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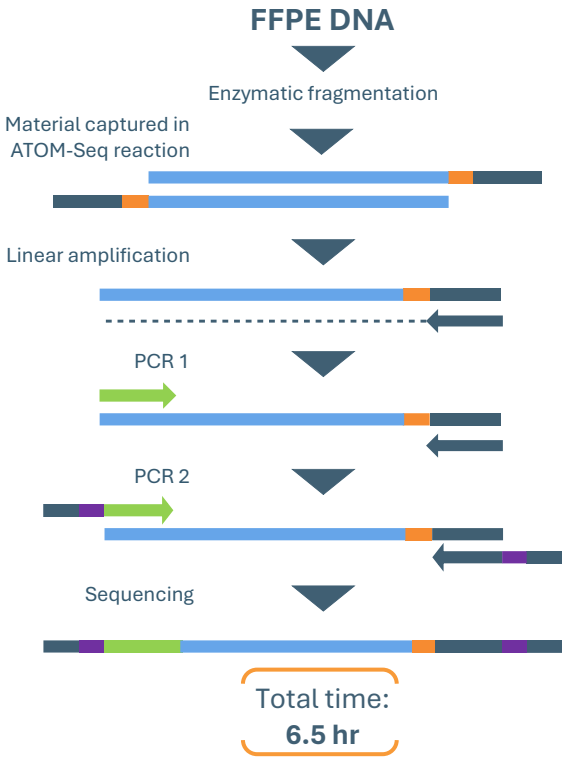
ATOM-Seq®

FFPE DNA/RNA Capture Workflows

NGS library preparation workflows for capturing and enriching FFPE DNA or FFPE RNA

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



Workflow benefits

Reduce false-positives by enzymatic removal of C→U deamination

Detect even the rarest clinical signatures by using both UMIs and unique, error-reducing workflow optimisations

Enrich any cfDNA molecule. All captured molecules are amplified, irrespective of length or breakpoint

Detect clinically relevant DNA alterations including SNVs, insertions, deletions, CNV and MSI

Highly versatile chemistry suitable with other enrichment applications

Identification of CRISPR genome edits

Eliminate ligation-based false positives because ATOM-Seq is 100% free of ligation steps

Localisation of viral integration sites

Identify all integration sites with target-specific primers in the viral sequence

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Known and Unknown Fusion Detection

Fusion detection workflow optimised to generate highest quality sequencing libraries using RNA from FFPE-preserved samples

Uniquely designed for challenging material

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- Efficient with low input quantities
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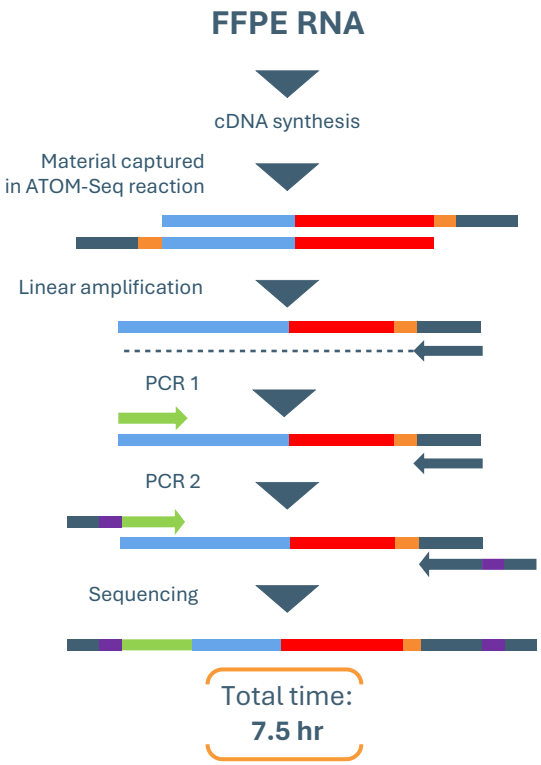

Identify all fusions, both known and unknown, using a single targeting primer for each conserved exon

Workflow benefits

Simple, single-day workflows generate high quality sequencing libraries from FFPE-preserved samples

Accurate counting of fusions by using UMI for reliable deduplication of PCR duplicates ensuring each cDNA molecule is counted

Detect clinically relevant RNA alterations including known and unknown fusions, exon skipping, expression and SNVs

FFPE DNA Workflows

FFPE RNA Workflows

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Custom Assay Development