KAPA EvoPrep Kits

KAPA EvoPrep Kits: every breakthrough begins with brilliant sample prep.

The **KAPA EvoPrep Kits** are the latest high-performance, streamlined, and automation-friendly library preparation solutions from Roche. The kits are validated with challenging sample inputs such as cell-free DNA, FFPET DNA, or mechanically sheared DNA, and developed to help reduce workflow steps. Their ReadyMix reagents are available in tube and plated formats for enhanced automatability and include the KAPA EvoT4 DNA Ligase (in the ligation ReadyMix). This new evolved ligase is specifically engineered to increase library conversion rates.

These and the many other advanced features of the **KAPA EvoPrep Kits** were thoughtfully designed to set new standards in NGS sample prep workflows and jumpstart the journey to your next big research breakthrough.

KAPA EvoPrep Kits offer a complete library preparation solution when combined with **KAPA Adapters** and **KAPA HyperPure Beads** (sold separately) and a complete target enrichment solution when combined with **KAPA HyperCap** or **KAPA HyperPETE workflows**. The kits are compatible with the Illumina sequencing platform and have been qualified with **automation methods**.

Benefits of the KAPA EvoPrep Workflow*

Simplified and streamlined workflow	Simplified, streamlined and automatable workflow with ReadyMix reagents, available in tube and plated format to increase efficiency and convenience
Exceptional library yields and sequencing quality	Designed to provide increased library conversion efficiency with the KAPA EvoT4 DNA Ligase in the Ligation ReadyMix, enabling higher sensitivity and more confident variant detection
Enable superior performance and sequencing efficiency	Optimal utilization of sequencing throughput with minimal sequence coverage bias, minimization in the presence of sequencing artefacts with more unique library molecules recovered

Constantly evolving, efficient, and complete solutions

*Compared to earlier KAPA DNA Library Prep chemistries. Data on file.
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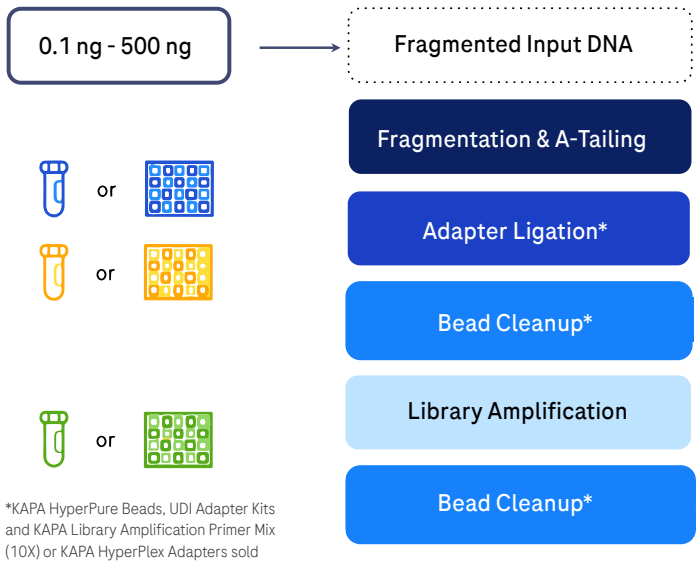
Simplified and streamlined workflow*

The **KAPA EvoPrep Kit** provides a simplified and streamlined workflow to remove the complexities and risk for human error by providing a **trusted library preparation** solution.

- Analyze more samples with a wide range of DNA inputs (0.1 ng-500 ng)
- PCR-free workflows starting from 50 ng of DNA input
- **ReadyMix formulations**, therefore fewer reagents and hands-on-time
- **Tubes and plated format** increase efficiency and convenience
- Manual and automation friendly protocol
- Ligation time of just 5 minutes, shortening workflow duration without compromising results
- Reduces complexity of workflow and provides greater peace of mind
- Validated with the **KAPA HyperCap Workflow** and the **KAPA HyperPETE Workflow**



*KAPA HyperPure Beads, UDI Adapter Kits and KAPA Library Amplification Primer Mix (10X) or KAPA HyperPlex Adapters sold separately

Figure 1: KAPA EvoPrep Workflow.

