Comprehensive testing for myeloid neoplasms

Enhance clinical decision-making for MDS and CMML using a guideline-driven comprehensive genomic profile

Comprehensive genomic profiling (CGP) plays a pivotal role in differentiating disease subtypes and resolving complex diagnostic challenges associated with MDS and CMML with greater clarity and confidence than traditional diagnostic testing.[1] Neo Comprehensive – Myeloid Disorders, a CGP assay, uses DNA and RNA NGS to detect relevant aberrations for diagnostic evaluation, prognosis, risk stratification, and therapy guidance for MDS, CMML, and other myeloid disorders, driving informed care.

Now providing the same trusted, comprehensive insights with improved turnaround time of as few as 8 days.*

Over 80% of patients with early MDS have no defining evidence of clonality by traditional diagnostic methods, and morphologic dysplasia is subtle, or often undetectable.[3,4]

Why CGP for MDS and CMML?

Establishing a diagnosis of MDS remains challenging, as cytopenias may result from a variety of non-neoplastic causes. Additionally, the genetic alterations found in MDS frequently overlap with those present in other myeloid disorders, further complicating an accurate diagnosis.[2]

To address these challenges, CGP offers broad genetic coverage, supporting the precise diagnosis and management of MDS and CMML, as well as accurate risk stratification, treatment selection, and monitoring. Expanded panels may also drive improved patient outcomes by identifying actionable alterations that expand therapeutic options, increase clinical trial eligibility, or provide a foundation for emerging targeted therapies.

48% of MDS patients have at least one clinically significant alteration detected through CGP.[1]

MDS = myelodysplastic neoplasms, CMML = chronic myelomonocytic leukemia, NGS = next-generation sequencing, MPN = myeloproliferative neoplasms

*Turnaround time for this test is 8-11 days

Neo Comprehensive – Myeloid Disorders is an NGS CGP solution for the effective management of MDS, CMML, and other myeloid neoplasms

DNA sequencing

SNVs/Indels (127 genes):
ABL1, ANKRD26, APC, ARAF, ASXL1, ATM, ATRX, BCOR, BCORL1, BLM, BRAF, BRCA1, BRCA2, BRIP1, CALR, CBL, CBLB, CBLC, CDKN2A, CEBPA, CHEK2, CSF3R, CTC1, CUX1, CXCR4, DDX41, DKC1, DNMT3A, ELANE, EPCAM, ERCC4, ETNK1, ETV6, EZH2, FANCA, FANCB, FANCC, FANCD2, FANCE, FANCF, FANCG, FANCI, FANCL, FANCM, FBXW7, FLT3, G6PC3, GATA1, GATA2, GFI1, GNAS, GNB1, HAX1, HRAS, IDH1, IDH2, IKZF1, IKZF3, ITPKB, JAK2, JAK3, KDM6A, KIT, KMT2A, KRAS, MAP2K1, MET, MLH1, MPL, MSH2, MSH6, MYD88, NF1, NHP2, NOP10, NOTCH1, NPM1, NRAS, PALB2, PDGFRA, PHF6, PIGA, PML, PMS2, PPM1D, PRPF8, PTEN, PTPN11, RAD21, RAD51C, RB1, RPL11, RPL35A, RPL5, RPS10, RPS17, RPS26, RPS7, RTEL1, RUNX1, SAMD9, SAMD9L, SBDS, SETBP1, SETD2, SF3B1, SH2B3, SLX4, SMC1A, SMC3, SRP72, SRSF2, STAG2, STAT3, STAT5B, SUZ12, TERC, TERT, TET2, TINF2, TP53, U2AF1, VHL, WAS, WRAP53, WT1, ZRSR2

CNV (17 genes):
ABL1, ASXL1, ATG2B, BRAF, CBFB, CDKN1B, CDKN2A, DNMT1, ETV6, EZH2, GSKIP, JAK2, KMT2A, KRAS, MYC, RAD21, TP53

RNA sequencing

Fusions (40 genes):
ABL1, AFDN, AFF1, ALK, BCL11B, CBFB, CEP43, CPSF6, CREBBP, DEK, ELL, EP300, ETV6, FGFR1, FLT3, GLIS2, JAK2, KMT2A, MECOM, MLLT1, MLLT3, MRTFA, MYB, MYH11, NTRK3, NUP214, NUP98, PCM1, PDGFRA, PDGFRB, PICALM, PML, PRDM16, RARA, RBM15, RPN1, RUNX1, RUNX1T1, TCF3, ZNF384

Turnaround time is 8-11 days.
Results are integrated into a final comprehensive report. If *FLT3* by PCR is ordered, it reports separately as soon as completed (approximately 5 days).

Specimen requirements

- **Bone marrow: 2-3 mL in EDTA tube**
- **Peripheral blood: 3-5 mL in EDTA tube**
- **FFPE tissue: Paraffin block**

Alternatively, send 1 H&E slide plus 10-14 unstained slides cut at 5 or more microns.

Please use positively-charged slides and 10% NBF fixative is the recommended fixative.

Do not use zinc or mercury fixatives (B5). Highly acidic or prolonged decalcification processes will not yield sufficient nucleic acid to accurately perform molecular studies.

We pride ourselves on our unparalleled Client Services team. If you have questions regarding test information, specimen requirements, turnaround times, test add-ons, or patient results, please email us at Client.Services@NeoGenomics.com or call 866.776.5907, option 3.

Note: FLT3 by PCR (via FLT3 Mutation Analysis) is available to be ordered as client-bill only, in conjunction with the Neo Comprehensive – Myeloid Disorders. It is reported separately from the Neo Comprehensive profile for the purpose of prompt therapy selection in patients with a new diagnosis of AML.

1. Puentes, R. The Importance of Comprehensive Testing in Myeloid Neoplasms: Insights from Real-World Genomics Data. NeoGenomics Laboratories; 2025. Accessed October 10, 2025. **2.** Weinberg OK, Hasserjian RP. Semin Hematol. 2019;56(1):15-21. **3.** Malcovati L, et al. Blood. 2013;122:2943-2964. **4.** Bejar R, et al. N Engl J Med. 2011;364(26):2496-2506.

NeoGenomics, Inc. is a premier cancer diagnostics company specializing in cancer genetics testing and information services. We offer one of the most comprehensive oncology-focused testing menus across the cancer continuum, serving oncologists, pathologists, hospital systems, academic centers, and pharmaceutical firms with innovative diagnostic and predictive testing to deliver timely, actionable insights that guide personalized care decisions. Headquartered in Fort Myers, FL, NeoGenomics operates a network of CAP-accredited and CLIA-certified laboratories for full-service sample processing and analysis services throughout the US and a CAP-accredited full-service sample-processing laboratory in Cambridge, England.

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