

# Two New Solutions for Nucleic Acid Fragmentation

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**Covaris**<sup>®</sup>  
the pre-analytical advantage™

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## Covaris – the established standard for DNA shearing

### Overview

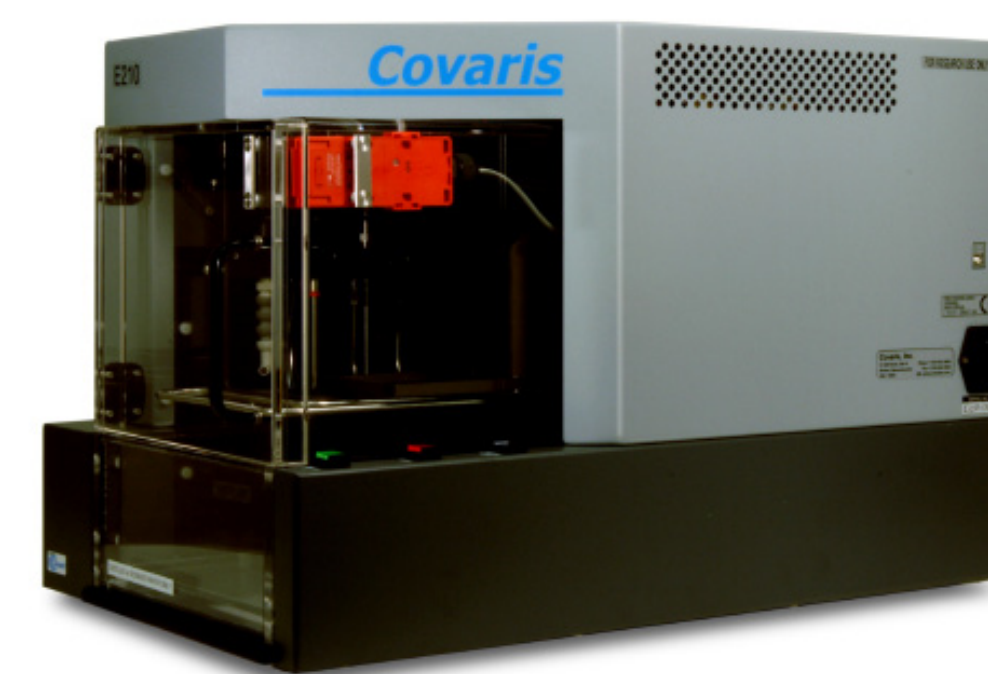
- The Covaris Adaptive Focused Acoustics (AFA™) technology enables unprecedented iso-thermal control over DNA shearing forces in the sample.
- The development of clinical applications requires high recovery, high reproducibility, robust systems and methodology, and automation capabilities.
- With the increasing resolution of genomic analytical techniques, high recovery, bias free DNA shearing becomes critical.

### S-series



- Manual
- Single
- Circular transducer
- Single sample processing

### E-series



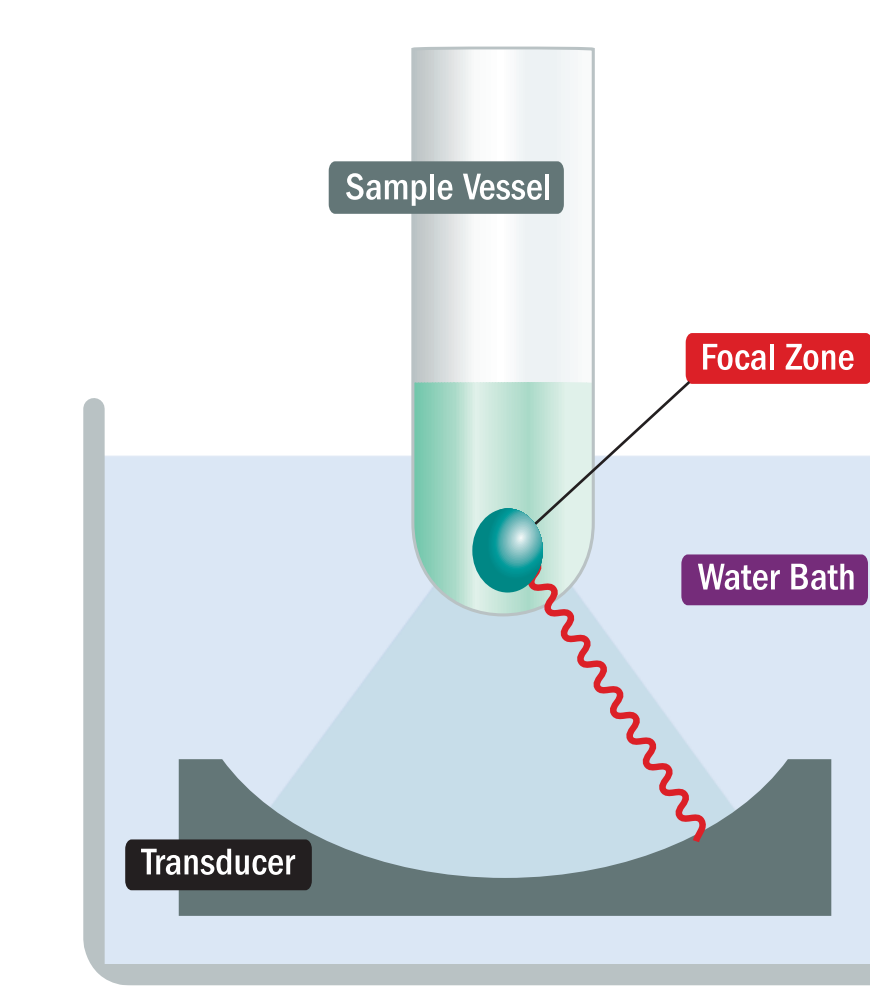
- Automated • Batch
- Circular transducer
- 24 to 96 sample processing
- Robot integration for full automation

