External request: Submission from Illumina Inc requesting the inclusion of Next-Generation Sequencing (NGS) when referring to various “molecular” related terminology and applications in the Guidelines. (see submission for detailed request)

Based on the data in the noted references, the panel consensus did not support the addition of these specific recommendations into the Guidelines.

Footnote a was modified during the update process:
A variety of gene mutations are associated with specific prognoses (category 2A) and may guide medical decision making (category 2B) (See AML-A). Currently, c-KIT, FLT3-ITD, FLT3-TKD, NPM1, CEBPA, IDH1/IDH2, and TP53 are included in this group; however, this field is evolving rapidly. While the above mutations should be tested in all patients, multiplex gene panels and next-generation sequencing analysis may be used to obtain a more comprehensive prognostic assessment (Papaemmanuil E, et al. Genomic classification and prognosis in acute myeloid leukemia. N Engl J Med 2016;374:2209-2221). The information obtained may have prognostic impact in AML, may influence medical decision making regarding consolidation with chemotherapy versus an allogeneic hematopoietic stem cell transplant, or determination for eligibility for clinical trial participation (see Discussion). If a test is not available at your institution, consult pathology prior to performing the marrow evaluation about preserving material from the original diagnostic sample for future testing at an outside reference lab. Circulating blasts from peripheral blood may alternatively be used to detect molecular abnormalities in patients with a minimum of 10% involvement by the myeloid neoplasm to prevent false-negative results.

See Submission for references.