

Patient Name: Sample Patient
D.O.B. & Gender:
Collection Date: 09/02/2014
Received Date: 09/04/2014
Report Date: 09/04/2014
Specimen Type: Bone Marrow BM-000-000

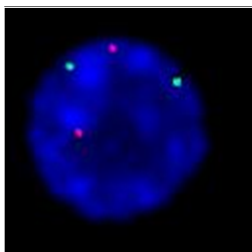
Ordering Physician:
Ordering Facility:
Referring Physician:
VantagePoint ID #:
VantagePoint Case #:
Medical Record #:

Fluorescence *in situ* Hybridization (FISH) Report Myelodysplastic Syndrome (MDS) Panel by FISH

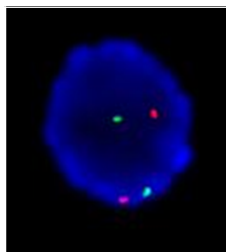
Clinical Indication: 72 year old Female with Anemia

Results: Negative by FISH testing.

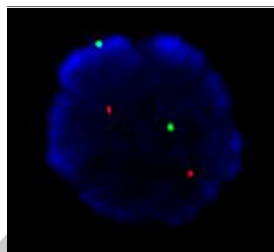
Note: The following probes were used to detect chromosomal aberrations: -5/5q-, -7/7q-, trisomy 8, and 20q-.



FSG14-000956-5q



FSG14-000956-7q



FSG14-000956-cep8-20q

Probe Name	Result	ISCN 2013
Chromosome 5: -5/5q-	Negative by FISH testing.	nuc ish(D5S23,D5S721,CSFR1)x2[200]
Chromosome 7: -7/7q-	Negative by FISH testing.	nuc ish(D7Z1,D7S486)x2[200]
Chromosome 8: trisomy 8	Negative by FISH testing.	nuc ish(D8Z2x2)[200]
Chromosome 20: 20q-	Negative by FISH testing.	nuc ish(D20S108x2)[200]

Interpretation: No chromosomal abnormalities were identified utilizing the probes in this MDS FISH panel assay. FISH analysis was performed on this patient's specimen using Vysis® DNA probes for the MDS profile. Two hundred interphase nuclei were examined for each probe and revealed that the signal pattern obtained did not differ significantly from the normal controls. No therapeutic action should be taken based solely upon these results. Genetic changes other than those assayed cannot be ruled out on the basis of this testing. Correlation with clinical, hematopathological and cytogenetic findings is recommended for a complete interpretation of the results.

Methodology: Interphase FISH is performed on cellular preparations which are adhered onto a glass slide. Appropriate controls are processed with each run of patient samples. The resulting specimen DNA is denatured to its single stranded form and then allowed to hybridize with the fluorescent-labeled DNA probes from Abbott Molecular, Inc., specific to the loci which identify the chromosomal aberrations -5/5q-, -7/7q-, trisomy 8, and 20q-. The slides are washed and then counterstained to identify the nuclei. Hybridization of the DNA probes is viewed using a fluorescence microscope. Enumeration of the signals is performed on a minimum of 200 nuclei.

Intended Use: It is indicated for use as an adjunct to standard cytogenetic analysis for identifying and enumerating the chromosomal aberrations associated with Myelodysplastic syndrome (MDS), via FISH technology in interphase nuclei. It is not intended to be used as a stand-alone assay for test reporting.

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Specimen Type: Bone Marrow BM-11-111 #1	Medical Record #:

Comments: Reference Range:
5q deletion:
Negative: Less than or equal to 3.53% of cells with 2G/10 signal pattern in 200 cells scored (7/200 cells).
Positive (Deletion): Greater than 3.53% of cells with 2G/10 signal pattern in 200 cells scored.
Monosomy 5:
Negative: Less than or equal to 0.94% of cells with 1G/10 signal pattern in 200 cells scored (2/200 cells).
Positive (Monosomy): Greater than 0.94% of cells with 1G/10 signal pattern in 200 cells scored.
7q deletion:
Negative: Less than or equal to 3.30% of cells with 2G/10 signal pattern in 200 cells scored (7/200 cells).
Positive (Deletion): Greater than 3.30% of cells with 2G/10 signal pattern in 200 cells scored.
Monosomy 7:
Negative: Less than or equal to 1.53% of cells with 1G/10 signal pattern in 200 cells scored (3/200 cells).
Positive (Deletion): Greater than 1.53% of cells with 1G/10 signal pattern in 200 cells scored.
Trisomy 8:
Negative: Less than or equal to 2.07% of cells with 3O signal pattern in 200 cells scored (4/200 cells).
Positive (Trisomy): Greater than 2.07% of cells with 3O signal pattern in 200 cells scored.
Deletion 20q:
Negative: Less than or equal to 5.10% of cells with 1O signal pattern in 200 cells scored (10/200 cells).
Positive (Deletion): Greater than 5.10% of cells with 1O signal pattern in 200 cells scored.

Electronically Signed by:



Rubio R. Punzalan, M.D., Ph.D.
Pathologist

END OF REPORT