KAPABIOSYSTEMS
evolving better science

NGS PCR qPCR

KAPA HYPER PLUS

NGS library preparation. Evolved.

The KAPA HyperPlus kit provides a streamlined workflow that includes fragmentation and library preparation in a single tube. Building on industry-leading library construction efficiencies, this integrated solution combines enzymatic fragmentation, similar in quality to mechanical shearing, with the speed and convenience of tagmentation-based workflows.

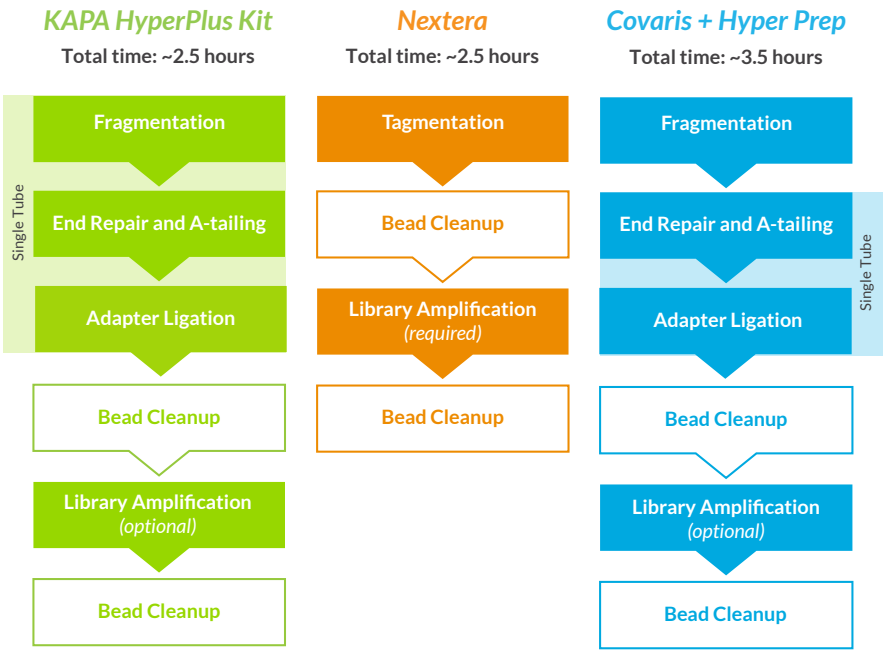
Benefits include:

- DNA fragmentation and library prep in 2.5 hours
- flexible DNA sample input from 1 ng - 1 ug
- reduced bias and more uniform sequence coverage
- PCR-Free workflows

Integrated Fragmentation and Library Preparation Solution

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

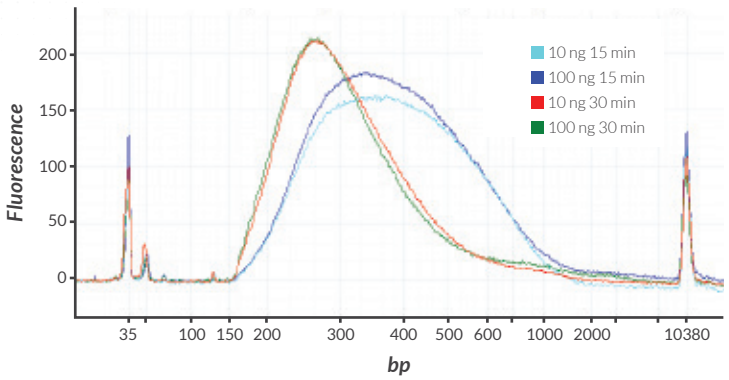
- Fragment DNA and construct libraries in 2.5 hours with a single-tube workflow
- Supports a wide range of DNA types and input amounts including challenging sample types such as FFPE
- Versatile kit works across many applications, including human exome and microbial whole genome sequencing
- Automation-friendly workflow



