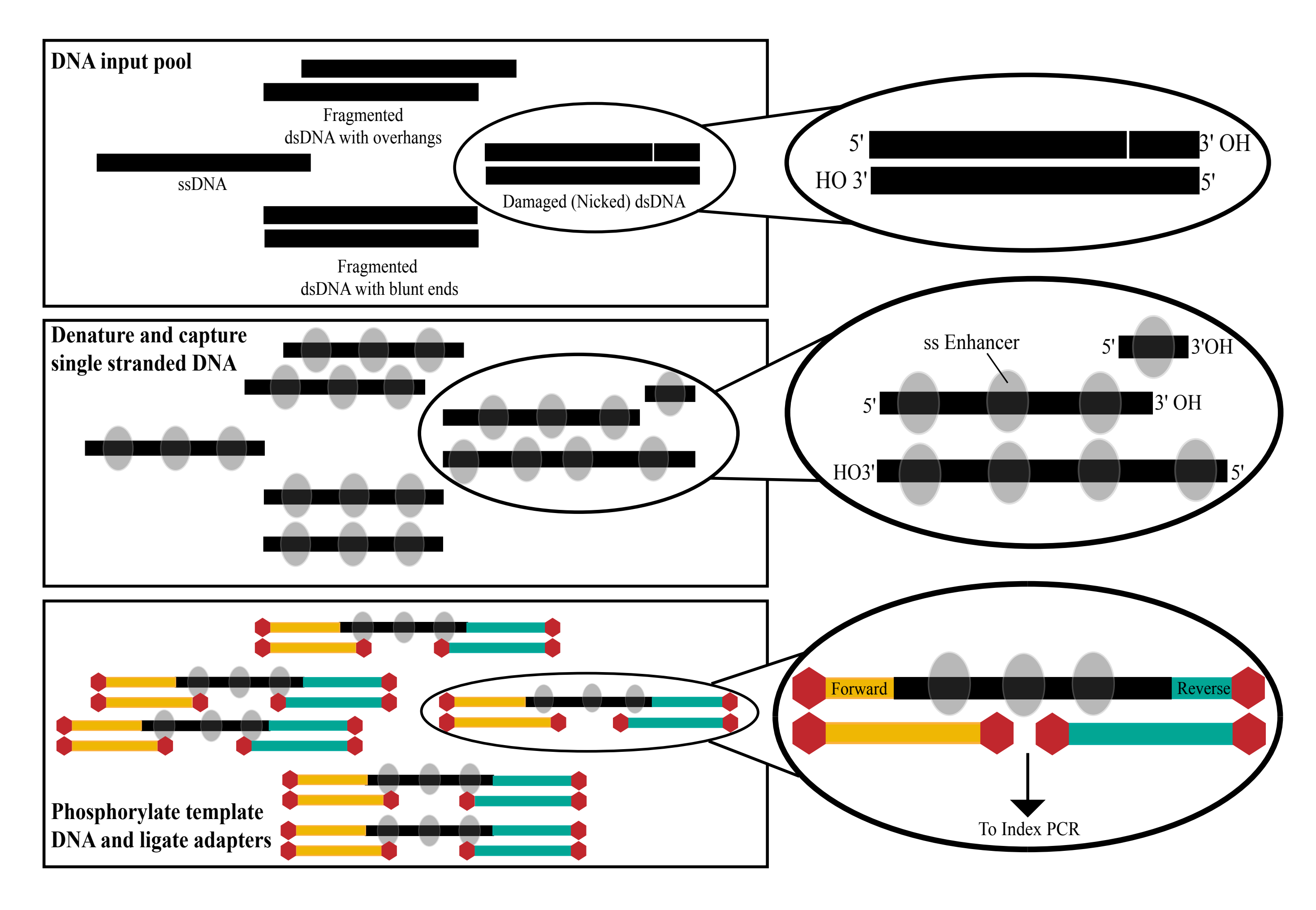


SRSLY™: A single-stranded approach to NGS library preparation for analyses of cell-free DNA fragments