### L-series

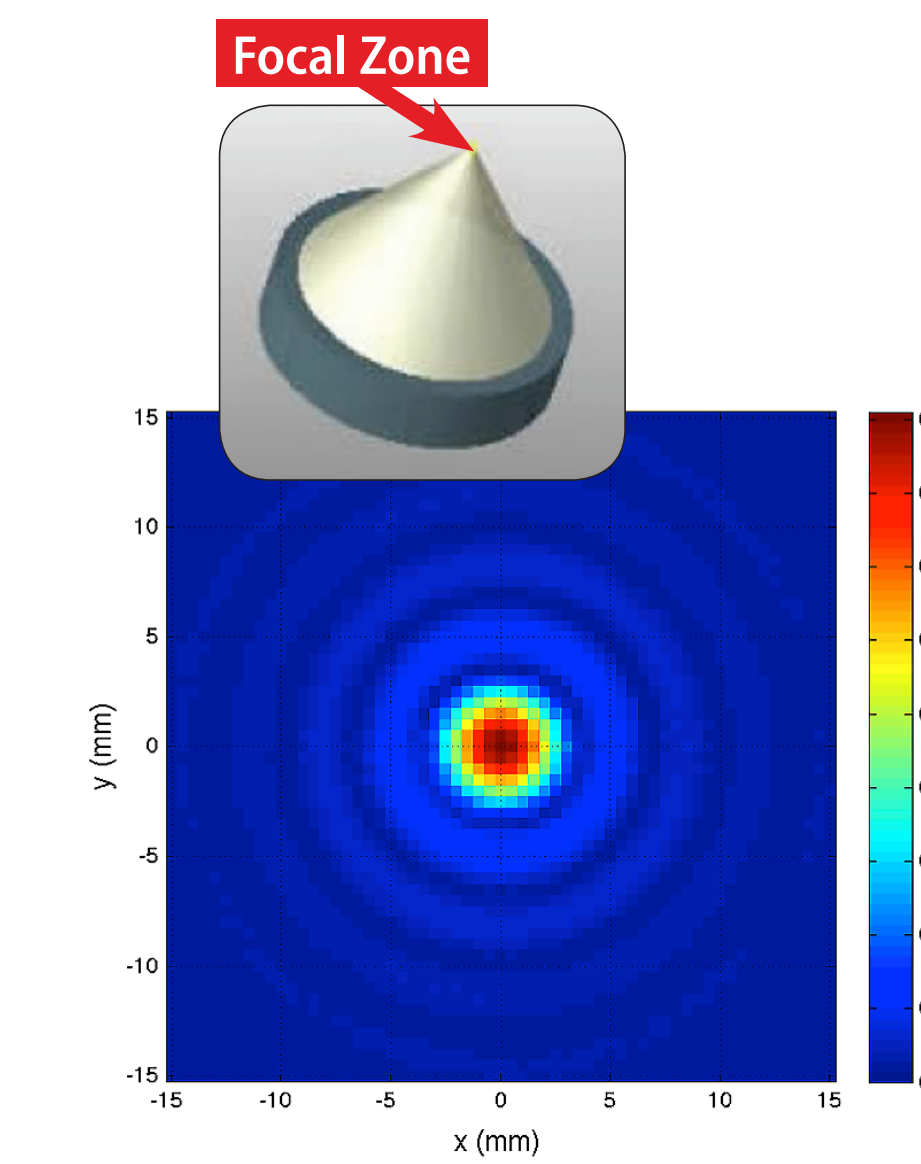


- Linear transducer – Parallel processing
- Highly uniform field along a row treats a full 96-w plate 8x faster