Exceptional library yields and sequencing quality

- Achieve **higher library yields** across a range of input DNA and sample types
- Fewer amplification cycles for downstream processing result in **lower duplication rates** and higher sequence coverage
- Achieve successful library construction with **biologically relevant samples** and PCR-free workflows (from as little as 50 ng)

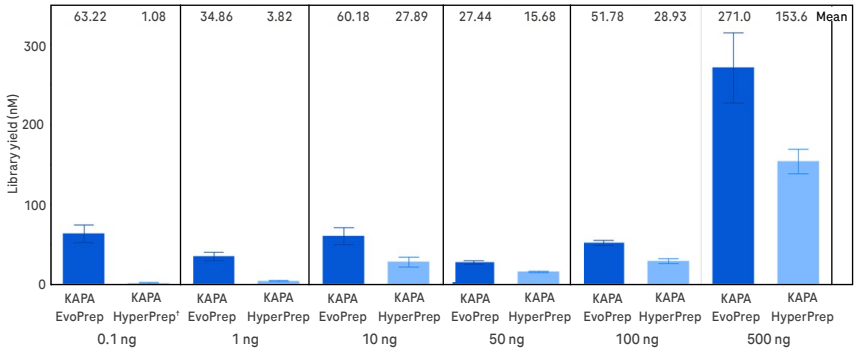


Figure 2: KAPA EvoPrep chemistry enables high library conversion across a range of input DNA. 0.1 ng - 500 ng of Covaris-sheared human genomic DNA was used to prepare libraries with KAPA Universal Adapters (with KAPA UDI Primer Mixes) at the recommended adapter:insert molar ratio following the KAPA EvoPrep and KAPA HyperPrep Kit Instructions for Use. Libraries were amplified for various cycles dependent on DNA input to enable visualization. Electropherograms were generated with LabChip GX Touch NGS 3K Assay.† Non-validated input (outside of the input range) for KAPA HyperPrep Kit - optimized cycle number for KAPA EvoPrep Kit inputs used.

Improved performance with challenging sample types

- Generate **more diverse libraries** from challenging sample types such as cfDNA
- **Higher confidence in data** generated due to reduction in sequencing artefacts

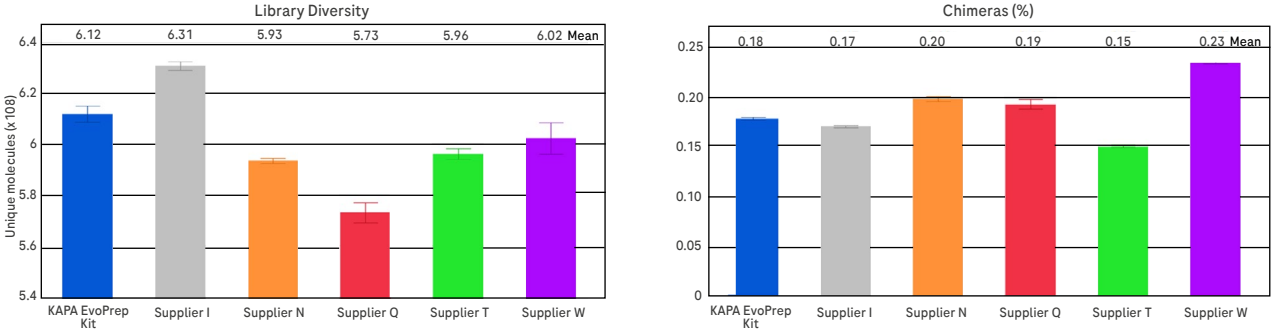


Figure 3: Improved sequencing performance - high number of unique library molecules, with reduced chimeras present. Whole genome sequencing libraries were prepared using 10 ng of cfDNA with the KAPA EvoPrep Kit, Supplier I, Supplier N, Supplier Q, Supplier T and Supplier W, following each supplier's instructions for use. KAPA EvoPrep Kit generated a higher number of unique library molecules compared to Supplier N, Supplier Q, Supplier T and Supplier W, resulting in higher library diversity and data confidence[1]. The KAPA EvoPrep Kit generated a low percentage of Chimeras present, resulting in higher data confidence[2], with Supplier N, Supplier Q and Supplier W generating a higher percentage of Chimeras present.

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Optimal utilization of sequencing throughput

- Minimal bias of sequencing coverage leading to **more uniform sequencing coverage and reduced sequencing costs**
- Improved sequencing metrics, allowing **higher confidence in data** due to reduction in sequencing artefacts