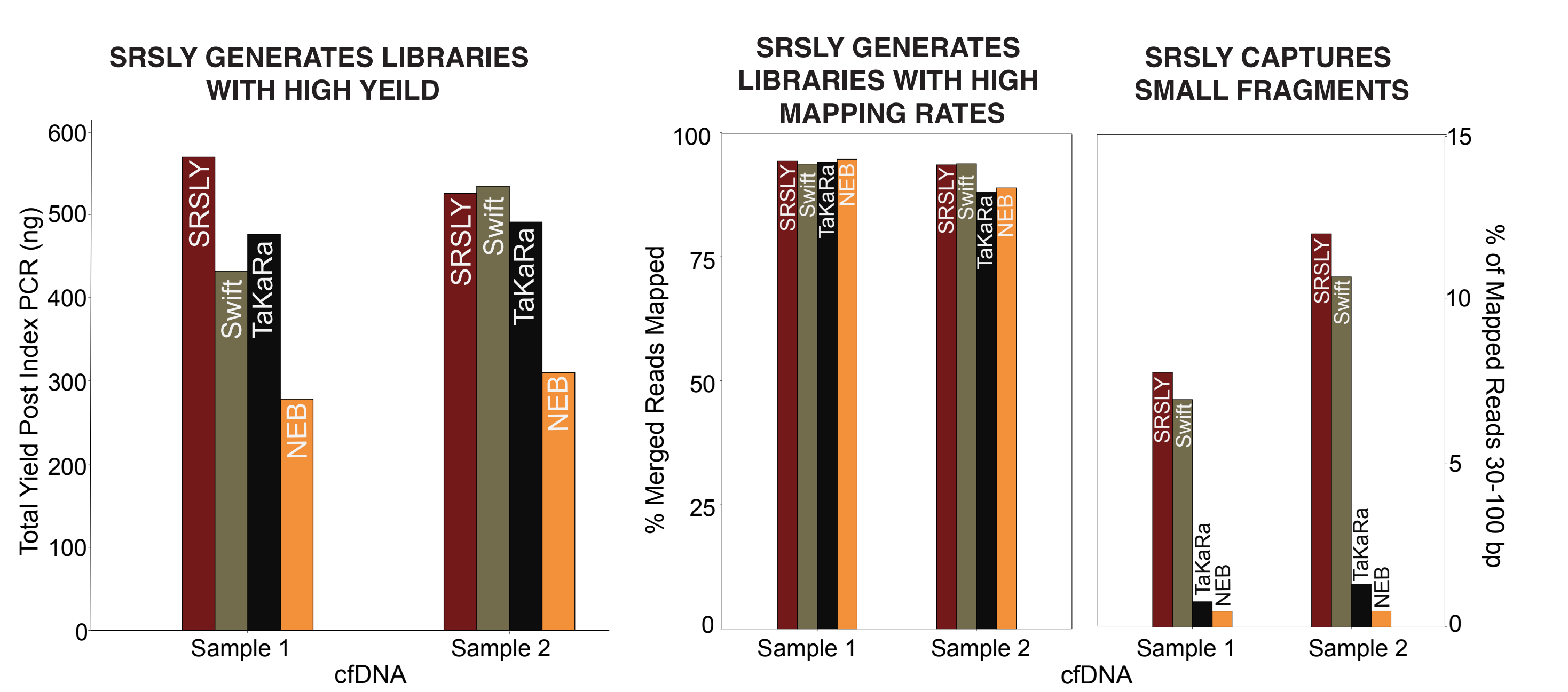
Christopher J. Troll¹, Kelly M. Harkins¹, Varsha Rao¹, Josh D. Kapp³, Colin Naughton¹, Jessica M. Morgan¹, Beth Shapiro³, and Richard E. Green²

