

## Acute Myeloid Leukemia Molecular Genetic Testing

Acute myeloid leukemias (AMLs) are a heterogeneous group of disorders characterized by the clonal expansion of myeloid precursors in the peripheral blood, bone marrow, and/or other tissues, which results in impaired hematopoiesis and bone marrow failure.<sup>1,2,3,4</sup> AML is the most common acute leukemia in adults (~80% of leukemia cases) and accounts for the largest number of annual deaths from leukemia in the United States.<sup>2,4</sup> Gene alterations, along with translocations and inversions, carry prognostic importance in AML. In addition to large chromosomal rearrangements, molecular changes have also been implicated in the development of AML. A comprehensive evaluation of several molecular markers, including *FLT3*, *NPM1*, *CEBPA*, *KIT*, *IDH1*, and *IDH2*, is important for risk assessment and prognostication in certain patients with AML, and may guide treatment decisions.<sup>2</sup>

For more information on next generation sequencing testing for AML, see [Myeloid Malignancies Mutation Panel by Next Generation Sequencing](#). For information on cytogenetic testing related to AML, see [Acute Myeloid Leukemia with Myelodysplastic Syndrome \(MDS\) or Therapy-Related MDS Panel by FISH](#).

### Testing Strategy

At diagnosis, the minimum AML workup includes a bone marrow aspirate for morphology, flow cytometric immunophenotyping, cytogenetics (eg, karyotyping and fluorescence in situ hybridization [FISH]), and appropriate molecular genetic testing.<sup>1,2,3</sup>

### Disease Overview

#### Incidence

>20,000 cases/year in the U.S.<sup>4</sup>

#### Age of Onset

Median is 67 years<sup>2</sup>

#### Symptoms

- Symptoms resulting from thrombocytopenia, neutropenia, and anemia due to the accumulation of blasts in the marrow<sup>2</sup>
- Morphologic hallmark: excessive accumulation of blasts (typically >20%) and other defined immature cells which affect one or more myeloid lineage<sup>2</sup>

### Test Interpretation

For more detailed information on the prognostic significance of molecular markers in AML, see the ARUP Consult [Acute Myeloid Leukemia](#) topic.

### Tests to Consider

**Detect and quantitate gene alterations/translocations/inversions. Use for minimal residual disease (MRD) and relapse risk monitoring.**

[CBFB-MYH11 inv\(16\) Detection, Quantitative 2011114](#)

**Method:** Reverse Transcription Quantitative Polymerase Chain Reaction

[NPM1 Mutation Detection by RT-PCR, Quantitative 3000066](#)

**Method:** Quantitative Reverse-Transcription Polymerase Chain Reaction

[PML-RARA Detection by RT-PCR, Quantitative 2002871](#)

**Method:** Reverse Transcription Polymerase Chain Reaction

[RUNX1-RUNX1T1 \(AML1-ETO\) t\(8;21\) Detection, Quantitative 2010138](#)

**Method:** Quantitative Reverse Transcription Polymerase Chain Reaction

**Use for diagnosis, prognosis, and management. Not intended for MRD monitoring.**

[FLT3 ITD and TKD Mutation Detection 3001161](#)

**Method:** Capillary Electrophoresis

[IDH1 and IDH2 Mutation Analysis, exon 4 2006444](#)

**Method:** Polymerase Chain Reaction/Sequencing

**Use for prognostication in cytogenetically normal AML (CN-AML).**

[CEBPA Mutation Detection 2004247](#)

**Method:** Polymerase Chain Reaction/Sequencing

**Use for prognostication in core-binding factor-related (CBF) AML.**

[KIT Mutations in AML by Fragment Analysis and Sequencing 2002437](#)

