

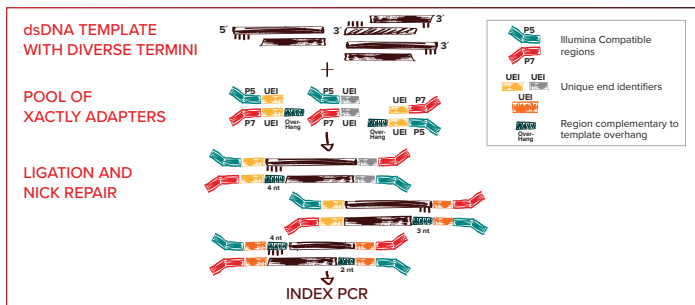
XACTLY™

DNA TERMINI PROFILING ASSAY FOR IMPROVED FRAGMENTOMICS

DNA fragmentation generates DNA molecules with a variety of termini, including blunt ends and single-stranded overhangs. Differential nuclease expression and activity may occur during disease progression resulting in altered DNA fragmentation patterns intra-cellularly and in cell-free DNA (cfDNA).

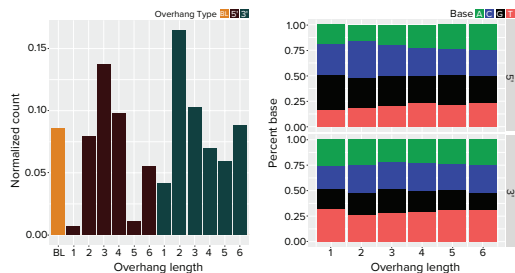
Deconvolution of the signal residing in DNA termini can reveal the genomic provenance of the fragment. Traditional library preparation approaches lose this vital information due to end repair. XACTLY is a novel double-stranded library preparation and data analysis approach that provides comprehensive DNA termini information while retaining the entire sequence, capturing the complete strand from beginning to end.

XACTLY WORKFLOW



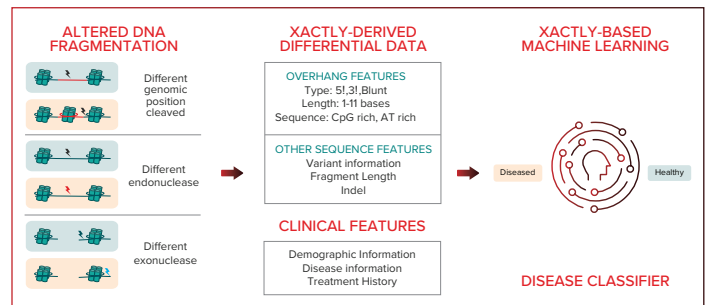
XACTLY generates dsDNA libraries without the conventional end-polishing step by ligating a pool of end-informative NGS adapters that contain Unique End Identifiers (UEI) to template DNA in a massively parallel reaction to generate sequence-ready libraries.

XACTLY DATA GENERATION



XACTLY data processing workflow enables deconvolution of overhang type, length and sequence information for every fragment (cfDNA from a healthy donor shown here) within the library while capturing sequence information from the entire library molecule.

XACTLY FOR CFDNA FRAGMENTOMICS



Dysfunctional nuclease activity, changes in transcription factor binding and nucleosome occupancy during cancer result in distinct genomic fragmentation patterns which are reflected in cfDNA. Combining the unique data type and bonafide sequence information captured by XACTLY with clinical data can potentially improve the predictive power of machine learning algorithms in cancer diagnosis.

OTHER APPLICATIONS

- Characterization of DNA shearing mechanisms
- Characterization of nuclease activity - restriction enzymes, apoptotic nucleases, other bioengineered nucleases
- Evaluation of DNA stability and degradation

CONTACT US for collaborative R&D opportunities