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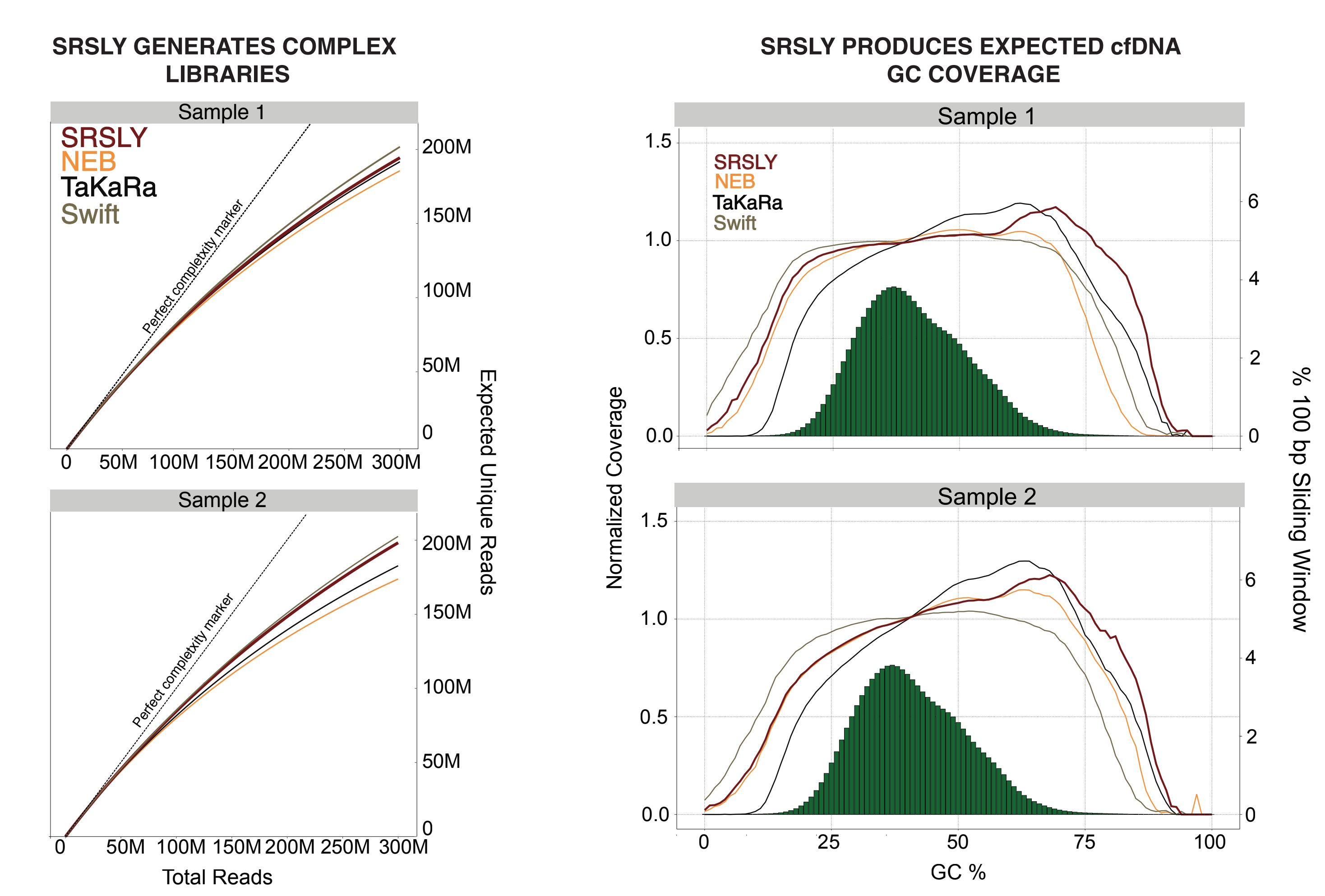
The SRSLY™ Workflow



SRSLY™ cfDNA Metrics Rival or Outperform Other Commercial Kits



Kit	Type of prep method	Input cfDNA amount	Total time through index PCR	Input cfDNA sample ID	Yield post 10c index PCR (Total)	Merged read pairs sequenced	Mapping rate	Mapped reads in 30-100bp bin
ClaretBio SRSLY™	Single-stranded	1ng	2.5hrs	Sample 1	569ng	73,077,812	94.35%	7.77%
				Sample 2	525ng	63,449,167	93.52%	12.0%
NEBNext® Ultra II™	Double-stranded	1ng	3hrs	Sample 1	278ng	78,705,033	94.66%	0.49%
				Sample 2	310ng	54,734,560	88.88%	0.49%
TaKaRa ThruPLEX® Plasma-Seq	Double-stranded	1ng	2.5hrs	Sample 1	476ng	74,429,274	94.01%	0.77%
				Sample 2	470ng	71,294,525	87.97%	1.32%
Swift Accel NGS® 1S Plus	Single-stranded	1ng	3.5hrs	Sample 1	432ng	78,018,897	93.66%	6.94%
				Sample 2	534ng	69,959,246	93.73%	10.68%



SRSLY™ is a simple, quick, and efficient ligation-based ssDNA library prep method that:

Produces complex libraries from low inputs of cfDNA

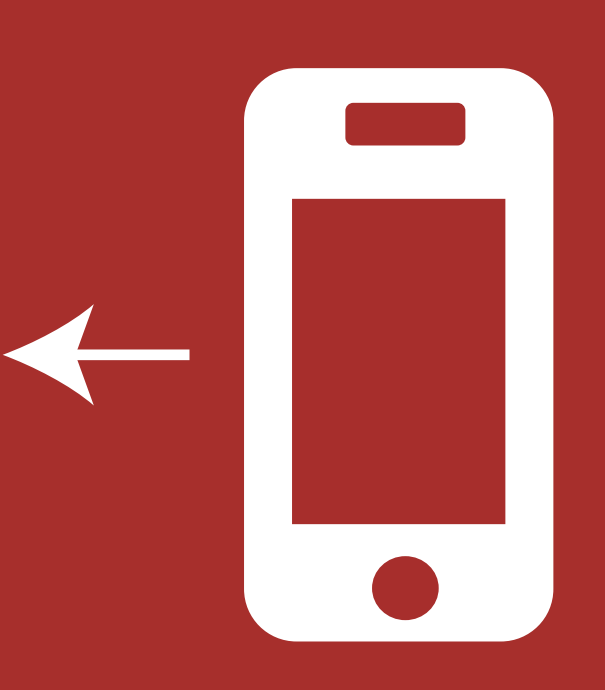
Does not alter the native ends of template molecules

