



Patient ID SA00170058	Patient Name TESTINGRNA, SAMPLEREPORT-CMAT	Birth Date 1990-08-28	Sex M	Age 33
Order Number SA00170058	Client Order Number SA00170058	Ordering Physician CLIENT,CLIENT	Report Notes	
Account Information C7028846 DLMP Rochester		Collected 25 Aug 2024 09:47		

Chromosomal Microarray, Tumor

Result Summary

MCR

Normal male

Nomenclature

MCR

arr(1-22)x2,(XY)x1

Interpretation

1 MCR

The result is normal. No clinically relevant copy number changes or regions with copy-neutral loss of heterozygosity were observed.

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

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.

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



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Released By

MCR

William R. Sukov, M.D.

Received: 26 Aug 2024 09:57

Reported: 26 Aug 2024 11:38

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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