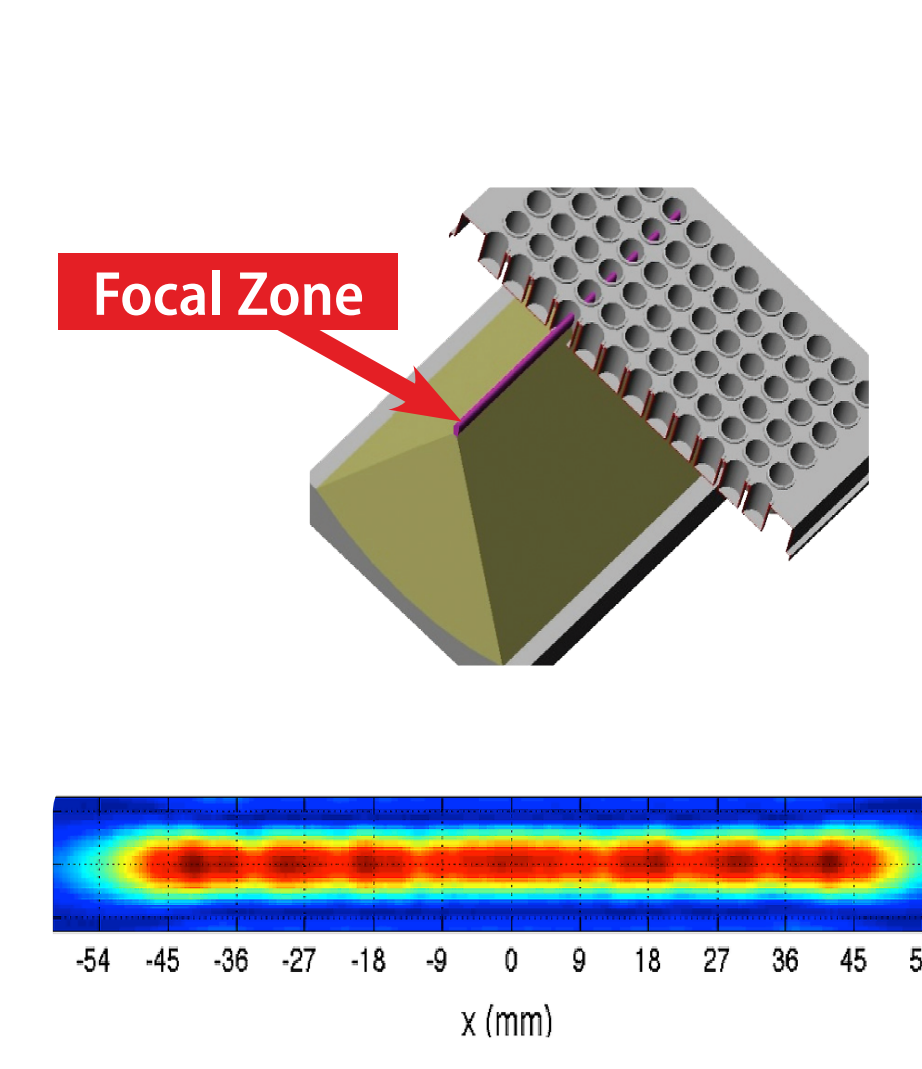
• 500 kHz Transducer technology



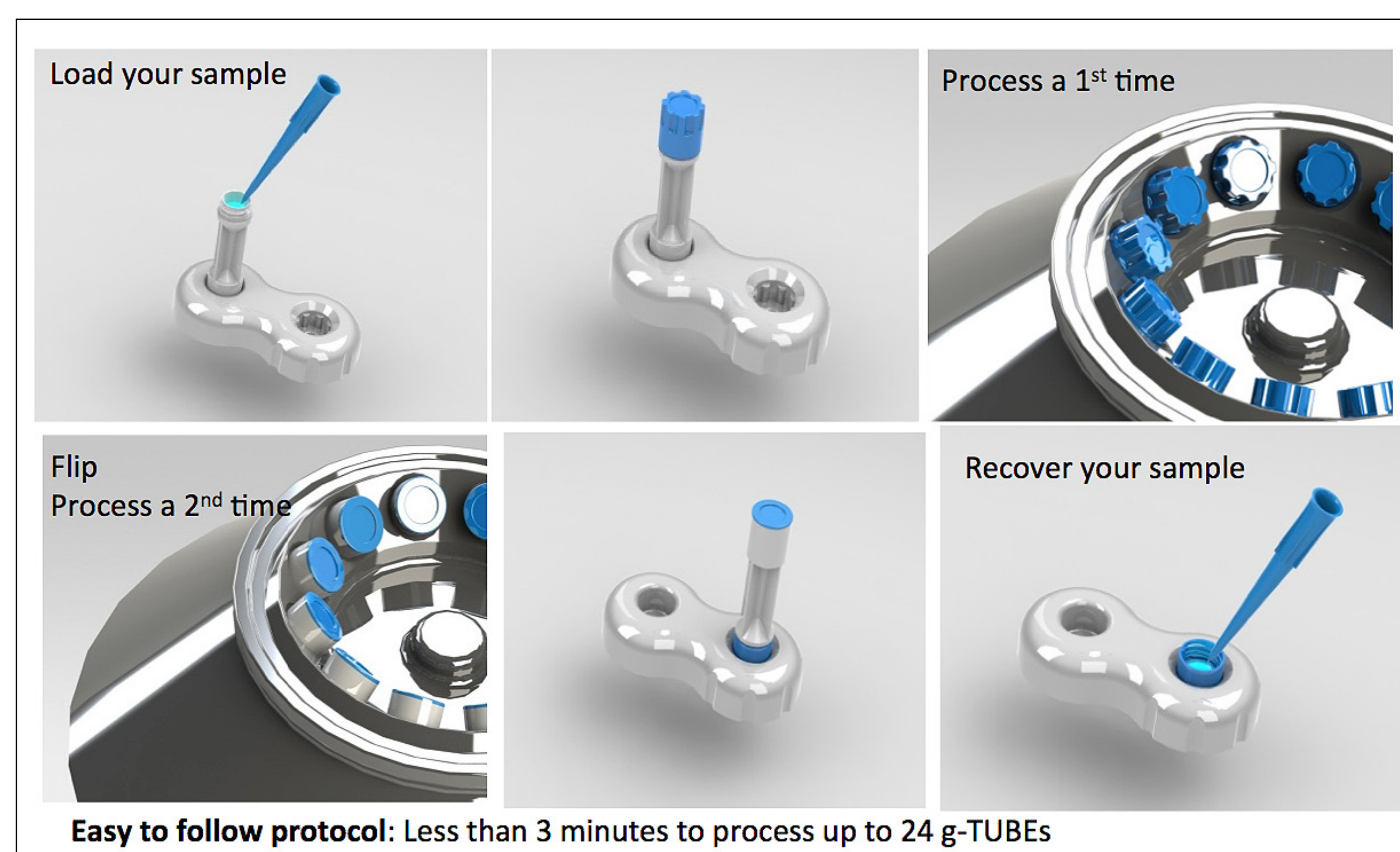
• Circular transducer  
• Serial processing



• Linear Transducer  
• Parallel processing



## g-TUBE – DNA fragmentation from 6kb to 20kb



**Versatile:** Ideal for direct sequencing, mate-pair libraries, and other applications that require longer DNA fragments.

