DNA Library Preparation > Enzymatic Fragmentation

KAPA EvoPlus Boost Kit

Streamline your enzymatic prep, boost your performance

Enhance your NGS sample prep workflow and increase sequencing performance with **KAPA EvoPlus Boost Kits**. Combine the high library conversion efficiencies and low sequencing artifacts of mechanical shearing-based DNA library prep kits with the convenience and ease of automation of enzymatic fragmentation-based methods. Now with an optimized amplification mix, the KAPA EvoPlus Boost Kits deliver enhanced performance and confidence for your WGS, WES, and targeted sequencing applications.

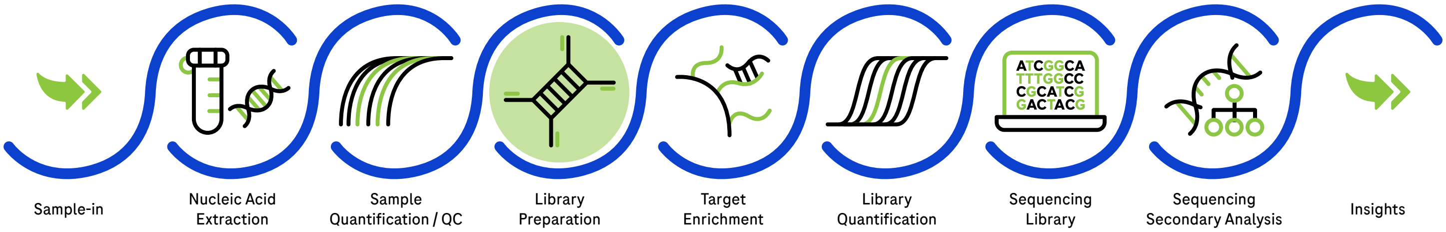
- **Increase efficiency and convenience** with all-in-one enzyme & buffer ReadyMixes—available in either automation-friendly reagent plates or tubes
- **Maximize sequencing efficiency** by ensuring high uniformity and fewer dropouts in difficult regions with an optimized low-bias PCR mix (KAPA EvoAmp ReadyMix)
- **Skip mechanical fragmentation** – **without the bias** often associated with enzymatic fragmentation

2 hrs
Workflow Time

30 min
Hands-on Time

0.1-500 ng
Input Amount

Constantly evolving, efficient, and complete solutions



Increase efficiency and convenience

- Simplify library prep and reduce the risk of human error with a simplified workflow, including one-step Fragmentation & A-tailing
- Decrease hands-on-time and the number of reagents required with ReadyMix formulations available in tubes or automation- friendly plates
- Produce sequencing-ready or target-capture-ready libraries in 2 hr

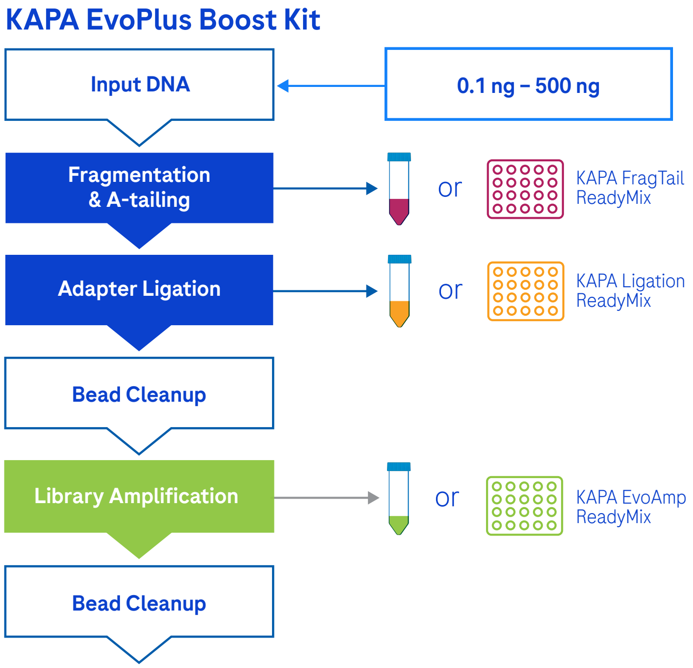


Figure 1: Streamline DNA library prep from 0.1-500 ng of input DNA with KAPA EvoPlus Boost Kits' ready-to-use master mixes. Avoid reagent preparation with master mixes available in tubes or pre-plated.

