

## Overview

### Useful For

Aiding in establishing diagnosis, refining prognosis, and potentially identifying targeted therapies for the optimal management of patients with chronic or low-grade B-cell lymphoid neoplasms

### Genetics Test Information

This test includes next-generation sequencing to evaluate the following 25 genes and select intronic regions: *ATM*, *BCL2*, *BIRC3*, *BRAF*, *BTG1*, *BTK*, *CCND1*, *CDKN2A*, *CXCR4*, *DDX3X*, *EZH2*, *FBXW7*, *KLF2*, *KRAS*, *MAP2K1*, *MYD88*, *NOTCH1*, *NOTCH2*, *NRAS*, *PIK3CA*, *PLCG2*, *SF3B1*, *TNFAIP3*, *TP53*, and *XPO1*. For a list of genes and exons targeted by this test, see [Targeted Genes Interrogated by MayoComplete Chronic Lymphoid Neoplasms Next-Generation Sequencing](#).

### Special Instructions

- [Hematopathology Patient Information](#)
- [Targeted Genes Interrogated by MayoComplete Chronic Lymphoid Neoplasms Next-Generation Sequencing](#)

### Highlights

This test utilizes next-generation sequencing for the detection of somatic mutations with diagnostic, prognostic, or therapeutic value in a set of genes associated with chronic or clinically "low grade" lymphoid neoplasms.

### Method Name

Next-Generation Sequencing (NGS)

### NY State Available

Yes

## Specimen

### Specimen Type

Varies

### Shipping Instructions

Whole blood, bone marrow aspirate, and body fluid specimens must arrive within 14 days of collection.

### Specimen Required

Submit only 1 of the following specimens:

**Specimen Type:** Bone marrow aspirate

**Container/Tube:**

**Preferred:** Lavender or pink top EDTA) or yellow top (ACD)

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**Acceptable:** Green top (sodium heparin)

**Specimen Volume:** 2 mL

**Collection Instructions:**

1. Invert several times to mix bone marrow.
2. Send bone marrow specimen in original tube. **Do not aliquot.**
3. Label specimen as bone marrow.

**Specimen Stability Information:** Ambient (preferred) 14 days/Refrigerate

**Specimen Type:** Whole blood

**Container/Tube:**

**Preferred:** Lavender or pink top (EDTA) or yellow top (ACD)

**Acceptable:** Green top (sodium heparin)

**Specimen Volume:** 3 mL

**Collection Instructions:**

1. Invert several times to mix peripheral blood.
2. Send whole blood specimen in original tube. **Do not aliquot.**
3. Label specimen as peripheral blood.

**Specimen Stability Information:** Ambient (preferred) 14 days/Refrigerate

**Specimen Type:** Paraffin-embedded tissue

**Container/ Tube:** Paraffin block

**Collection Instructions:**

1. Send 1 representative slide stained with hematoxylin and eosin
2. Minimum amount of tumor nuclei is 20%
3. Required amount of tissue area is at least 25 mm<sup>2</sup>
4. Tissue should be fixed in 10% neutral-buffered formalin. Other fixatives are not acceptable.
5. Decalcified specimens (eg, bone marrow core biopsies) are not acceptable.

**Specimen Stability Information:** Ambient

**Specimen Type:** Tissue slide

**Slides:** 10 unstained slides

**Container/ Tube:** Transport in plastic slide holders.

**Collection Instructions:**

1. Send 10 unstained, nonbaked slides with 5-micron thick sections of tissue and 1 representative slide stained with hematoxylin and eosin.
2. Minimum amount of tumor nuclei is 20%
3. Required amount of tissue area is at least 25 mm<sup>2</sup>
4. Tissue should be fixed in 10% neutral-buffered formalin. Other fixatives are not acceptable.
5. Decalcified specimens (eg, bone marrow core biopsies) are not acceptable.

