Prep *EFFICIENTLY*

KAPA EvoPlus: Embrace the new standard in library prep.

The **KAPA EvoPlus Kits** offer improved fragmentation performance, insensitivity to fragmentation inhibitors, and reduced sequencing artefacts through a streamlined and fully automatable workflow. This **new and upgraded enzymatic fragmentation and library prep solution** enables researchers to achieve higher confidence with increased sequencing efficiency.

KAPA EvoPlus Kits offer a complete library preparation solution when combined with KAPA Adapters and KAPA HyperPure Beads (sold separately). The kits are compatible with the Illumina sequencing platform and have been qualified with automation methods.

Benefits of the KAPA EvoPlus Workflow

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Superior performance and sequencing results	Drastically reduced sequencing artefacts, with insensitivity to inhibitors, fully tunable fragmentation, and improved library prep performance
Simplified and streamlined workflow	Simplified, streamlined, and automatable workflow with combined Fragmentation and A-tailing step in ReadyMix formulations
Scalable and automation friendly	Tubes and plated format increases efficiency and convenience
Tunable and trusted	Compatible with a wide range of sample types and inputs, and flexible with respect to fragment size, adapter design and library amplification

Automation & Connectivity

Sample ▶ ... ▶ Sequencing Ready Library
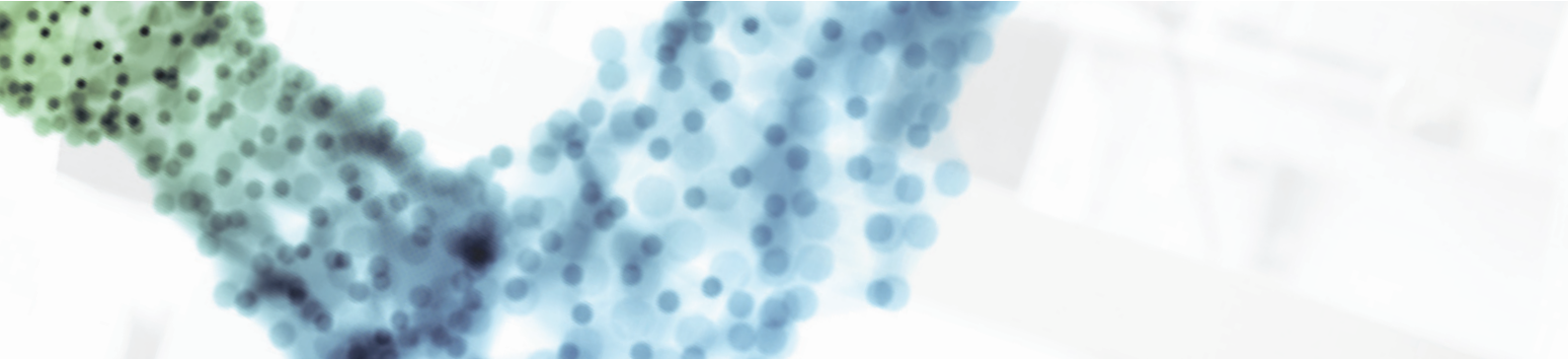
Enable superior performance and sequencing results

- KAPA EvoPlus Kits provide the benefits of enzymatic fragmentation without any drawbacks

- Improved sequencing metrics allow higher confidence in data due to reduction in sequencing artefacts
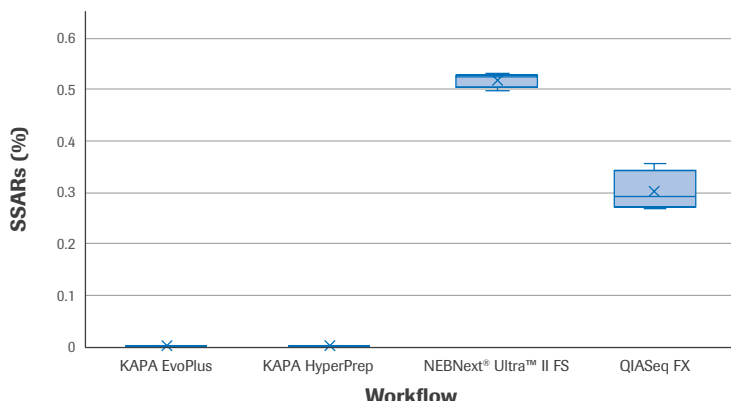

