MEDGENOME

3rd Floor, Narayana Netralaya Building, Narayana Health City,
#258/A, Bommasandra, Hosur Road, Bengaluru, Karnataka 560099,
India.
T : +91(0)80 67154990/991 W : www.medgenome.com

Fluorescent In Situ Hybridization (FISH) REPORT: FISH for Multiple Myeloma with reflex Common IGH Breakapart

Patient Name	Kathirgamathamby Anandarajah	**Requesting Clinician**	Dr. Mahendra Perera
Gender	Male	**Hospital Information**	Aegle Omics Private Limited
Age/Date of Birth	71 Years	**Sample Source**	Peripheral blood in sodium heparin.
Sample ID	9030906	**Samples Collected(Date & Time)**	11/03/2025
Order ID(s)	1236038	**Samples Received(Date & Time)**	20-03-2025 11:00:00
Clinical Indication	Multiple myeloma under evaluation	**Report Date**	25-03-2025 7:00 pm

Sl no	Probe Name	FISH Result	ISCN 2020
1	C-MYC(8q24.21) rearrangement	Negative	nuc ish(C-MYC)x2[190/200]
2	5p15/9q22/15q22 (Hyperdiploidy markers)	Negative	nuc ish(D5S1976,D9S1783,SMAD6)x2[192/200]
3	IGH Gene Rearrangement	Negative	nuc ish(IGH)x2[190/200]
4	CDKN2C/CKS1B(1p32/1q21)	Negative	nuc ish(CDKN2C,CKS1B)x2[196/200]
5	Del 13q	Negative	nuc ish(DLEU1,LAMP1)x2[196/200]
6	TP53/CEP17 (Del17p)	Negative	nuc ish(TP53,NF1)x2[196/200]

Interpretation:

FISH test is negative for CDKN2C/CKS1B ((1p loss/1q gain), 5p15/9q22/15q22 ((Hyperdiploidy markers), C-MYC(8q24.21) rearrangement, Del13q, IGH Gene Rearrangement and Deletion 17p.
Kindly refer to the table 1 in this report to asses the risk stratification.

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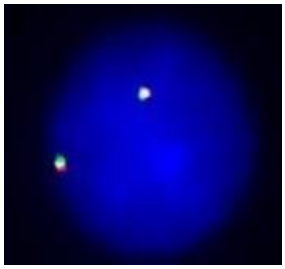
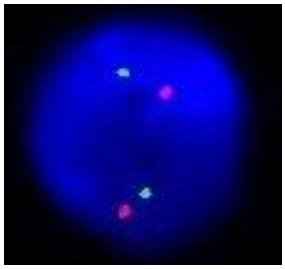
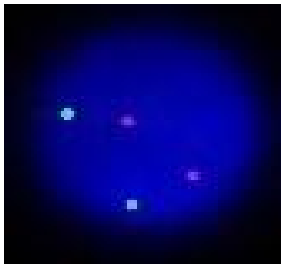
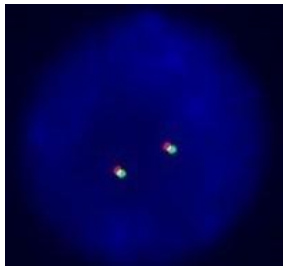
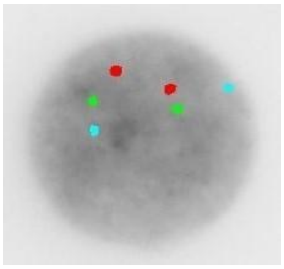
Collection Center/ Partner Lab			


IGH Gene Rearrangement


CDKN2C/CKS1B (1p32/1q21)


Del 13q


C-MYC(8q24.21) rearrangement


5p15/9q22/15q22 (Hyperdiploidy markers)

1) IGH(14q32) :

Spectrum Green (G)	5' IGH	Spectrum Orange (O)	3' IGH

Loci Analyzed	Signal Pattern	Normal Cut Off (%)	Percentage of Cells showing signal pattern	Result
IGH(14q32)	1F/1G/1O	>= 7 %	5 %	Negative

2) CDKN2C/CKS1B :

