KAPA HyperPlus Kits

NGS library preparation. Evolved.

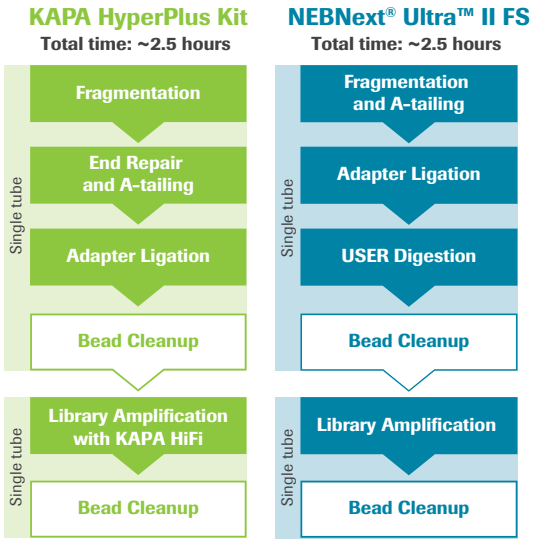
The KAPA HyperPlus Kit provides a streamlined, single-tube workflow from DNA fragmentation through library construction. This integrated solution combines the industry-leading library construction efficiency and library quality of the KAPA HyperPrep Kit with the speed and convenience of enzymatic fragmentation.

- **Improve sequencing performance** by reducing artifacts associated with sample preparation: use the newly included KAPA HyperPlus End Repair & A-Tailing Enzyme Mix to further reduce the chimeric reads often seen with library prep kits employing enzymatic fragmentation.[1]
- **Save time with the 2.5-hour workflow**, inclusive of DNA fragmentation
- **Maximize library prep flexibility** with a range of DNA inputs (1 ng – 1 µg), tunable DNA fragmentation, and both with-PCR and PCR-free workflows that are compatible with various liquid-handling instruments
- **Reduce bias, increase library complexity, and improve coverage uniformity** with industry-leading conversion rates—particularly for FFPE DNA
- **Order all of your library prep reagents from one trusted vendor**—including sequencing adapters, quantification and QC reagents, clean-up beads, and target enrichment solutions

Integrated fragmentation and library preparation solution

The **KAPA HyperPlus Kit** includes low-bias enzymatic fragmentation, eliminating the need for mechanical DNA shearing methods that require expensive instrumentation and are difficult to automate.

- Fragment DNA and construct libraries in 2.5 hours with a single-tube, automation-friendly workflow
- Achieve high success rates from a wide range of DNA input amounts and sample types, including challenging samples such as FFPE
- Use with a variety of sequencing applications, including human exome and microbial whole-genome sequencing
- Rely on the newly included KAPA HyperPlus End Repair & A-Tailing Enzyme Mix to further reduce the chimeric reads often seen with enzymatic fragmentation methods[1]



Tunable and reproducible fragmentation

- Adjust library insert sizes from 150 – 800 bp by varying fragmentation time
- Consistently generate desired insert sizes across a range of GC content and DNA input amounts

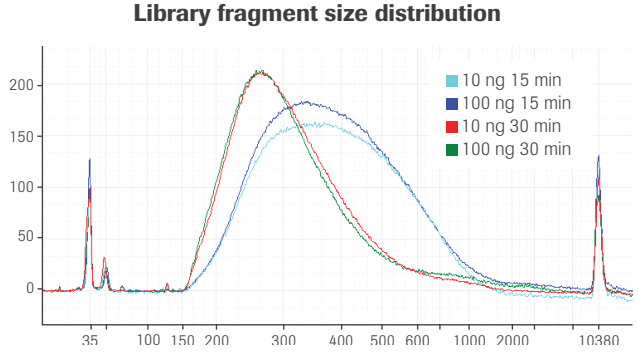


Figure 1. Reproducible library fragment size distributions are obtained with different DNA inputs. Various input amounts of *Escherichia coli* gDNA were processed using the KAPA HyperPlus Kit with fragmentation times of 15 or 30 minutes at 37ºC. After library amplification and a single bead cleanup, samples were analyzed using an Agilent® High Sensitivity DNA Assay.

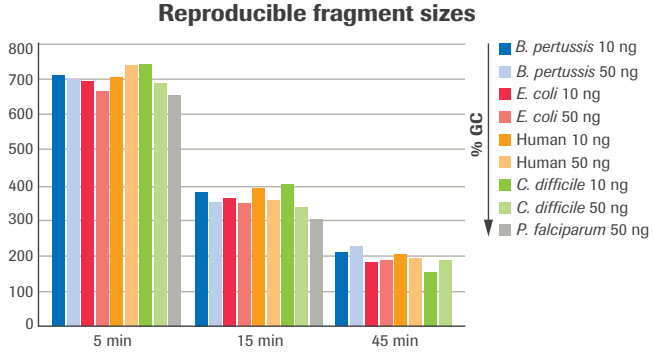


Figure 2. Defined fragmentation parameters yield consistent library insert sizes for samples from multiple species across a wide range of GC content. 10 ng or 50 ng of *Bordetella pertussis* (68% GC), *Clostridium difficile* (29% GC), *Escherichia coli* (51% GC), *Plasmodium falciparum* (20% GC), or human gDNA were fragmented for 5, 15, or 45 minutes. These fragmentation times yielded average library insert sizes of approximately 700 bp, 350 bp, and 200 bp, respectively; regardless of GC content and input amount. All fragmentation reactions were performed at 37ºC.