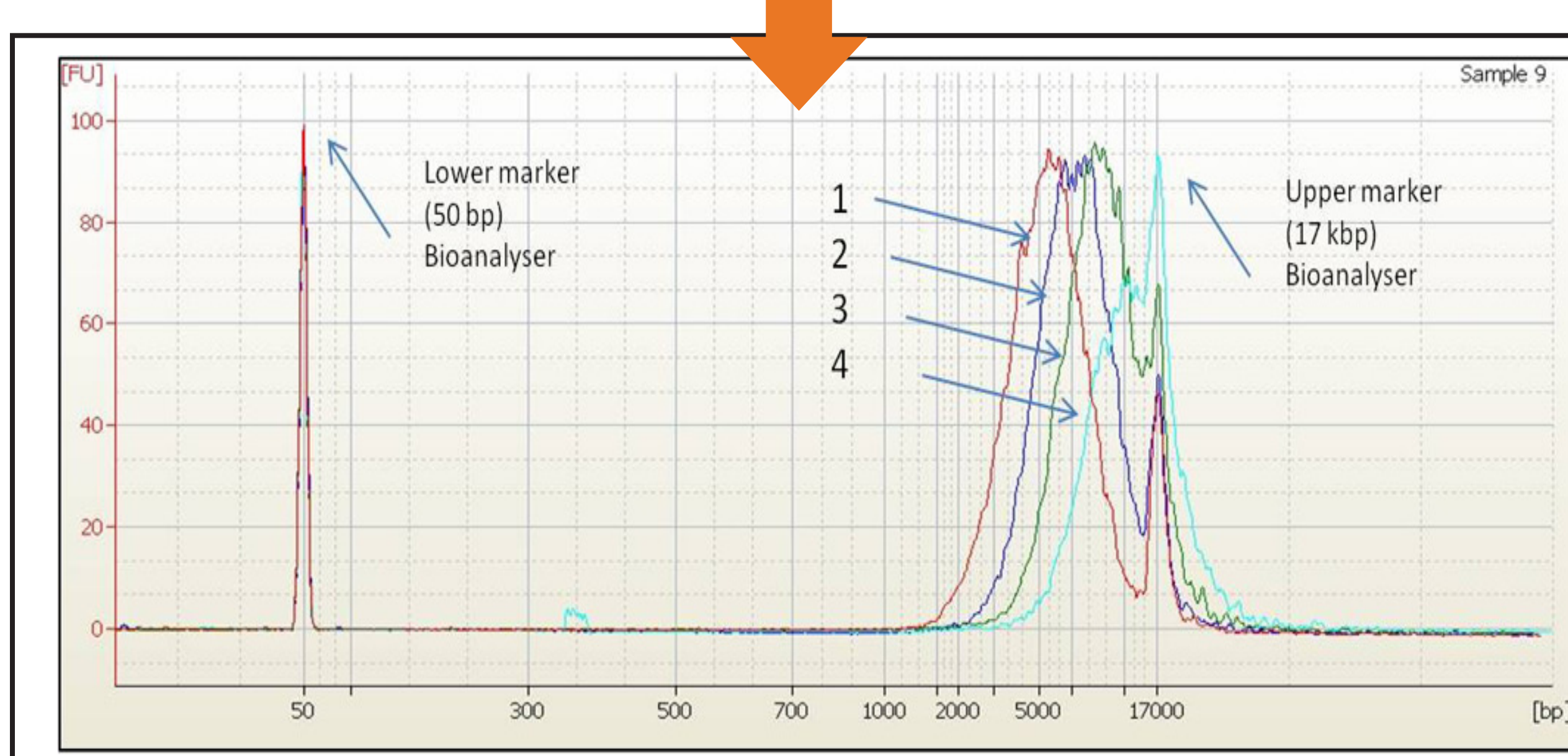
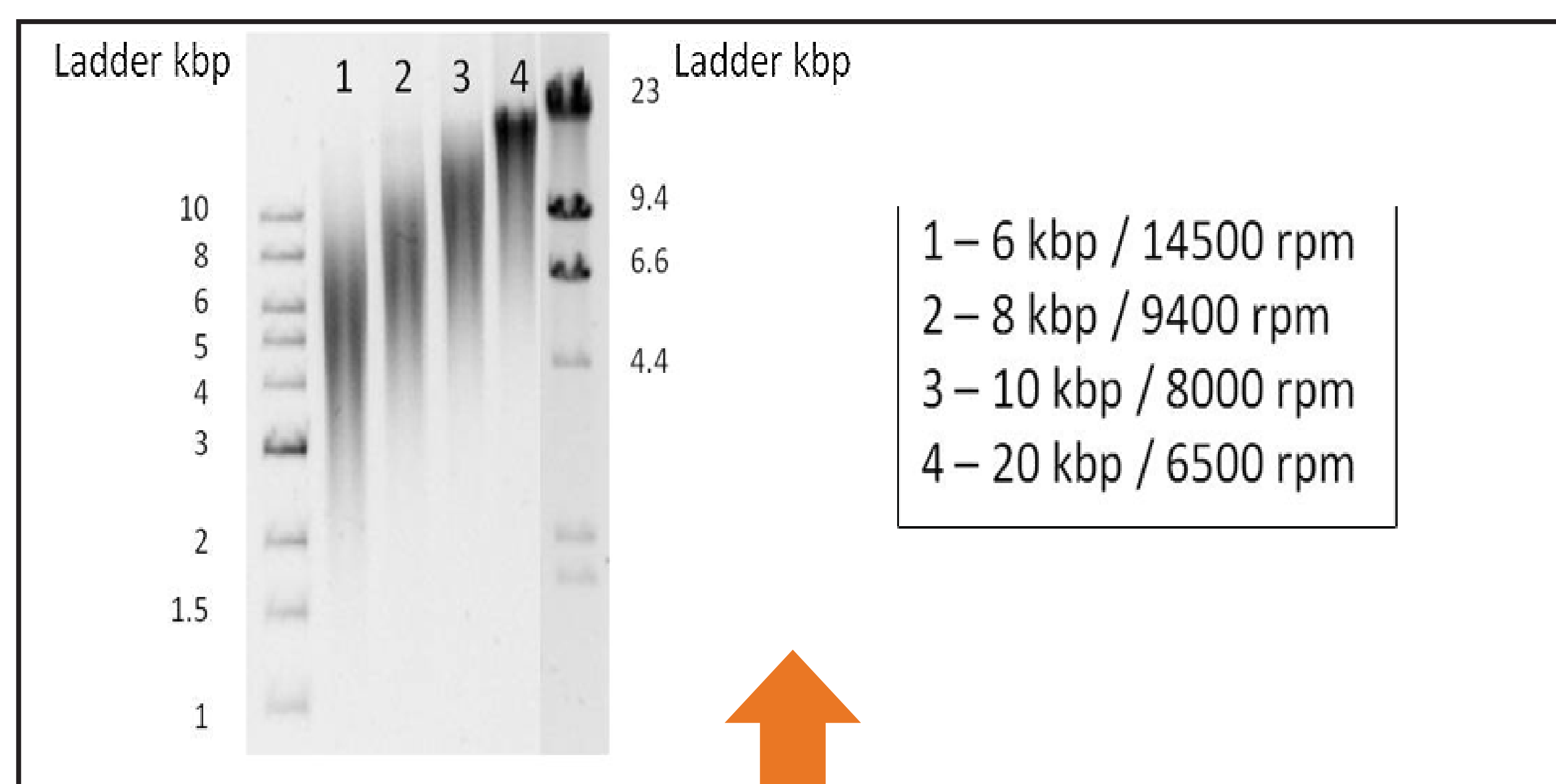
**Selectable Fragment Size:** g-TUBE shears DNA in user-selectable fragment sizes ranging from 6kb to 20kb.

