



- For DNA qualitative and quantitative QC
- Direct HSAFM imaging, single molecule resolution
- 100 bp to 500 kbp+ sizing, pg input
- Single consumable chip, no cold chain
- Fast workflow and analysis

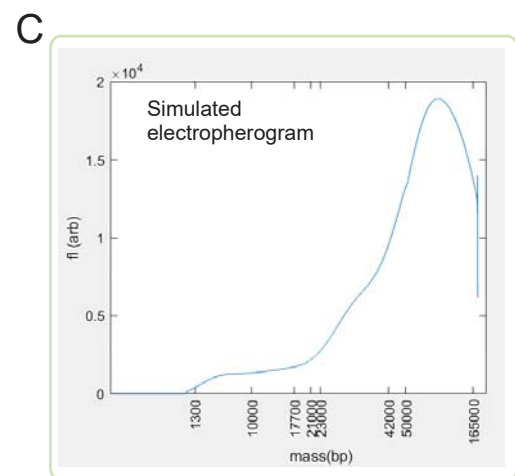
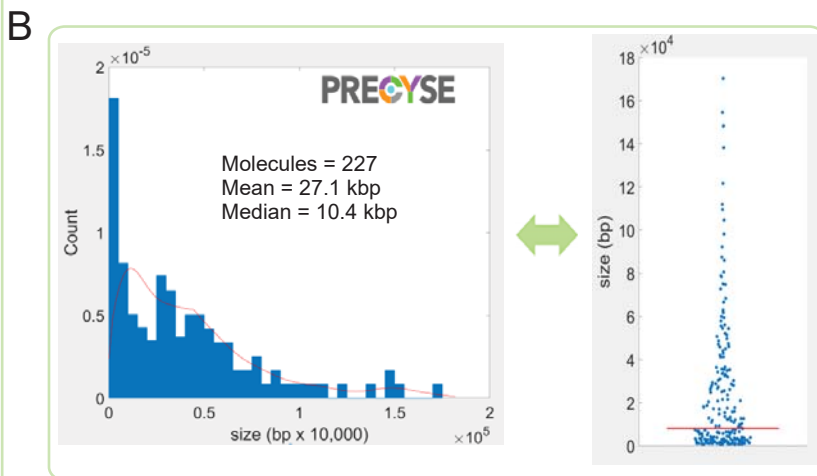
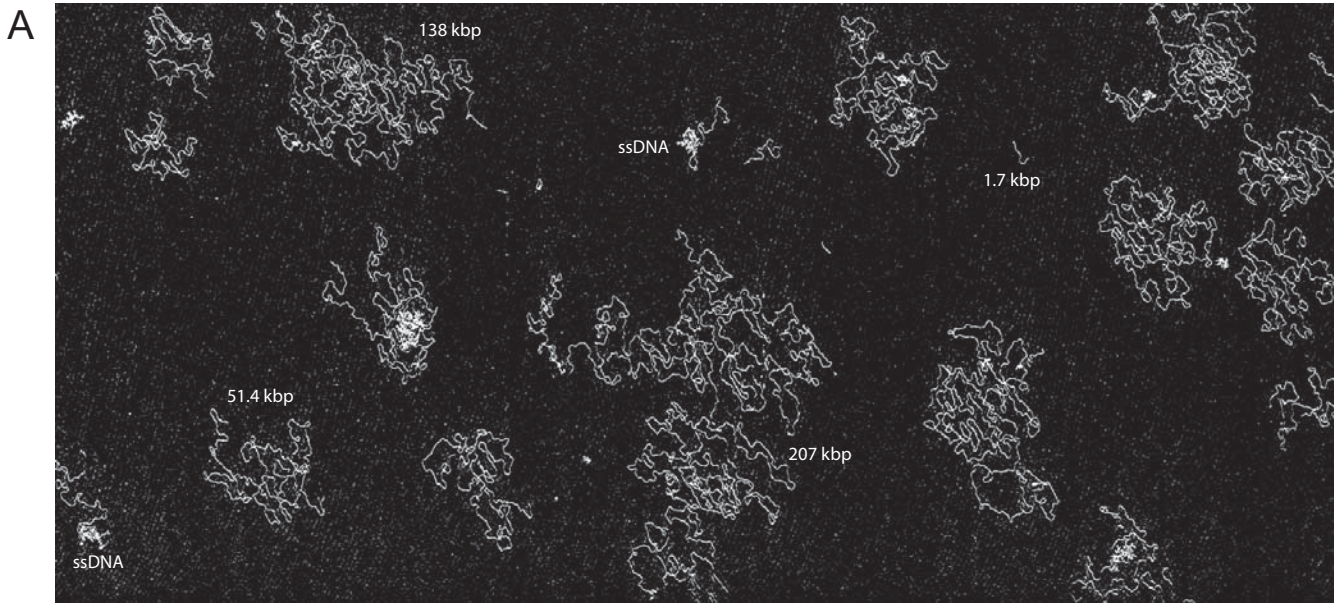