Data on file.

Industry-leading conversion and library yield

The new and improved KAPA HyperPlus Kits combine the efficiency of KAPA HyperPrep Kits with the convenience of enzymatic fragmentation, delivering higher library yields that ultimately improve library diversity and quality.

- Achieve the highest post-ligation library yields with KAPA HyperPlus
- Create PCR-free libraries from as little as 50 ng input DNA
- Generate high-quality libraries from low-input samples without the need for additional, specialized reagents

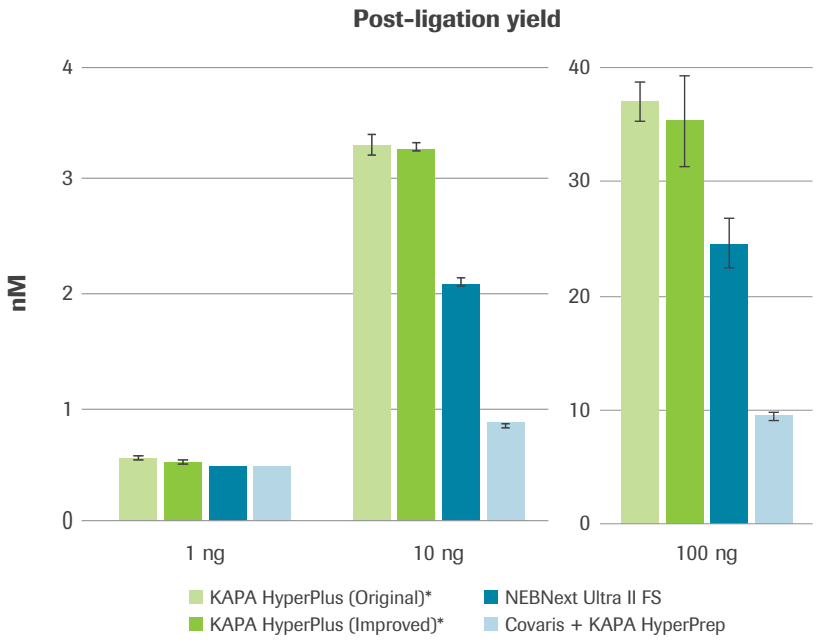


Figure 3. KAPA HyperPlus Kits produce the highest yields from a range of input amounts. The KAPA HyperPlus Kit—both the Original formulation employing the HyperPrep End Repair and A-Tailing Enzyme Mix, as well as the Improved formulation, which also contains the new KAPA HyperPlus End Repair and A-Tailing Enzyme Mix—converts more input DNA to adapter-ligated library than NEBNext® Ultra™ II FS Kits or Covaris shearing combined with KAPA HyperPrep. PCR-free libraries were prepared from 1 ng, 10 ng, and 100 ng *E. coli* gDNA using KAPA UDI Adapters and KAPA HyperPure Beads for all workflows, including NEBNext Ultra II FS Kits. Libraries (the average of three replicates) were quantified after ligation using the KAPA Library Quantification Kit.

Superior sequencing results

- Reduce duplication rates
- Detect variants with confidence

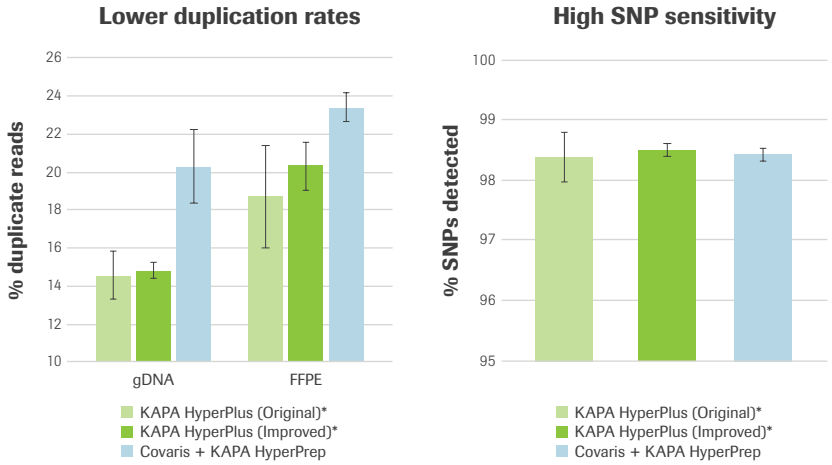


Figure 4. The updated/improved KAPA HyperPlus Kit yields fewer duplicate reads while maintaining high SNP sensitivity. Whole human exome libraries were prepared using 100 ng inputs with the original KAPA HyperPlus Kit, the improved KAPA HyperPlus Kit, or the KAPA HyperPrep Kit (with mechanical shearing). Captures were performed with the SeqCap EZ MedExome panel.