**Highly Reproducible:** DNA shearing results with g-TUBE are reproducible assay-to-assay, lab-to-lab, day-to-day.

**Fast and Scalable:** Shear 6kb - 20kb fragments in 2 minutes or less. Runs multiple samples simultaneously.

**Efficient:** High sample recovery (90%+) with a closed vessel process.

**Economical:** Use an Eppendorf® "MiniSpin® plus" microcentrifuge - no other equipment needed.



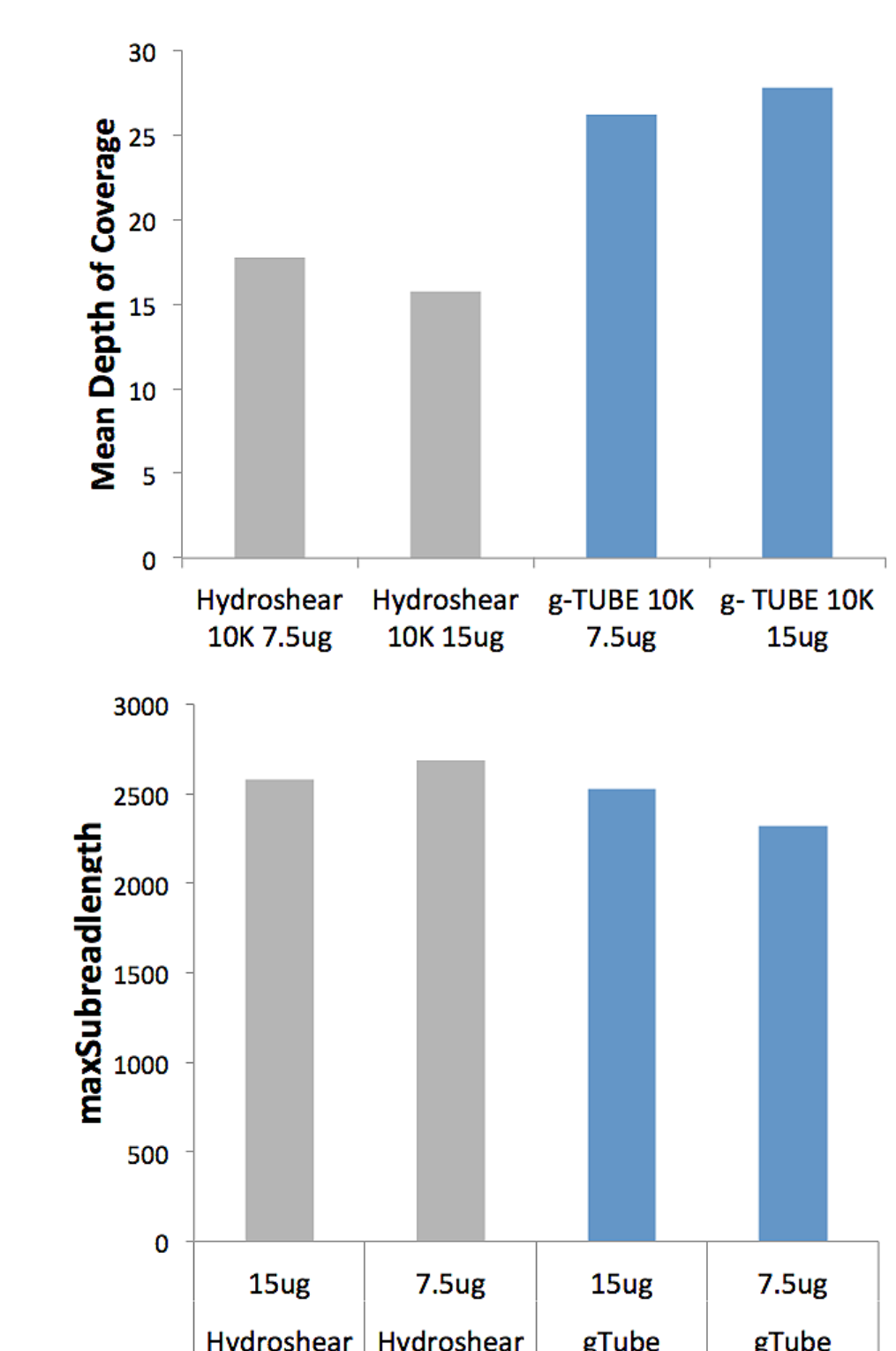
### From DNA to sequencing with Covaris g-TUBEs and PacBio RS

