

# MayoComplete B-Cell Lymphoma, Next-Generation Sequencing, Varies

**Test ID:** NGBCL

## Useful for:

Aiding in establishing diagnosis, refining prognosis, and potentially identifying targeted therapies for the optimal management of patients with B-cell lymphomas

## Genetics Information

This test includes next-generation sequencing to evaluate the following 45 genes and select intronic regions: ARAF, ARID1A, ATM, B2M, BCL2, BIRC3, BRAF, BTG1, BTK, CARD11, CCND1, CCND3, CD79A, CD79B, CDKN2A, CREBBP, CSF1R, CXCR4, DDX3X, EP300, EZH2, FBXW7, FOXO1, ID3, KLF2, KMT2D, KRAS, MAP2K1, MEF2B, MYD88, NOTCH1, NOTCH2, NRAS, NSD2, PIK3CA, PIM1, PLCG2, PRDM1, PTEN, SF3B1, STAT6, TCF3, TNFAIP3, TNFRSF14, TP53, and XPO1. For a list of genes and exons targeted by this test, see [Targeted Genes Interrogated by MayoComplete B-cell Lymphoma 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 low-grade and aggressive B-cell non-Hodgkin lymphomas

## Methods:

Next-Generation Sequencing (NGS)

## Reference Values:

An interpretive report will be provided.

## Specimen Requirements:

**Submit only 1 of the following specimens:**

**Specimen Type:** Bone marrow aspirate

**Container/Tube:**

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

**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 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(2)
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(2)
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

**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

## Specimen Stability Information:

Specimen Type	Temperature	Time
Varies	Varies	14 days

## Cautions:

This test is a targeted next-generation sequencing (NGS) panel assay that encompasses 45 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 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%).

## CPT Code:

81450

**Day(s) Performed:** Monday through Friday

**Report Available:** 16 to 21 days

## Questions

Contact Connie Penz, Laboratory Resource Coordinator at 800-533-1710.