KAPA EvoPrep Kits Guide to Success

Simplify high-performance library prep from mechanically fragmented DNA.

Roche

Optimize amplification cycles for your downstream application

Input DNA	Number of cycles to generate ≥4 nM* of library (if using KAPA UDI Adapters)	Number of cycles to generate ≥4 nM* of library (if using truncated KAPA Universal Adapter & KAPA UDI Primer Mixes)
0.1 ng	10 - 12	11 - 13
1 ng	7 - 9	8 - 10
10 ng	3 - 5	5 - 7
50 – 500 ng	0 (PCR free)	3

* The number of cycles needed depends on the specific adapter and amplification primer design, as well as input type and quality

1 INPUT DNA

Fragmented dsDNA or cfDNA

Setup is at 4°C

2 END REPAIR & A-TAILING (ERAT)

30 min

Incubate at 35°C

30 min

Followed by 65°C

ReadyMixes are already prepared for all KAPA EvoPrep library steps

3 ADAPTER LIGATION

5 min

Incubate at 20°C

Adapter concentration depends on input DNA

4 0.93X POST-LIGATION BEAD CLEANUP

PCR-free Whole Genome Sequencing

5 LIBRARY AMPLIFICATION

6 1X POST-AMP BEAD CLEANUP

7 SECOND POST-AMP CLEANUP (OPTIONAL)

Only if using KAPA Universal Adapter & KAPA UDI Primer Mixes

Proceed to target enrichment or Whole Genome Sequencing
Visit us at sequencing.roche.com/support

Is my library of sufficient quality and quantity to proceed?
Assess both the size and concentration of the library with an appropriate quantification method.

YES → **Proceed to sequencing**

NO → **Visit us at** sequencing.roche.com/support

How much DNA do I need?

Application	Sample type	Input
WGS	High quality gDNA	0.1 – 500 ng
	Low quality FFPET-derived DNA	≥ 50 ng*
WGS (PCR-free)	High quality gDNA	≥ 50 ng (no-SS)** 500 ng (with SS)**
Targeted Sequencing	High quality gDNA	100 ng
	Cell-free/circulating tumor DNA (cfDNA/ctDNA)	10 ng – 50 ng

* Reach out to Technical Support for possible workflow modifications when using this sample type.
** SS = double-sided size selection; a requirement when performing WGS on patterned flow cells but may result in sample losses of 60 – 95%, irrespective of whether a bead- or gel-based technique is used. For PCR-free workflows, due to the inherent sample losses, performing double-sided size selection with inputs <500 ng (into library prep) is not recommended.

How much adapter do I need?

Adapter concentration affects ligation efficiency, as well as adapter and adapter-dimer carry-over during the post-ligation cleanup.

Input DNA	Adapter stock concentration*
<10 ng	3 µM
10 ng - 500 ng	15 µM

*Adapter stock concentration remains unchanged, regardless of whether KAPA UDI Adapter (full length) or KAPA Universal Adapter (truncated) are used.