Patient ID	Patient Name		Birth Date	Sex	Age
SA00170059	TESTINGRNV, SAMPLEREPORT-CMAT		1990-11-03	M	33
Order Number	Client Order Number	Ordering Physician	Report Notes		
SA00170059	SA00170059	CLIENT,CLIENT			
Account Information		Collected			
C7028846 DLMP Rochester		25 Aug 2024 09:48			

Chromosomal Microarray, Tumor

Result Summary

MCR

See Interpretation

Result

MCR

CHANGE	REGION	GENOME COORDINATES	SIZE (Mb)
Gain	11q13.4q24.1	chr11:72685981–121416262	48.7
Loss	11q24.1q25	chr11:121423048–134938470	13.5

Nomenclature

MCR

arr[hg19]
11q13.4q24.1(72,685,981–121,416,2620)x3,11q24.1q25(121,423,0 48–134,938,470)x1

Interpretation

1 MCR

An abnormal molecular karyotype was observed. Major clonal abnormalities include a complex chromosome 11q aberration characterized by a 48.7 Mb interstitial one copy gain of 11q13.4–11q24.1 (including the PAFAH1B2 gene), followed by a 13.5 Mb telomeric loss of 11q24.1q25 (including the FLI1 and ETS1 genes). The ATM and MLL(KMT2A) genes are located in the region of gain.

The 11q abnormalities identified in this patient are consistent with the WHO subset of lymphomas defined as "Burkitt-like lymphoma with 11q aberration" (Swerdlow et al., WHO Classification of Tumours of Haematopoietic and Lymphoid Tissues. IARC Press:Lyon 2017; p. 334–335). Similar aberrations involving chromosome 11q have been described in a subset of high-grade B cell lymphomas with morphological and clinical features of Burkitt lymphoma (Salaverria, et al. Blood. 123: 1187–1198, 2014) but with absence of MYC translocation, as seen in this patient (MYC negative). Emerging literature supports that patients with MYC-negative B-cell lymphoma with 11q abnormalities do not have a significantly different prognosis compared to MYC-positive Burkitt lymphoma patients.

Clinical and pathologic correlation is recommended.

This assay does not rule out balanced chromosome abnormalities or imbalances of chromosomal regions not represented by probes on the array. This assay may not detect tetraploidy, low level mosaicism, or minor subclones. A normal result does not exclude the diagnosis of any of the disorders tested for on this array.

Reason for Referral

MCR

tumor

Specimen

MCR

Tissue, Lymph Node

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

MAYO CLINIC LABORATORIES

Patient ID	Patient Name		Birth Date	Sex	Age
SA00170059	TESTINGRNV, SAMPLEREPORT-CMAT		1990-11-03	M	33
Order Number	**Client Order Number**	**Ordering Physician**	**Report Notes**		
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C7028846 DLMP Rochester		25 Aug 2024 09:48			

Source

MCR

Lymph node

Method

MCR

Chromosomal microarray (CMA) analysis was performed using both copy number and single-nucleotide polymorphism (SNP) probes on a whole genome array (Thermo Fisher Scientific) CytoScan HD Accel platform; 2.0 million copy number probes and 750,000 SNPs) using in silico controls. The genome-wide functional resolution of this array is approximately 30 kilobases for non-mosaic deletions and 60 kilobases for non-mosaic duplications. However, functional resolution of this array varies significantly dependent upon size of the abnormality, probe density in region, percentage of abnormal cells, and quality of the DNA obtained. Mosaic clonal abnormalities, especially those that are represented in a minor fraction of the sample, may not be detected. Deletions larger than 1.0 megabase, duplications larger than 2.0 megabases, and copy neutral loss of heterozygosity (cnLOH) larger than 10 megabases are generally reported. However, complex genomic alterations may be reported in aggregate, and well documented pathogenic constitutional and/or acquired abnormalities of any size may also be reported. All data were analyzed and reported using the February 2009 NCBI human genome build 37.1 (hg19). The genome coordinates described are best estimates and may not represent precise breakpoints, especially for abnormalities detected in a low percentage of cells.

Released By

MCR

William R. Sukov, M.D.

Received: 26 Aug 2024 09:57 **Reported:** 26 Aug 2024 11:40

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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