Tunable and Reproducible Fragmentation

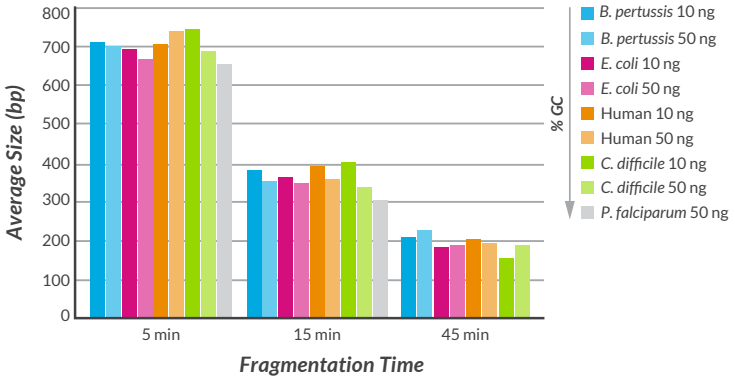
- Adjust library insert sizes from 150 - 800 bp by varying fragmentation time
- Reproducible insert sizes across a range of GC content and DNA input amounts

Library Fragment Size Distribution



Reproducible library fragment size distributions are obtained from a variety of DNA sample inputs. Various input amounts of *E. coli* gDNA, were processed using the HyperPlus Kit with fragmentation times of 15 or 30 minutes at 37˚C. After library amplification and a single 1x SPRI® bead cleanup, samples were analysed using an Agilent High Sensitivity DNA Assay™.

Reproducible Fragment Sizes



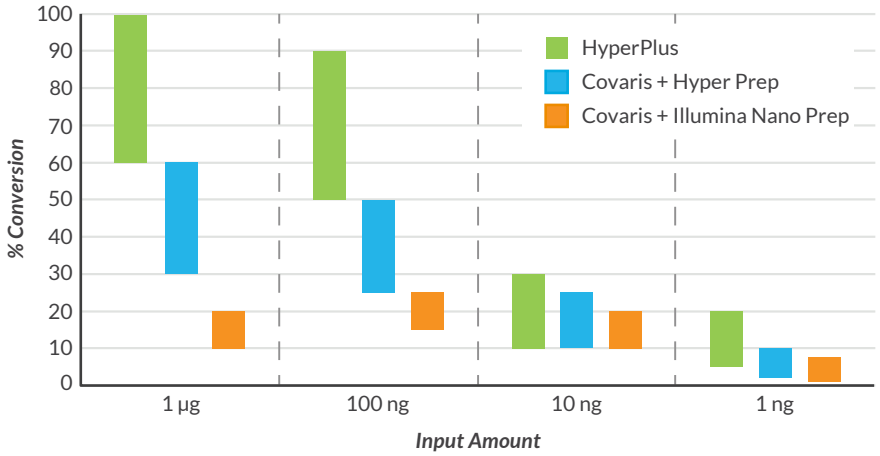
Defined fragmentation parameters yield consistent library insert sizes using samples from multiple species across a wide range of GC content. 10 ng or 50 ng of *Bordetella pertussis* (68% GC), *Clostridium difficile* (29% GC), *Escherichia coli* (51% GC), *Plasmodium falciparum* (20% GC) or human gDNA were fragmented for 5, 15 or 45 minutes, yielding average insert fragment sizes of ~700, ~350 or ~200 bp respectively. Fragmentation reaction performed at at 37°C.

Industry Leading Library Yields…

Conversion rate, defined as % input DNA converted to sequenceable, adapter-ligated library, is a key library construction metric, which ultimately determines library diversity and quality.

