KAPA HyperPrep Kits

Shift your workflow into hyperdrive

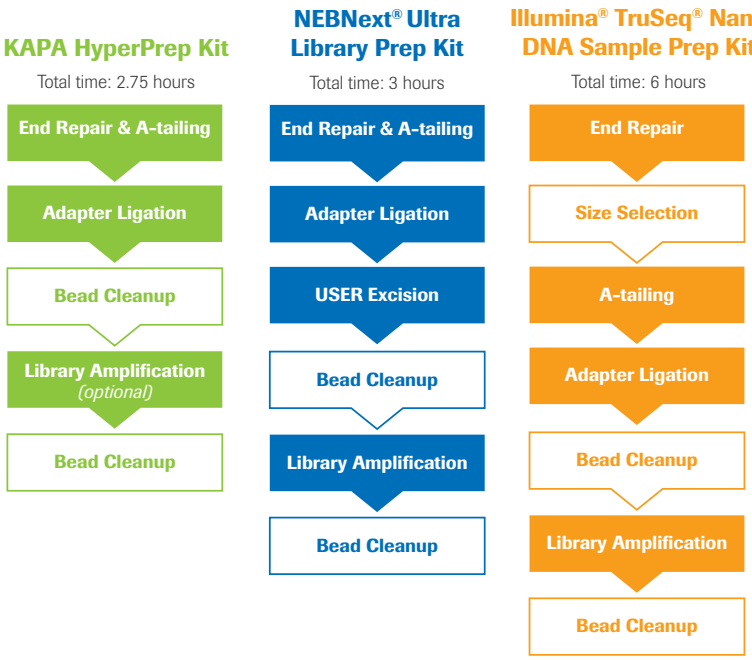
The KAPA HyperPrep Kit provides a streamlined, versatile library preparation solution that significantly reduces sequencing library preparation time. The novel, single-tube chemistry offers improvements to library construction efficiency, particularly for challenging samples such as FFPE and cell-free DNA.

- Superior speed and convenience
- Lower duplication rates and higher sequencing coverage
- Improved performance with low-input samples
- High-quality library construction from FFPE samples
- Choice of PCR or PCR-free workflows
- Qualified automation methods

Superior speed and convenience

The streamlined, one-tube KAPA HyperPrep protocol offers rapid turnaround times, with reduced hands-on time.

- Complete library construction in less than 3 hours
- Omit library amplification for PCR-free workflows, if desired
- Incorporate bead-based size-selection steps to achieve the appropriate final library fragment-size distribution



High library yields and sequencing quality

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

- Achieve higher library yields across a range of input DNA and sample types
- Employ fewer amplification cycles for downstream processing, resulting in lower duplication rates and higher sequence coverage
- Achieve successful library construction with challenging samples and PCR-free workflows

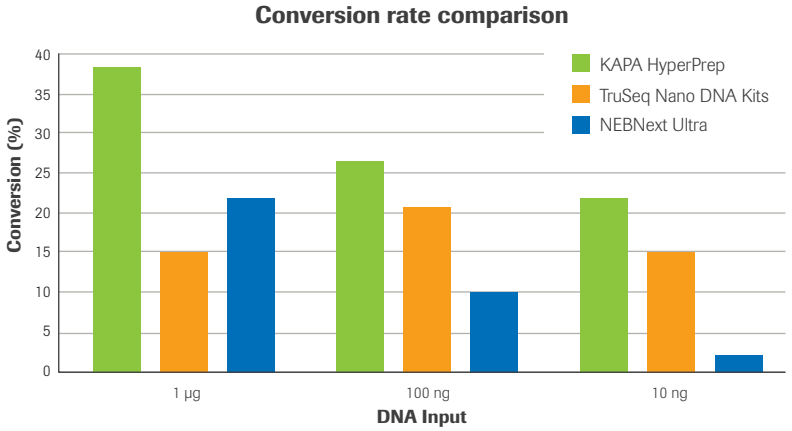


Figure 1. Conversion rates for libraries prepared for target capture from different amounts of Covaris-sheared DNA, using the KAPA HyperPrep or competitor library construction kits. Libraries were prepared according to manufacturer's instructions. Input DNA was quantified by Qubit®, whereas the qPCR-based KAPA Library Quantification Kit was used to determine KAPA HyperPrep and TruSeq Nano library yields after adapter ligation. Conversion rates for NEBNext libraries cannot be measured directly using the KAPA Library Quantification Kit and were derived from post-amplification yields.

