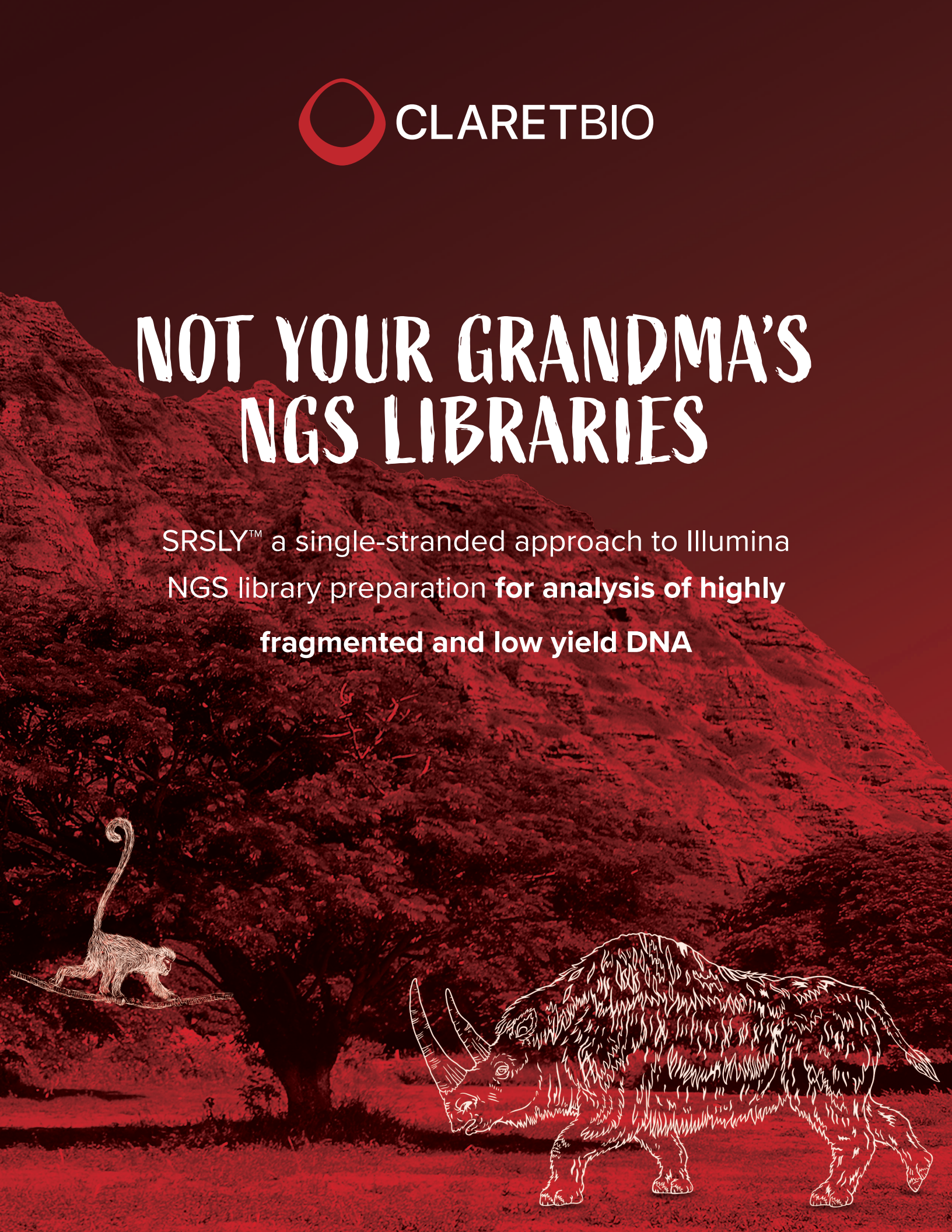
CLARETBIO

NOT YOUR GRANDMA'S NGS LIBRARIES

SRSLY™ a single-stranded approach to Illumina NGS library preparation **for analysis of highly fragmented and low yield DNA**



Short-read NGS sequencing technology revolutionized the way we explore the living world. Yet certain sample types like rootless hair contain DNA so highly fragmented and in such low amounts, it was long thought not to exist at all. By retaining the shortest molecules and pushing efficiency to its limit, the **SRSLY PicoPlus NGS library preparation method** can do the impossible in under 3 hours, from mammoth to modern organisms and more.

