MAYO CLINIC LABORATORIES

Test Definition: NGSMC

Comprehensive Myeloid Panel,
Next-Generation Sequencing, Varies

Overview

Useful For

Evaluating known or suspected hematologic neoplasms, specifically of myeloid origin (eg, acute myeloid leukemia, myelodysplastic syndrome, myeloproliferative neoplasm, myelodysplastic/myeloproliferative neoplasm, unexplained cytopenias) at the time of diagnosis or, possibly, disease relapse

As an aid in determining diagnostic classification using blood or bone marrow specimens

Providing prognostic or therapeutic information for guiding clinical management

Determining the presence of new clinically important gene mutation changes at relapse

Genetics Test Information

This test includes next-generation sequencing to evaluate for the following 52 genes for mutation detection: *ABL1, ANKRD26, ASXL1, BCOR, BCORL1, BRAF, CALR, CBL, CEBPA, CSF3R, DDX41, DNMT3A, ETNK1, ETV6, EZH2, FLT3, GATA1, GATA2, HRAS, IDH1, IDH2, IKZF1, JAK2, KIT, KRAS, MPL, MYD88, NF1, NPM1, NRAS, PHF6, PPM1D, PRPF8, PTPN11, RAD21, RB1, RUNX1, SETBP1, SF3B1, SH2B3, SMC1A, SMC3, SRSF2, STAG2, STAT3, STAT5B, TET2, TP53, U2AF1, UBA1, WT1*, and *ZRSR2*.

Additionally, 35 fusion driver genes are evaluated, allowing sequencing of over 700 unique fusion transcripts: *ABL1, ABL2, BCL2, BRAF, CCND1, CREBBP, EGFR, ETV6, FGFR1, FGFR2, FUS, HMGA2, JAK2, KAT6A (MOZ), KAT6B, KMT2A, KMT2A PTDs, MECOM, MET, MLLT10, MRTFA (MKL1), MYBL1, MYH11, NTRK2, NTRK3, NUP214, NUP98, PAX5, PDGFRA, PDGFRB, RARA, RUNX1, TCF3, TFE3,* and *ZNF384*.

Method Name

Next-Generation Sequencing (NGS)

NY State Available

No

Specimen

Specimen Type

Varies

Shipping Instructions

Specimen must arrive within 5 days of collection.

Necessary Information

The following information is required:

1. Pertinent clinical history
2. Clinical or morphologic suspicion
3. Date of collection
4. Specimen source
5. Indication for test
6. Purpose for test

Specimen Required

Submit only 1 of the following specimens:

Specimen Type: Bone marrow aspirate
Container/Tube:
Preferred: Lavender top (EDTA)
Acceptable: Yellow top (ACD-B)
Specimen Volume: 3 mL
Collection Instructions:
1. Invert several times to mix bone marrow with anticoagulant.
2. Send bone marrow in original tube. **Do not aliquot**.
3. Label specimen as bone marrow.

Specimen Type: Whole blood
Container/Tube:
Preferred: Lavender top (EDTA)
Acceptable: Yellow top (ACD-B)
Specimen Volume: 4 mL
Collection Instructions:
1. Invert several times to mix blood with anticoagulant.
2. Send whole blood specimen in original tube. **Do not aliquot.**
3. Label specimen as blood.

Specimen Minimum Volume

Whole blood: 2 mL; Bone marrow: 1 mL

Reject Due To

Gross hemolysis	Reject
Moderately to severely clotted	Reject
Extracted DNA/RNA from outside institution	Reject

Specimen Stability Information

Specimen Type	Temperature	Time	Special Container
Varies	Refrigerated (preferred)	5 days	
	Ambient	5 days	

Clinical & Interpretive

Clinical Information

This next-generation sequencing test provides a comprehensive genomic profile, including gene mutations and fusions, for myeloid neoplasms in a single assay. Many hematologic neoplasms are characterized by morphologic or phenotypic similarities but can have characteristic somatic mutations in many genes or a specific gene fusion that enables specific disease classification. In addition, many myeloid neoplasms lack a clonal cytogenetic finding at diagnosis (normal karyotype) but can be diagnosed, confirmed, and classified according to the gene mutation profile. Patients with unexplained cytopenias may harbor acquired genetic alterations in hematopoietic cells (clonal cytopenias of uncertain significance) that may carry risk of developing overt myeloid malignancies. Detection of a specific gene fusion or gene mutations in known or suspected myeloid neoplasm can provide critical diagnostic, prognostic, and therapeutic information to help guide management for the patient's physician or other healthcare professional.

Reference Values

An interpretive report will be provided.

Interpretation

Detailed variant assessment and interpretive comments will be provided for all reportable genetic alterations.

If this test is ordered in the setting of erythrocytosis and suspicion of polycythemia vera, interpretation requires correlation with a concurrent or recent bone marrow or peripheral blood evaluation.

Cautions

This test is a targeted next-generation sequencing (NGS) assay that encompasses 52 genes with variable full exon, partial region (including select intronic or noncoding regions) or hot spot coverage (depending on specific locus), and 35 targeted fusion driver genes. 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), small insertions or deletions as well as gene fusions, but it does not detect copy number alterations or large scale (segmental chromosome region) deletions and complex changes.

This assay does not distinguish between somatic mutations and germline variants in analyzed gene regions, particularly with variant allele frequencies near 50% or 100%. If nucleotide alterations in genes associated with germline variant syndromes are present and there is a strong clinical suspicion or family history of malignant disease predisposition, additional genetic testing and appropriate counseling may be indicated. 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); these may not be clearly distinguishable from tumor-associated mutations.

Some apparent mutations classified as variants of uncertain significance may represent rare or low-frequency alterations (ie, polymorphisms).