**Method:** Capillary Electrophoresis

## Recurrent Genetic Abnormalities in AML<sup>2,4,5</sup>

Molecular Genetic Alteration	Prognostic Significance
<i>CEBPA</i>	Biallelic mutations confer favorable prognosis
<i>FLT3</i> ITD and TKD	Poor prognosis associated with <i>FLT3</i> ITD mutation; <i>FLT3</i> TKD mutation has unclear prognosis
<i>IDH1</i> and <i>IDH2</i>	Unfavorable prognosis; targeted therapy is available for AML with <i>IDH1</i> or <i>IDH2</i> mutation
<i>KIT</i>	Poor prognosis, usually associated with core binding factor leukemias; increased risk of relapse
<i>NPM1</i>	Favorable prognosis in patients with normal karyotype and without <i>FLT3</i> ITD mutation; poor prognosis if present with <i>FLT3</i> ITD and <i>DNMT3A</i> mutations
<i>CBFB-MYH11</i> <sup>a</sup>	Usually associated with high rate of CR and long-term, disease-free survival when treated with intensive consolidation therapy
<i>PML-RARA</i> <sup>a</sup>	More favorable prognosis than any other AML cytogenetic subtype when treated appropriately
<i>RUNX1-RUNX1T1</i> <sup>a</sup>	Usually associated with a high rate of CR and long-term, disease free survival when treated with intensive consolidation therapy

<sup>a</sup>These fusions can initially be screened by FISH but are also useful in monitoring for MRD.

CR, complete remission

Sources: NCCN, 2019<sup>2</sup>; De Kouchkovsky, 2016<sup>4</sup>; WHO, 2017<sup>5</sup>

## Related Next Generation Sequencing Tests

[Acute Myeloid Leukemia Mutation Panel by Next Generation Sequencing 3002714](#)

**Method:** Massively Parallel Sequencing

[Myeloid Malignancies Mutation Panel by Next Generation Sequencing 2011117](#)

**Method:** Massively Parallel Sequencing

## Sensitivity/Specificity

Gene	Methodology	Analytical Sensitivity	Analytical Specificity (%)
<i>CEBPA</i>	PCR/sequencing	40% mutated cells	100
<i>FLT3</i> ITD and TKD	PCR/CE	Signal ratio of 0.05 for ITD and 0.05 for TKD D835	100
<i>IDH1</i> and <i>IDH2</i>	PCR/sequencing	40% mutated cells	100
<i>KIT</i>	PCR/fragment analysis/sequencing	30% mutated cells for exon 17 5% mutated cells for exon 8	100
<i>NPM1</i>	Quantitative reverse transcription PCR	1:100,000	100
<i>CBFB-MYH11</i> <sup>a</sup>	Quantitative reverse transcription PCR	1:10,000	100
<i>PML-RARA</i> <sup>a</sup>	Quantitative reverse transcription PCR	1:10,000	85
<i>RUNX1-RUNX1T1</i> <sup>a</sup>	Quantitative reverse transcription PCR	1:100,000	100

Gene	Methodology	Analytical Sensitivity	Analytical Specificity (%)
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<sup>a</sup>These fusions can initially be screened by FISH but are also useful in monitoring for MRD.

CE, capillary electrophoresis; PCR, polymerase chain reaction

## Limitations

- Variants outside the targeted regions or below the limit of detection will not be identified
- Results must always be interpreted within the patient's clinical context and in conjunction with other relevant data and should not be used alone for a diagnosis of malignancy

## References

1. Arber DA, Borowitz MJ, Cessna M, et al. [Initial diagnostic workup of acute leukemia: guideline from the College of American Pathologists and the American Society of Hematology](#). Arch Pathol Lab Med. 2017;141(10):1342-1393. PubMed
2. National Comprehensive Cancer Network. [NCCN clinical practice guidelines in oncology: acute myeloid leukemia](#), Version 3.2020. [Last update: Dec 2019; Accessed: Sep 2020]
3. Weinberg OK, Sohani AR, Bhargava P, et al. [Diagnostic work-up of acute myeloid leukemia](#). Am J Hematol. 2017;92(3):317-321. PubMed
4. De Kouchkovsky I, Abdul-Hay M. ['Acute myeloid leukemia: a comprehensive review and 2016 update'](#). Blood Cancer J. 2016;6(7):e441. PubMed
5. Swerdlow S, Campo E, Jaffe E, et al. WHO Classification of Tumours of Haematopoietic and Lymphoid Tissues, Revised 4th ed. International Agency for Research on Cancer, 2017.

## Related Information

### [Acute Myeloid Leukemia - AML](#)

ARUP Laboratories is a nonprofit enterprise of the University of Utah and its Department of Pathology, 500 Chipeta Way, Salt Lake City, UT 84108  
 (800) 522-2787 | (801) 583-2787 | aruplab.com | arupconsult.com  
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