- Attain up to 100% conversion rates
- Superior performance across a range of DNA input amounts
- High library yields enable PCR-free workflows from as little as 50 ng starting material

Conversion Rate Ranges

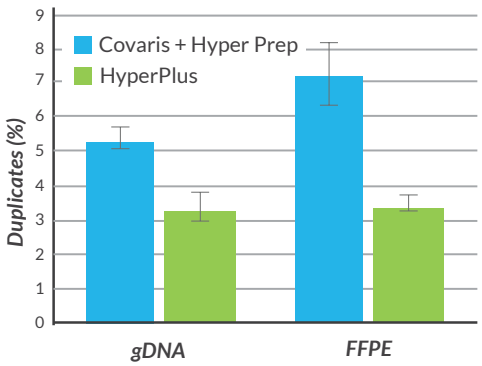


Conversion rates vary widely for commercial library construction products. The HyperPlus integrated workflow results in greater conversion of input DNA to adapter-ligated library compared to Covaris-sheared DNA processed using the Illumina TruSeq Nano Prep Kit, or the KAPA Hyper Prep Kit. Conversion rates are highest for the KAPA HyperPlus Kit for both high- and low-input applications.

…Enable Superior Sequencing Results

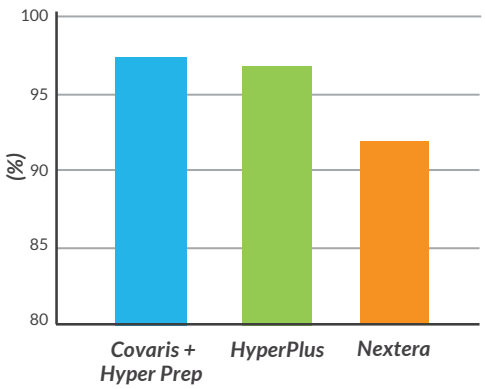
- Higher conversion rates results in fewer amplification cycles and lower duplication rates
- Detect low-frequency mutations with high confidence due to greater library diversity and more uniform sequence coverage

Duplication Rates



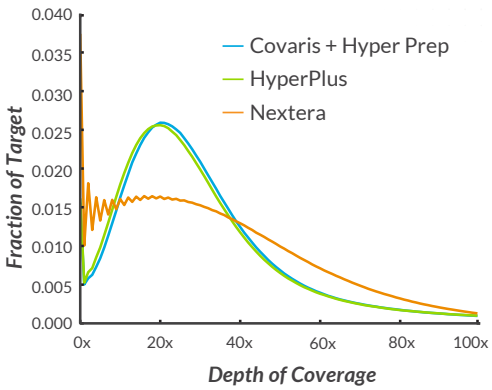
Low duplication rates. % duplicates from exome sequencing experiments using HyperPlus, or Covaris and Hyper Prep. Libraries were prepared from 50 ng hgDNA or 50 ng FFPE DNA and captured with the Nimblegen SeqCap EZ HGSC VCRome panel.

Sensitivity of SNP Detection



Single nucleotide polymorphism (SNP) detection sensitivity indicates better sequencing quality. Libraries prepared for capture using the Nimblegen SeqCap EZ HGSC VCRome panel, 50 ng input, standard capture protocol. SNPs were called using LoFreq with default settings and a minimum per-base depth of coverage cut-off of 10. Sensitivity (true positive rate) was calculated as the ratio of true positives divided by the sum of true positives and false negatives. The total number of SNPs analyzed was greater than 25,000.