**Specimen Stability Information:** Ambient

**Specimen Type:** Frozen tissue

**Container/Tube:** Plastic container

**Specimen Volume:** 100 mg

**Collection Instructions:** Freeze tissue within 1 hour of collection

**Specimen Stability Information:** Frozen

**Specimen Type:** Body fluid

**Container/Tube:** Sterile container

**Specimen Volume:** 5 mL

**Specimen Stability Information:** Refrigerated 14 days/Frozen

**Specimen Type:** Extracted DNA

**Container/Tube:** 1.5- to 2-mL tube

**Specimen Volume:** Entire specimen

**Collection Instructions:**

1. Label specimen as extracted DNA and source of specimen.
2. Indicate volume and concentration of DNA on label.

**Specimen Stability Information:** Frozen (preferred)/Refrigerated/Ambient

## Forms

[Hematopathology Patient Information](#) (T676)

## Specimen Minimum Volume

Whole blood, bone marrow aspirate, body fluid: 1 mL; Frozen tissue: 50 mg; Extracted DNA: 100 microliters (mL) at 20 ng/mL

## Reject Due To

Gross hemolysis	Reject
Gross lipemia	OK
Specimens that have been decalcified (all methods) Bone marrow core biopsies Paraffin shavings Fixatives other than 10% neutral-buffered formalin for paraffin-embedded tissue Moderately to severely clotted bone	Reject

marrow aspirate	
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**Specimen Stability Information**

Specimen Type	Temperature	Time	Special Container
Varies	Varies	14 days	

**Clinical & Interpretive**

**Clinical Information**

This test is intended to evaluate a targeted set of genes involved in a heterogeneous group of chronic lymphoid neoplasms that includes chronic lymphocytic leukemia (CLL) and various low-grade B-cell lymphomas. The test includes actionable targets to aid in the differential diagnosis of low-grade B-cell lymphomas (eg, hairy cell leukemia, lymphoplasmacytic lymphoma, splenic marginal zone lymphoma), predict prognosis (eg, risk stratification in CLL), and evaluate therapeutic options or efficacy (eg, ibrutinib therapy in CLL, EZH2 [enhancer of zeste homolog 2] inhibitors in follicular lymphoma). Genomic analysis by next-generation sequencing is complementary to the standard evaluation in the classification and management of patients with chronic lymphoid neoplasms.

**Reference Values**

An interpretive report will be provided.

**Interpretation**

Genomic variants detected by this test will be documented in a detailed laboratory-issued report. This report will contain information regarding the detected alterations and their associations with prognosis or possible therapeutic implications in chronic lymphoid neoplasms. The information in the clinical report may be used by the patient’s clinician to help guide decisions concerning management. Final interpretation of next-generation sequencing results requires correlation with all relevant clinical, pathologic, and laboratory findings and is the responsibility of the managing clinician.

**Cautions**

This test is a targeted next-generation sequencing (NGS) panel assay that encompasses 25 genes with variable full exon, partial region (including select intronic or noncoding regions), or hot spot coverage (depending on specific genetic locus). Therefore, this test will not detect other genetic abnormalities in genes or regions outside the specified target areas. The test detects single-base substitutions (ie, point mutations), as well as small insertion or deletion type events. This test is not configured to detect structural genomic rearrangements (ie, translocations), gene fusions, copy number alterations, or large-scale (segmental chromosome region) deletions and other complex genomic changes.

This assay does not distinguish between somatic and germline alterations in analyzed gene regions, particularly with variant allele frequencies near approximately 50% or 100%. If nucleotide alterations in genes associated with germline mutation syndromes are present and there is a strong clinical suspicion or family history of malignant disease predisposition, additional genetic testing and appropriate counseling may be indicated. Some apparent mutations classified as variants of undetermined significance may represent rare or low population frequency polymorphisms.

Prior treatment for hematologic malignancy could affect the results obtained in this assay. Particularly, a prior allogeneic hematopoietic stem cell transplant may cause difficulties in either resolving somatic or polymorphic alterations or assigning variant calls correctly to donor and recipient fractions, if pertinent clinical or laboratory information (eg, chimerism engraftment status) is not provided.

Inadequate samples (eg, insufficient DNA quantity or quality) will preclude further testing and will be noted in the interpretive report. For formalin-fixed, paraffin-embedded specimens, NGS testing should not be pursued if the quality of the biopsy specimen is poor (eg, limited sample size, presence of extensive necrosis or fibrosis), or the target tumor cell population is low (<20%).

