ARUP LABORATORIES

800-522-2787 | aruplab.com
500 Chipeta Way, Salt Lake City, UT 84108-1221
Tracy I. George, MD, Chief Medical Officer

Client: Example Client ABC123
123 Test Drive
Salt Lake City, UT 84108
UNITED STATES

Physician: Doctor, Example

Patient: Patient, Example

DOB	10/24/1945
Gender:	Female
Patient Identifiers:	01234567890ABCD, 012345
Visit Number (FIN):	01234567890ABCD
Collection Date:	01/01/2017 12:34

Cytogenomic SNP Microarray - Oncology

ARUP test code 2006325

Cytogenomic Microarray SNP - Oncology	Normal	(Ref Interval: Normal)

H=High, L=Low, *=Abnormal, C=Critical

Unless otherwise indicated, testing performed at:

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500 Chipeta Way, Salt Lake City, UT 84108-1221
Tracy I. George, MD, Laboratory Director

Specimen Received
Specimen Type: Bone Marrow
Reason for Referral: Anemia, Thrombocytopenia
Test Performed: CMA ONC

TEST RESULT

The cytogenomic microarray analysis showed no clinically significant DNA copy number changes or copy neutral long contiguous stretches of homozygosity.

Sex chromosome complement: XX (female)

Test Information:
Chromosomal microarray analysis (CMA) was performed using Affymetrix CytoScan HD microarray. This microarray consists of 2,696,550 oligonucleotide probes across the genome, including 1,953,246 unique non-polymorphic probes, and 743,304 SNP (single nucleotide polymorphism) probes. Patient hybridization parameters are normalized to a reference set derived from 100 individuals with normal microarray results. Genomic linear positions are given relative to NCBI build 37 (hg19). Detected aberrations are reported when found to have clear or suspected clinical relevance; aberrations devoid of relevant gene content or reported as common findings in the general population may not be reported.

This microarray and associated software (Chromosome Analysis Suite) are manufactured by Affymetrix and used by ARUP Laboratories for the purpose of identifying DNA copy number gains and losses associated with large chromosomal imbalances. This analysis will not detect all forms of polyploidy, balanced rearrangements (e.g. inversions and balanced chromosomal translocations), small deletions, point mutations, and some mosaic conditions. While this assay has been extensively validated by ARUP Laboratories and other clinical laboratories per ACMG guidelines, it is not feasible to validate every potential genomic imbalance in the human genome. Furthermore, this technique only identifies the regions of imbalance; it does not provide information regarding the arrangement or mechanisms responsible. For these reasons, we may recommend that some chromosomal microarray results be characterized by fluorescence in situ hybridization (FISH) or standard chromosome analysis.

The functional resolution of this assay varies across different samples dependent upon the size of the abnormality, probe density, tumor content and quality of the DNA obtained. On average, the limit of detection will vary from less than 100 kilobases for samples with high tumor content (generally greater than 70 percent) to several megabases for samples with lower tumor content (25-35 percent). The limit of detection for loss of heterozygosity (LOH) is approximately 3 megabases.

This result has been reviewed and approved by [redacted],
[redacted]

INTERPRETIVE INFORMATION: Cytogenomic Microarray
SNP - Oncology
Test developed and characteristics determined by ARUP Laboratories. See Compliance Statement B: aruplab.com/CS

EER CMA ONC

EERUnavailable

H=High, L=Low, *=Abnormal, C=Critical

VERIFIED/REPORTED DATES

Procedure	Accession	Collected	Received	Verified/Reported
Cytogenomic Microarray SNP - Oncology	20-076-142077	3/16/2020 10:01:00 AM	3/27/2020 6:04:05 PM	4/4/2020 5:15:00 PM
EER CMA ONC	20-076-142077	3/16/2020 10:01:00 AM	3/27/2020 6:04:05 PM	4/4/2020 5:15:00 PM

END OF CHART