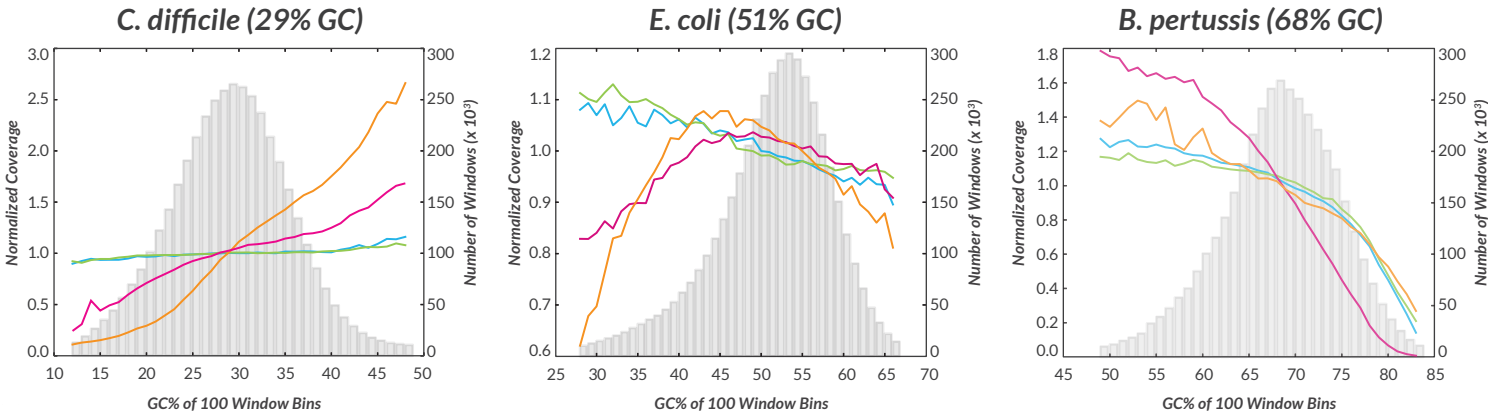
Sequence Coverage Uniformity



Sequence coverage uniformity comparison. Data for all libraries were down-sampled to equal number of reads. Roche Nimblegen capture libraries prepared with HyperPlus or Covaris and Hyper Prep were compared to libraries prepared with Nextera™ Rapid Capture. Coverage distribution was similar for Covaris and HyperPlus libraries, while Nextera libraries displayed much broader coverage distribution. A sharper peak and smaller tails indicate more uniform coverage.

Minimal Sequence Coverage Bias

- Lower sequence bias when compared to tagmentation and other enzymatic fragmentation methods
- Equivalent performance to mechanical shearing
- Less bias leads to more uniform sequencing coverage and reduced sequencing costs



GC bias comparison. GC bias for *C. difficile* (left), *E.coli* (middle) *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 Covaris and Hyper Prep, HyperPlus, NEBNext® Ultra™ and Nextera™ workflows, using Picard CollectGCBiasMetrics. Libraries were prepared from 1 ng of input DNA. In the absence of sequencing bias, all bins would be equally represented, indicated by a horizontal distribution centred on a normalized coverage of 1. Distribution of GC content in the genome is indicated by the grey histograms.

Ordering Information

Kit Code	Description	Kit Size
KK8510	KAPA HyperPlus Kit with Library Amplification	8 reactions
KK8512	KAPA HyperPlus Kit with Library Amplification	24 reactions
KK8514	KAPA HyperPlus Kit with Library Amplification	96 reactions
KK8511	KAPA HyperPlus Kit, PCR-free	8 reactions
KK8513	KAPA HyperPlus Kit, PCR-free	24 reactions
KK8515	KAPA HyperPlus Kit, PCR-free	96 reactions

Contact Sales by:

Calling us at **781.497.2933**

Visiting our website at **kapabiosystems.com**

Emailing us at **sales@kapabiosystems.com**

Contact Technical Support by:

Calling us at **781.497.2933**

Emailing us at **support@kapabiosystems.com**

@KapaBiosystems KapaBiosystems KapaBiosystems

Headquarters
Wilmington, Massachusetts, United States
Tel: 781.497.2933
Fax: 781.497.2934
sales@kapabiosystems.com

International Office
Cape Town, South Africa
Tel: +27.21.448.8200
Fax: +27.21.448.6503
sales@kapabiosystems.com

United Kingdom Office
London, England
Tel: +44.845.512.0641
Fax: +44.203.745.5862
uksales@kapabiosystems.com