MAYO CLINIC LABORATORIES

1-800-533-1710

HSCHP

High Sensitivity Clonal Hematopoiesis Panel, Next-Generation Sequencing, Blood

Patient ID	Patient Name		Birth Date	Sex	Age
321	IMPLEMENTATION, TEST T		2001-05-01	F	24
Order Number	**Client Order Number**	**Ordering Physician**	**Report Notes**		
X100522512	X100522512	UNKNOWN,PROVIDER			
Account Information		**Collected**			
C7028846 DLMP Rochester		16 Feb 2026 10:00			

HS Clonal Hematopoiesis Panel

Result

MCR

Reason for referral: Testing

No reportable sequence variants were detected within the analyzed regions of the tested genes listed in the method description.

Interpretation

MCR

These results should be interpreted in correlation with the clinico-radiological findings. Referral to the Mayo Clinic Clonal Hematopoiesis Clinic for clinical evaluation and treatment recommendations may be considered.

No clinically significant gene mutations were identified within the analyzed genes. Test results should be interpreted in the context of clinical findings and other laboratory data. If results obtained do not match other clinical or laboratory findings, please contact the laboratory. An abnormality involving the genes evaluated in this panel is not excluded since sequence variants and fusions/transcript variants involving non-targeted gene regions, and genomic abnormalities not detectable by this method (e.g. genomic copy number alterations, epigenetic changes) may be present.

Additional Information

MCR

CLINICAL TRIALS

Possible clinical trials of benefit for this patient can be found at the following sites:
1) ClinicalTrials.gov:
www.clinicaltrials.gov/ct2/search/advanced
2) Mayo Clinic: www.mayo.edu/research/clinical-trials/ 3) National Cancer Institute: www.cancer.gov/clinicaltrials/search

Specimen

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WB Whole Blood

Method

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Next generation sequencing is performed to test for the presence of a mutation within all coding regions and exon/intron boundaries of the following 37 targeted genes: ASXL1, ATM, BARD1, BCOR, BCORL1, BRAF, BRCA1, BRCA2, BRIP1, CBL, CHEK2, DNMT3A, EZH2, GATA2, IDH1, IDH2, JAK2, KRAS, NRAS, PALB2, PHF6, PPM1D, PTPN11, RAD21, RAD51C, RAD51D, RUNX1, SETBP1, SF3B1, SMC1A, SMC3, SRSF2, STAG2, TET2, TP53, U2AF1, and ZRSR2.

Variant nomenclature is based on build GRCh37 (hg19). For details about gene transcripts (RefSeq accession numbers), specific targeted regions of each gene, and additional information on this test, see www.mayocliniclabs.com (Test ID HSCHP).

Disclaimer

1 MCR

This test may not differentiate between somatic and germline alterations. Additional testing may be necessary to clarify the significance of results if there is a potential hereditary risk.

DNA variants of uncertain significance may be identified.

A negative (ie, wildtype) result does not rule out the presence of an alteration that may be present but below the limits of detection of this assay. Validation studies demonstrated a limit of detection of 0.25% variant allele frequency (VAF) for SNVs and DELINS, supported by a minimum deduplicated coverage depth of equal to or greater than 500X and a minimum DNA input of 40 ng. Variants with observed VAFs as low as 0.15% may be reported.

Point mutations and small insertion/deletion mutations will be detected in the 37 genes. This test does not detect multi-exon deletions, duplications, larger-scale genomic copy number variants, copy neutral loss of heterozygosity (LOH), or epigenetic modifications such as promoter methylation. This test does not reliably detect insertions larger than approximately 119 base pairs and deletions larger than approximately 129 base pairs.

Variant allele frequency (VAF) is the percentage of sequencing

Test Environment
LTCSEQ Template

Performing Site Legend

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

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reads supporting a specific variant divided by the total sequencing reads at that position. In somatic testing, VAF should be interpreted in the context of several factors including, but not limited to: clonal size/heterogeneity/copy number status (ploidy, gains/losses, loss of heterozygosity) and sequencing artifact/ misalignment [PMID: 27144058, PMID: 29769535].

Rare polymorphisms may be present that could lead to false-negative or false-positive results.

The presence or absence of a variant may not be predictive of response to therapy in all patients.

Test results should be interpreted in the context of clinical laboratory data. If results obtained do not match other clinical or laboratory findings, contact the laboratory for discussion. Misinterpretation of results may occur if the information provided is inaccurate and/or incomplete.

Reliable results are dependent on adequate specimen collection and processing. This test has been validated on whole blood samples; other types of samples are discouraged. Improper treatment of samples may cause PCR failure.

Released By MCR

Gang Zheng, M.D., Ph.D.

Received: 17 Feb 2026 14:44 **Reported:** 27 Feb 2026 11:57

Test Environment LTCSEQ Template

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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