

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

|                            |                                   |                                           |                                     |
|----------------------------|-----------------------------------|-------------------------------------------|-------------------------------------|
| <b>Patient Name</b>        | Mr. Kathirgamathamby Anandarajah  | <b>Requesting Clinician</b>               | Dr. Mahendra Perera                 |
| <b>Gender</b>              | Male                              | <b>Hospital Information</b>               | Aegle Omics Private Limited         |
| <b>Age/Date of Birth</b>   | 71 Years                          | <b>Sample Source</b>                      | Peripheral blood in sodium heparin. |
| <b>Sample ID</b>           | 9018045                           | <b>Samples Collected(Date &amp; Time)</b> | 11/03/2025                          |
| <b>Order ID(s)</b>         | 1228669                           | <b>Samples Received(Date &amp; Time)</b>  | 13-Mar-25 11:15:00                  |
| <b>Clinical Indication</b> | Multiple myeloma under evaluation | <b>Report Date</b>                        | 19-03-2025 7:00 pm                  |

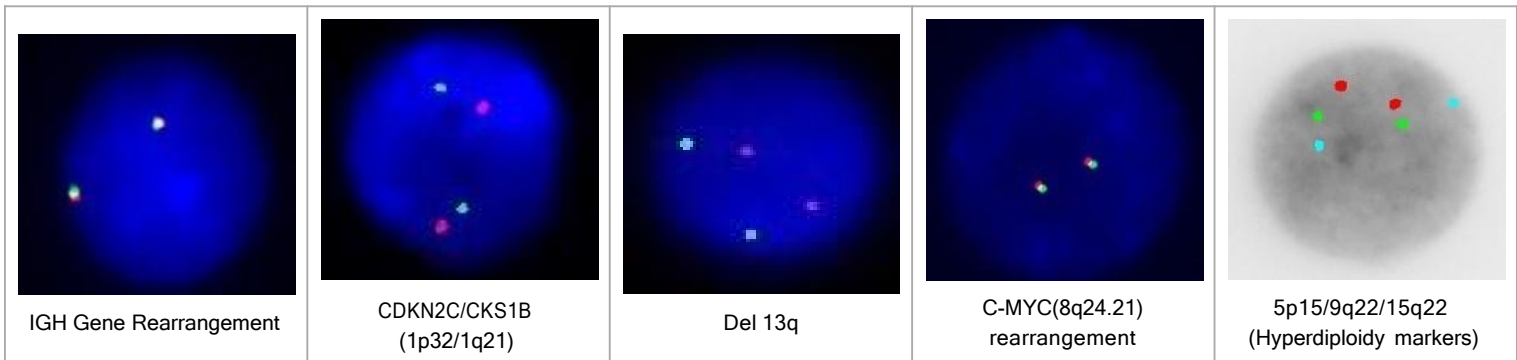
| Sl no | Probe Name                              | FISH Result | ISCN 2020                                 |
|-------|-----------------------------------------|-------------|-------------------------------------------|
| 1     | C-MYC(8q24.21) rearrangement            | Negative    | nuc ish(C-MYC)x2[190/200]                 |
| 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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| <b>Collection Center/ Partner Lab</b> |                                   |                                           |                                     |



### 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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| Gender              |  | Male                              |         | Hospital Information           |  | Aegle Omics Private Limited        |  |
| Age/Date of Birth   |  | 71 Years                          |         | Sample Source                  |  | Peripheral blood in sodium heparin |  |
| Sample ID           |  | 9018045                           |         | Samples Collected(Date & Time) |  | 11-03-2025                         |  |
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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 "EasySep™ Human WB", "BM CD138 Positive Selection Cocktail" and "EasySep™ Whole Blood Magnetic Particles" (Stemcell Technologies™) 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 or 17p |

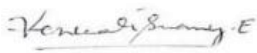
### References:

1. Jian-1Yong Li, Fanny Gaillard, Anne Moreau, Jean-Luc Harousseau, Christian Laboissee, 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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**Dr. E. Venkataswamy, PhD**  
**Lab Director**  
**End of Report**

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

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