Overview

Useful For
Prognostic assessment of acute myeloid leukemias with core-binding factor translocations (inv16 or t[16;16] CBFB-MYH11 or t[8;21] RUNX1-RUNX1T1)

Aids in establishing the diagnosis in some cases of mastocytosis

Genetics Test Information
This test is intended to detect KIT gene mutations in exons 8 through 11 and 17 that occur in hematologic malignant neoplasms, including specifically acute myeloid leukemia (AML) and mastocytosis. This test identifies somatic (acquired) mutations in these tumors.

Highlights
KIT mutations have been associated with adverse prognosis in “core-binding factor” (CBF) acute myeloid leukemias (AML) characterized by inv16 or t(16;16) CBFB-MYH11 or t(8;21) RUNX1-RUNX1T1 genetic abnormalities.

KIT mutations are involved in the pathogenesis of mastocytosis and detection of the common KIT mutation p.Asp816Val (D816V) is an important minor diagnostic criterion for systemic mastocytosis; however, other KIT mutations can be seen in a small number of cases negative for the D816V.

This test is intended primarily for detection of KIT mutations in CBF AML and may be useful in some cases of mastocytosis. However, if systemic mastocytosis is suspected, the more sensitive allele-specific PCR method to specifically identify the KIT D816V abnormality is strongly recommended prior to KIT sequencing (available as KITB / KIT Asp816Val Mutation Analysis, Blood; KITBM / KIT Asp816Val Mutation Analysis, Qualitative PCR, Bone Marrow; or KITAS / KIT Asp816Val Mutation Analysis, Qualitative PCR), given that mast cell abundance in bone marrow samples is often very limited (see Cautions).

Testing Algorithm
See Acute Myeloid Leukemia: Testing Algorithm in Special Instructions

Special Instructions
- Hematopathology Patient Information
- Acute Myeloid Leukemia: Testing Algorithm

Method Name
Mutation Detection in DNA Using Sanger Sequencing

NY State Available
Yes

Specimen

Specimen Type
Varies

Advisory Information
This test is intended for detection of KIT mutations in “core-binding factor” (CBF) acute myeloid leukemias (AML). For systemic mastocytosis see:
Test Definition: KITE
KIT Mutation, Hematologic Neoplasm

-KITB / KIT Asp816Val Mutation Analysis, Blood
-KITBM / KIT Asp816Val Mutation Analysis, Qualitative PCR, Bone Marrow
-KITAS / KIT Asp816Val Mutation Analysis, Qualitative PCR

Shipping Instructions
Specimen must arrive within 7 days (168 hours) of collection.

Necessary Information
The following information is required:
1. Pertinent clinical history
2. Clinical or morphologic suspicion
3. Date and time of collection
4. Specimen source

Specimen Required
Submit only 1 of the following specimens:

Specimen Type: Blood
Container/Tube: EDTA (lavender top) or ACD (yellow top)
Specimen Volume: 3 mL

Collection Instructions:
1. Invert several times to mix blood.
2. Send specimen in original tube.
3. Label specimen as blood.

Specimen Stability Information: Ambient (preferred)/Refrigerate

Specimen Type: Bone marrow
Container/Tube: EDTA (lavender top) or ACD (yellow top)
Specimen Volume: 2 mL

Collection Instructions:
1. Invert several times to mix bone marrow.
2. Send specimen in original tube.
3. Label specimen as bone marrow.

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

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

**Container/Tube:** 1.5- to 2-mL tube

**Specimen Volume:** Entire specimen

**Collection Instructions:** Label specimen as extracted DNA from blood or bone marrow with an indication of volume and concentration of the DNA.

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

**Specimen Type:** Paraffin-embedded tissue

**Container/Tube:** Paraffin block

**Specimen Volume:** Entire block

**Additional Information:** Tissue must demonstrate involvement by a hematologic neoplasm (eg, AML), not solid tumors.

**Specimen Stability Information:** Ambient

**Specimen Type:** Paraffin-embedded bone marrow aspirate clot

**Container/Tube:** Paraffin block

**Specimen Volume:** Entire block

**Specimen Stability Information:** Ambient

**Specimen Type:** Tissue

**Slides:** Unstained slides

**Specimen Volume:** 10 Slides

**Additional Information:** Tissue must demonstrate involvement by a hematologic neoplasm (eg, AML), not solid tumors.

**Specimen Stability Information:** Ambient

**Forms**

1. [Hematopathology Patient Information](#) (T676) in Special Instructions

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

**Specimen Minimum Volume**

Blood, bone marrow: 1 mL

Extracted DNA from blood or bone marrow: 50 microliters (mcL) at 20 ng/mcL

**Reject Due To**

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<tr>
<td>Gross hemolysis</td>
<td>Reject</td>
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<tr>
<td>Other</td>
<td>Bone marrow core biopsies Paraffin shavings Frozen tissues Moderately to severely clotted</td>
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**Specimen Stability Information**

