MAYO CLINIC LABORATORIES

1-800-533-1710

CXLPL

CXCR4 Mutation in B-cell Lymphoma

Patient ID	Patient Name		Birth Date	Gender	Age
SA00105295	TESTINGRNV, CXLPLMOLHEME		1984-01-01	M	34
Order Number	**Client Order Number**	**Ordering Physician**	**Report Notes**		
SA00105295	SA00105295	CLIENT, CLIENT			
Account Information		**Collected**			
C7028846 DLMP Rochester		15 Mar 2018 00:00			

CXCR4 Mutation in B-cell Lymphoma

Specimen Type

MCR

Peripheral blood

CXLPL Result

MCR

see interpretation

Final Diagnosis

[1] MCR

Peripheral blood, CXCR4 mutation analysis :

Positive. The following pathogenic nonsense mutation was detected in CXCR4: g.136872485G>C, c.1013C>G,

This translates into the following predicted protein change: p.Ser338*

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-WHIM molecular signature is associated with similar overall survival, lower response to ibrutinib in previously treated patients, similar or higher bone marrow disease burden and serum IgM levels, and less adenopathy in comparison to those with a MYD88-L265P/CXCR4-WT (wild type) molecular signature. CXCR4 WHIM-like somatic mutations have also been described in approximately 6–20% IgM-MGUS and a small percentage of splenic marginal zone lymphoma, nodal marginal zone lymphoma and rarely, diffuse large B-cell lymphoma (Treon et al., 2014, 24553177; 2015, 25853747; Poulain et al., 2016, 26490317; Roccaro et al., 2014, 24711662; Cao et al., 2017, 28280994). Interpretation of the result in 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 Review of the sequence data is performed using a combination of automated calls and manual inspection (Unpublished Mayo method).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 14:28 **Reported:** 16 Mar 2018 14:50

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
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