Maximize sequencing efficiency

- Increase sequencing efficiency by enhancing coverage uniformity and accuracy
- Deliver high-quality sequencing results with low error rates and minimal artifact generation for reliable outputs

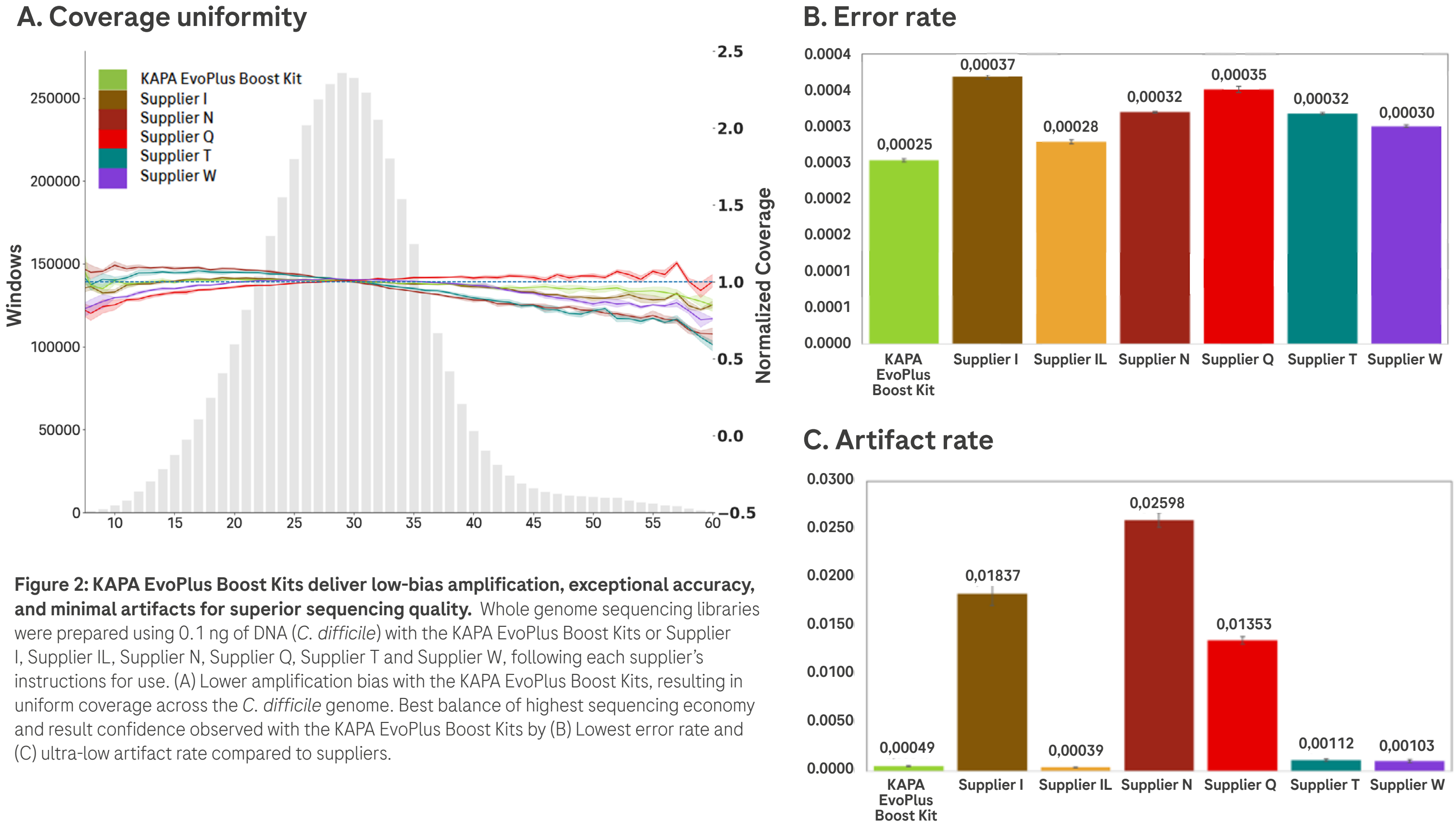


Figure 2: KAPA EvoPlus Boost Kits deliver low-bias amplification, exceptional accuracy, and minimal artifacts for superior sequencing quality. Whole genome sequencing libraries were prepared using 0.1 ng of DNA (*C. difficile*) with the KAPA EvoPlus Boost Kits or Supplier I, Supplier IL, Supplier N, Supplier Q, Supplier T and Supplier W, following each supplier's instructions for use. (A) Lower amplification bias with the KAPA EvoPlus Boost Kits, resulting in uniform coverage across the *C. difficile* genome. Best balance of highest sequencing economy and result confidence observed with the KAPA EvoPlus Boost Kits by (B) Lowest error rate and (C) ultra-low artifact rate compared to suppliers.

Skip mechanical fragmentation – without the bias

- Achieve higher sequencing efficiency with exceptional specificity and duplex molecule recovery
- Minimize sequencing artifacts and boost result confidence compared to mechanical fragmentation methods

