Overview

Useful For
Evaluation of acute myeloid leukemia (AML) using a focused 11-gene panel at the time of diagnosis or possibly at relapsed/refractory disease, to assist in appropriate classification, prognosis, and therapeutic management of patients.

Evaluation to determine if a different gene mutation profile is present at the time of AML relapse.

Genetics Test Information
This test includes next-generation sequencing to evaluate for the following 11 genes: CEBPA, DNMT3A, FLT3, IDH1, IDH2, KIT, KRAS, NPM1, NRAS, RUNX1, and TP53.

Testing Algorithm
For a list of the genes and exons targeted by this test see Targeted Genes Interrogated by Next-Generation Sequencing, Acute Myeloid Leukemia, 11-Gene Panel.

Special Instructions
- Hematopathology Patient Information
- Targeted Genes Interrogated by Next-Generation Sequencing, Acute Myeloid Leukemia, 11-Gene Panel

Highlights
Next-generation sequencing detection of somatic gene mutations, including type, pattern, and distribution, has diagnostic, prognostic, and potential therapeutic implications for patients with hematologic cancers, such as acute myeloid leukemia (AML).

This test enables more accurate classification and prognostic assessment of AML.

Method Name
Next-Generation Sequencing (NGS)

NY State Available
Yes

Specimen
Specimen Type
Varies

Ordering Guidance
This test focuses specifically on the gene mutations that are most prevalent and clinically significant in acute myeloid leukemias (AML) and is a subset of NGSHM / OncoHeme Next-Generation Sequencing for Myeloid Neoplasms, Varies. If a wider gene mutation analysis is desired or the indication is for a myeloid malignancy other than AML, order NGSHM.

Shipping Instructions
Bone marrow and peripheral blood specimens must arrive within 14 days of collection.

Necessary Information
The following information is required:

1. Clinical diagnosis

2. Pertinent clinical history, including disease phase (diagnostic, remission, relapse/refractory) and therapy status (especially if patient has received a hematopoietic stem cell transplant).

3. Clinical or morphologic suspicion

4. Date of collection

5. Specimen source

Specimen Required
Submit only 1 of the following specimens:

Specimen Type: Bone marrow aspirate (preferred)

Container/Tube:

Preferred: Lavender top (EDTA) or yellow top (ACD)

Acceptable: Green top (heparin)

Specimen Volume: 2 mL

Collection Instructions:

1. Invert several times to mix bone marrow.

2. Send bone marrow specimen in original tube. Do not aliquot
3. Label specimen as bone marrow.

**Specimen Stability:** Ambient (preferred)/Refrigerate

**Specimen Type:** Peripheral blood

**Container/Tube:**

**Preferred:** Lavender top (EDTA) or yellow top (ACD)

**Acceptable:** Green top (heparin)

**Specimen Volume:** 3 mL

**Collection Instructions:**

1. Invert several times to mix blood.

2. Send whole blood specimen in original tube. **Do not aliquot** 3. Label specimen as blood.

**Specimen Stability:** Ambient (preferred)/Refrigerate

**Specimen Type:** Extracted DNA from blood or bone marrow

**Container/Tube:** 1.5-2 mL tube with indication of volume and concentration of the DNA

**Specimen Volume:** Entire specimen

**Collection Instructions:** Label specimen as extracted DNA and source of specimen

**Specimen Stability:** Frozen (preferred)/Refrigerated/Ambient

**Forms**

1. [Hematopathology Patient Information](#) (T676)

2. If not ordering electronically, complete, print, and send a [Hematopathology/Cytogenetics Test Request](#) (T726) with the specimen.

