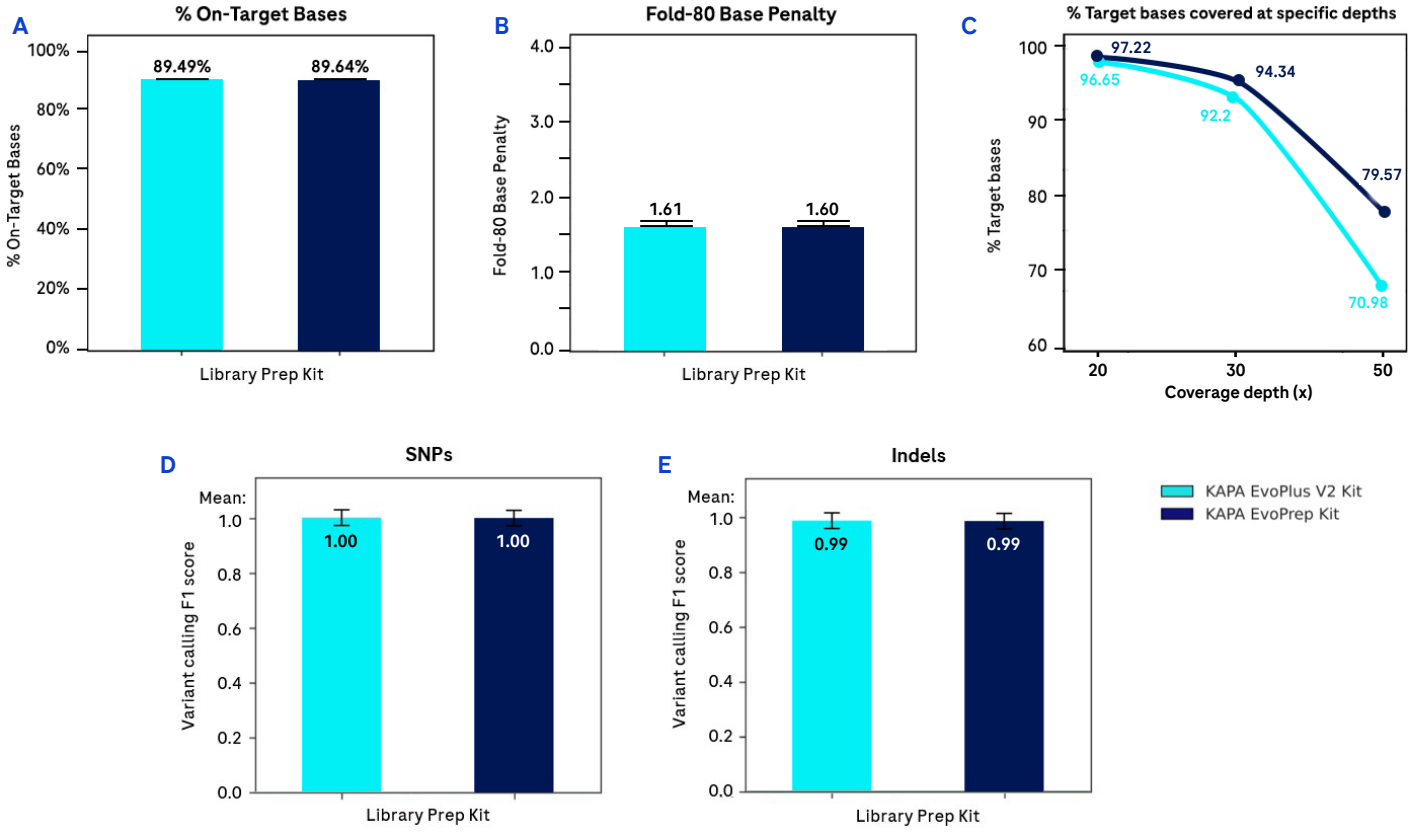


Figure 1. Highly efficient WES with the KAPA HyperCap Evolved Workflow, KAPA HyperExome V2 Probes, and the Element Biosciences Trinity Workflow. (A) Exceptional on-target rates, and **(B)** high coverage uniformity (low fold-80 penalty values) translate to high base coverage at different minimum coverage depths **(C)** These key metrics enable accurate, high-confidence variant calling **(D)** Libraries (n=8) were prepared from each of two reference samples (NA12878 and NA24385; Coriell Institute for Medical Research) using the KAPA EvoPlus Kit V2 (enzymatic fragmentation; light blue) or KAPA EvoPrep Kit (mechanical shearing, dark blue). Both kits contain the KAPA EvoT4 DNA Ligase, which offers exceptional ligation efficiency with only 15 min of ligation time. Libraries were prepared as described in the KAPA HyperCap Evolved Workflow v5.0 Instructions for Use. However, KAPA Universal Adapters and KAPA UDI Primer Mixes were replaced with xGen™ Stubby Adapter-UDI Primers for Element (Integrated DNA Technologies) to ensure compatibility with the AVITI sequencer. Exome capture with KAPA HyperExome V2 Probes was initiated as described. The KAPA HyperCap Evolved Workflow v4.0 was concluded after the overnight hybridization step. Trinity targeted sequencing was subsequently performed as described in the Element Biosciences Trinity Sequencing User Guide (July 2025). The sequencing run was configured to target 60 million reads (2 x 75 bp) per library. Data analysis was performed using the Roche KAPA TE Germline RUO Pipeline (v1.0) on DNAnexus.

