

Rapid Acute Myeloid Leukemia Targeted Therapy Mutation Panel

Last Literature Review: March 2024 Last Update: January 2026

[Acute myeloid leukemia](#) (AML) is a clonal disorder of hematopoietic progenitor cells. Recent studies have identified recurrently mutated genes with diagnostic, prognostic, and therapeutic significance in AML. The presence of certain variants may inform clinical management.

This multigene panel can be used upon initial diagnosis or overt relapse of AML to assess molecular changes, including single nucleotide variants (SNVs) and small insertions and deletions (indels) in select hotspots of relevant genes via massively parallel sequencing (MPS; also referred to as next generation sequencing [NGS]). This test has a fast turnaround time, which is critical in the timely identification of prognostic markers and advantageous in immediate patient management. In addition, it is more cost-effective than the use of multiple single gene tests and can be used to complement the morphologic and cytogenetic workup of AML. For testing for subsequent or more comprehensive analyses, refer to the [Myeloid Malignancies Mutation and Copy Number Variation Panel by Next Generation Sequencing Test Fact Sheet](#).

This test is NOT intended to detect minimal residual disease (MRD).

Featured ARUP Testing

[Rapid Acute Myeloid Leukemia Targeted Therapy Mutation Panel 3017050](#)

Method: Massively Parallel Sequencing

For more information on ARUP's myeloid malignancies panel, which includes the genes in this panel and additional genes relevant to other myeloid malignancies, refer to the [Myeloid Malignancies Mutation and Copy Number Variation Panel by Next Generation Sequencing Test Fact Sheet](#).

Disease Overview

Diagnostic, Prognostic, and Treatment Issues

Identification of one or more clonal genetic abnormalities, variants, or patterns of variants in patients with AML may:

- Aid in establishing the diagnosis of certain subtypes of AML
- Aid in the determination of prognosis and identification of therapeutic targets
- Inform clinical management

Genetics

Genes Tested

Rapid Acute Myeloid Leukemia Targeted Therapy Mutation Panel: Genes Tested			
Gene	Transcript (NM)	Covered Exon(s)	Covered Region(s)
<i>CEBPA</i>	NM_004364	1	chr19:33792244-33793320
<i>FLT3</i>	NM_004119	14, 15, 16, 20, intron 14	chr13:28608014-28608361 chr13:28602305-28602435 chr13:28592594-28592736
<i>IDH1</i>	NM_005896	4 ^a	chr2:209113083-209113292
<i>IDH2</i>	NM_002168	4	chr15:90631809-90631984

Gene	Transcript (NM)	Covered Exon(s)	Covered Region(s)
<i>KIT</i>	NM_000222	8, 9, 10, 11, 17	chr4:55589740-55589874 chr4:55592023-55592226 chr4:55593374-55593500 chr4:55593572-55593718 chr4:55599226-55599368
<i>KRAS</i>	NM_004985	2, 3, 4	chr12:25398198-25398318 chr12:25380158-25380356 chr12:25378538-25378717
<i>NPM1</i>	NM_002520	11 ^a	chr5:170837521-170837569
<i>NRAS</i>	NM_002524	2, 3, 4	chr1:115258661-115258781 chr1:115256411-115256609 chr1:115252180-115252359
<i>TP53</i>	NM_000546	All coding (noncoding exon 1 is not covered)	chr17:7579837-7579912 chr17:7579690-7579731 chr17:7579302-7579600 chr17:7578361-7578564 chr17:7578167-7578291 chr17:7577489-7577615 chr17:7577009-7577165 chr17:7576843-7576936 chr17:7573917-7574043 chr17:7572926-7573017

^aIndicated exons are partially targeted (for hotspots only) and not reportable in full.

Test Interpretation

Results

Reported variants are classified into two categories:

- Variants with known clinical significance in hematologic malignancies
- Variants of unknown clinical significance in hematologic malignancies

Limitations

Variants Not Detected

- Some variants may not be identified due to technical limitations in the presence of pseudogenes, in GC-rich regions, in repetitive or homologous regions, or in regions overlapping with primers designed for target enrichment.
- Variants at exon-intron boundaries may not be detected.
- Variants in regions that are not included in the targeted coding regions of the preferred transcript for the targeted genes
- Copy number variants (losses or gains)
- Loss of heterozygosity
- RNA variants
- Gene fusions, balanced translocations, and other structural variants

Variants Not Reported

- Benign or likely benign variants in the preferred transcript
- Variants other than hotspot mutations may not be reported

Additional Limitations

- This test is not intended to detect MRD.
- Interpretation of this test result may be impacted if this patient has had an undisclosed allogeneic bone marrow transplant or stem cell transplant.
- This test does not distinguish between somatic and germline variants

Limit of Detection

- SNVs and small variants <25 base pairs (bp): 5% variant allele fraction (VAF)
 - Variants >25 bp: may be detected at limit of detection (LOD), but analytic sensitivity may be reduced
- *FLT3* internal tandem duplications (ITDs) (3-126bp): 10% VAF

Analytic Sensitivity

Variant Class	Analytic Sensitivity (PPA) ^a Estimate (%)	Analytic Sensitivity (PPA) 95% Credibility Region ^a (%)
SNVs	98.9	95.2-99.8
Insertions/duplications/MNVs (1-25bp)	100	96.2-99.9
FLT3 ITDs	97.7	90.0-99.7

^aGenes included on this test are a subset of a larger methods-based validation from which the PPA values are derived.

bp, base pairs; ITDs, internal tandem duplications; MNVs, multinucleotide variants; PPA, positive percent agreement