Captures highest % of short fragments

Is sequence ready in <2.5 hrs

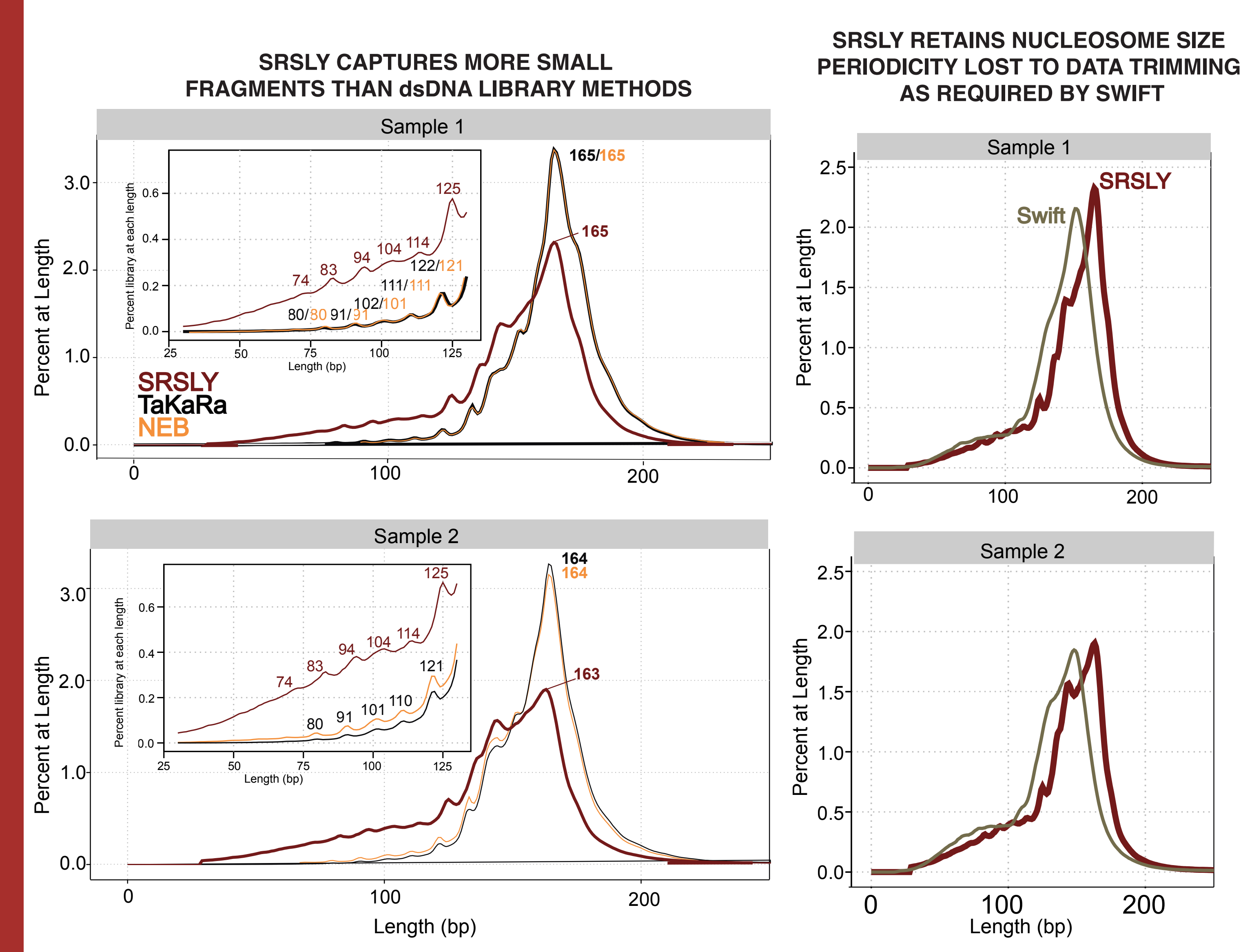


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 Santa Cruz, Ca, 95060

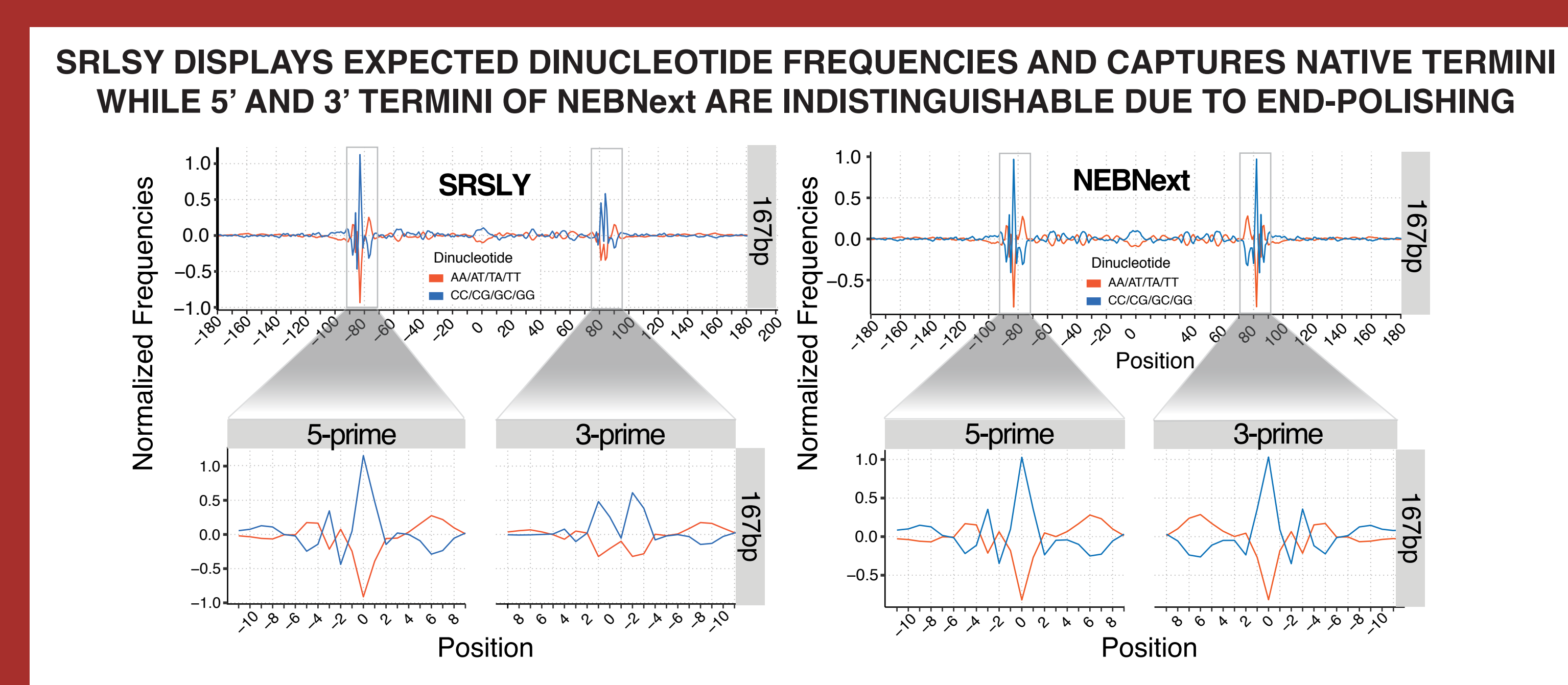


Scan the QR code to visit www.claretbio.com to learn more about us, other applications for SRSLY, and additional Claret technologies

