

# KAPA EvoPrep Kits Guide to Success



Streamlined sample prep workflow using the next evolved generation of KAPA DNA Library Prep Reagents.

**Work smarter, not harder.**  
Optimize amplification cycles for your downstream application

Input DNA	Number of cycles to generate $\geq 4$ nM* of library (if using KAPA UDI Adapters)	Number of cycles to generate $\geq 4$ 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



## How much DNA do I need?

Application	Sample type	Input
WGS	High quality gDNA	0.1 - 500 ng
	Low quality FFPE-derived DNA	$\geq 50$ ng*
WGS (PCR-free)	High quality gDNA	$\geq 50$ ng (no-SS)** 500 ng (with SS)**
	High quality gDNA	100 ng
Targeted Sequencing	High quality gDNA	100 ng
	Cell-free/circulating tumour DNA (cfDNA/ctDNA)	10 ng - 50 ng

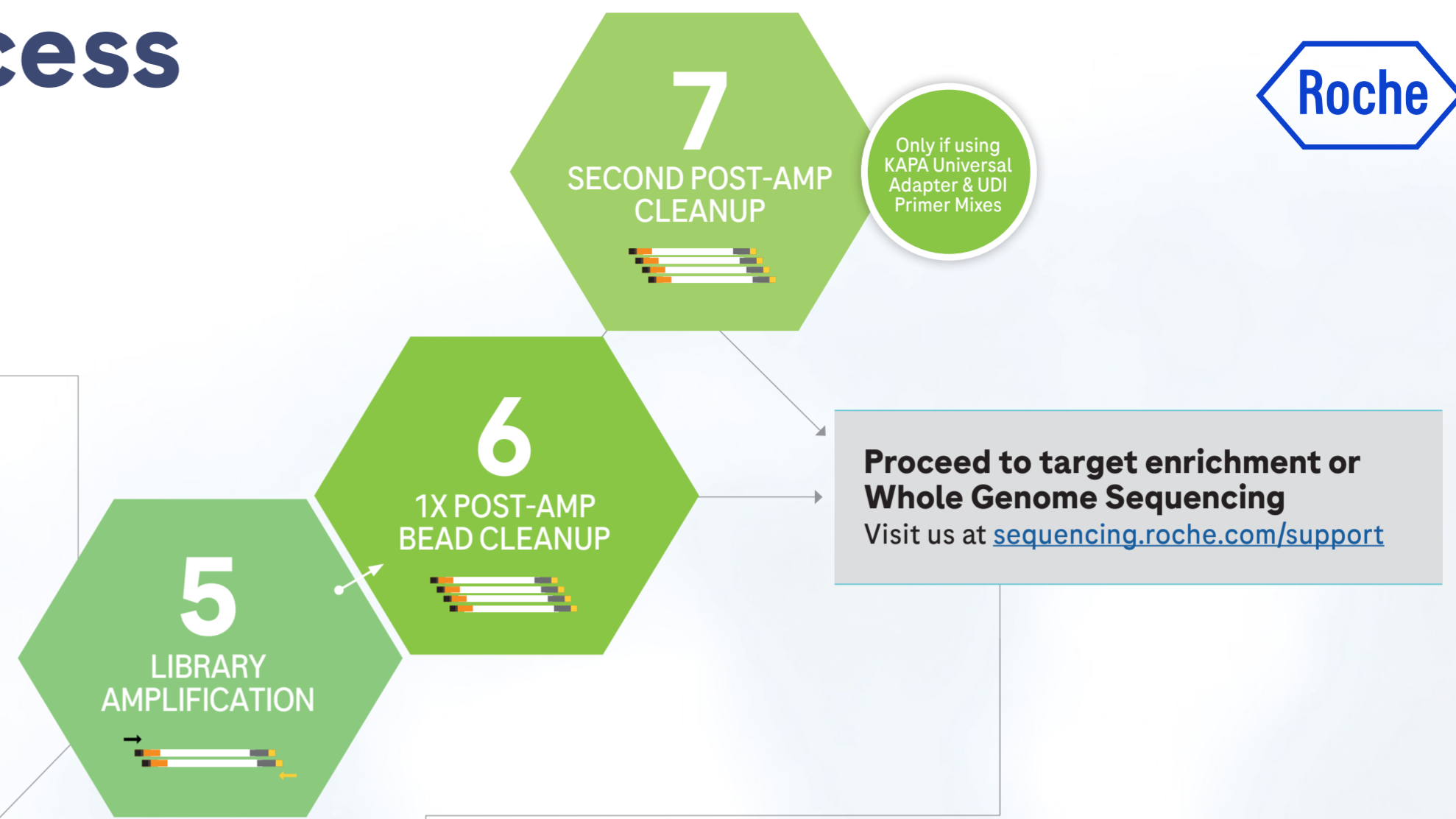
\*Reach out to Technical Support for possible workflow modifications when using this sample type.  
\*\*SS = double-sided size selection; a requirement when performing WGS on patterned flow cells but may result in sample losses of 60 - 95%, irrespective of whether a bead- or gel-based technique is used. 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 $\mu$ M
10 ng - 500 ng	15 $\mu$ M

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



**Proceed to target enrichment or Whole Genome Sequencing**  
Visit us at [sequencing.roche.com/support](https://sequencing.roche.com/support)

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

**YES** → Sequence the library.

**NO** → Visit us at [sequencing.roche.com/support](https://sequencing.roche.com/support)

**You have succeeded with KAPA EvoPrep Kits!**  
Visit us at [sequencing.roche.com](https://sequencing.roche.com) or contact your local sales representative to order more!





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