Figure 1. Improved sequencing performance – reduction of strand–split artefact reads (SSARs). Human whole-genome libraries were prepared using 500 ng inputs (double-sided size selection performed) with the KAPA EvoPlus Kit, KAPA HyperPrep Kit, NEBNext® Ultra™ II FS, and QIAseq FX. The percentage SSARs present for KAPA EvoPlus libraries are equivalent to KAPA HyperPrep libraries (considered industry gold-standard)—near zero (0.002%). The competitor kits have a higher percentage of SSARs present. SSARs represent chimeric reads that appear to be derived from non-contiguous portions of the genome.[1]
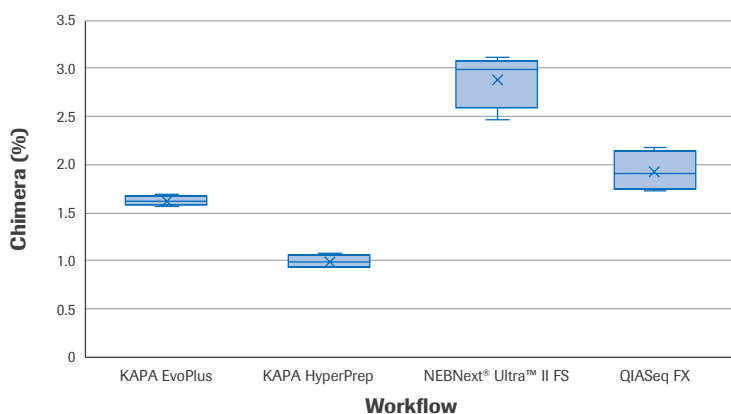

Figure 2. Improved sequencing performance – reduction of chimeras. Human whole-genome libraries were prepared using 500 ng inputs (double-sided size selection performed) with the KAPA EvoPlus Kit, KAPA HyperPrep Kit, NEBNext® Ultra™ II FS, and QIAseq FX. The percentage chimeras present for KAPA EvoPlus libraries is similar to the KAPA HyperPrep libraries (considered industry gold-standard). The competitor kits have a higher percentage of chimeras present.
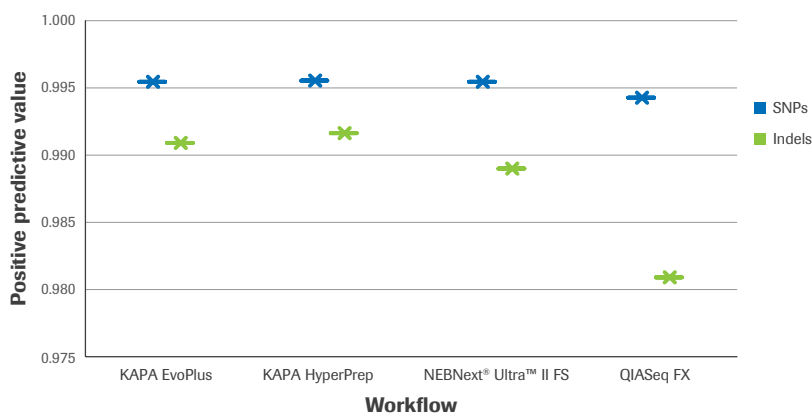

Figure 3. Improved sequencing performance – high positive predictive values (PPVs). This metric relates to the precision of calling the fraction of confirmed SNPs and indels, among all variants called. This would be opposite of the number of false SNPs or indels. The higher this metric, the better. Human whole-genome libraries were prepared using 500 ng inputs (double-sided size selection performed) with the KAPA EvoPlus Kit, KAPA HyperPrep Kit, NEBNext® Ultra™ II FS, and QIAseq FX. The PPVs for the KAPA EvoPlus libraries are similar to the KAPA HyperPrep libraries (considered industry gold-standard). The competitor kits have lower PPVs.

[1]Source: 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*, 2019, 47,2. doi: 10.1093/nar/gky1142.

Simplified and streamlined workflow

The KAPA EvoPlus Kit provides a simplified and streamlined workflow to remove the complexities and risk for human error by providing a trusted enzymatic fragmentation solution.

