

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

Physician: Doctor, Example

Patient: Patient, Example

10/13/2020
Female
01234567890ABCD, 012345
01234567890ABCD
00/00/0000 00:00

Cytogenomic Molecular Inversion Probe Array FFPE Tissue - Oncology

ARUP test code 3004275

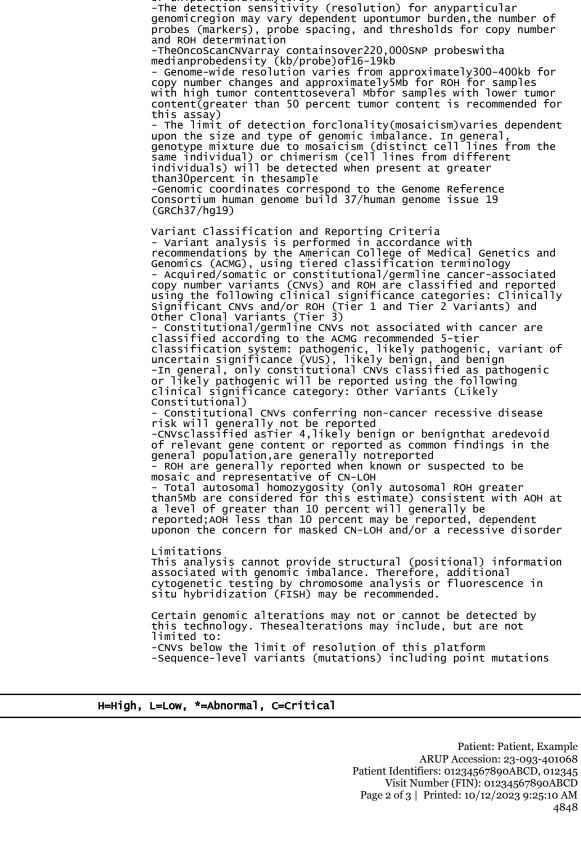
Cytogenomic MIP Array, FFPE	Abnormal * (Ref Interval: Normal)
	Test Performed:CytogenomicMolecular Inversion Probe Array, FFPE Tissue - Oncology(FFPEARRAY) Specimen Type:Core Biopsy EstimatedTumorContent: 100 percent Indication for Testing:B Lymphoblastic Leukemia
	RESULT SUMMARY
	Abnormal Microarray 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)
	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

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

4848

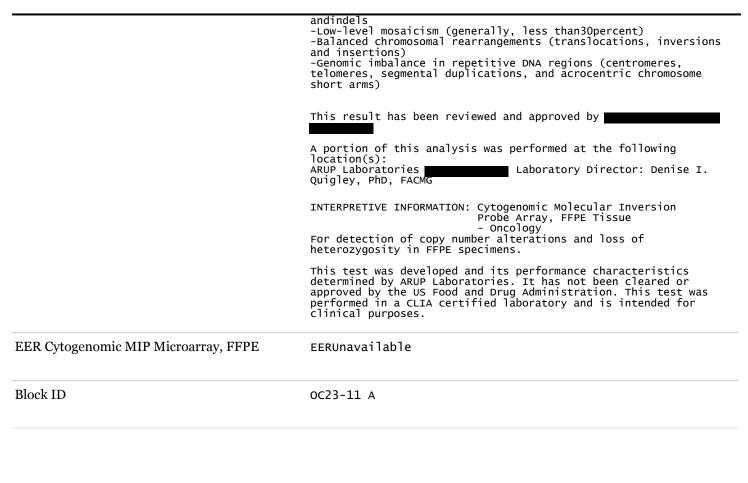
Assay(ThermoFisher Scientific) according to validated protocols within the Genomic Microarray Laboratory at ARUP Laboratories

witnin 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 any particular



ss otherwise indicated testing perform

ARUP LABORATORIES | 800-522-2787 | aruplab.com 500 Chipeta Way, Salt Lake City, UT 84108-1221 Jonathan R. Genzen, MD, PhD, Laboratory Director



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

Unless otherwise indicated, testing performed at: