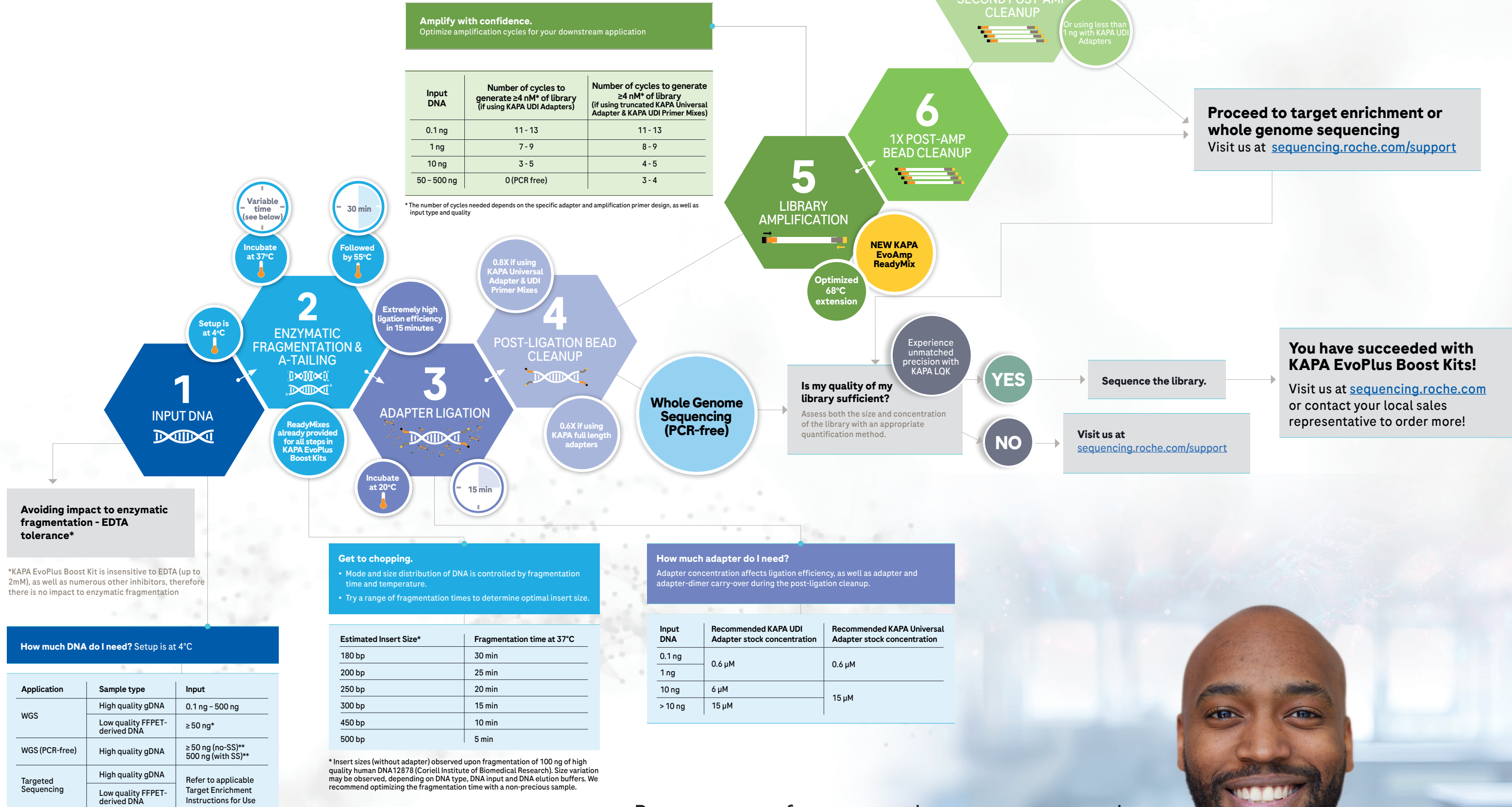


KAPA EvoPlus Boost Kits Guide to Success

With integrated highly tunable enzymatic DNA shearing.



Streamlined sample prep workflow using the next evolved generation of KAPA DNA Library Prep Reagents featuring the KAPA EvoT4 DNA Ligase and KAPA EvoAmp ReadyMix.



Avoiding impact to enzymatic fragmentation - EDTA tolerance*

*KAPA EvoPlus Boost Kit is insensitive to EDTA (up to 2mM), as well as numerous other inhibitors, therefore there is no impact to enzymatic fragmentation

How much DNA do I need? Setup is at 4°C

Application	Sample type	Input
WGS	High quality gDNA	0.1 ng - 500 ng
	Low quality FFPE-derived DNA	≥ 50 ng*
WGS (PCR-free)	High quality gDNA	≥ 50 ng (no-SS)** 500 ng (with SS)**
Targeted Sequencing	High quality gDNA	Refer to applicable Target Enrichment Instructions for Use
	Low quality FFPE-derived DNA	

Get to chopping.

- Mode and size distribution of DNA is controlled by fragmentation time and temperature.
- Try a range of fragmentation times to determine optimal insert size.

Estimated Insert Size*	Fragmentation time at 37°C
180 bp	30 min
200 bp	25 min
250 bp	20 min
300 bp	15 min
450 bp	10 min
500 bp	5 min

*Insert sizes (without adapter) observed upon fragmentation of 100 ng of high quality human DNA12878 (Coriell Institute of Biomedical Research). Size variation may be observed, depending on DNA type, DNA input and DNA elution buffers. We recommend optimizing the fragmentation time with a non-precious sample.

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	Recommended KAPA UDI Adapter stock concentration	Recommended KAPA Universal Adapter stock concentration
0.1 ng	0.6 μ M	0.6 μ M
1 ng		
10 ng	6 μ M	15 μ M
> 10 ng	15 μ M	

* 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.

Boost your performance, advance your research.





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