- Streamlined library prep with combined Fragmentation and A-tailing step
- ReadyMix formulations, therefore fewer reagents and hands-on-time
- Tubes and plated format increases efficiency and convenience
- Manual and automation friendly
- Reduces complexity of workflow and provides greater peace of mind
- Validated with the KAPA HyperCap Workflow and KAPA HyperPETE Workflow
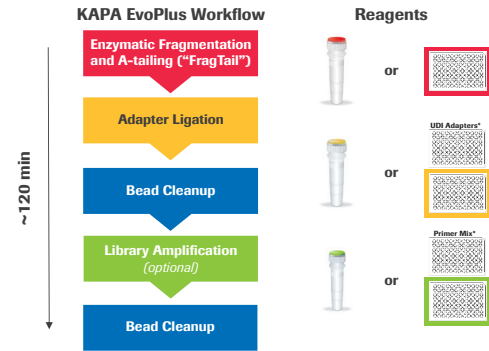

Figure 4. The KAPA EvoPlus Workflow.

*KAPA UDI Adapter Kits and KAPA Library Amplification Primer Mix (10X) sold separately.

Tunable and trusted fragmentation

- Library insert sizes adjustable by varying fragmentation time
- Reproducible insert sizes across a range of GC content and DNA input amounts
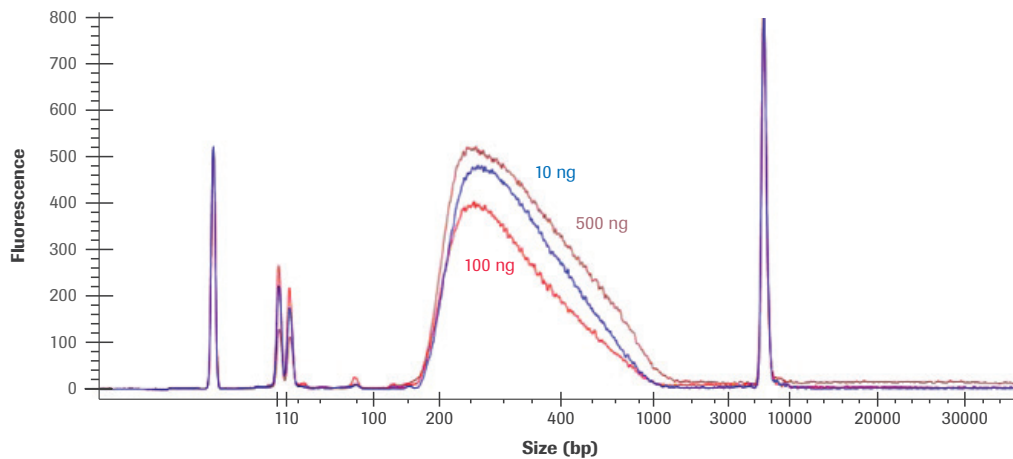- No impact to fragmentation—insensitive to EDTA (up to 2 mM), as well as numerous other inhibitors

Figure 5. The KAPA EvoPlus chemistry enables reproducible enzymatic fragmentation across different input amounts. Human genomic DNA (10 ng, 100 ng and 500 ng) was fragmented at 37°C to achieve mode library insert size of approximately 300 bp. The KAPA EvoPlus workflow was completed without any size selection using full-length adapters (KAPA UDI Adapters) and 2 cycles of amplification. Final libraries were analyzed using a LabChip GX Touch HT instrument and HT DNA HiSens Reagent Kit (PerkinElmer).
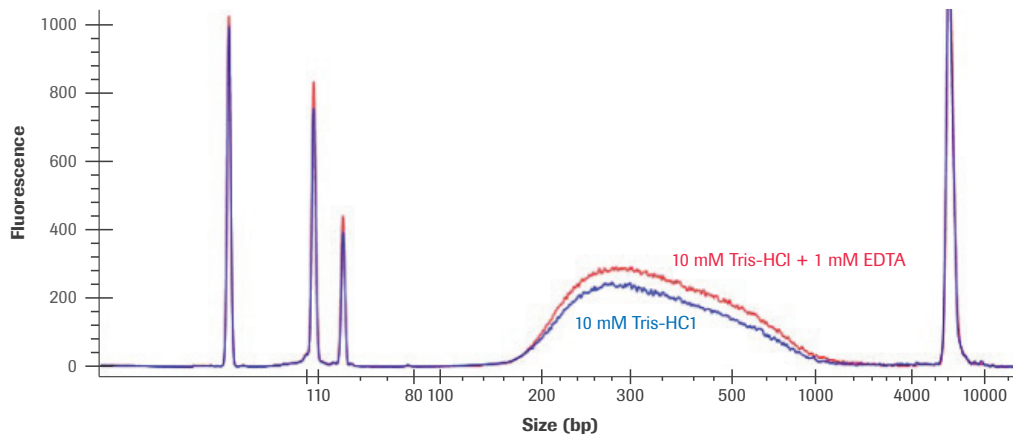