Figure. Commercially available human female gDNA from Promega imaged and analyzed by PRECYSE. Sample diluted in water to 500 pg/uL. (A) One frame scan (12 x 24 microns). Blue tracing of molecule backbones and sizing is performed in real time by onboard Molecular Explorer software. ssDNA in sample is easily distinguished from dsDNA and excluded from the sizing analysis. (B) Histogram sizing analysis of sample spanning 6 frames, totaling 227 molecules, generated a median of 8.1 kbp. Swarm plot of same sizing data to emphasize 'tail' of large molecules indicative of intact high quality gDNA. (C) Simulated Femto pulse (Agilent Technologies) electropherogram from PRECYSE data. Conversion to mass-based electropherogram was done by comparing migration behavior of known sizing and concentration of the Femto Pulse standard ladder provided by Harvard University Bauer Center Genomics Core Facility. PRECYSE provides direct visual and individual molecule analysis, eliminating mass-based fluorescent bias, for improved downstream application QC.

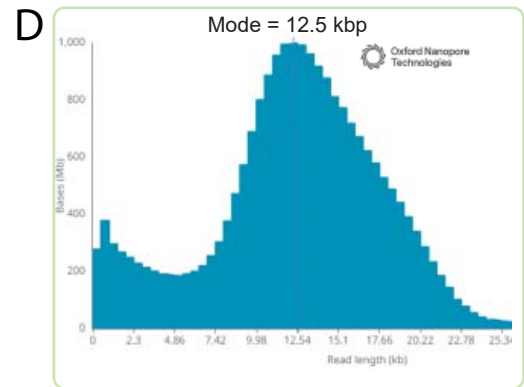
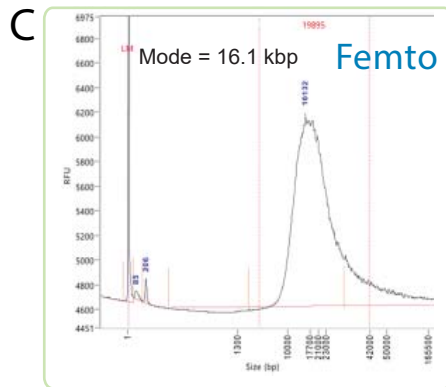
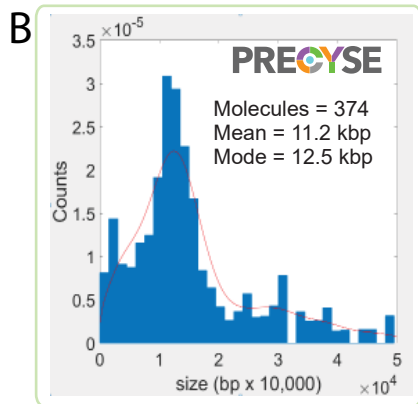
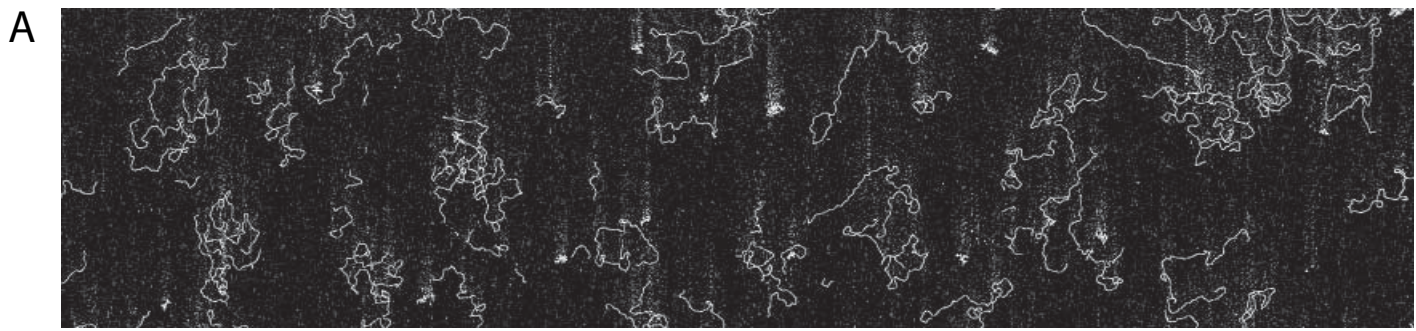


Figure. Sheared Mouse gDNA provided by Harvard University Bauer Center. Target shear size of 10-12 kbp utilizing a Megaruptor 3 (Hologic). (A) Partial image of frame 1 scan by PRECYSE showing ideal molecule separation at 250 pg/uL. ssDNA contamination is clearly visible. (B) Software analysis of 4 scanned frames and 374 molecules generated a median of 11.2 kbp and mode at 12.5 kbp. (C) Femto pulse (Agilent Technologies) electropherogram generated a mean size of 19.9 kbp and mode at 16.1 kbp. (D) ONT sequencing generated a mode at ~12.5 kbp with an N50 of 13.0 kbp. Comparison between PRECYSE and Femto data shows how mass-based fluorescence electrophoresis can significantly overestimate the true sizing of DNA. Sizing histogram modes were identical between PRECYSE and ONT.