Spectrum Green (G)	CKS1B	Spectrum Orange (O)	CDKN2C

Loci Analyzed	Signal Pattern	Normal Cut Off (%)	Percentage of Cells showing signal pattern	Result
CDKN2C/CKS1B	2G/2O	>= 98 %	98 %	Negative

3) DLEU/LAMP1 :

Spectrum Green (G)	13q34/LAMP1	Spectrum Orange (O)	13q14.2/DLEU1

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DLEU1/LAMP1	2G/2O	>= 98 %	98 %	**Negative**

4) C-MYC :

Spectrum Green (G)	**distal to the breakpoint in the MYC gene region at 8q24**	**Spectrum Orange (O)**	**proximal to the breakpoint in the MYC gene region at 8q24**

Loci Analyzed	Signal Pattern	Normal Cut Off (%)	Percentage of Cells showing signal pattern	Result
C-MYC	1F/1G/1O	>= 7 %	5 %	**Negative**

5) 5p15/9q22/15q22 :

Spectrum Green (G)	**5p15**	**Spectrum Orange (O)**	**9q22**	**Spectrum Aqua (A)**	**15q22**

Loci Analyzed	Signal Pattern	Normal Cut Off (%)	Percentage of Cells showing signal pattern	Result
5p15/9q22/15q22	>2G/>2O/>2A	>= 2 %	0 %	**Negative**

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TP53/CEP17 (Del17p)

6) TP53/CEP17 (Del17p) :

Spectrum Green (G)	CEP17	Spectrum Orange (O)	TP53

Loci Analyzed	Signal Pattern	Normal Cut Off (%)	Percentage of Cells showing signal pattern	Result
TP53/CEP17 (Del17p)	2G2O	>= 98 %	98 %	Negative

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involves co-denaturation and hybridization of fluorescent labelled specific DNA probes to target DNA sequence in the cells. The excess unbound probe is removed during post hybridization washes. The sample is stained with a DAPI (4',6-Diamidino-2-phenylindole) counter-stain to demarcate the nuclei. Each fluorescent labelled probe that hybridizes to region of interest in plasma cells is visualized as signal using suitable optical filters under Epi fluorescent microscope. Plasma cells were enriched using the "EasySepTM Human WB", "BM CD138 Positive Selection Cocktail" and "EasySepTM Whole Blood Magnetic Particles" (Stemcell TechnologiesTM) kits. 200 plasma cells were counted for each probe. Interpretation of results are done based on the signal patterns observed and the cut off value for each probe has been defined as per the iFISH Myeloma workshop.

RISK STRATIFICATION OF CYTOGENETIC ABNORMALITIES IN MULTIPLE MYELOMA ACCORDING TO IMWG AND R-ISS FOR MYELOMA:(i) R-ISS (ISS: International staging system)

Prognosis	Cytogenetic markers
Low risk	del13 or 13q-
Intermediate risk	t(11;14)
High risk	t(4;14), t (14;16), 1q gain, 1p loss or17p

References:

1. Jian-1Yong Li, Fanny Gaillard, Anne Moreau, Jean-Luc Harousseau, Christian Laboisse, Noël Milpied, Régis Bataille, and Hervé Avet-Loiseau "Detection of Translocation t(11;14)(q13;q32) in Mantle Cell Lymphoma by Fluorescence in Situ Hybridization"Am J Pathol: Vols. 1 to 188; 1925 to 2018.
2. R. Fonseca et al. International Myeloma Working Group molecular classification of multiple myeloma: spotlight review. Leukaemia (2009) 23, 2210-2221.
3. Nikhil C. Munshi,1,2 Kenneth C. Anderson,1 P. Leif Bergsagel,3 John Shaughnessy,4 Antonio Palumbo,5 Brian Durie, "Consensus recommendations for risk stratification in multiple myeloma: report of the International Myeloma Workshop Consensus Panel 2"; DOI 10.1182/blood-2010-10- 300970.

Disclaimers:

1. This test was developed, and its performance characteristics determined by MedGenome. It has not been cleared or approved by the US Food and Drug Administration.
2. The finding of this test must be correlated with other clinical, haematopathological and cytogenetic findings for complete analysis.
3. Genetic changes other than those assayed cannot be ruled out on the basis of this testing.

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Lab Director

Dr. Syed Muqlisur Rehman, MD
Molecular Pathologist KMC Reg No. - 71468

End of Report

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