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<tr>
<th>Specimen Type</th>
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<tr>
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**Clinical and Interpretive**

**Clinical Information**

Acquired mutations in the *KIT* gene are identified in a subset of acute myeloid leukemias (AML) characterized by inv16 or t(16;16) *CBFB-MYH11* or t(8;21) *RUNX1-RUNX1T1* genetic abnormalities (approximately 10%-20% of cases) and in this setting, the additional presence of *KIT* gene mutation has been described as an adverse prognostic factor in some studies. *KIT* mutations in AML tend to involve exons 8 through 11 and 17, although the p.Asp816Val (D816V) variant that is highly prevalent in systemic mastocytosis is less common in AML. Mastocytosis is a hematologic disorder characterized by abnormal mast cell expansion in the bone marrow and extramedullary organ sites (eg, skin, gastrointestinal tract). Disease can be localized to skin (ie, cutaneous mastocytosis) or present systemically, with variable features of disease aggressiveness and symptomatology. Mutations in the *KIT* gene are identified in a large majority of patients with both cutaneous mastocytosis (CM) and systemic mastocytosis (SM). The D816V abnormality is identified in most patients with SM and this finding represents an important minor diagnostic criterion in the 2008 WHO classification. The D816V is less commonly seen in CM, although single nucleotide variants are present in other *KIT* exons. Rare cases of familial mastocytosis are also described with *KIT* mutations involving exons 8 and 9. Although *KIT* gene mutation represents an important diagnostic marker for SM, the number of bone marrow mast cells is often limited in aspirate samples. Therefore, if SM is clinically and pathologically suspected, KIT testing should first proceed with a sensitive and specific screen for the D816V (*KIT* / *KIT* Asp816Val Mutation Analysis, Blood; *KITBM* / *KIT* Asp816Val Mutation Analysis, Qualitative PCR, Bone Marrow; or *KITAS* / *KIT* Asp816Val Mutation Analysis, Qualitative PCR) prior to consideration of *KIT* gene sequencing, based on the greatly enhanced sensitivity of the PCR test for this particular variant. In AML, *KIT* sequencing is preferred, given the wider spectrum of mutations in other *KIT* exons.

**Reference Values**

An interpretive report will be provided

**Interpretation**

Mutations detected or not detected. An interpretive report will be provided.

**Cautions**

This test is intended to evaluate for the presence of somatically acquired *KIT* mutations in hematologic malignant
neoplasms, specifically core-binding factor (CBF) acute myeloid leukemia with t(8;21)/RUNX1-RUNX1T1 or inv(16) or t(16;16)/CBFB-MYH11, although it may be useful in some cases of mastocytosis. This test does not detect mutations in the entire KIT gene, but is limited to alterations in exons 8, 9, 10, 11, and 17. The analytic sensitivity of this assay is approximately 20%. It is important to note that in many instances of systemic mastocytosis (SM), mast cell abundance in bone marrow aspirates is very limited and this test may result a false-negative for KIT mutation. Therefore, if SM is suspected clinically or pathologically, testing for the specific p.Asp816Val (D816V) by allele-specific PCR method should be strongly considered as the initial test (KITB / KIT Asp816Val Mutation Analysis, Blood; KITBM / KIT Asp816Val Mutation Analysis, Qualitative PCR, Bone Marrow; or KITAS / KIT Asp816Val Mutation Analysis, Qualitative PCR), prior to pursuing KIT sequencing.

The test is not intended for KIT mutation evaluation in solid tumors (eg, melanoma, gastrointestinal stromal tumor); for these indications, refer to specific tests offered by Molecular Genetics laboratory at Mayo Clinic.

Clinical Reference

Performance

Method Description
Total DNA is extracted from the sample and exons 8, 9, 10, 11, and 17 of the KIT gene are amplified by PCR followed by Sanger sequencing with evaluation by capillary electrophoresis. Review of the sequence data is performed using a combination of automated calls and manual inspection.(Unpublished Mayo method)

PDF Report
No

Day(s) and Time(s) Test Performed
Monday through Friday

Analytic Time
5 days

Maximum Laboratory Time
8 days

Specimen Retention Time
DNA 3 months
Performing Laboratory Location
Rochester

Fees and Codes

Fees
- Authorized users can sign in to Test Prices for detailed fee information.
- Clients without access to Test Prices can contact Customer Service 24 hours a day, seven days a week.
- Prospective clients should contact their Regional Manager. For assistance, contact Customer Service.

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 U.S. Food and Drug Administration.

CPT Code Information
81272-KIT (v-kit Hardy-Zuckerman 4 feline sarcoma viral oncogene homolog) (eg, gastrointestinal stromal tumor [GIST], acute myeloid leukemia, melanoma), gene analysis, targeted sequence analysis (eg, exons 8, 11, 13, 17, 18)

LOINC® Information

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