Scientific Relevance

• Tumor-sequencing studies have demonstrated that most cancers are driven by either single-nucleotide variants (SNV) or structural variants (SV).

• Shallow Whole Genome Sequencing (sWGS), also known as Low Coverage (LC) WGS, allows researchers to determine SV with 0.1 to 0.2X low sequencing coverage.

• Low cost sWGS is emerging as a promising clinical sequencing strategy for SV-driven tumors.

• sWGS can be used for clinically relevant structural variants such as oncogenic amplification, tumor-suppressor deletion, and genomic instability.

• sWGS can be applied to DNA originating from Formalin-Fixed Paraffin-Embedded tissue (FFPE), blood, or cfDNA.

Challenges

• Protocol requires library construction from DNA of different qualities and origins.

• Uniform coverage of the genome is challenging to obtain due to bias in sequencing technology.

Workflow

Fig 1: sWGS workflow enabled by AFA energetics from extraction to data analysis. AFA-Energetics are used for extraction of multiple sample types such as FFPE, cfDNA, and DBS. Post-extraction, samples are sheared with a Focused-ultrasonicator before library construction. After sequencing, reads are binned to genomic regions then additional bioinformatics is performed.

Advantages of Adaptive Focused Acoustics® (AFA®)

AFA technology is the gold standard for mechanical DNA shearing.

• Highly reproducible results

• Unbiased fragmentation regardless of GC content

• Compatible with all DNA inputs, quality, and origin, including FFPE samples

• Automation friendly options (LE220R-plus paired with AFA-TUBE consumables)

Suggested Covaris Products

• Covaris Focused-ultrasonicator (M-Series, S-Series, E-Series, or LE-Series)

• 96 AFA-TUBE TPX Plate (PN 520291)

• 8 AFA-TUBE TPX Strip (PN 520292)

• truXTRAC FFPE

• truXTRAC cfDNA (PN 520221)

Citations


