Patient ID	Patient Name		Birth Date	Sex	Age
SA00164244	TESTING, NGAML NORMAL		2001-01-01	F	22
Order Number	**Client Order Number**	**Ordering Physician**	**Report Notes**		
SA00164244	SA00164244	CLIENT,CLIENT			
Account Information		**Collected**			
C7028846 DLMP Rochester		25 Oct 2023 00:00			

AML, 11 Gene, NGS, V

Specimen Type

MCR

Peripheral blood

Pathogenic Mutations Detected

MCR

None. See below for Variants of Unknown Significance and Additional Notes. Please see the section of "Panel Gene List" below for the complete list of genes tested.

This NGS assay evaluates a subset of genes from a 47 gene myeloid neoplasm panel. If evaluation of the remaining gene regions is clinically indicated, NGSFX (Reanalysis, AML 4 or 11 Gene Panel) could be performed. This reflex analysis option is available within 6 months of the initial testing by contacting Mayo Clinic Laboratories at 800–533–1710.

Interpretation

MCR

No pathogenic genetic alteration is detected in the listed gene regions. This finding does not exclude the presence of a genetic alteration occurring at an allele frequency below our established detection limit of 2–4%, or other genetic alterations present in untested gene regions.

Variants of Unknown Significance

MCR

None

The VUS variants listed here (with approximate variant allele %) are not sufficiently characterized in the current literature and are therefore of uncertain clinical significance at this time. They are reported here for future reference in the event they become clinically significant in the light of new scientific data.

Clinical Trials

MCR

Information regarding possible clinical trials for this patient can be found at the following sites:

1). ClinicalTrials.gov:
http://clinicaltrials.gov/ct2/search/advanced
2). Mayo Clinic:
http://www.mayo.edu/research/clinical-trials
3). National Cancer Institute:
http://www.cancer.gov/clinicaltrials/search
4). The Leukemia and Lymphoma Society's Clinical Trial Support Center https://www.hematology.org/education/clinicians/clinical-trial-support-center

Additional Notes

MCR

None

Performing Site Legend

Code	Laboratory	Address	Lab Director	CLIA Certificate
MCR	Mayo Clinic Laboratories - Rochester Main Campus	200 First Street SW, Rochester, MN 55905	William G. Morice M.D. Ph.D	24D0404292

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Method Summary

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DNA is extracted from peripheral blood or bone marrow specimens. Library preparation for Next Generation Sequencing (NGS) is performed followed by probe hybridization and capture. Sequencing of the final sample library is performed on a NGS instrument. Following bioinformatic processing of the sequencing data, the sequencing results are interpreted to provide a final clinical report. Genomic alterations are called according to human genome reference build GRCh37 (hg19).

Performance characteristics of NGS panel:
Single base substitutions: accuracy >99%; reproducibility 100% (intra- and interassay); sensitivity 2–4% variant allele fraction with a minimum depth of coverage of 500X. Small insertion/deletion events (up to 500 bp): accuracy >99%; reproducibility 100% (intra- and interassay); sensitivity 2–4.99% variant allele fraction with a minimum depth of coverage of 500X. Larger single gene insertion/deletion events with sizes between ≥ 501 bp and ≤ 5 kb with a variant allele fraction ≥ 5% and minimum depth of coverage of 500X* will be reported. Variants involving multiple genes or single gene events ≥ 1 kb with variant allele fractions between 2–5% will not be reported. Events ≥ 5 kb with a variant allele fraction ≥ 5% within a single gene may be identified and if present, general information on gene, chromosome, and event type will be provided in the Additional Notes section, with suggestion for confirmatory testing. *Some genetic or genomic alterations such as very large insertion/deletion events, copy number alterations (CNA) and gene translocation events are not detected by this assay.

Disclaimer

MCR

CLINICAL DISCLAIMER

The finding of a genetic alteration does not necessarily indicate the presence of a myeloid neoplasm. Some apparent mutations classified as VUS may represent very low population frequency polymorphisms. Hematopoietic cells in some individuals may have age-related genetic alterations associated with myeloid neoplasms in the absence of a hematologic malignancy (clonal hematopoiesis of indeterminate potential, CHIP, also known as age-related clonal hematopoiesis, ARCH). In addition, patients with unexplained cytopenias may also harbor similar myeloid neoplasm-associated gene mutations (clonal cytopenias of uncertain significance, CCUS) [PMIDs: 25931582, 30482770, 31672865, and 30759825]. Distinction between CHIP or CCUS and a myeloid malignancy requires correlation with clinical, pathologic, and other laboratory findings. Prior treatment for hematologic malignancy could affect the results obtained in this assay. In particular, prior allogeneic hematopoietic stem cell transplant (HSCT) 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 (e.g. chimerism engraftment status) is not provided. This assay does not distinguish between somatic and germline alterations in analyzed gene regions, particularly with VAF near 50% or 100%. If nucleotide alterations in genes associated with germline mutation syndromes are present and there is also a strong clinical suspicion or family history of malignant disease predisposition, additional genetic testing and appropriate counseling may be indicated. This report interpretation is based on current medical and scientific literature, but clinical significance may not be completely established for all reported target gene abnormalities identified. Correlation with clinical, histopathologic and additional laboratory findings is required for final interpretation of these results. The final interpretation of results for clinical management of the patient is the responsibility of the managing physician.

TECHNICAL DISCLAIMER

The depth of sequencing coverage may be variable for some target regions, but assay performance below the minimum acceptable criteria, or for failed regions are noted. Analysis of rare (low allele frequency) polymorphisms may be problematic in some cases. A low tumor cell percentage in the sample may affect the true mutation VAF and/or sensitivity. Suboptimal-performing regions (i.e. less than the expected minimum depth of coverage) may affect analytic sensitivity for detecting lower level mutations. This is a qualitative test. The variant read

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C7028846 DLMP Rochester		25 Oct 2023 00:00			

fractions are provided for information only and represent a relative proportion of mutated alleles, but do not indicate a measure of analytical sensitivity for the given genes; assay sensitivity is as stated in the method summary. Some genetic or genomic alterations, such as very large insertion/deletion events, copy number alterations (CNA) and gene translocation events are not detected by this assay.

AML Panel Gene List

MCR

CEBPA (NM_004364.4) exon 1, DNMT3A (NM_022552.4) exons 8–23, FLT3 (NM_004119.2) exons 14–20 and intron 14, IDH1 (NM_005896.3) exons 4, 6–8, IDH2 (NM_002168.3) exons 3–4, 6–8, KIT (NM_000222.2) exons 8–11 and 17, KRAS (NM_033360.3) exons 2–4, NPM1 (NM_002520.6) exons 9–11, intron 10 start 3 bp before exon 11, NRAS (NM_002524.4) exons 2–4, RUNX1 (NM_001754.4) exons 1–9, intron 7 start 13 bp before exon 8, TP53 (NM_000546.4) exons 4–11.

Unless otherwise noted, intronic coverage surrounding exons is ±10 bp.

For some genes, the transcript IDs used in this analysis may differ from those present in cancer mutation databases or other similar sources.

Variants will be reported out using HGVS nomenclature per the documentation version available at varnomen.hgvs.org at the time of the report.

Reviewed By

MCR

Signing Pathologist: LAUREN SCHULTZ

NGAML Result

MCR

see interpretation

Received: 25 Oct 2023 11:18 **Reported:** 25 Oct 2023 11:22

Laboratory Notes

[1] 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.

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