genefirst

Multiomic Sequencing

Multiomic ATOM-Seq®

Sample scarcity limits multiomic analyses

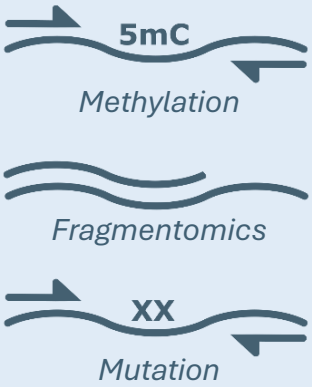
Limited cfDNA starting sample:

30ng cfDNA

Sample split, 10ng per assay:

33% sample representation per assay

3x drop in sensitivity per assay:



ATOM-Seq empowers high-sensitivity multiomics

Whole-sample capture and amplification:

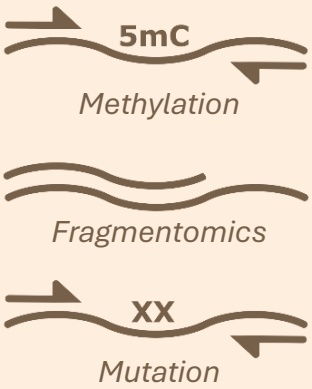
UMI-tagged copies of original molecules

Amplified sample split between assays:

Near 100% sample representation per assay

**assay and combination dependent*

Each assay achieves maximum sensitivity:



ATOM-Seq can interrogate many possible combinations of multiomic datasets from a single sample

Target Enrichment

Mutations
Copy number variation
Known gene fusions
Unknown gene fusions

Microbiome
Pathogen detection
Viral integration

Expression
Microsatellite instability
Exon splicing

Methylation (Bisulphite)

Whole genome
GC-enriched genome
Target Enrichment

Total Sample

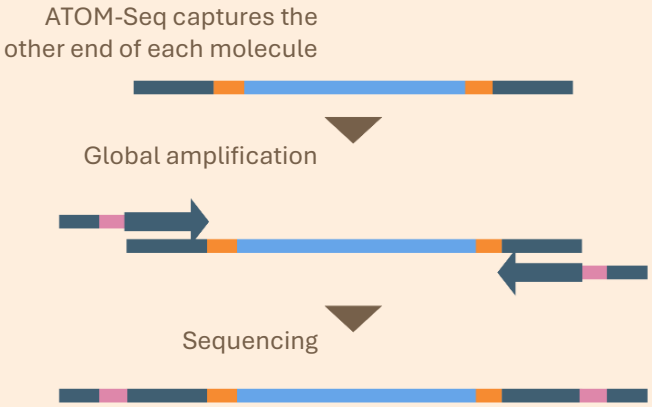
Copy number variation
Mutations
Fragmentomics

Example Multiomic ATOM-Seq Workflow

Sample capture and amplification

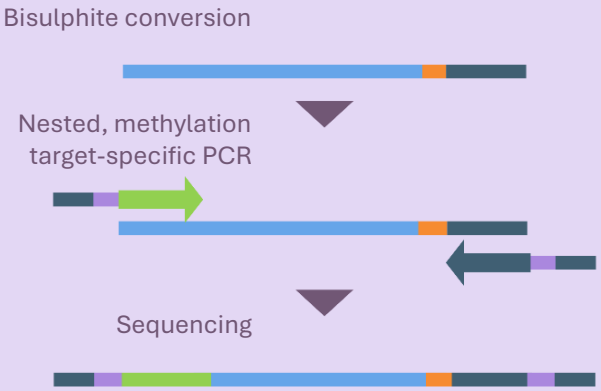
Downstream genetic analyses

e.g. mutation and fragmentomics



Downstream epigenetic analyses

e.g. targeted methylation



Build powerful and flexible workflows

No DNA end-repair step required, for efficient capture of cfDNA, FFPE DNA or high-quality DNA

Allows multiomic detection of methylation, mutations, fragmentomics and CNV **from a single liquid biopsy sample**

Eliminate false-positive calls, suppressing PCR artefacts via UMIs and linear amplification

Simple, single-day workflows

Enriches all target molecules regardless of length or breakpoint via use of a single targeting primer

Maximum sample retention and minimal hands-on time, due to minimal purification steps.

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