MAYO CLINIC LABORATORIES

1-800-533-1710

CXLPL

CXCR4 Mutation in B-cell Lymphoma

Patient ID	Patient Name		Birth Date	Gender	Age
SA00105296	TSTINGRNV, CXLPLMOLHEME		1984-09-11	M	33
Order Number	**Client Order Number**	**Ordering Physician**	**Report Notes**		
SA00105296	SA00105296	CLIENT, CLIENT			
Account Information		**Collected**			
C7028846 DLMP Rochester		15 Mar 2018 00:00			

CXCR4 Mutation in B-cell Lymphoma

Specimen Type

MCR

Bone marrow

CXLPL Result

MCR

see interpretation

Final Diagnosis

[1] MCR

Bone marrow, CXCR4 mutation analysis :

Negative. No pathogenic variant is detected in the region tested in CXCR4.

A negative result does not exclude the presence of a hematologic neoplasm. In lymphoplasmacytic lymphoma/ Waldenstrom's macroglobulinemia (LPL/WM), WHIM-like somatic mutations (C-terminus nonsense/frameshift mutations) of CXCR4 have been reported in approximately 30% of cases, commonly coexisting with a MYD88 L265P mutation. A MYD88-L265P/ CXCR4-WT (wild type) molecular signature is associated with similar overall survival, higher response to ibrutinib in previously treated patients, more adenopathy, and similar or lower bone marrow disease burden and serum IgM levels in comparison to those with co-occurring MYD88-L265P/CXCR4-WHIM mutations. In contrast, rare cases of apparent LPL with MYD88-WT/CXCR4-WT molecular signature have demonstrated inferior overall survival, lower response to ibrutinib therapy in previously treated patients, and lower bone marrow disease burden and serum IgM levels in comparison to those harboring a MYD88 L265P mutation (Treon et al., 2014, 24553177; 2015, 25853747; Poulain et al., 2016, 26490317). Interpretation of the result in the context of all available clinical laboratory and morphologic information is recommended.

Method Summary - The C-terminus end of CXCR4 (NM_003467.2, c.898–1059) is amplified from extracted genomic DNA by polymerase chain reaction (PCR), followed by Sanger sequencing and capillary electrophoresis analysis. Review of the sequence data is performed using a combination of automated calls and manual inspection (Unpublished Mayo method). The hotspot mutation c.1013 C>A/G (p.S338X) is examined using bridge nucleic acids (BNA) clamping-enhanced Sanger sequencing with an analytic sensitivity of 1%. All other genetic variants in the test region are examined by regular Sanger sequencing with the analytic sensitivity of 15–20%.

Signing Pathologist: BENJAMIN BAILEY

Received: 16 Mar 2018 14:27 **Reported:** 16 Mar 2018 14:51

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.

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