Data on file at Roche.

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Element Biosciences™ Trinity™ Targeted Sequencing Workflow

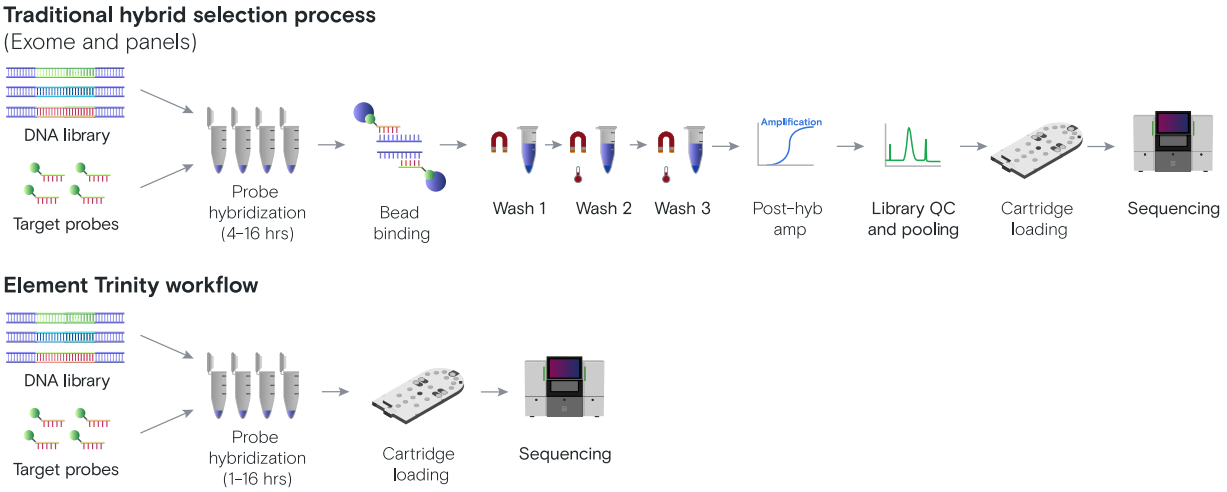

Figure 2. Ultra-streamlined exome capture with KAPA library preparation and Trinity targeted sequencing. KAPA EvoPlus V2 and KAPA EvoPrep Kits enable the preparation of sample libraries in <2 hours with minimal hands-on time. Minor protocol modifications are required to ensure compatibility with the Trinity Workflow.* After overnight hybridization to KAPA HyperExome V2 Probes, subsequent target enrichment steps and sequencing are performed on the Trinity sequencing cartridge, thereby eliminating laborious and error-prone steps required for traditional hybrid capture protocols and greatly reducing the time from sample to result.

**Please contact Element Biosciences regarding modifications required for your specific workflow.*

Summary

KAPA EvoPlus V2 and KAPA EvoPrep Kits utilize an **evolved ligase**, **readymixes**, and a **streamlined protocol** to enable rapid construction of highly complex sample libraries for exome sequencing. Combined with the Trinity on-sequencer targeted sequencing workflow, exome sequencing can be completed in **<48 hours with minimal hands-on time**.

The most relevant genomic databases were utilized in the design of KAPA HyperExome V2 Probes to achieve coverage of the **most challenging exonic regions** in a **compact capture target** (43.2 Mb) with low sequencing requirements. Performance was carefully **optimized using real-world samples** in the streamlined KAPA HyperCap Workflow.

The innovative, on-sequencer Trinity Workflow **reduces loss of sample material (preserves library complexity), eliminates temperature-sensitive wash steps** required in traditional protocols, and **mitigates the risk of small-volume pipetting errors**. This ensures **faster, robust and reproducible** sequencing results.

Discover more...

with **KAPA EvoPlus V2 or KAPA EvoPrep Kits** and **KAPA HyperExome V2 Probes** using the Trinity Workflow.

Click here or scan the code below:

1. Rabbani *et al*. The promise of whole-exome sequencing in medical genetics. 2014, J of human genetics, 59, 5-15.

Data on file at Roche.
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