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HLID#: PATIENT NAME:
PATIENT ID#: DOB : SEX:
NPI: ORDERING PHYSICIAN:
SPECIMEN TYPE: Bone Marrow Aspirate
COLLECTION DATE: RECEIPT DATE:
REPORT DATE: ICD-9: UNITS: 1 FISH – MM panel
CLINIC ID#: ACCOUNT:
NUMBER OF PROBES/HYBRIDIZATIONS : A-8/2
CPT:

Patient XY, HLID#

Specimen Type: CD138+ enriched cell population from Bone Marrow Aspirate

Clinical History/Indications: A xx year old male with a listed clinical history of Multiple Myeloma. Flow cytometric studies revealed the presence of **0.2%** monoclonal plasma cells (see separate report). Cytogenetic studies reveal a normal karyotype (see separate report). Previous FISH studies without plasma cell enrichment were normal.

FISH (fluorescence in situ hybridization) Result: ABNORMAL

evidence of gain of 11q or trisomy 11
gain of IGH (14q32) or presence of alternate IGH gene rearrangement
gain of FGFR3 (4p16)

nuc ish (IGHx2-3),(FGFR3x2-3)[38/200]/(MLLx3)[53/200]/(D13S319x2),(TP53x2,CEP17x2)[200]

Interpretation:

- **These findings reveal the presence of an aberrant CD138+ plasma cell population harboring a gain of 4p (or trisomy 4), 11q (or trisomy 11) as well as a gain of 14q32 (or alternate IGH translocation).**
- *In order to further investigate the presence of an alternate IGH gene rearrangement, additional analysis using the CCND1/IGH probe set for t(11;14) and the MAF/IGH probe set for t(14;16) may be used since both translocation have been reported in Multiple Myeloma (please contact HematoLogics for add-on testing).*
- Clinical and hematopathology information is required for interpretation.

CD138+ plasma cells were isolated by magnetic-activated cell sorting using anti-CD138 immunobeads and a magnetic-activated cell sorter (MACS, Miltenyi Biotec) separation system. Interphase FISH (fluorescent in situ hybridization) was performed to assess this specimen for the presence of cytogenetic aberrations in the non-dividing cell population. Hybridization was performed with the MLL gene probe (11q23), D13S319 (13q14) and TP53 (17p13.1) to look for deletion/loss of these regions or chromosomes and the FGFR3/IgH probe set to look for the t(4;14) or alternate IgH gene rearrangement. The 13q34 probe was run as the control for D13S319 and to distinguish between deletion 13q and monosomy 13.

Please note, that this analysis cannot be used for quantification purposes of the aberrant cell population since only CD138+ purified cells were analyzed.

A total of 200 interphase cells were analyzed for each probe; of these, the MLL gene probe showed 3 hybridization signals in 26.5% of cells examined, consistent with a gain of 11q or trisomy 11. The FGFR3/IGH probe set revealed 2-3 hybridization signals for both loci in 19% of cells examined, consistent with either an alternate IGH gene rearrangement or trisomy 14 and trisomy 4/4p. All other analyses fell within normal limits for this specimen type.

FISH Analysis Summary:

Number of Cells Analyzed: 200

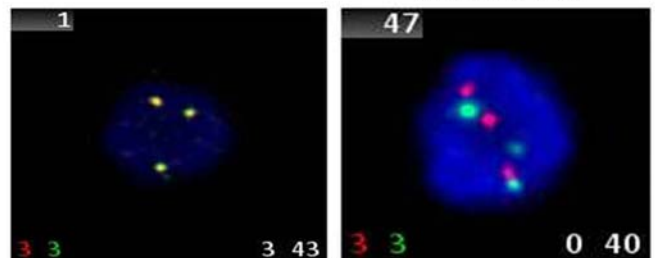
Cells Analyzed: Interphase

Probes Utilized: TP53/Cen17, FGFR3/IGH, D13S319/13q34, MLL Source and Lot Number: Abbott, 425332, 423402, 423499, 425265

Control Probe Utilized: database

MLL (11q23) break-apart
3F [53/200]: 26.5% gain of 11q23

IGH (G) /FGFR3 (R):
2-3R2-3G [38/200]:
19% gain of 4p16 and IGH (14q32)
or alternate rearrangement



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