E coli DNA was sheared to 10 kbp with both Covaris g-TUBE and Hydroshear. Experiment was repeated for 2 different inputs of DNA.

Libraries built following PacBio RS protocols and sequenced on PacBio RS instrument.

Sample ID	Starting ng	% Yield
g-TUBE 10K SB 7.5ug - 10uL	5000	14%
g-TUBE 10K SB 15ug - 10uL	5000	13%
Hydroshear 10K SB 7.5ug R1 - 10uL	5000	14%
Hydroshear 10K SB 15ug - 10uL	5000	11%

Job Metric	gTUBE		Hydroshear SC13	
	10K 7.5ug	10K 15ug	10K 7.5ug	10K 15ug
% Adapter Dimer (0-10bp)	0.16	0.07	0.56	1.09
% Short Insert (11-100bp)	0.02	0.08	0.06	0.12
# of Movies	3	3	3	3
Pre-Filter # of Bases	323492808	400785167	393724278	377533951
Post-Filter # of Bases	172001266	192748644	125869867	117074824
Pre-Filter # of Reads	225459	225459	225459	225459
Post-Filter # of Reads	48707	47989	30202	28672
Pre-Filter Mean Readlength	637	686	441	409
Post-Filter Mean Readlength	2899	3154	3226	3148
Pre-Filter Mean Read Quality	0.177	0.173	0.168	0.162
Post-Filter Mean Read Quality	0.819	0.811	0.801	0.802
# of Post-Filter Reads	48707	47989	30202	28672
Mean Mapped Subread Readlength	2072	2173	2355	2247
# of Mapped Reads	47374	46045	28575	28550
Mean Mapped Readlength	2769	3025	3099	3001
# of Mapped Subreads	62407	62948	37377	34838
95th Percentile Mapped Readlength	7155	7692	7858	7857
# of Mapped Bases	131175408	138293492	89322471	79606616
Maximum Mapped Readlength	12196	12767	13087	12408
Mean Mapped Subread Accuracy	84.26	83.59	82.53	82.68
Mean Depth of Coverage	26.21	27.79	17.76	15.75
% Missing Bases	0	0	0	0