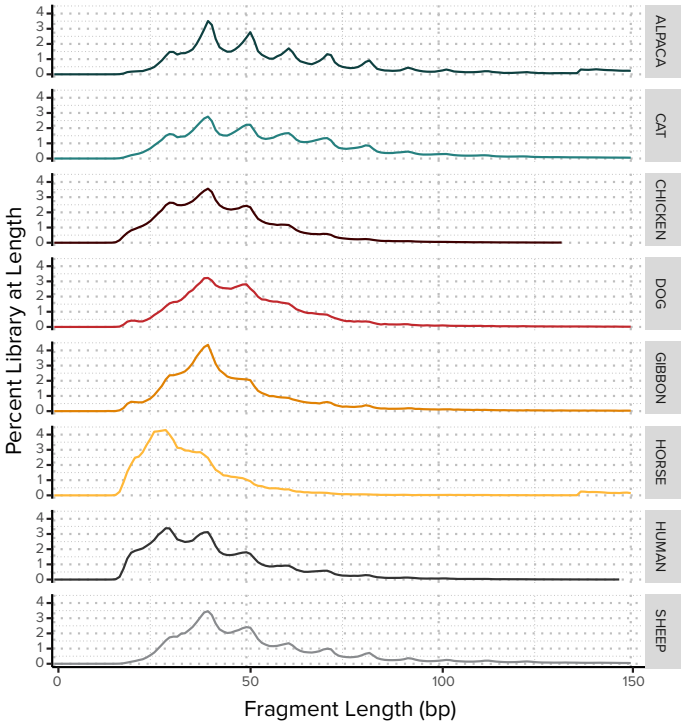
WHY SEQUENCE DNA FROM ROOTLESS HAIR?

Opens up new possibilities for non-invasive wildlife sampling, cracking cold cases, or unlocking evolutionary mysteries.

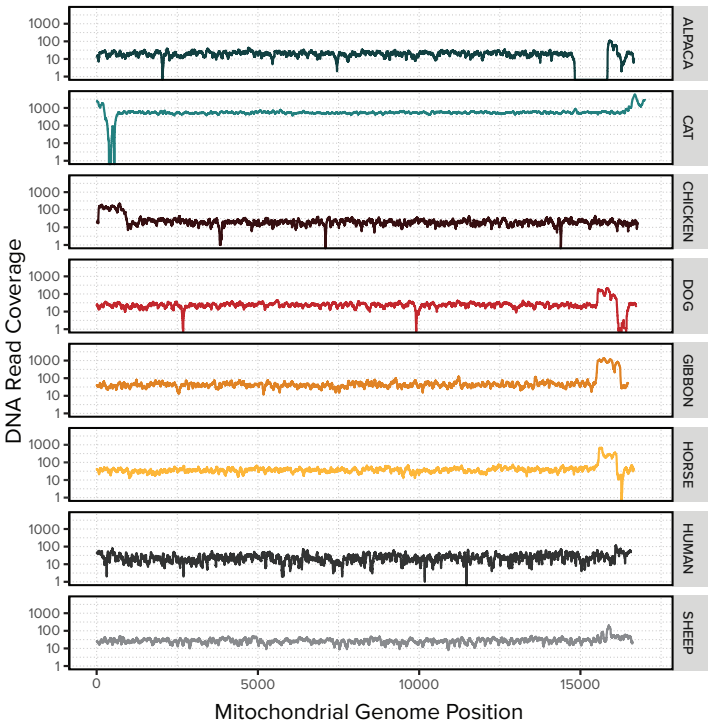
Convert picograms of DNA from a few strands of rootless hair or a single feather to Illumina NGS libraries

Rootless Hair Collected From	Input DNA Amount into SRSLY	PCR Cycles	Total DNA Yield Post Index PCR	Total Read Pairs Sequenced	Average Mitochondrial Coverage
Alpaca	220 pg	15	183.2 ng	3,779,907	13x
Cat	350 pg	14	1276 ng	3,636,029	324x
Chicken	600 pg	12	234 ng	3,062,552	20x
Dog	200 pg	15	510 ng	1,680,182	14x
Gibbon	200 pg	15	382 ng	1,831,741	51x
Horse	250 pg	15	360 ng	3,610,330	25x
Sheep	2000 pg	12	1492 ng	2,711,282	18x

Capture the shortest DNA fragments, lost to standard preparation



Reconstruct mitogenomes with low coverage data



WHAT ABOUT ANCIENT HAIR SAMPLES?