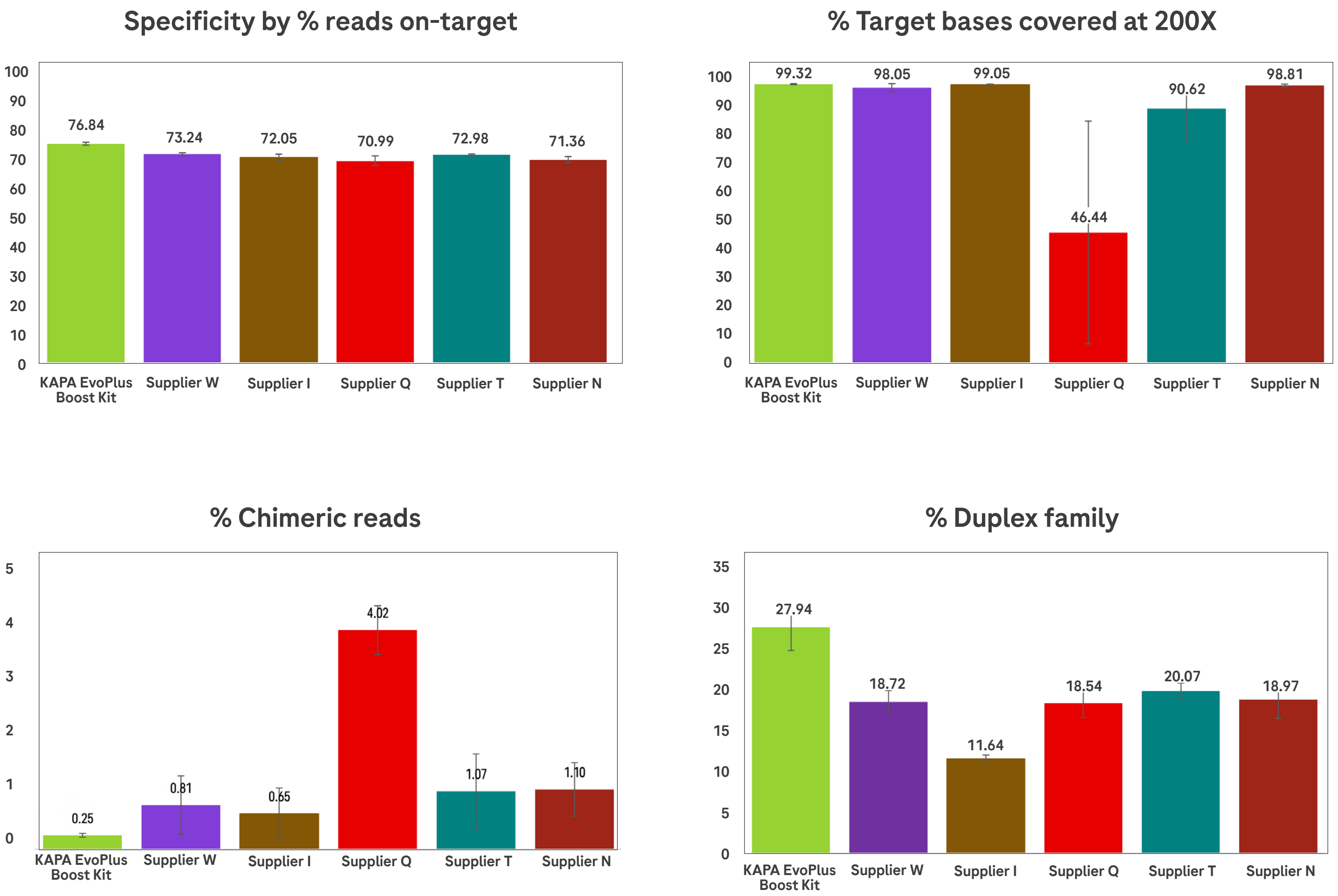


Figure 3. Improved sequencing performance in target capture workflow utilizing FFPET DNA. 50 ng of low quality FFPET DNA was used to prepare triplicate libraries with the KAPA EvoPlus Boost Kit and mechanical fragmentation kits of Supplier I, Supplier N, Supplier Q, Supplier T and Supplier W, following each supplier's instructions for use. Libraries were enriched with the KAPA HyperCap Oncology Panel (214 Kb), following the KAPA HyperCap FFPET Evolved workflow instructions[1]. (A) The KAPA EvoPlus Boost Kit had one of the highest percentage of reads on-target compared to mechanical fragmentation suppliers and (B) very high percentage of target bases covered by at least 200X compared to mechanical fragmentation suppliers, thereby showcasing the optimal utilization of sequencing throughput. (C) The KAPA EvoPlus Boost Kit had the lowest percentage of Chimeras present and (D) the highest duplex recovery, resulting in higher data confidence[2] compared to mechanical fragmentation suppliers (Supplier I, Supplier N, Supplier Q, Supplier T and Supplier W).

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1. KAPA EvoPlus Boost Kit data generated in 2025, separate from other supplier data generated in 2024.