Figure 6. The KAPA EvoPlus chemistry enables reproducible enzymatic fragmentation across DNA diluted in different buffer types. Human genomic DNA (500 ng) diluted in 10 mM Tris-HCl and 10 mM Tris-HCl, 1 mM EDTA was fragmented at 37°C to achieve mode library insert sizes of approximately 300 bp. The KAPA EvoPlus workflow was completed without any size selection using full-length adapters (KAPA UDI Adapters) and 2 cycles of amplification. Final libraries were analyzed using a LabChip GX Touch HT instrument and HT DNA HiSens Reagent Kit (PerkinElmer).

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

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Minimal sequence coverage bias

- Lower sequence bias when compared to other enzymatic fragmentation methods

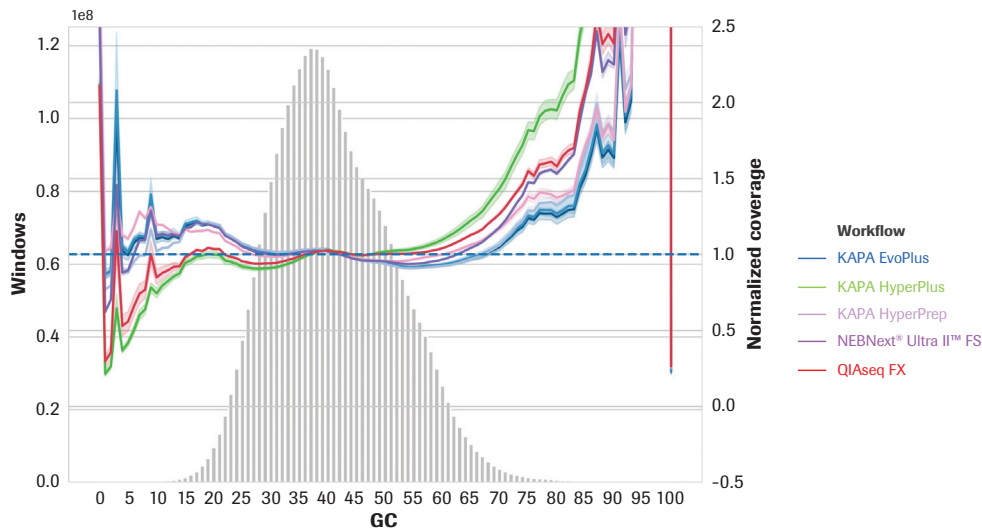- Less bias leads to more uniform sequencing coverage and reduced sequencing costs

Figure 7. Bias associated with enzymatic fragmentation in the KAPA EvoPlus workflow had no impact on overall coverage depth and uniformity, or GC bias—which were virtually identical for KAPA EvoPlus and KAPA HyperPrep workflows. The QIAseq FX workflow struggles with both AT- and GC-rich regions, whereas NEBNext® Ultra™ II FS workflow performs worse with GC-rich regions—presumably as the result of more biased fragmentation. This results in lumpy coverage and coverage hotspots, i.e., over-representation of "easy" (more GC-balanced) regions and under-representation of "difficult" (AT- and GC rich) regions. With these methods, more sequencing has to be performed to achieve the requisite coverage for these regions, which increases cost and turnaround times.

Ordering Information

Roche cat. no.	Description	Kit size
09420037001	KAPA EvoPlus Kit	24 rxn
09420053001	KAPA EvoPlus Kit	96 rxn
09420339001	KAPA EvoPlus Kit	384 rxn
09420428001	KAPA EvoPlus Kit (96-well plate)	96 rxn
09420045001	KAPA EvoPlus Kit, PCR-free	24 rxn
09420304001	KAPA EvoPlus Kit, PCR-free	96 rxn
09420371001	KAPA EvoPlus Kit, PCR-free	384 rxn
09420436001	KAPA EvoPlus Kit, PCR-free (96-well plate)	96 rxn
09420398001	KAPA HiFi HotStart ReadyMix	9.6 mL
09420410001	KAPA Library Amp Primer Mix	384 rxn
09420479001	KAPA Library Amp Primer Mix (96-well plate)	96 rxn

Learn more at
sequencing.roche.com