MAYO CLINIC LABORATORIES

1-800-533-1710

BCLL

IGH Somatic Hypermutation in B-CLL

Patient ID	Patient Name		Birth Date	Gender	Age
SA00100555	TESTINGRNV, REPORT		1999-11-11	M	17
Order Number	**Client Order Number**	**Ordering Physician**	**Report Notes**		
SA00100555	SA00100555	CLIENT, CLIENT			
Account Information		**Collected**			
C7028846 DLMP Rochester		08 Nov 2017 06:00			

IGH Somatic Hypermutation in B-CLL

BCLL Result

MCR

see interpretation

Specimen Type

MCR

Peripheral blood

Final Diagnosis

[1] MCR

Peripheral blood, IGH somatic hypermutation analysis:

A mutated IGH V rearrangement was identified. The level of mutation identified was 5%.

The IGH V allele identified was 3–21*03.

VH3–21 family rearrangements have been associated with relatively adverse clinical outcome regardless of somatic mutation status (Reference: Zent CS, et al. Leuk Lymphoma 2006;47(9):1738–1746).

Somatic hypermutation of the immunoglobulin heavy chain gene variable region (IGH-V) status is a recognized prognostic marker in chronic lymphocytic leukemia. Mutated CLL is defined by the presence of >2% IGH-V somatic mutation (or <98% identity to the closest germline sequence) and is independently associated with a relatively favorable prognosis. In contrast, unmutated IGH-V status, defined as ≤2% somatic mutation (or ≥98% germline sequence identity) is associated with relatively adverse prognosis (Oscier D et al, 2002, 12149195). Correlation of these results with clinical, pathologic and other pertinent laboratory data is required for final interpretation.

Signing Pathologist: Melissa Tricker-Klar

ADDITIONAL INFORMATION

Method Summary - IGH V-region (IGHV) somatic mutation analysis: DNA is extracted and IGH gene rearrangements are amplified by PCR method using leader and/or FR1 forward primers. Next generation sequencing of the PCR product clonal IGH variable (IGHV) region is performed. Sequences of functional IGHV rearrangements are compared to a germline IGH sequence database to determine the closest IGHV gene exon and percent nucleobase identity. Mutated IGHV status is assigned when the analyzed clonal sequence is greater than 2% different from the germline reference and unmutated status is defined as 2% or less deviation from the referene.

Received: 08 Nov 2017 16:13 **Reported:** 08 Nov 2017 17:16

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