

Highlights

- Unrivalled Library Complexity - powered by ATOM-Seq® capture technology
- Developed for liquid biopsy samples
- Enhanced Error Correction - Error suppression protocol and unique molecular identifiers (UMI)
- Rapid Protocol With High Sample Retention – Minimal bead purification and hands on time

Our XCeloSeq® Lung Cancer cfDNA Kit employs our patented ATOM-Seq technology (Adaptor Template Oligo-Mediated Sequencing), which uses a simple and elegant chemistry to capture DNA, using sample DNA molecules as primers themselves, where their 3' ends are extended by a polymerase.

ATOM-Seq adds Unique Molecular Identifiers (UMIs) and universal adapter sequences directly to available 3' ends of every original sample molecule meaning that all original fragments can be captured. A universal primer is then used for rounds of linear amplification, allowing for the sequencing of both sense- and antisense-strands when the linear product is divided between two reactions thereby further improving error correction.

This unique approach is ligation free and is set apart from conventional PCR-based approaches by requiring only a single target-specific primer for enrichment. This offers numerous advantages that make ATOM-Seq particularly well suited to challenging clinical material such as cell-free DNA (cfDNA) from liquid biopsies or FFPE-preserved DNA.

The approach employed by ATOM-Seq along with unique protocol enhancements for sensitivity, specificity, and error correction allows for the highest sample retention and capture efficiency with no compromises on sensitivity and performance.

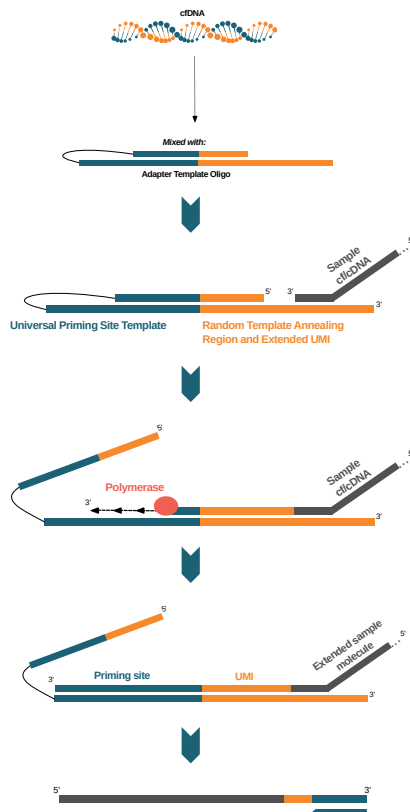
Specifications

Up to 50 ng Input Quantity*	300 Targeting Primers**	15 Gene Targets
4.5 million Recommended Reads Per Sample***	1.5 Hours Hands-On Time	<6 hours Total Protocol Time

*Higher quantities within the range will improve maximum sensitivity, recommended maximum is 50 ng. Enzymatically fragmented FFPE is also supported as an alternative starting material, when 50 ng should be used.

**Targeting primers are split between the sense and antisense DNA strands.

***Suggested read number for cfDNA samples. Reads should be divided equally between Pool 1 and Pool 2 Libraries. Read numbers can be optimised by users for different uses. For example, for FFPE libraries fewer reads may be sufficient. When using FFPE enzymatic digestion is required.



ATOM-Seq Workflow

Sample DNA is combined with the Adapter Template Oligo. The DNA molecules anneal to the 3' end of the ATO and a polymerase extends the original molecule, using the ATO sequence as a template to add a Unique Molecular Identifier (UMI) and a universal priming site to the end of the captured molecule.



Summary

The Lung Cancer cfDNA Kit is powered by our ATOM-Seq chemistry and is for use with cell-free DNA extracted from liquid biopsy blood samples. This kit is designed to target selected hotspots across 15 of the most frequently mutated genes in cancers and allows for high sensitivity and specificity detection of mutations including SNPs, insertions, deletions.

When used in conjunction with XCellSeq Unique Dual Indexing Sets, these allow for the enrichment of nucleic acids to generate high quality, high-complexity next-generation sequencing libraries suitable for use with Illumina® next-generation sequencing (NGS) instruments.

Ordering Information

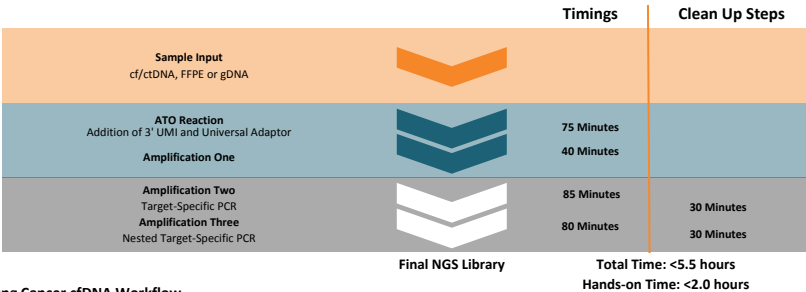
Product	No. of Samples	Catalog No.
XCellSeq® Lung Cancer cfDNA Kit	8	SEQ010

Learn more

For more information including the protocol please visit www.genefirst.com

Further Information

Dunwell TL, Dailey SC, et al. Adaptor Template Oligo-Mediated Sequencing (ATOM-Seq) is a new ultra-sensitive UMI-based NGS library preparation technology for use with cfDNA and cfRNA. Sci Rep. 2021 Feb 4;11(1):3138. doi: 10.1038/s41598-021-82737-9. PMID: 33542447; PMCID: PMC7862664.



XCellSeq® Lung Cancer cfDNA Workflow.

AKT	BRAF	ERBB3	HRAS	KRAS	MET	PIK3CA	ROS1	STK11	TP53*
ALK	EGFR	ESR1	KEAP1	MAP2K1	NRAS	RET			

XCellSeq® Lung Cancer cfDNA Kit Assay Targets. Selected target regions are enriched for the above genes (*Whole Coding Region Coverage).



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