



<u>Procedure</u>	<u>Result</u>	<u>Units</u>	<u>Ref Interval</u>	<u>Accession</u>	<u>Collected</u>	<u>Received</u>	<u>Reported/</u> <u>Verified</u>
DDIT3 FISH Result	Negative f			18-346-900108	12-Dec-18 09:56:00	12-Dec-18 09:56:00	18-Dec-18 17:41:30
DDIT3 FISH Reference Number	123			18-346-900108	12-Dec-18 09:56:00	12-Dec-18 09:56:00	18-Dec-18 17:41:30
DDIT3 FISH Source	Other			18-346-900108	12-Dec-18 09:56:00	12-Dec-18 09:56:00	18-Dec-18 17:41:30
Total Cell Count	50			18-346-900108	12-Dec-18 09:56:00	12-Dec-18 09:56:00	18-Dec-18 17:41:30
Scoring Method	Manual			18-346-900108	12-Dec-18 09:56:00	12-Dec-18 09:56:00	18-Dec-18 17:41:30

12-Dec-18 09:56:00 DDIT3 FISH Result:

This result has been reviewed and approved by Joshua F. Coleman, M.D. Controls performed as expected.

12-Dec-18 09:56:00 DDIT3 FISH Result:

METHODOLOGY AND TEST INFORMATION:

Fluorescence in situ hybridization (FISH) analysis was performed on a section from a paraffin embedded tissue block using differentially labeled fluorescent probes targeting the upstream (5') and downstream (3') flanking regions of the DDIT3 (CHOP) gene (Abbott Molecular). Cells were evaluated from regions of tumor identified on histopathologic review of a matching hematoxylin and eosin stained section. Controls performed appropriately.

This test is designed to detect rearrangements involving the DDIT3 (CHOP) gene, but it does not identify a specific partner gene. An abnormal signal pattern seen in 25 percent or more of the tumor cells evaluated is considered a positive result.

Identification of a rearrangement of the DDIT3 gene locus is useful for distinguishing myxoid liposarcoma/round cell liposarcoma from other soft tissue tumors in the differential diagnosis.

Reference:

Fletcher DM, Bridge JA, Hogendoorn P, Mertens F, Eds. WHO Classification of Tumours of Soft Tissue and Bone, 4th Ed. Lyon, France: IARC, 2013.

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