Patient ID	Patient Name		Birth Date	Sex	Age
SA00179768	TESTINGRNV, MPCDS-ABNORMAL		1983-10-16	F	42
Order Number	**Client Order Number**	**Ordering Physician**	**Report Notes**		
SA00179768	SA00179768	CLIENT,CLIENT			
Account Information		**Collected**			
C7028846 DLMP Rochester		08 Apr 2026 13:29			

MPCDS Pre-Analysis Cell Sorting, BM

MPCDS Pre-Analysis Cell Sort

1 MCR

Performed

ADDITIONAL INFORMATION

Flow cytometric cell selection was performed with antibodies to the following antigens: CD19, CD38, CD45, CD56, CD138, and CD319.

Specimen enrichment for certain cell types is necessary, in order to enhance the sensitivity of genetic/molecular abnormalities detection in the cell population of interest, and to avoid unwanted contamination from other cell types. Flow cytometric cell sorting is the most direct and robust method of obtaining a pure population for subsequent genetic/molecular analysis, through assessment of a characteristic combination of cell surface antigens.

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Performing Site Legend

Code	Laboratory	Address	Lab Director	CLIA Certificate
MCR	Mayo Clinic Laboratories - Rochester Main Campus	200 First Street SW, Rochester, MN 55905	Nikola Baumann Ph.D.	24D0404292

Patient ID	Patient Name		Birth Date	Sex	Age
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Order Number	**Client Order Number**	**Ordering Physician**	**Report Notes**		
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mSMART Eval, PCPDs, FISH

mSMART Result Summary

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Standard-Risk

mSMART Evaluation

MCR

Based on the mSMART algorithm, this patient is in the STANDARD-RISK category. Plasma cell FISH studies identified a t(11;14) and the Monotypic Plasma Cells S-phase (MSMRT) result was <2.0% (reported separately).

Mayo Stratification for Myeloma and Risk Adapted Therapy (mSMART 4.0, https://www.msmart.org/mm-treatment-guidelines.html) algorithm classifies patients into standard or high-risk categories based on the results of 2 assays. Please note that the risk stratification for any follow up testing on samples previously evaluated using the mSMART 2.0 or 3.0 algorithms may have changed using the updated mSMART 4.0 algorithm. This risk adjustment does not necessarily imply disease progression.

The High-Risk group includes patients with a Monotypic Plasma Cells S-phase (MSMRT) result of ≥ 2.0%. or patients with any of the six following abnormalities defined by FISH: 1) Heterozygous or biallelic 17p deletion (TP53 deletion), 2) biallelic 1p deletion, 3) t(4;14) PLUS EITHER 1q gain/amplification OR heterozygous 1p deletion,
4) t(14;16) PLUS EITHER 1q gain/amplification OR heterozygous 1p deletion, 5) t(14;20) PLUS EITHER 1q gain/amplification OR heterozygous 1p deletion, 6) 1q gain/amplification PLUS heterozygous 1p deletion. Double-Hit Myeloma = Patients meeting criteria for high-risk myeloma with presence of two or more high risk qualifying cytogenetic abnormalities as listed above.

The Standard-Risk group includes patients with all remaining results, including: Monotypic Plasma Cells S-phase (MSMRT) <2.0%, Monotypic Plasma Cells DNA Ploidy (MSMRT) result that is hyperdiploid suggestive of multiple trisomies and FISH abnormalities including multiple trisomies, the following translocations in isolation; t(11;14), t(6;14), t(14;20), t(14;16), t(4;14), and 1q gain/amplification or heterozygous 1p deletion in isolation.

This classification is best used for active multiple myeloma. The interpretation may not be appropriate in amyloidosis, monoclonal gammopathy of undetermined significance (MGUS), smoldering multiple myeloma (SMM) or plasmacytoma.

Interpretation

MCR

The result is abnormal and indicates a plasma cell clone with IGH::CCND1 fusion, usually representing a t(11;14). In multiple myeloma, this clone represents a Standard-Risk cytogenetic abnormality (1–4).

In monoclonal gammopathy of undetermined significance (MGUS), smoldering multiple myeloma (SMM), plasmacytoma or amyloidosis, the prognostic significance is less well defined. For amyloidosis, the prognostic significance may be influenced by treatment.

The overall risk assessment should be done in the context of other risk factors.

Testing for TP53, a high-risk molecular genetics abnormality, may be considered using test, NGPCM [MayoComplete Plasma Cell Myeloma, Next-generation Sequencing].

For monitoring response to treatment, highly sensitive flow cytometry testing is recommended, test MSMRD [Myeloma Stratification and Risk-Adapted Therapy with Reflex to Minimal Residual Disease, Bone Marrow].

