NGS Disease Research Panels

ClearSeq AML

Access Targets Identified by Experts in Acute Myeloid Leukemia Research

Benefits

Expert-defined content

- Designed in collaboration with Dr. Robert Ohgami and Dr. Daniel Arber at Stanford University
- Targets 20 key genes frequently mutated in AML

Premium Performance You Can Trust

- Provides 99.9% design coverage of targeted exons
- Library-prep free target enrichment in less than a day

Comprehensive Workflow Solution

- Get from raw data to mutation report in 3 simple steps using SureCall analysis software
- Obtain all reagents for sample preparation, QC and automation tools from one trusted partner

Overview

Acute myeloid leukemia (AML) is the most common myeloid neoplasm affecting adults and the role of chromosomal structural variations in its molecular pathogenesis have been well-established[1]. In recent years, next generation sequencing has led to a revolution in the study of hematological malignancies and shown that mutations and indels play an essential part in the pathogenesis of AML.

The ClearSeq AML, designed in collaboration with Dr. Robert Ohgami and Dr. Daniel Arber at Stanford University, targets 48 selected exons in 20 genes found to be commonly mutated in AML. Research has also shown these genes to be associated with myelodysplastic syndromes, myelodysplastic/myeloproliferative neoplasms and myeloproliferative neoplasms.

Gene List (targeted exons)			
ASXL1	12	**MPL**	10
CSF3R	14, 17	**NPM1**	11
CBL	8, 9	**NRAS**	2, 3
CEBPA	1	**RUNX1**	3, 4, 8
DNMT3A	4, 8, 13, 15, 16, 18 19, 20, 22, 23	**SETBP1**	3
		SF3B1	13–15, 17
EZH2	8, 17, 18	**SRSF2**	1
FLT3	14, 20	**TET2**	3, 9, 10, 11
IDH1	4	**TP53**	5–8
IDH2	4	**U2AF1**	2, 6
JAK2	12, 14		

1: Betz BL, Hess JL. Acute myeloid leukemia diagnosis in the 21st century. Arch Pathol Lab Med. 2010; 134:1427–1433.

Excellent Performance for Accurate Variant Calling

The ClearSeq AML was designed for full coverage of targeted regions and provides ≥ 90% coverage at 20X depth, ensuring that important variants are not missed (Figure 1). Furthermore, multiple amplicon coverage of the target regions, a key feature of the HaloPlex technology, confers superior sensitivity and accuracy when compared to other PCR-based methods, eliminating false positive calls (Figure 2). The combination of an optimized design and library-prep free, single-tube amplification workflow allows the clinical researcher to accurately identify somatic variants faster. The panel can also be easily customized by the addition of genes using SureDesign.

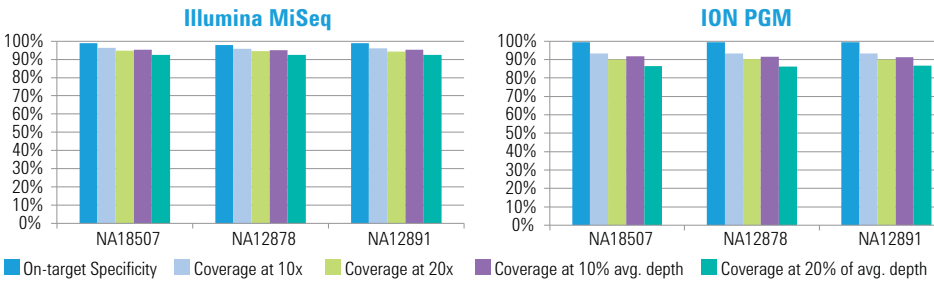

Figure 1. The ClearSeq AML provides excellent on-target specificity and uniform coverage of target regions so important mutations are not missed.

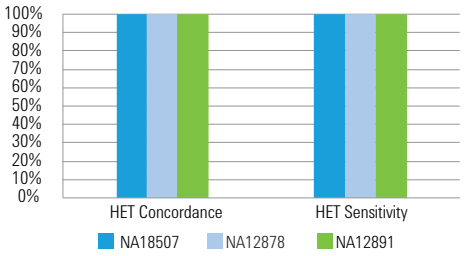

Figure 2. Multiple amplicon coverage of the target regions confers superior sensitivity and accuracy when compared to other PCR-based methods, eliminating false positive calls

Comprehensive Sample-to-Analysis Solution

The ClearSeq AML is ideally suited for analysis using SureCall, a NGS data analysis software developed to address the critical bioinformatics needs of clinical researchers. Using pre-configured cancer analysis workflows, go from raw data to a mutation report containing categorized known variants of interest within minutes, greatly reducing time-to-results. Together with robust sample QC and throughput scalability by automation, ClearSeq AML accelerates the confident detection of disease-associated variants.

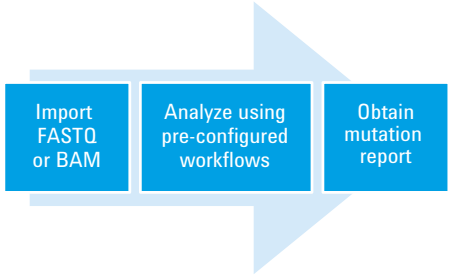

Figure 3. Accelerate time-to-results with a simplified 3-step analysis workflow using SureCall. Starting from FASTQ or BAM files, obtain a report of categorized variants within minutes.

Ordering Info

Part Number	Description
G9913A	ClearSeq AML, Illumina Sequencer, 16 Samples
G9913B	ClearSeq AML, Illumina Sequencer, 96 Samples
G9914A	ClearSeq AML, ION PGM Sequencer, 16 Samples
G9914B	ClearSeq AML, ION PGM Sequencer, 96 Samples

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