SRSLY™ Recovers Expected cfDNA Length Profiles

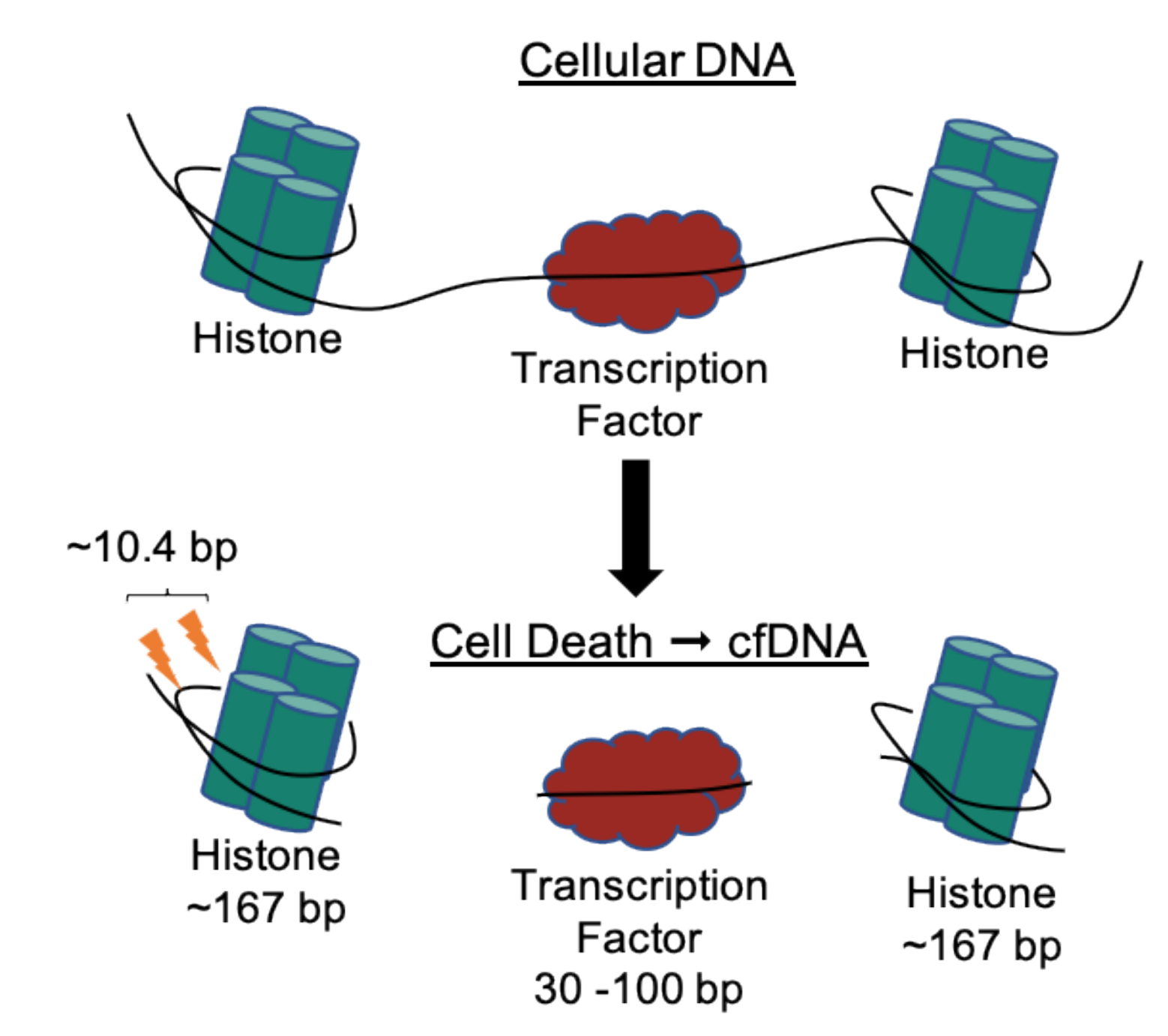


SRSLY™ Captures Native Termini

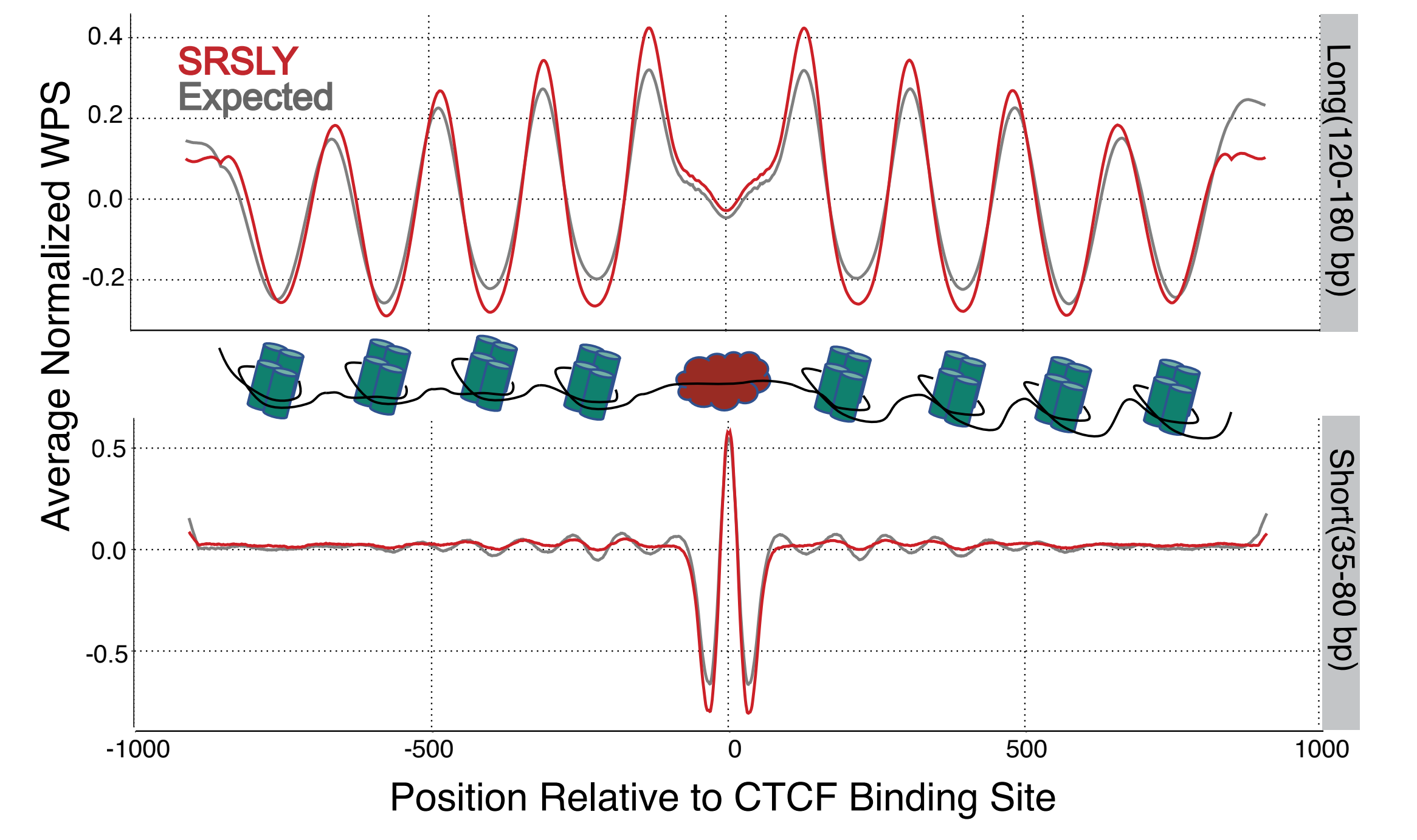


SRSLY™ Facilitates Biological Analysis of Long and Short Fragments

SHORT AND LONG cfDNA FRAGMENTS CONTAIN VALUABLE BUT DISTINCT BIOLOGICAL INFORMATION



SRSLY FACILITATES ANALYSIS OF NUCLEOSOME AND TRANSCRIPTION FACTOR BOUND FRAGMENTS



Note: WPS score methods and expected distribution data from Snyder et al 2016, Cell 164, 57-68