**Reject Due To**

<table>
<thead>
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<th>Gross hemolysis</th>
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<tr>
<td>Gross lipemia</td>
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Test Definition: NGAML
Next Gen Sequencing, AML, 11 Gene

Bone marrow biopsies
Slides
Paraffin shavings or frozen tissues
Paraffin-embedded tissues
Paraffin-embedded bone marrow aspirates
Moderately to severely clotted

Specimen Minimum Volume
Blood, Bone Marrow: 1 mL

Extracted DNA: 100 mcL at 20 ng/mcL concentration

Specimen Stability Information

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Clinical & Interpretive

Clinical Information
Next-generation sequencing is a comprehensive molecular diagnostic methodology that can interrogate multiple regions of genomic tumor DNA in a single assay. Many hematologic neoplasms, including acute myeloid leukemia (AML), are characterized by morphologic or phenotypic similarities but can have characteristic somatic mutations in many genes. In addition, many cases of AML lack a clonal cytogenetic finding at diagnosis (normal karyotype) and can be better classified according to gene mutation profile. The presence and pattern of gene mutations in AML can provide critical prognostic information and may help in guiding therapeutic management decisions by physicians, particularly if targeted therapies are available.

Reference Values
An interpretive report will be provided.

Interpretation
Mutations (gene alterations) identified, if present, using human reference genome build GRCh37 (hg19). An interpretive report will be provided.

Cautions
This test is a targeted next-generation sequencing assay that encompasses 11 genes with variable full exon, partial region (including select intronic or noncoding regions), or hot spot coverage (depending on specific locus). Therefore, this test will not detect other genetic abnormalities in genes or regions outside the specified target areas. The test detects single base substitutions (ie, point mutations), as well as small insertion or deletion type events, but it does not detect gene rearrangements (ie, translocations), gene fusions, copy number alterations, or large scale (segmental chromosome region) deletions and complex changes.
This assay does not distinguish between somatic and germline alterations in analyzed gene regions, particularly with variant allele frequencies (VAF) near 50% or 100%. If nucleotide alterations in genes associated with germline variant syndromes are present and there is also a strong clinical suspicion or family history of malignant disease predisposition, additional genetic testing and appropriate counseling may be indicated. Mutation cells detected between 5% and 10% VAF may indicate low-level (ie, subclonal) tumor populations, although the clinical significance of these findings may not be clear. A low incidence of gene mutations associated with myeloid neoplasms can be detected in nonmalignant hematopoietic cells in individuals with advancing age (clonal hematopoiesis of indeterminate potential), and these may not be clearly distinguishable from tumor-associated mutations. Some apparent mutations classified as variants of undetermined significance may represent rare or low-frequency polymorphisms.

Prior treatment for hematologic malignancy could affect the results obtained in this assay. In particular, a prior allogeneic hematopoietic stem cell transplant may cause difficulties in resolving somatic or polymorphic alterations or in assigning variant calls correctly to donor and recipient fractions, if pertinent clinical or laboratory information (eg, chimerism engraftment status) is not provided.

Correlation with clinical, histopathologic, and additional laboratory findings is required for final interpretation of these results. The final interpretation of results for clinical management of the patient is the responsibility of the managing physician.

Clinical Reference
Method Description

Next-generation sequencing is performed to test for the presence of a mutation in targeted regions of the following 11 genes: CEBPA, DNMT3A, FLT3, IDH1, IDH2, KIT, KRAS, NPM1, NRAS, RUNX1, and TP53. See Targeted Genes Interrogated by Next-Generation Sequencing, Acute Myeloid Leukemia, 11-Gene Panel for details regarding the targeted gene regions identified in this test. This is a laboratory-developed test using research use only reagents. Extracted DNA from the clinical specimen is fragmented, adapter ligated, and a sequence library of fragments is prepared using a custom capture hybridization method. Individual patient samples are indexed (“bar-coded”) for identification and the library is sequenced on an Illumina platform. Sequence data are processed through a bioinformatics pipeline and a variant call file is generated for final analysis and reporting. (Unpublished Mayo method)

PDF Report

No

Specimen Retention Time

DNA 3 months

Performing Laboratory Location

Rochester

Fees & Codes

Test Classification

This test was developed, and its performance characteristics determined by Mayo Clinic in a manner consistent with CLIA requirements. This test has not been cleared or approved by the US Food and Drug Administration.

CPT Code Information

81450

LOINC® Information

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