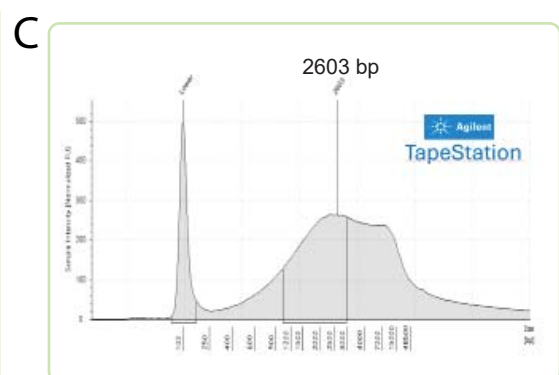
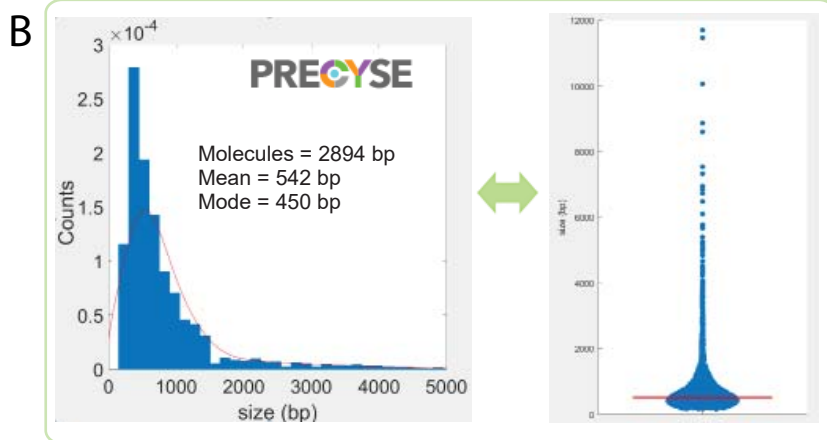
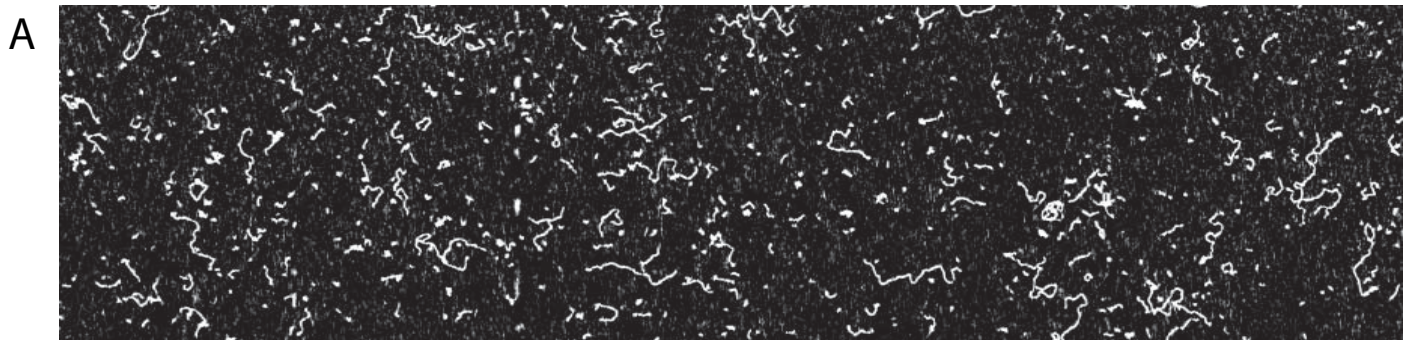


Figure. gDNA extracted from Human FFPE tissue provided by the Jackson Laboratory for Genomic Medicine. (A) PRECYSE partial image scan of frame 1 showing significant crosslinking (backbone branching) and contaminants/proteins (smaller brighter white objects). (B) Histogram sizing analysis of 5 frames and 2894 molecules generated a median of 542 bp and mode at 450 bp. Swarm plot clearly shows a long tail of larger molecules extending out to near 12 kbp with majority of molecules <1.5 kbp. (C) TapeStation (Agilent Technologies) analysis generated a very broad curve with a mode near 2.6 kbp. Electrophoretic migration was likely impacted by the DNA crosslinking and bound protein from the FFPE.