Shallow Whole Genome Sequencing Workflow - sWGS

Scientific Relevance

- Tumor-sequencing studies have demonstrated that most cancers are driven by either single-nucleotide variants (SNV) or structural variants (SV).1
- 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.1
- sWGS can be used for clinically relevant structural variants such as oncogenic amplification, tumor-suppressor deletion, and genomic instability.2
- sWGS can be applied to DNA originating from Formalin-Fixed Paraffin-Embedded tissue (FFPE), blood, or cfDNA.3

Challenges

- Protocol requires library construction from DNA of different qualities and origins.5
- Uniform coverage of the genome is challenging to obtain due to bias in sequencing technology.5

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 oneTUBE-10™ consumables)

Suggested Covaris Products

- Covaris Focused-ultrasonicator® (M-Series, S-Series, E-Series, or LE-Series)
- 96 oneTUBE-10 AFA Plate (PN 520249)
- 8 oneTUBE-10 Strip AFA Strip (PN 520225)
- truXTRAC FFPE
- truXTRAC cfDNA (PN 520221)

Citations