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**		
SA00179438	SA00179438	CLIENT,CLIENT			
Account Information		**Collected**			
C7028846 DLMP Rochester		04 Mar 2026 00:00			

HS Clonal Hematopoiesis Panel

Result

MCR

Reason for referral: not provided

The following CLINICALLY RELEVANT variants were detected:

CLONAL HEMATOPOIESIS OF INDETERMINATE POTENTIAL

(CHIP - variant allele fractions greater than or equal to 2%)
Gene: TET2
DNA change: c.2586dup (exon 3)
Amino Acid change: p.His863Alafs*9 (p.H863Afs*9)
Variant Allele Fraction: 25.9%

CLONAL HEMATOPOIESIS

(CH - variant allele fraction less than 2%)
Gene: ASXL1
DNA change: c.1636C>T (exon 12)
Amino Acid change: p.Gln546* (p.Q546*)
Variant Allele Fraction: 0.4%

The following VARIANT OF UNCERTAIN SIGNIFICANCE variant was
detected:
Gene: BRIP1
DNA change: c.3158G>A (exon 20)
Amino Acid change: p.Cys1053Tyr (p.C1053Y)
Variant Allele Fraction: 0.3%

No other reportable sequence variants were detected within the analyzed regions of the tested gene(s) 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.

CLONAL HEMATOPOIESIS OF INDETERMINATE POTENTIAL (CHIP)

Operationally defined as the detection of somatic oncogenic driver mutations in hematopoietic stem and progenitor cells, present at a variant allele fraction of greater than or equal to 2%, with the potential to expand under selection pressures, in apparently healthy individuals, without diagnostic abnormalities in their blood counts. Clonal hematopoiesis refers to the detection of somatic oncogenic driver mutations in hematopoietic stem and progenitor cells, with the potential to expand under selection pressures, regardless of blood count abnormalities or variant allele fractions.

Somatic clones in hematopoietic stem and progenitor cells with a variant allele fraction of less than 2% are sometimes referred to as micro clonal hematopoiesis (micro CH). While these variants may not be consequential in healthy aging individuals, under dynamic selection pressures such as genotoxic exposures, they can rapidly expand with clinical consequences.

Detection of a genetic alterations in genes interrogated on this panel, usually as solitary abnormality, can also be seen with increasing age in individuals without a myeloid neoplasm, representing a clonal hematopoiesis of indeterminate potential (CHIP); this finding has been associated with an increased risk of developing a subsequent hematologic malignancy. In patients with unexplained cytopenia(s) despite adequate clinical evaluation, this finding may be consistent with clonal cytopenia(s) of undetermined significance (CCUS) [PMID: 8424163]. Clinical and pathologic correlation is suggested in this setting.

1) TET2 c.2586dup (p.H863Afs*9) (exon 3)

TET2 encodes methylcytosine dioxygenase, a tumor suppressor that plays a role in DNA methylation [PMID:22240200, PMID: 19372391, PMID: 25510268]. Loss of function mutations are common in myeloid and lymphoid malignancies [PMID: 24220273, PMID: 26099018, PMID: 27848178]. TET2 mutations have also been detected in individuals with clonal hematopoiesis with no evidence of hematologic disease [PMID: 23001125].

Pathogenic somatic alterations in TET2 are frequently associated with clonal hematopoiesis in the context of normal aging or exposure to radiation or chemotherapy.

CLONAL HEMATOPOIESIS (CH)

The operational cutoff for clonal hematopoiesis of indeterminate

Test Environment LTCSE Online

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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potential is greater than or equal to 2% variant allele fraction given the inability for conventional NGS assays to accurately detect CH variants below that number. The current assay, with error corrected sequencing, is designed to detect micro CH clones, with the lower reportable range of the assay being 0.15% variant allele fraction.

1) ASXL1 c.1636C>T (p.Q546*) (exon 12)

ASXL1 encodes Asxl1, a member of the Asxl family of proteins involved in the recruitment of chromatin remodeling and histone modifying enzymes to genetic loci. Asxl1 may be found as a member of various transcriptional complexes, and its function has been shown to be context-dependent; therefore, Asxl1 may activate oncogenes or repress tumor suppressor expression [PMID:23736028].

Pathogenic somatic alterations in ASXL1 are frequently associated with clonal hematopoiesis in the context of normal aging or exposure to radiation or chemotherapy.

VARIANT OF UNCERTAIN SIGNIFICANCE

One variant of uncertain significance was detected. The variant was not observed at significant frequency in population germline/cancer somatic variant databases nor predicted to be functionally significant based on variant type/in silico algorithm results. Additionally, there was no convincing published evidence of cancer association. Therefore, the clinical significance of the detected variant is unknown.

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

REFERENCE TRANSCRIPTS

Sequence variant nomenclature is based on the following RefSeq accession numbers (build GRCh37 (hg19)):ASXL1 NM_015338, BRIP1 NM_032043 and TET2 NM_001127208.

Specimen MCR

WB Whole Blood

Method MCR

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.

Test Environment LTCSF Template

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Variant allele frequency (VAF) is the percentage of sequencing 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: 04 Mar 2026 15:34 **Reported:** 04 Mar 2026 15:49

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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