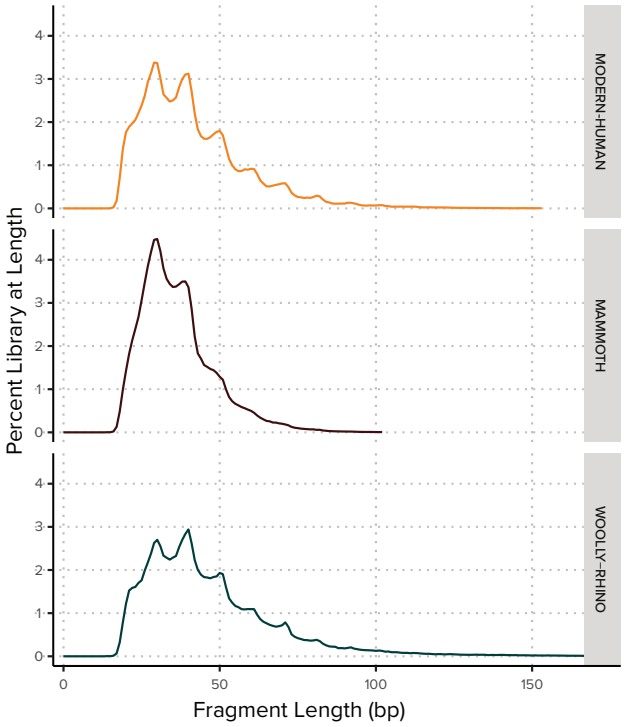
SRSLY with as little as 100 pg DNA from a few strands of hair from ancient animals...

Make sequence-ready libraries

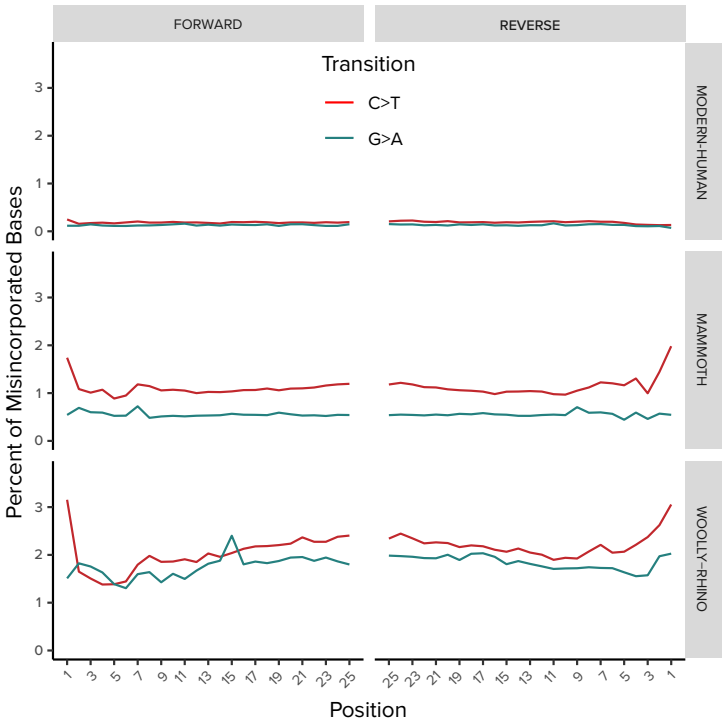
Rootless Hair Collection From	Input DNA Amount into SRSLY	Total DNA Yield Post Index PCR	Reference Genome Mapped to	Total Read Pairs Sequenced	Mapping Rate to Reference Genome	Average Mitochondrial Coverage
Yuka Mammoth	100pg	57.6ng	African Elephant	2,250,849	47.4%	39X
Woolly Rhino	100pg	72.4ng	White Rhinoceros	3,179,680	31.5%	36.2X

Library yields and shotgun sequencing metrics for rootless ancient hair SRSLY libraries, in collaboration with UCSC Paleogenomics Lab.

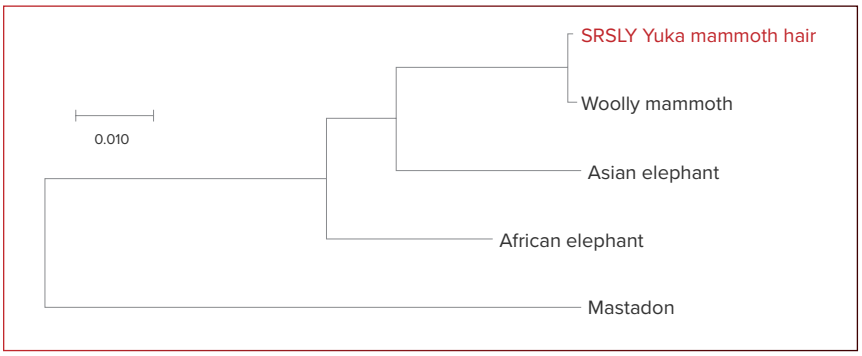
Capture highly fragmented DNA from extinct and extant animals