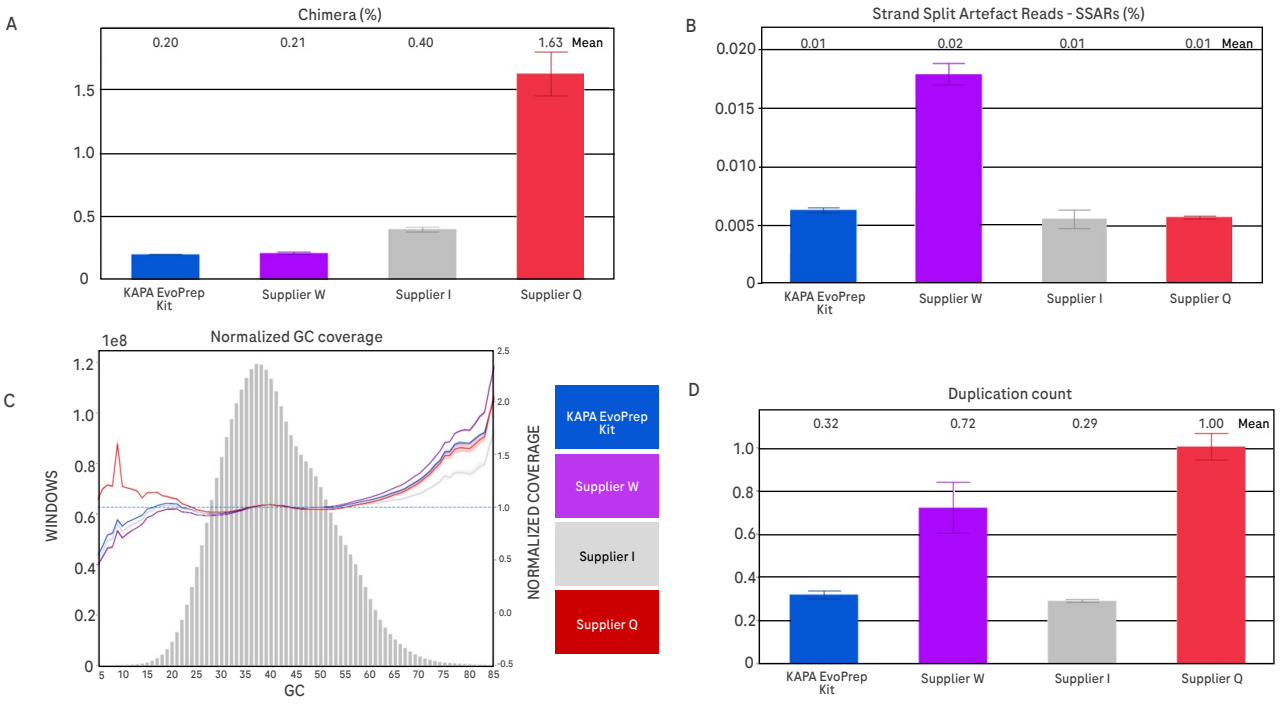

Figure 4: Improved sequencing performance - uniform coverage with reduction in sequencing artefacts. PCR-free whole genome libraries were prepared using 100 ng of Covaris-sheared human genomic DNA (NA12878) with the KAPA EvoPrep Kit, Supplier I, Supplier Q and Supplier W, following each supplier's instructions for use. (A) The KAPA EvoPrep Kit had the lowest percentage of Chimeras present, resulting in higher data confidence[2] compared to Supplier I, Supplier Q and Supplier W having a higher percentage of Chimeras present. (B) The ultra low percentage of SSARs present for KAPA EvoPrep Kit was equivalent to Supplier I and Supplier Q, with Supplier W having the highest percentage of SSARs present. SSARs represent chimeric reads that appear to be derived from non-contiguous portions of the genome[3]. (C) The KAPA EvoPrep Kit had uniform coverage and low AT- or GC-bias. Supplier I had slightly better uniform coverage in the GC-rich region and Supplier Q had lumpy coverage and coverage hotspots i.e., over-representation of AT- rich region. This could require more sequencing to be performed to achieve the requisite coverage for these regions, which increases cost and turnaround times. (D) KAPA EvoPrep Kit had very low duplication count compared to Supplier Q and Supplier W, thereby having more unique library molecules present[1].

Exceptional performance and sequencing results

- **High specificity** combined with the **highest percent of target coverage at ≥ 1000x**
- Best combination of **high uniformity and unique molecule recovery**