*KAPA HyperPlus (Original) refers to kits containing the HyperPrep End Repair & A-Tailing Enzyme Mix, originally included with the KAPA HyperPlus Kits. KAPA HyperPlus (Improved) refers to kits containing the new HyperPlus End Repair & A-Tailing Enzyme Mix, which is now also included in the KAPA HyperPlus Kit.

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

Minimal sequence coverage bias and chimeric reads

- Reduce sequence bias compared to other enzymatic fragmentation methods
- Increase coverage uniformity and reduce sequencing costs
- Rely on the newly included KAPA HyperPlus End Repair & A-Tailing Enzyme Mix to further reduce the chimeric reads often seen with enzymatic fragmentation methods (Figure 6)

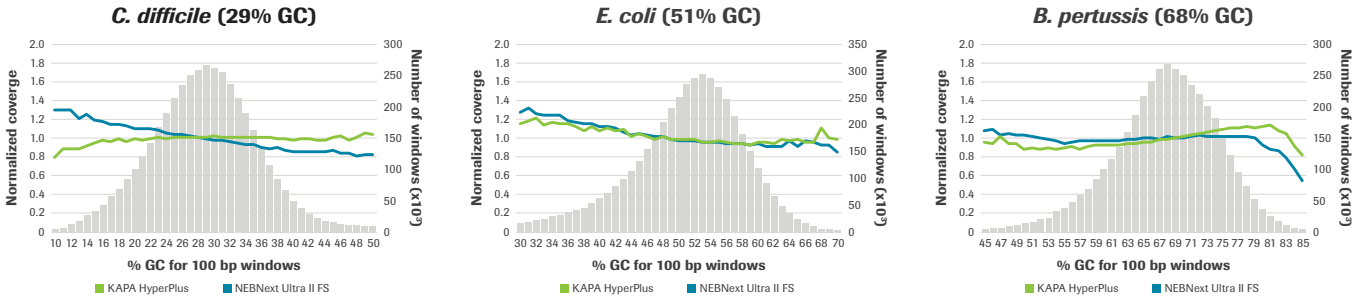


Figure 5. Reduce GC bias with the HyperPlus workflow. GC bias for *C. difficile* (left), *E. coli* (middle) and *B. pertussis* (right) was assessed by calculating the GC content of the reference in 100 bp bins and plotting normalized coverage across these bins for the KAPA HyperPlus and NEBNext® Ultra™ II FS workflows using Picard CollectGCBiasMetrics. Libraries were prepared from 10 ng of input DNA. In the absence of sequencing bias, all bins would be equally represented, indicated by a horizontal distribution centered on a normalized coverage of 1. Distribution of GC content in the genome is indicated by the grey histograms.

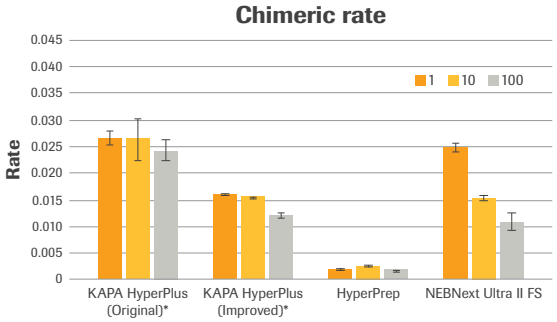


Figure 6. Achieve lower chimeric rates than with other enzymatic fragmentation kits. The rate of chimeric reads obtained with any enzymatic fragmentation-based kit is higher than rates obtained with kits that use mechanically sheared DNA as input, such as the KAPA HyperPrep Kit. While still higher than the low chimeric rates yielded by the KAPA HyperPrep Kit, the chimeric rate obtained with the Improved version of the KAPA HyperPlus Kit is lower than either the Original KAPA HyperPlus Kit formulation or the NEB Ultra II FS Kit.

Ordering information

Roche cat. no.	KAPA code	Description	Kit size
07962380001	KK8510	KAPA HyperPlus Kit with Library Amplification	8 reactions
07962401001	KK8512	KAPA HyperPlus Kit with Library Amplification	24 reactions
07962428001	KK8514	KAPA HyperPlus Kit with Library Amplification	96 reactions
07962398001	KK8511	KAPA HyperPlus Kit, PCR-Free	8 reactions
07962410001	KK8513	KAPA HyperPlus Kit, PCR-Free	24 reactions
07962436001	KK8515	KAPA HyperPlus Kit, PCR-Free	96 reactions
08861919702	KK8727	KAPA Unique Dual-Indexed Adapter Kit (15 µM, incl. KAPA Adapter Dilution Buffer)	384 reactions
08278539001	KK8721	KAPA Adapter Dilution Buffer (Available for purchase separately)	25 mL
08963835001	KK8007	KAPA HyperPure Beads	5 mL
08963843001	KK8008	KAPA HyperPure Beads	30 mL
08963851001	KK8009	KAPA HyperPure Beads	60 mL
08963878001	KK8011	KAPA HyperPure Beads	4 x 60 mL
08963860001	KK8010	KAPA HyperPure Beads	450 mL

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[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.

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