Prior treatment for hematologic malignancy could affect the results obtained in this assay. Particularly, 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 NGS results and is the responsibility of the managing physician.

Clinical Reference

1. National Comprehensive Cancer Network (NCCN): NCCN Guidelines. Acute Myeloid Leukemia. NCCN; Version 3.2024. Accessed January 19, 2026. Available at www.nccn.org/guidelines/guidelines-detail?category=1&id=1411
2. National Comprehensive Cancer Network (NCCN): NCCN Guidelines. Myeloproliferative Neoplasms. NCCN;. Version 2.2024. Accessed January 19, 2026. Available at www.nccn.org/guidelines/guidelines-detail?category=1&id=1477
3. National Comprehensive Cancer Network (NCCN): NCCN Guidelines. Myelodysplastic Syndromes. NCCN; Version 1.2025. Accessed January 19, 2026. Available at www.nccn.org/guidelines/guidelines-detail?category=1&id=1446
4. He R, Chiou J, Chiou A, et al. Molecular markers demonstrate diagnostic and prognostic value in the evaluation of myelodysplastic syndromes in cytopenia patients. Blood Cancer J. 2022;12(1):12. doi:10.1038/s41408-022-00612-w
5. Malcovati L, Galli A, Travaglino E, et al. Clinical significance of somatic mutation in unexplained blood cytopenia. Blood. 2017;129(25):3371-3378. doi:10.1182/blood-2017-01-763425
6. Dohner H, Estey E, Grimwade D, et al. Diagnosis and management of AML in adults: 2017 ELN recommendations from an international expert panel. Blood. 2017;129(4):424-447. doi:10.1182/blood-2016-08-733196
7. Smith CC. The growing landscape of FLT3 inhibition in AML. Hematology Am Soc Hematol Educ Program. 2019;2019(1):539-547. doi:10.1182/hematology.2019000058
8. Kennedy JA, Ebert BL. Clinical implications of genetic mutations in myelodysplastic syndrome. J Clin Oncol. 2017;35(9):968-974. doi:10.1200/JCO.2016.71.0806
9. Daver N, Schlenk RF, Russell NH, Levis MJ. Targeting FLT3 mutations in AML: review of current knowledge and evidence. Leukemia. 2019;33(2):299-312
10. Khoury JD, Solary E, Abla O, et al. The 5th ed of the World Health Organization classification of haematolymphoid tumors: myeloid and histiocytic/dendritic neoplasms. Leukemia. 2022:36(7):1703-1719

Performance

Method Description

This assay includes DNA-based sequencing for 52 genes, including the hotspots of 32 genes and 20 full genes, and RNA-based sequencing for 35 fusion driver genes, which allows detection of over 700 unique fusions.

DNA and RNA are extracted from blood or bone marrow samples. After library preparation using Ion AmpliSeq technology, the samples are subjected to Ion Torrent next-generation sequencing (NGS) with post-sequencing analysis on an NGS instrument, Genexus. NGS bioinformatics is performed using the software provided by Thermo Fisher.

Genomic alterations are called according to the Genome Reference Consortium Human Build 37 (GRCh37), hg19, described using standard nomenclature, and interpreted using the current standards and guidelines recommended by Association of Molecular Pathology, American Society of Clinical Oncology and College of American Pathologists.

Test validation has shown greater than 99% accuracy, 100% (intra- and interassay) reproducibility, and a sensitivity of detection of 5% variant allele fraction with a minimum depth coverage of 250X for single base substitutions, deletion-insertion events (including FLT3-ITD), and gene fusions for the targeted gene mutations and fusions included in the validation design.(Unpublished Mayo method)

Genes analyzed: *ABL1, ANKRD26, ASXL1, BCOR, BCORL1, BRAF, CALR, CBL, CEBPA, CSF3R, DDX41, DNMT3A, ETNK1, ETV6, EZH2, FLT3, GATA1, GATA2, HRAS, IDH1, IDH2, IKZF1, JAK2, KIT, KRAS, MPL, MYD88, NF1, NPM1, NRAS, PHF6, PPM1D, PRPF8, PTPN11, RAD21, RB1, RUNX1, SETBP1, SF3B1, SH2B3, SMC1A, SMC3, SRSF2, STAG2, STAT3, STAT5B, TET2, TP53, U2AF1, UBA1, WT1*, and *ZRSR2*
Included fusion-drive genes: *ABL1, ABL2, BCL2, BRAF, CCND1, CREBBP, EGFR, ETV6, FGFR1, FGFR2, FUS, HMGA2, JAK2, KAT6A (MOZ), KAT6B, KMT2A, KMT2A PTDs, MECOM, MET, MLLT10, MRTFA (MKL1), MYBL1, MYH11, NTRK2, NTRK3, NUP214, NUP98, PAX5, PDGFRA, PDGFRB, RARA, RUNX1, TCF3, TFE3,* and *ZNF384*

PDF Report
Supplemental

Day(s) Performed
Monday through Friday

Report Available
3 to 9 days

Specimen Retention Time
Whole blood, bone marrow: 2 weeks; DNA/RNA: 1 year

Performing Laboratory Location
Mayo Clinic Jacksonville Clinical Lab

Fees & 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 account representative. 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. It has not been cleared or approved by the US Food and Drug Administration.

Test Definition: NGSMC

Comprehensive Myeloid Panel,
Next-Generation Sequencing, Varies

CPT Code Information

81455

LOINC® Information

Test ID	Test Order Name	Order LOINC® Value
NGSMC	Comprehensive NGS Myeloid Panel	99961-5

Result ID	Test Result Name	Result LOINC® Value
622767	Specimen Type	31208-2
622768	Indication for Test	42349-1
622770	Interpretation	59465-5
622777	Reviewed By	19139-5