### Clinical Reference

1. Swerdlow S, Campo E, Harris NL, et al, eds. WHO Classification of Tumours of Haematopoietic and Lymphoid Tissues. 4th ed. IARC Press; 2017. WHO Classification of Tumours, Vol 2
2. Onaindia A, Medeiros LJ, Patel KP. Clinical utility of recently identified diagnostic, prognostic, and predictive molecular biomarkers in mature B-cell neoplasms. *Mod Pathol*. 2017;30(10):1338-1366. doi:10.1038/modpathol.2017.58
3. Jajosky AA, Havens NP, Sadri N, et al. Clinical utility of targeted next-generation sequencing in the evaluation of low-grade lymphoproliferative disorders. *Am J Clin Pathol*. 2021;156(3):433-444
4. Davis AR, Stone SL, Oran AR, et al. Targeted massively parallel sequencing of mature lymphoid neoplasms: assessment of empirical application and diagnostic utility in routine clinical practice. *Mod Pathol*. 2021;34(5):904-921
5. Stewart JP, Gazdova J, Darzentas N, et al. Validation of the EuroClonality-NGS DNA capture panel as an integrated genomic tool for lymphoproliferative disorders. *Blood Adv*. 2021;5(16):3188-3198
6. Treon SP, Cao Y, Xu L, Yang G, Liu X, Hunter ZR. Somatic mutations in MYD88 and CXCR4 are determinants of clinical presentation and overall survival in Waldenstrom macroglobulinemia. *Blood*. 2014;123(18):2791-2796. doi:10.1182/blood-2014-01-550905
7. Morin RD, Arthur SE, Assouline S. Treating lymphoma is now a bit EZ-er. *Blood Adv*. 2021;5(8):2256-2263
8. Thangavadivel S, Byrd JC. Gly101Val BCL2 Mutation: One step closer to understanding Venetoclax resistance in CLL. *Cancer Discov*. 2019;9(3):320-322. doi:10.1158/2159-8290.CD-19-0029
9. Lee J, Wang YL. Prognostic and predictive molecular biomarkers in chronic lymphocytic leukemia. *J Mol Diagn*. 2020;22(9):1114-1125
10. Liebers N, Roider T, Bohn JP, et al. BRAF inhibitor treatment in classic hairy cell leukemia: a long-term follow-up study of patients treated outside clinical trials. *Leukemia*. 2020;34(5):1454-1457

### Performance

#### Method Description

This is a target-enriched next-generation sequencing (NGS) panel. DNA is extracted from validated specimen sources including, but not limited to, peripheral blood, bone marrow aspirate, and formalin-fixed paraffin embedded tissues. Library preparation for 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). (Unpublished Mayo method)

**PDF Report**

No

**Day(s) Performed**

Monday through Friday

**Report Available**

16 to 21 days

**Specimen Retention Time**

Bone marrow aspirate/whole blood: 2 weeks; DNA: 3 months; Tissue: 1 month; FFPE tissue: Unused portions of blocks will be returned to the client. Unstained slides/body fluid: Not retained

**Performing Laboratory Location**

Rochester

**Fees & Codes**
**Fees**

- Authorized users can sign in to [Test Prices](#) for detailed fee information.
- Clients without access to Test Prices can contact [Customer Service](#) 24 hours a day, seven days a week.
- Prospective clients should contact their account representative. For assistance, contact [Customer Service](#).

**Test Classification**

This test was developed and its performance characteristics determined by Mayo Clinic in a manner consistent with CLIA requirements. It has not been cleared or approved by the US Food and Drug Administration.

**CPT Code Information**

81450

**LOINC® Information**

Test ID	Test Order Name	Order LOINC® Value
NGCLN	Chronic Lymphoid Neoplasms, NGS, V	104238-1

Result ID	Test Result Name	Result LOINC® Value
MP065	Specimen Type	31208-2
MP066	Indication for Test	42349-1
618485	NGCLN Result	No LOINC Needed
618486	Pathogenic Mutations Detected	82939-0
618487	Interpretation	69047-9

618489	Variants of Unknown Significance	93367-1
618490	Additional Information	48767-8
618488	Clinical Trials	82786-5
618491	Method Summary	85069-3
618492	Disclaimer	62364-5
618493	Panel Gene List	36908-2
618494	Reviewed By	18771-6