genefirst

XCeloSeq® DNA Testing

Explore how ATOM-Seq excels with next generation sequencing of challenging clinical samples

NGS Library Preparation

Clinical samples pose technical challenges to NGS due to their biological origin and the preservation processes:

cfDNA

- **Low DNA yields** ➔ limit mutation sensitivity
- **Highly fragmented DNA** ➔ poorly captured by NGS workflows
- **Abundant wild-Type DNA** ➔ mutations are highly diluted

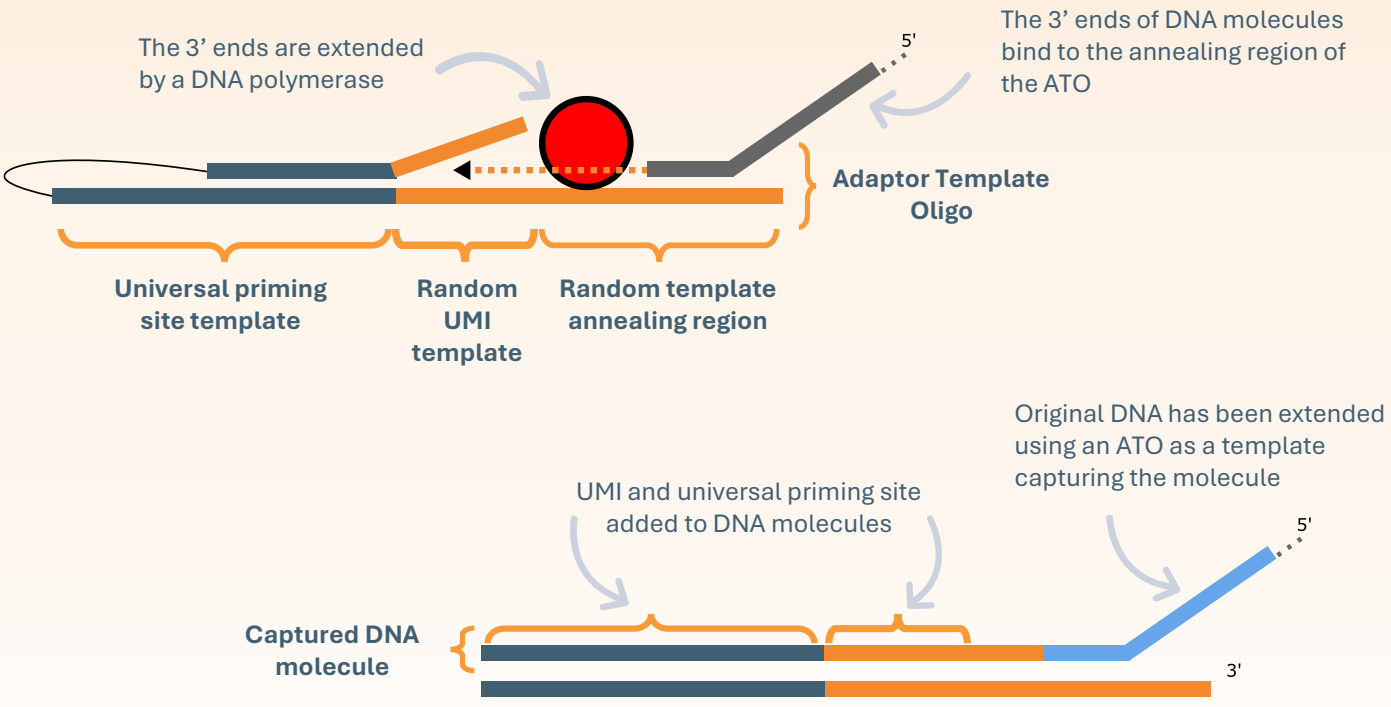
FFPE DNA

- **Variable tissue mass** ➔ can limit DNA yield
- **Inconsistent preservation** ➔ variable assay performance
- **Formalin damage/degradation** ➔ reduces mutation sensitivity

GeneFirst NGS library preparation technology is uniquely designed with these challenges in mind