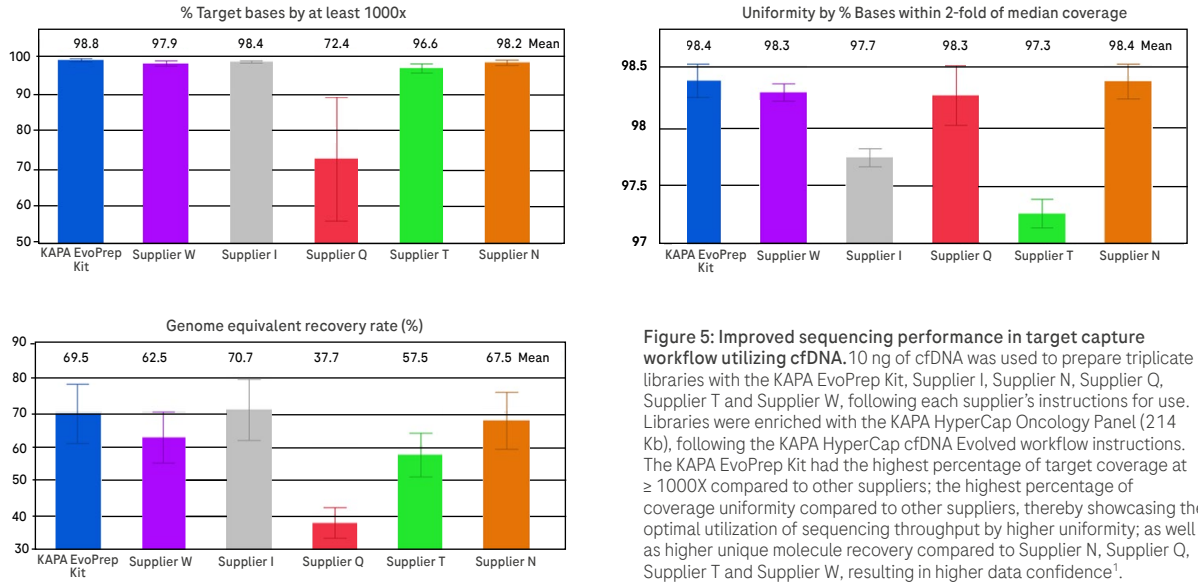

Figure 5: Improved sequencing performance in target capture workflow utilizing cfDNA. 10 ng of cfDNA was used to prepare triplicate libraries with the KAPA EvoPrep Kit, Supplier I, Supplier N, Supplier Q, Supplier T and Supplier W, following each supplier's instructions for use. Libraries were enriched with the KAPA HyperCap Oncology Panel (214 Kb), following the KAPA HyperCap cfDNA Evolved workflow instructions. The KAPA EvoPrep Kit had the highest percentage of target coverage at ≥ 1000X compared to other suppliers; the highest percentage of coverage uniformity compared to other suppliers, thereby showcasing the optimal utilization of sequencing throughput by higher uniformity; as well as higher unique molecule recovery compared to Supplier N, Supplier Q, Supplier T and Supplier W, resulting in higher data confidence[1].

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Ordering information

Roche cat. no.	Description	Pack size
10154039001	KAPA EvoPrep Kit (24rxn)	24 rxn
10096039001	KAPA EvoPrep Kit (96rxn)	96 rxn
10153849001	KAPA EvoPrep Kit (384rxn)	384 rxn
10153865001	KAPA EvoPrep Kit, plated format (96rxn)	96 rxn
10153806001*	KAPA EvoPrep Kit, PCR-free (24rxn)	24 rxn
10153814001*	KAPA EvoPrep Kit, PCR-free (96rxn)	96 rxn
10153857001*	KAPA EvoPrep Kit, PCR-free (384rxn)	384 rxn
10154284001*	KAPA EvoPrep Kit, PCR-free, plated format (96rxn)	96 rxn
09420398001	KAPA HiFi HS RM (9.6ml)	9.6 mL
09420444001	KAPA HiFi HS RM 96 well plate (96rxn)	96 rxn
09420410001	KAPA Library Amp Primer Mix (384 rxn)	384 rxn
09420479001	KAPA Library Amp Primer Mix 96-well plate (96rxn)	96 rxn
10212233702**	KAPA EvoPrep Kit + Lib Amp Primers (24rxn)	24 rxn
10212250702**	KAPA EvoPrep Kit + Lib Amp Primers (96rxn)	96 rxn
10212268702**	KAPA EvoPrep Kit + Lib Amp Primers (384rxn)	384 rxn
10212276702**	KAPA EvoPrep Kit+Lib Amp Primers 96plate	96 rxn

* KAPA Library Amplification Primer Mix (10X) not included.

** Virtual kits.

1. McNulty, *et al.* (2020). Impact of reducing DNA input on next-generation sequencing library complexity and variant detection. The journal of Molecular Diagnostics, Volume 22, Issue 5, May 2020, Pages 720-727.

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.

3. Haile, *et al.* (2019). Sources of erroneous sequences and artifact chimeric reads in next generation sequencing of genomic DNA from formalin-fixed paraffin-embedded samples. Nucleic Acids Research, 47,2. doi: 10.1093/nar/gky1142.

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