2. Chen, *et al.* (2024). Characterization and mitigation of artifacts derived from NGS library preparation due to structure-specific sequences in the human genome. *BMC Genomics* 25:227.

Ordering Information

Roche Cat. No	Description	Kit size	Format
10613696001	KAPA EvoPlus Boost (24rxn)*	24 reactions	Tube
10613700001	KAPA EvoPlus Boost (96rxn)*	96 reactions	Tube/Bottle
10613718001	KAPA EvoPlus Boost (384rxn)*	384 reactions	Bottle
10613726001	KAPA EvoPlus Boost, plated format (96rxn)*	96 reactions	Plate
07958994001	KAPA Library Amplification Primer Mix (250rxn)	250 reactions	Tube
09420410001	KAPA Library Amplification Primer Mix (384 rxn)	384 reactions	Bottle
09420479001	KAPA Library Amplification Primer Mix 96-well plate (96rxn)	96 reactions	Plate

*KAPA full-length UDI adapters are only available in 96-well plates. KAPA Universal Adapters, which are used in combination with KAPA UDI Primer Mixes and require amplification, are available in tube format. KAPA HyperPure Beads, UDI Adapter Kits & KAPA Library Amplification Primer Mix (10X) are sold separately.

Contact your local representative to request an evaluation.

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