Figure. Use of Laboratory Testing in AML Diagnosis and Prognosis Assessment

**Individuals with Clinical Features Suggestive of AML**

Comprehensive Hematopathology Report (17734X) includes morphology evaluation and, at the discretion of the hematopathologist, may also include immunophenotyping, chromosome analysis, FISH, and/or PCR.

- ≥20% myeloid blasts in PB or BM
- <20% myeloid blasts in PB or BM

**AML diagnosed**

- At least 1 of the following present:
  - Myeloid sarcoma
  - AML1/ETO t(8;21)
  - PML/RARA t(15;17)
  - CBFB/MYH11 inv(16) or t(16;16)

- Absence of all of the following:
  - Myeloid sarcoma
  - AML1/ETO t(8;21)
  - PML/RARA t(15;17)
  - CBFB/MYH11 inv(16) or t(16;16)

**Consider myelodysplastic syndrome or other leukocyte disorder**

- AML with chromosomal abnormalities
  - AML1/ETO t(8;21) or CBFB/MYH11 inv(16)/t(16;16)
  - PML/RARA t(15;17)

- c-KIT gene mutation analysis [19960X, 19961]
  - +8

**AML without chromosomal abnormalities**

- NPM1 or double CEBPA mutations
- FLT3-ITD mutations

- No NPM1, double CEBPA, or FLT3-ITD mutations

**DIAGNOSIS**

**PROGNOSIS**

This algorithm is intended as a guide for using Quest Diagnostics laboratory tests to diagnose, classify, and assess prognosis in patients suspected of having AML. The algorithm is based on the World Health Organization and National Comprehensive Cancer Network (NCCN) guidelines for AML. According to the NCCN guidelines, AML patients with chromosomal abnormalities not currently associated with better or poor risk should be assigned to the “intermediate risk” prognostic category. PB indicates peripheral blood; BM, bone marrow; NPM1, nucleophosmin 1 gene; FLT3-ITD, fms-like tyrosine kinase-internal tandem duplication; and CEBPA, CCAAT/enhancer-binding protein-alpha gene.