ARUP LABORATORIES
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Jonathan R. Genzen, MD, PhD, Chief Medical Officer

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

Physician: Doctor, Example

Patient: Patient, Example

DOB	10/13/2020
Gender:	Female
Patient Identifiers:	01234567890ABCD, 012345
Visit Number (FIN):	01234567890ABCD
Collection Date:	00/00/0000 00:00

Cytogenomic Molecular Inversion Probe Array FFPE Tissue - Oncology

ARUP test code 3004275

Cytogenomic MIP Array, FFPE

Abnormal * (Ref Interval: Normal)

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Test Performed:CytogenomicMolecular Inversion Probe Array, FFPE
Tissue - Oncology(FFPEARRAY)
Specimen Type:Core Biopsy
EstimatedTumorContent: 100 percent
Indication for Testing:B Lymphoblastic Leukemia
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RESULT SUMMARY

Abnormal Microarray Result (Female)

Clinically Significant CNVs and/or ROH (Tier 1 and Tier 2
Variants):

High Hyperdiploid Genomic Profile

- Hyperdiploidy (Gain of Chrs X, 4, 6, 14, 17, and 21)

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RESULT DESCRIPTION
The above abnormalities were observed at 60 percent in the
sample, consistent with a somatic (acquired) origin.

INTERPRETATION
High hyperdiploidy (51-67 chromosomes) is a recurrent genomic
finding in childhood B-cell acute lymphoblastic leukemia
(B-ALL). Typical chromosome gains involve X, 4, 6, 10, 14, 17,
18, and 21, consistent with this genomic profile. In B-ALL, high
hyperdiploidy is associated with a favorable prognosis. Please
correlate this result with clinical and other laboratory
findings.

Recommendation:
Monitor for hyperdiploidy by chromosome, FISH and/or genomic
microarray analysis in future studies.

References:
1) Paulsson et al. The genomic landscape of high hyperdiploid
childhood acute lymphoblastic leukemia. Nat Genet. 2015
Jun;47(6):672-6. PMID: 25961940.
2) Paulsson et al. Genetic landscape of high hyperdiploid
childhood acute lymphoblastic leukemia. Proc Natl Acad Sci U S
A. 2010 Dec 14;107(50):21719-24. PMID: 21098271.

Cytogenomic Nomenclature (ISCN):
arr(X,4,6,14,17,21)x2-3

TechnicalInformation
-This assay was performed using theOncoScan(TM)CNV
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H=High, L=Low, *=Abnormal, C=Critical

Assay(ThermoFisher 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 an absence- or loss-of-heterozygosity (AOH or LOH)
- 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 uniparentaldisomy(UPD)
-The detection sensitivity (resolution) for anyparticular genomicregion may vary dependent upontumor burden,the number of probes (markers), probe spacing, and thresholds for copy number and ROH determination
-TheOncoScanCNVarray containsover220,000SNP probeswitha medianprobedensity (kb/probe)of16-19kb
- Genome-wide resolution varies from approximately300-400kb for copy number changes and approximately5Mb for ROH for samples with high tumor contenttoseveral Mbfor samples with lower tumor content(greater than 50 percent tumor content is recommended for this assay)
- The limit of detection forclonality(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 than30percent in thesample
-Genomic coordinates correspond to the Genome Reference Consortium human genome build 37/human genome issue 19 (GRCh37/hg19)

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
-CNVsclassified asTier 4,likely benign or benignthat aredevoid of relevant gene content or reported as common findings in the general population,are generally notreported
- ROH are generally reported when known or suspected to be mosaic and representative of CN-LOH
- Total autosomal homozygosity (only autosomal ROH greater than5Mb 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 uponon 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. Thesealterations may include, but are not limited to:
-CNVs below the limit of resolution of this platform
-Sequence-level variants (mutations) including point mutations

	andindels -Low-level mosaicism (generally, less than30percent) -Balanced chromosomal rearrangements (translocations, inversions and insertions) -Genomic imbalance in repetitive DNA regions (centromeres, telomeres, segmental duplications, and acrocentric chromosome short arms) This result has been reviewed and approved by [redacted] A portion of this analysis was performed at the following location(s): ARUP Laboratories [redacted] Laboratory Director: Denise I. Quigley, PhD, FACMG 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.
EER Cytogenomic MIP Microarray, FFPE	EERUnavailable
Block ID	OC23-11 A

VERIFIED/REPORTED DATES

Procedure	Accession	Collected	Received	Verified/Reported
Cytogenomic MIP Array, FFPE	23-093-401068	00/00/0000 00:00	00/00/0000 00:00	00/00/0000 00:00
EER Cytogenomic MIP Microarray, FFPE	23-093-401068	00/00/0000 00:00	00/00/0000 00:00	00/00/0000 00:00
Block ID	23-093-401068	00/00/0000 00:00	00/00/0000 00:00	00/00/0000 00:00

END OF CHART

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