References:
1. WHO Classification of Tumours: Haematolymphoid Tumours; Lyon (France): 2024, 5th ed, p. 603–630 ; ISBN-13: 978–9283245209
2. The International Consensus Classification of Myeloid and Lymphoid Neoplasms; Philadelphia, PA (USA): 2025, p.384–396 ; ISBN-13: 978–1975222598
3. PMID: 40489728
4. PMID: 40533444

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Result Table

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Abnormality Name	Result	#Abn	Total Cells
14q32(IGH sep)	Abnormal	50	50
t(11;14) IGH::CCND1 fusion	Abnormal	50	50
-17p13.1(TP53x1,D17Z1x2)	Normal	0	50
-17(TP53,D17Z1)x1	Normal	0	50
-1p32.3(CDKN2Cx1,1q22x2)	Normal	0	50
-1p32.3/+1q22(CDKN2Cx1,1q22x3)	Normal	0	50
+1q22(CDKN2Cx2,1q22x3)	Normal	0	50
8q24.21(MYC sep)	Normal	0	50

Result

MCR

nuc ish (CCND1,IGH)x3(CCND1 con IGH)x2

Reason for Referral

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Plasma cell proliferative disorder (PCPD)

Specimen

MCR

Bone Marrow

Source

MCR

Left iliac crest

Method

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Locus and probes	[Strategy;#Nuclei;Vendor]
1p32.3(CDKN2C), 1q22(1q22)	[COPY#;50;LDT]
8q24.21(5'MYC,3'MYC)	[BAP;50;AM]
11q13(CCND1), 14q32(IGH)	[DFISH;50;AM]
14q32(3'IGH,5'IGH)	[BAP;50;LDT]
17p13(TP53), 17CEN(D17Z1)	[COPY#;50;AM]

Probe strategies include:
DFISH=dual color, double fusion;
BAP=break-apart probe;
COPY#=region gain and loss.
Scoring Method: Manual

Probe vendors include:
LDT = Mayo Clinic Developed
AM = Abbott Molecular, Inc (Des Plaines, IL)

Disclaimer

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Applicable to Analyte Specific Reagent (ASR) and Laboratory Developed Tests (LDT). This test was developed and its performance characteristics determined by Mayo Clinic in a manner consistent with CLIA requirements. It has not been cleared or approved by the U.S. Food and Drug Administration. This FISH test does not rule out other chromosome abnormalities.

Released By

MCR

Xinjie Xu, Ph.D.

Received: 09 Apr 2026 13:30 **Reported:** 09 Apr 2026 15:55

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MCR	Mayo Clinic Laboratories - Rochester Main Campus	200 First Street SW, Rochester, MN 55905	Nikola Baumann Ph.D.	24D0404292

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Order Number	**Client Order Number**	**Ordering Physician**	**Report Notes**		
SA00179768	SA00179768	CLIENT,CLIENT			
Account Information		**Collected**			
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mSMART Algorithmic Testing, BM

Final Diagnosis

[1] MCR

Bone marrow, flow cytometric immunophenotyping:

1. Plasma cells express: monotypic kappa cytoplasmic immunoglobulin light chains, CD38 and CD138. They do not express: CD19 or CD45.

Comment:
If the S-phase is ≥2%, it implies a less favorable prognosis in patients with multiple myeloma. It implies high-risk by mSMART stratification, in the absence of cytogenetic abnormalities. Correlation with plasma cell FISH results is recommended. For further details please see msmart.org.

Plasma cells, (monoclonal/monotypic and polyclonal/polytypic) are detected by immunoglobulin light chain restriction, surface immunophenotype, and DNA content. If present, the light chain expressed by the monotypic plasma cells is indicated. The percentage of clonal plasma cells estimated by flow cytometry is affected by specimen processing and antigen loss with specimen aging. Manual differential counting remains the accepted standard for determining the bone marrow plasma cell percentage.

The percentage of monotypic plasma cells in S-phase of the cell cycle is determined by quantitative DNA analysis. The DNA index is a calculated value. The presence of more than one value indicates the presence of cell populations with differing DNA contents within the monotypic plasma cells.

Method:
Plasma cell analysis was performed with antibodies to the following antigens: CD19, CD38, CD45, CD138, kappa and lambda cytoplasmic immunoglobulin light chains and DAPI.

Reviewed by: JENNIFER MAIN

Monotypic Plasma Cells:

MCR

Monotypic kappa plasma cells present.

Reference Value
None detected.

Monotypic PC per Total Events

MCR

12.21 %

Monotypic Plasma Cells S-phase

MCR

2.2 %

Monotypic Plasma Cells DNA Index

MCR

1.24

Reference Value
0.95–1.05

Monotypic Plasma Cells DNA Ploidy

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Hyperdiploid

Reference Value
Diploid

Polytypic PC per Total Events

MCR

< 0.1 %

Polytypic PC per All Plasma Cells

MCR

< 5.0 %

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Laboratory Notes

[1] This test was developed and its performance characteristics determined by Mayo Clinic in a manner consistent with CLIA requirements. This test has not been cleared or approved by the U.S. Food and Drug Administration.

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