ATOM-Seq®
An Alternative to Ligation-Based DNA Capture

A reimagined way of processing patient samples, combining advantages and overcoming limitations of common library preparation approaches

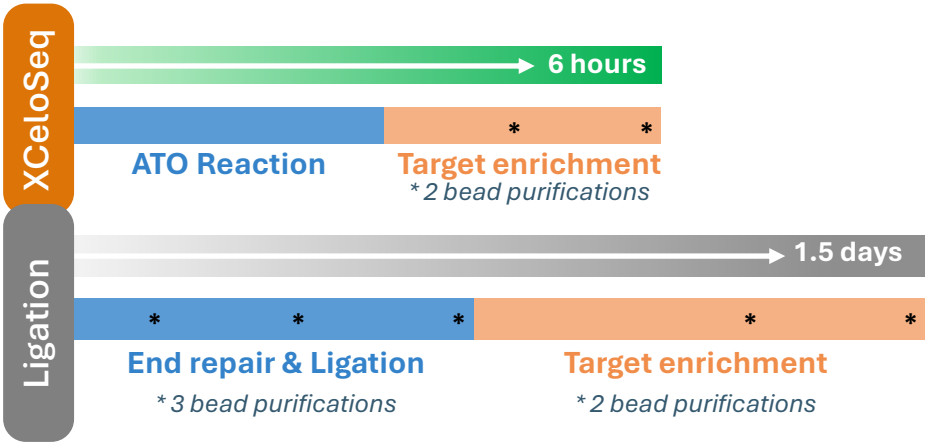


Targeted DNA Enrichment Workflow

Optimised for success with liquid biopsy cfDNA samples and damaged, poor quality FFPE DNA samples

Uniquely designed for challenging material

- Simple, ligation-free approach with no DNA end-repair
- Captures all single- and double-strand DNA
- Captures short and degraded material
- Efficient with low input quantities
- Single primer enrichment to maximise capture regardless of DNA breakpoint
- Unique molecular identifies for error suppression
- Minimal bead purification steps



Simple NGS workflows powered by ATOM-Seq

- Single-day workflow
- Fewer bead purifications and less hands-on time
- Easy customisation

Workflow benefits

FFPE false-positives reduced by enzymatic removal of C→U deamination

Excels with short, fragmented DNA as PCR enrichment requires only one target-specific primer

Call mutations with confidence with Unique Molecular Identifiers

Whole-sample representation as sample is PCR amplified before purification

Simple, single-day protocols, leveraging the simplicity and efficiency of DNA polymerases

Broad compatibility with Illumina, Ion Torrent, Element Bioscience and MGI sequencers

Comparative Data

The ATOM-Seq capture chemistry was **compared to a ligation-based chemistry** from a leading molecular biology company.

The **same input mass** of cfDNA was used for both workflows. Samples were processed following all recommended protocol, sequencing, and data analysis steps.

The ATOM-Seq workflow **captured 179%** the number of cfDNA molecules relative to the ligation-based workflow.

The average number of cfDNA molecules captured by the two competitor replicates is defined as 100%. The three ATOM-Seq replicates captured 179% as many molecules on average.

XCeloSeq targeted DNA enrichment kits

cfDNA

Product Code	Product Name
SEQ030	XCeloSeq Pan Cancer Panel - V2
SEQ031	XCeloSeq Colon Cancer cfDNA kit - V2
SEQ032	XCeloSeq Lung Cancer cfDNA kit - V2
SEQ033	XCeloSeq Breast Cancer cfDNA kit - V2

FFPE DNA

Product Code	Product Name
SEQ028	XCeloSeq Colon Cancer High-Sensitivity FFPE Kit - V2
SEQ035	XCeloSeq Lung Cancer High-Sensitivity FFPE Kit - V2
SEQ036	XCeloSeq Breast Cancer High-Sensitivity FFPE Kit - V2
SEQ038	XCeloSeq Pan Cancer High-Sensitivity FFPE Kit - V2

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ATOM-Seq

Custom Assay Development