Reduce amplification bias

- In workflows where amplification is required, rely on KAPA HiFi to reduce amplification bias, resulting in more uniform sequence coverage
- Choose kits without an amplification module for PCR-free workflows

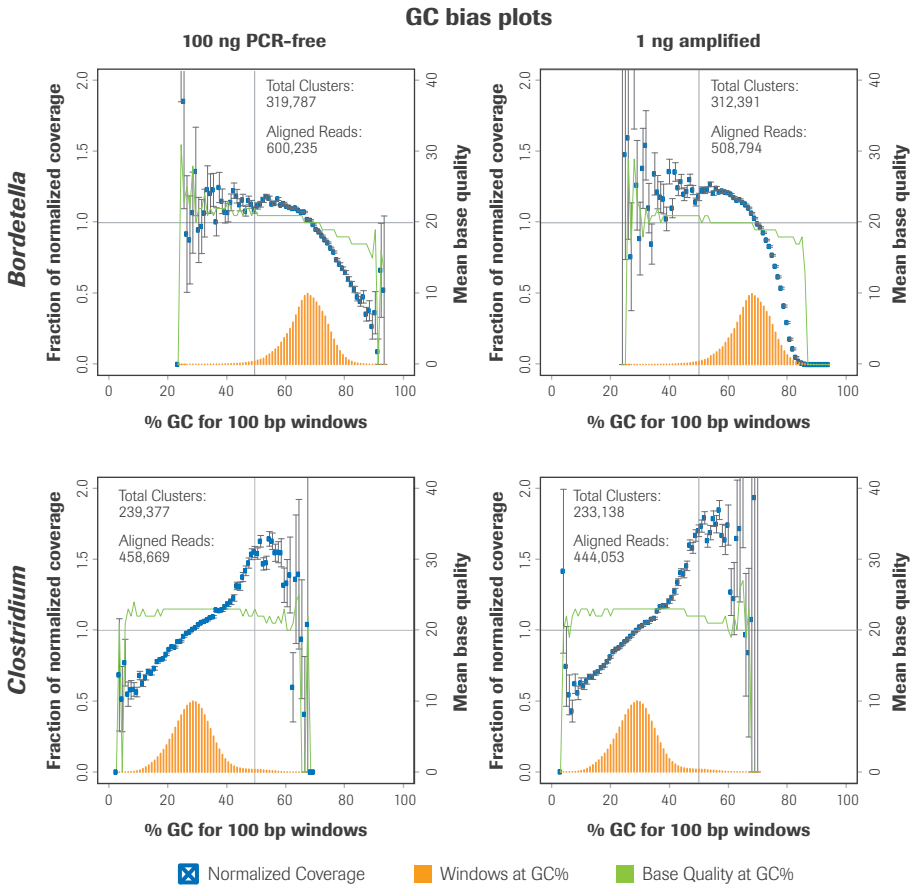


Figure 2. GC bias plots for libraries prepared for whole-genome shotgun sequencing of bacteria with extreme genomic GC content. Libraries were prepared with the KAPA HyperPrep Kit from 100 ng or 1 ng DNA, Covaris-sheared to an average size of ~200 bp, and sequenced without amplification, or after amplification with KAPA HiFi HotStart ReadyMix. Sequencing (2 x 300 bp) was performed on an Illumina® MiSeq® instrument and data analyzed using Picard.

High-quality library construction from FFPE samples

- Detect low-frequency mutations as a result of lower duplication rates and high sequence coverage
- More unique adapter-ligated library fragments from low-quality sample types translate to higher library diversity

