

Specimen Collected: 13-Sep-21 12:23

Cytogenomic MIP Array FFPE | **Received: 13-Sep-21 12:23** | **Report/Verified: 14-Sep-21 09:23**
Oncology

Procedure	Result	Units	Reference Interval
Cytogenomic MIP Array, See Note ^{f1 i1}			Normal
FFPE			
EER Cytogenomic MIP	EERUnavailable		
Microarray, FFPE			

Cytogenomic MIP Array FFPE | **Received: 14-Sep-21 09:43** | **Report/Verified: 14-Sep-21 09:44**
Oncology

Procedure	Result	Units	Reference Interval
Block ID	SP21-1234 1A		

Result Footnote

f1: Cytogenomic MIP Array, FFPE
 Test Performed: Cytogenomic SNP Microarray - Oncology (CMA ONC)
 Specimen Type: Bone marrow /Peripheral blood
 Indication for Testing: _

RESULT SUMMARY

Normal Microarray Result (Male)

RESULT DESCRIPTION

No clinically significant copy number changes or regions of homozygosity were detected.

INTERPRETATION

This analysis showed a normal result.

Cytogenomic Nomenclature (ISCN):

arr(X,Y)x1,(1-22)x2

Technical Information

- This assay was performed using the CytoScan(TM) HD Suite (Thermo Fisher Scientific) according to validated protocols within the Genomic Microarray Laboratory at ARUP Laboratories
- This assay is designed to detect alterations to DNA copy number state (gains and losses) as well as copy-neutral alterations (regions of homozygosity; ROH) that indicate a loss- or absence-of-heterozygosity (LOH or AOH)
- Copy-neutral LOH (CN-LOH) may be present due to acquired UPD (segmental or whole chromosome)
- AOH may be present due to parental relatedness (consanguinity) or uniparental disomy (UPD)
- The detection sensitivity (resolution) for any particular genomic region may vary dependent upon tumor burden, the number of probes (markers), probe spacing, and thresholds for copy number and ROH determination
- The CytoScan HD array contains 2.67 million markers across the genome with average probe spacing of 1.15 kb, including 750,000 SNP probes and 1.9 million non-polymorphic probes
- Genome-wide resolution varies from approximately 25-50 kb for copy number changes and approximately 3 Mb for ROH for samples with high tumor content (generally greater than 70 percent), to several Mb for samples with lower tumor content (20-30 percent)
- The limit of detection for clonality (mosaicism) varies dependent upon the size and type of genomic imbalance. In general, genotype mixture due to mosaicism (distinct cell lines from the same individual) or chimerism (cell lines from different individuals) will be detected when present at greater than 20-30 percent in the sample
- Genomic coordinates correspond to the Genome Reference Consortium human genome build 37/human genome issue 19 (GRCh37/hg19)

*=Abnormal, #=Corrected, C=Critical, f=Result Footnote, H-High, i-Test Information, L-Low, t-Interpretive Text, @=Performing lab

Unless otherwise indicated, testing performed at:

ARUP Laboratories

500 Chipeta Way, Salt Lake City, UT 84108

Laboratory Director: Tracy I. George, MD

ARUP Accession: 21-256-900194

Report Request ID: 15048459

Printed: 16-Sep-21 15:07

Result Footnote

f1: Cytogenomic MIP Array, FFPE
 Variant Classification and Reporting Criteria
 - Variant analysis is performed in accordance with recommendations by the American College of Medical Genetics and Genomics (ACMG), using tiered classification terminology
 - Acquired/somatic or constitutional/germline cancer-associated copy number variants (CNVs) and ROH are classified and reported using the following clinical significance categories: Clinically Significant CNVs and/or ROH (Tier 1 and Tier 2 Variants) and Other Clonal Variants (Tier 3)
 - Constitutional/germline CNVs not associated with cancer are classified according to the ACMG recommended 5-tier classification system: pathogenic, likely pathogenic, variant of uncertain significance (VUS), likely benign, and benign
 - In general, only constitutional CNVs classified as pathogenic or likely pathogenic will be reported using the following clinical significance category: Other Variants (Likely Constitutional)
 - Constitutional CNVs conferring non-cancer recessive disease risk will generally not be reported
 - CNVs classified as Tier 4, likely benign or benign that are devoid of relevant gene content or reported as common findings in the general population, are generally not reported
 - ROH are generally reported when known or suspected to be mosaic and representative of CN-LOH
 - Total autosomal homozygosity (only autosomal ROH greater than 3 Mb are considered for this estimate) consistent with AOH at a level of greater than 10 percent will generally be reported; AOH less than 10 percent may be reported, dependent upon on the concern for masked CN-LOH and/or a recessive disorder

Limitations

This analysis cannot provide structural (positional) information associated with genomic imbalance. Therefore, additional cytogenetic testing by chromosome analysis or fluorescence in situ hybridization (FISH) may be recommended.

Certain genomic alterations may not or cannot be detected by this technology. These alterations may include, but are not limited to:

- CNVs below the limit of resolution of this platform
- Sequence-level variants (mutations) including point mutations and indels
- Low-level mosaicism (generally, less than 20-30 percent)
- Balanced chromosomal rearrangements (translocations, inversions and insertions)
- Genomic imbalance in repetitive DNA regions (centromeres, telomeres, segmental duplications, and acrocentric chromosome short arms)

Test Information

i1: Cytogenomic MIP Array, FFPE
 INTERPRETIVE INFORMATION: Cytogenomic Molecular Inversion
 Probe Array, FFPE Tissue
 - Oncology

For detection of copy number alterations and loss of heterozygosity in FFPE specimens.

This test was developed and its performance characteristics determined by ARUP Laboratories. It has not been cleared or approved by the US Food and Drug Administration. This test was performed in a CLIA certified laboratory and is intended for clinical purposes.

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