Estimate ancient DNA damage patterns

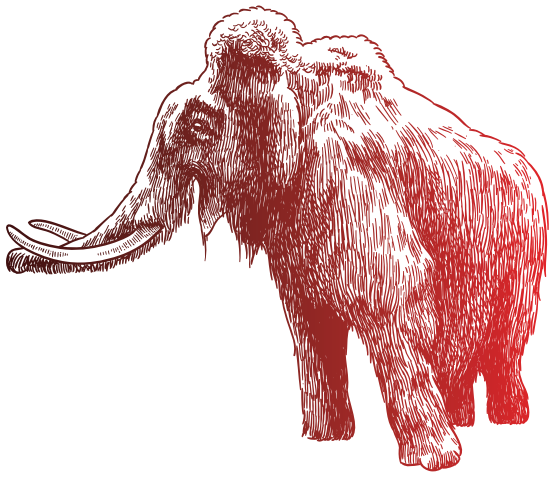


Perform evolutionary analyses...



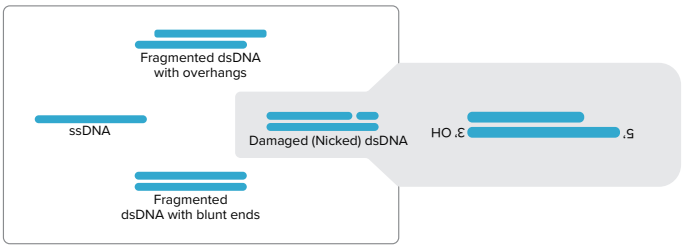
SRSLY hair mitogenome reconstructed using MIA mapped to M. primegenius. Phylogenetic ML tree built from complete mitogenome alignments; branch lengths measured in the number of substitutions per site.

and much more!

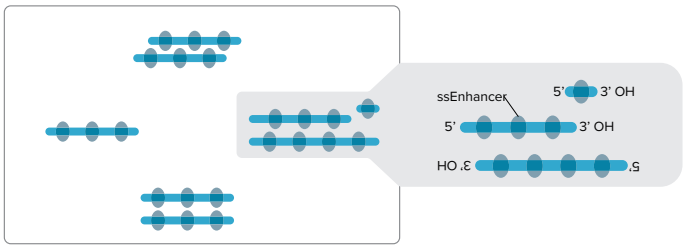


SRSLY HOW SIMPLE IS OUR WORKFLOW?

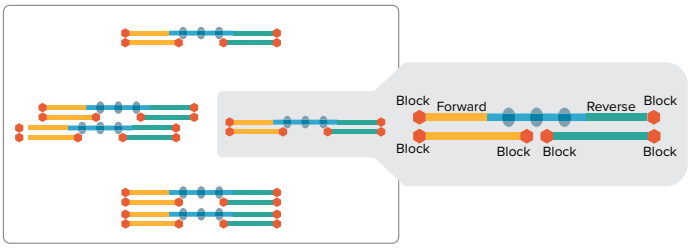
1. DNA input pool



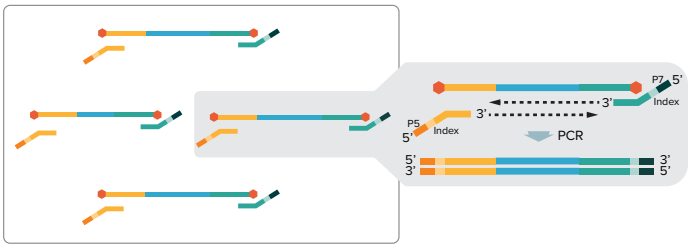
2. Denature and capture single-stranded DNA



3. Phosphorylate template DNA and ligate adapters



4. Index PCR



What else do you gain using a single-stranded approach to library prep?

Input DNA Molecule Type	SRSLY™ Kits	dsDNA Kits
dsDNA	✓	✓
ssDNA	✓	✗
Nicked/Abasic dsDNA	✓	✗
Native ends at 3' overhangs	✓	✗

Other SRSLY Validated Applications

- Clinical samples like cell-free DNA and FFPE
- First-strand cDNA for RNAseq workflows
- QC synthetic oligos
- Bisulfite-treated DNA
- Use upstream of targeted enrichment

Kit specifications

	SRSLY PicoPlus	SRSLY NanoPlus
Input range	250 pg – 10 ng	2 ng – 50 ng
Input max volume	18 µl	18 µl
Protocol time	~2.5 hours	2.5 hours
Recommended uses	cfDNA, aDNA, hair	FFPE, oligos, cDNA

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