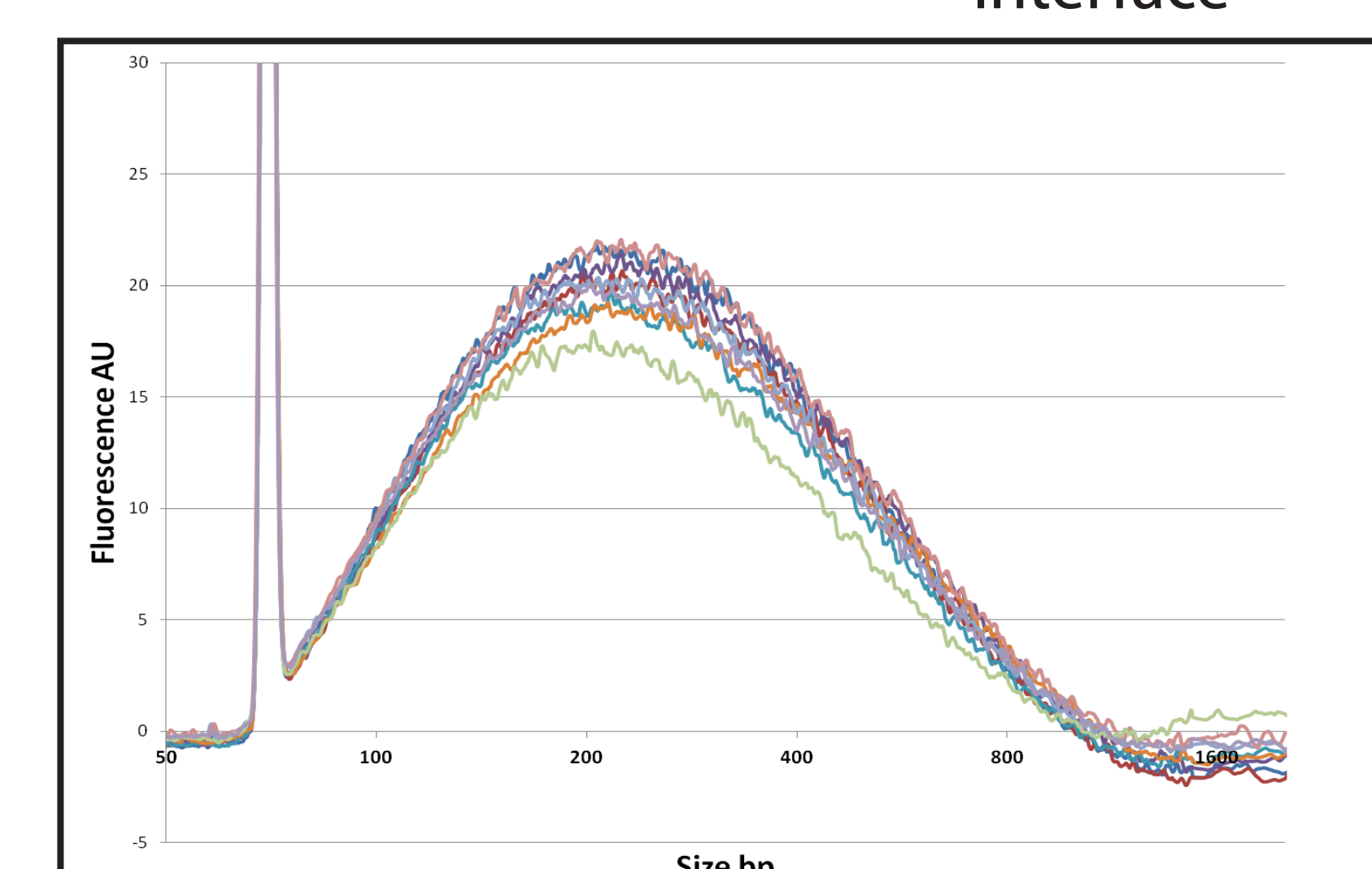
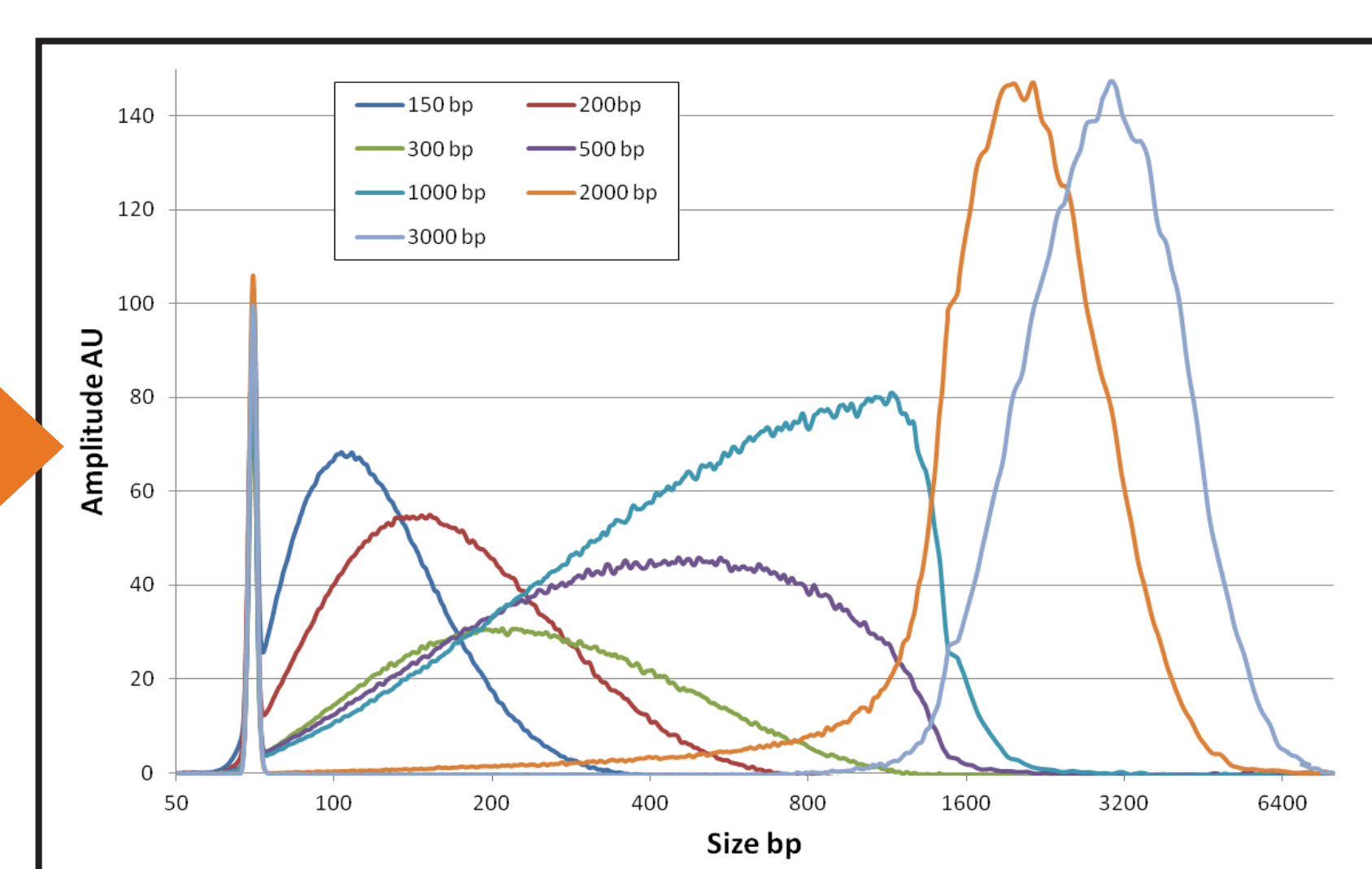
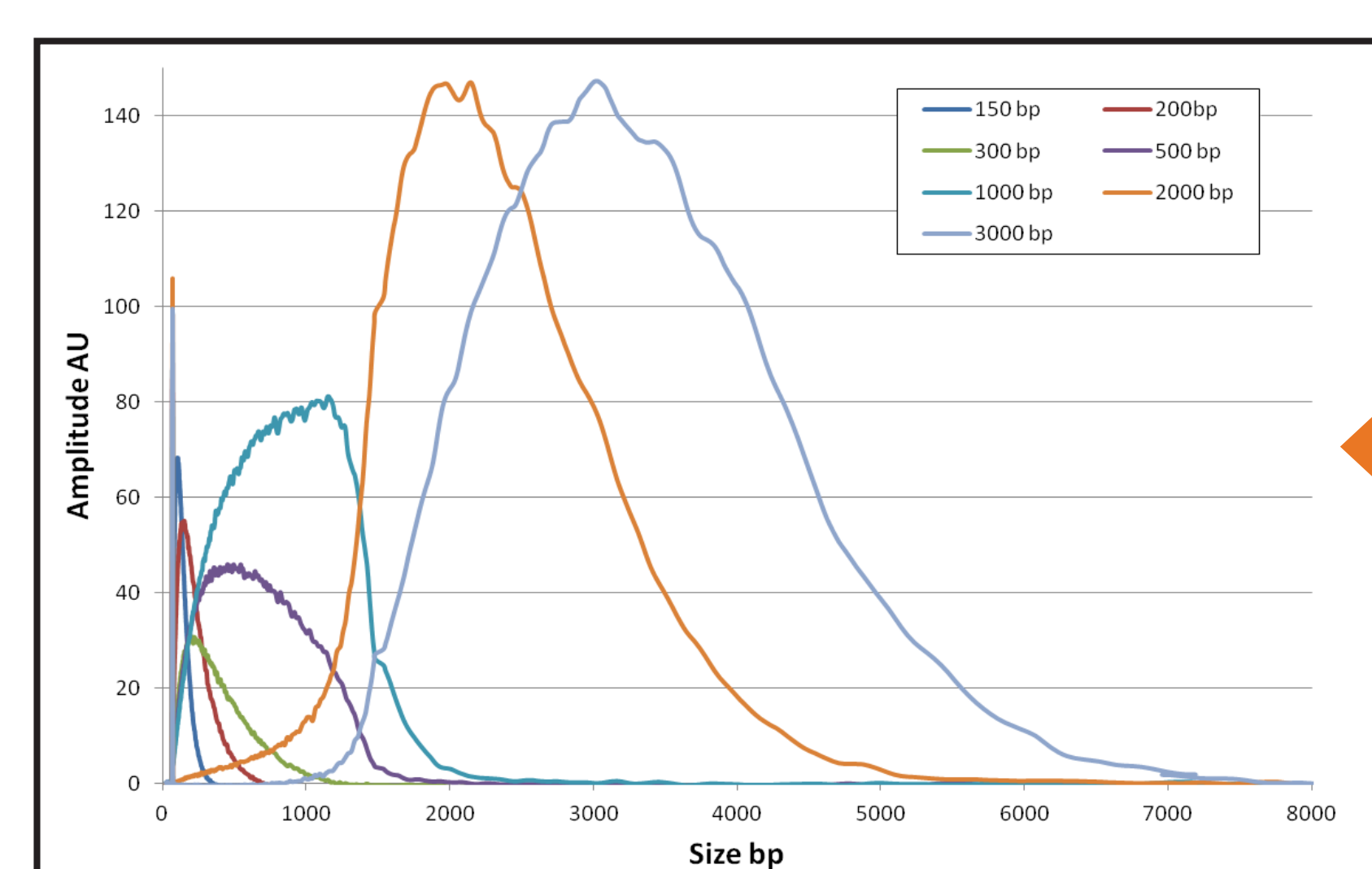


Data courtesy of Susana Wang, Swati Ranade and Kevin Travers, Pacific Biosciences, Menlo Park, CA

Post sequencing metrics for both Hydroshear and g-TUBEs libraries. Mean depth of coverage (top) and mean of maximum subread length (bottom)

## M220 Personal Fragmenter – Compact instrument for 150bp to 3kb

- 15ml Water bath volume
- Ready to use in <10 minutes after power-up
- Integrated Peltier thermo-electric cooling
- Pre-loaded shearing conditions: click and go
- Small footprint, no external chiller
- Ideal companion for bench-top NGS instruments
- Comparable to industry-standard AFA instruments
- Provides isothermal and bias-free DNA shearing
- Compatible with Covaris microTUBES and miniTUBES
- Robust construction and simple user interface



**High reproducibility:** 10 replicates of DNA samples sheared with M220 following a 300bp protocol



**Versatile:** AFA provides fine control of the energy delivered to the sample and enables tight fragment size distributions with a mean selected between 150bp and 3 kb. Left side, electropherogram from Agilent Bioanalyser 2100 plotted on a linear scale. On the right, same data plotted on a logarithmic scale.