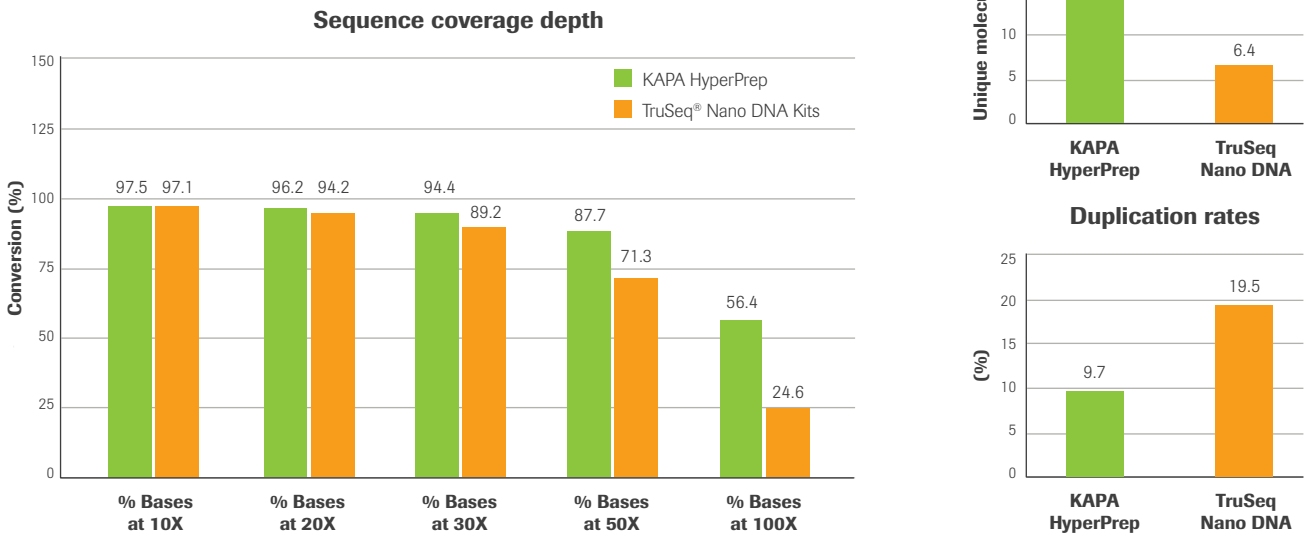


Figure 3. Sequencing metrics for libraries prepared from 100 ng FFPE DNA for target capture, using either the KAPA HyperPrep Kit or TruSeq Nano DNA Sample Prep Kit (Illumina). Captures were performed with the SeqCap EZ Comprehensive Cancer Design (4 Mb) according to the manufacturer's instructions, with the exception that the number of pre-capture amplification cycles for each library type was optimized based on post-ligation yields (10 cycles for KAPA HyperPrep vs. 14 cycles for TruSeq Nano DNA libraries). All libraries were amplified for 13 cycles after capture. Sequencing (2 x 75 bp) was performed on an Illumina HiSeq® instrument. Sequencing reads were down-sampled to ~14 million per library prior to analysis with Picard.

Improve performance with low-input samples

- Generate more diverse libraries from limited amounts of input DNA
- Use high adapter:insert molar ratios to increase library construction efficiency

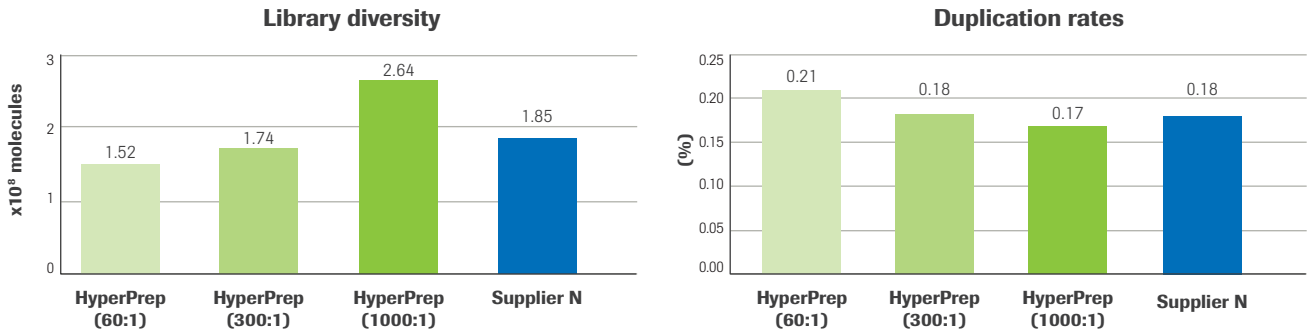


Figure 4. Library diversity and duplication rates for libraries prepared from 2 ng of cell-free DNA. Libraries were constructed with the KAPA HyperPrep Kit or another supplier's kit optimized for low-input library construction, according to manufacturer's instructions. Standard ligation parameters were used. KAPA HyperPrep libraries were prepared with a range of adapter:insert molar ratios. Sequencing (2 x 150 bp) was performed on an Illumina® MiSeq® instrument and data analyzed using Picard.

Ordering information

Roche cat. no.	KAPA code	Description	Kit size
07962312001	KK8500	KAPA HyperPrep Kit with Library Amplification	8 rxn
07962347001	KK8502	KAPA HyperPrep Kit with Library Amplification	24 rxn
07962363001	KK8504	KAPA HyperPrep Kit with Library Amplification	96 rxn
07962339001	KK8501	KAPA HyperPrep Kit, PCR-free	8 rxn
07962355001	KK8503	KAPA HyperPrep Kit, PCR-free	24 rxn
07962371001	KK8505	KAPA HyperPrep Kit, PCR-free	96 rxn
08963835001	KK8007	KAPA HyperPure Beads	5 mL
08963843001	KK8008	KAPA HyperPure Beads	30 mL
08963851001	KK8009	KAPA HyperPure Beads	60mL
08963878001	KK8011	KAPA HyperPure Beads	4 x 60 mL
08963860001	KK8010	KAPA HyperPure Beads	450 mL
08861919702	KK8727	KAPA Unique Dual-Indexed Adapters Kit 15 µM	384 rxn

Published by:

Roche Sequencing and Life Science
9115 Hague Road
Indianapolis, IN 46256

sequencing.roche.com

go.roche.com/HyperPrep

MC-US-09043 SS106001 A750 5/23