



<u>Procedure</u>	<u>Result</u>	<u>Units</u>	<u>Ref Interval</u>	<u>Accession</u>	<u>Collected</u>	<u>Received</u>	<u>Reported/Verified</u>
BCL2 FISH Result	Negative f			18-360-900043	26-Dec-18 13:37:00	26-Dec-18 13:37:00	26-Dec-18 13:46:24
BCL2 FISH Reference Number	S18-123			18-360-900043	26-Dec-18 13:37:00	26-Dec-18 13:37:00	26-Dec-18 13:46:24
BCL2 FISH Source	Tissue			18-360-900043	26-Dec-18 13:37:00	26-Dec-18 13:37:00	26-Dec-18 13:46:24
Total Cell Count	250			18-360-900043	26-Dec-18 13:37:00	26-Dec-18 13:37:00	26-Dec-18 13:46:24
Scoring Method	Computer Assisted			18-360-900043	26-Dec-18 13:37:00	26-Dec-18 13:37:00	26-Dec-18 13:46:24

26-Dec-18 13:37:00 BCL2 FISH Result:

Controls were run and performed as expected. This result has been reviewed and approved by Tracy George, M.D.

26-Dec-18 13:37:00 BCL2 FISH Result:

METHODOLOGY AND TEST INFORMATION:

IGH-BCL2 fluorescent in situ hybridization (FISH) analysis is designed to detect the IGH-BCL2 fusion associated with t(14;18)(q32;q21). Differentially labeled fluorescent probes directed against IGH and BCL2 were used (Abbott Molecular).

Fused signals within a cell are considered abnormal signal patterns and are consistent with IGH-BCL2 fusion. If a sample contains single fused signals seen in 21 percent or more of the cells, or two or more fused signals in 6 percent or more of the cells evaluated, it is considered a positive result.

IGH-BCL2 fusion is seen in a variety of B-cell lymphomas including follicular lymphomas, diffuse large B-cell lymphomas (DLBCL), and "double hit" or "triple hit" lymphomas. Results should be correlated with clinical, morphologic and immunophenotypic data.

Fluorescence in situ hybridization (FISH) analysis was performed on a section from a paraffin-embedded tissue block. The area(s) for analysis were selected by histopathologic review of a matching hematoxylin and eosin stained section.

Controls performed appropriately.

Test developed and characteristics determined by ARUP Laboratories. See Compliance Statement A: aruplab.com/CS.

* Abnormal, # = Corrected, C = Critical, f = Footnote, H = High, L = Low, t = Interpretive Text, @ = Reference Lab