

Patient ID SA00164235	Patient Name TESTING, NGSHM NORMAL	Birth Date 2001-01-01	Sex F	Age 22
Order Number SA00164235	Client Order Number SA00164235	Ordering Physician CLIENT,CLIENT	Report Notes	
Account Information C7028846 DLMP Rochester		Collected 25 Oct 2023 00:00		

Myeloid Neoplasms, NGS, V

Specimen Type

Peripheral blood

MCR

Indication for Test

AML

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Pathogenic Mutations Detected

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.

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Interpretation

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.

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Variants of Unknown Significance

None

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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

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

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- 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

None

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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

Report Status: Final

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Method Summary

1 MCR

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 $\geq 5\%$ 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 $\geq 5\%$ 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

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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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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.

OncoHeme Panel Gene list

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ANKRD26 (NM_014915.2) 5'UTR, start at c.-172, exons 1–4, ASXL1 (NM_015338.5) exons 10–13, BCOR (NM_001123385.1) exons 4–15, BCORL1 (NM_001184772.2) exons 1–13, BRAF (NM_004333.4), exons 11 and 15, CALR (NM_004343.3) exon 9, CBL (NM_005188.3) intron 7 last 100bp before start of exon 8, exon 8, intron 8, and exon 9, CEBPA (NM_004364.4) exon 1, CSF3R (NM_000760.3) exons 4, 13–14 and 17, DDX41 (NM_016222.2) exons 1–17, DNMT3A (NM_022552.4) exons 8–23, ELANE (NM_001972.2) exons 1–5, ETNK1 (NM_018638.4) exons 2–5, ETV6 (NM_001987.4) exons 3–8, EZH2 (NM_004456.4) exons 2–20, FLT3 (NM_004119.2) exons 14–20 and intron 14, GATA1 (NM_002049.3) exons 2 and 4, start at c.-19–30 before exon 2, GATA2 (NM_032638.4) exons 1–6, intron 4, c.1017+1 - 1017+870, IDH1 (NM_005896.3) exons 4, 6–8, IDH2 (NM_002168.3) exons 3–4, 6–8, JAK2 (NM_004972.3) exons 12–20, KDM6A (UTX) (NM_021140.3) exons 1–29, KIT (NM_000222.2) exons 8–11 and 17, KRAS (NM_033360.3) exons 2–4, MPL (NM_005373.2) exons 1–12, NF1 (NM_001042492.2), exons 1–58, NPM1 exons 9–11, intron 10 start 3 bp before exon 11, NRAS (NM_002524.4) exons 2–4, PHF6 (NM_001015877.1) exons 2–10, PPM1D (NM_003620.3) exons 1–6, PTPN11 (NM_002834.3) exons 3–4 and 12–13, RAD21 (NM_006265.2) exons 1–2, 4–7, 9–11, 13–14, intron 9 start 3 bp before exon 10, RUNX1 (NM_001754.4) exons 1–9, intron 7 start 13 bp before exon 8, SETBP1 (NM_015559.2) partial exon 4; amino acids 400–950, SH2B3 (LNK) (NM_005475.2) exon 2–8, SF3B1 (NM_012433.2) exons 13–16, SMC3 (NM_005445.3) exons 7–8, 13, 17, 19, 21, and 29, SRSF2 (NM_003016.4) exons 1–2, STAG2 (NM_001042750.1) exons 4–34, exons 12 and 17 start at -3 in preceding introns, STAT3 (NM_139276.2), exons 2–24, TERT (NM_198253.2) exons 2–16, TET2 (NM_001127208.2) exons 3–11, TP53 (NM_000546.4) exons 4–11, U2AF1 (NM_001025203.1) exons 2, 6, and 8, UBA1 (NM_003334.3) exons 2–26, WT1 (NM_024426.2) exons 1–10, and ZRSR2 (NM_005089.3) exons 1–11.

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

NGSHM Result

MCR

See Interpretation

Received: 25 Oct 2023 10:20

Reported: 25 Oct 2023 10:23

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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