

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

Physician: Doctor, Example

Patient: Patient, Example

DOB: 1/29/1997
Gender: Female
Patient Identifiers: 01234567890ABCD, 012345
Visit Number (FIN): 01234567890ABCD
Collection Date: 00/00/0000 00:00

Cytogenomic SNP Microarray - Fetal

ARUP test code 2002366

Maternal Contamination Study Fetal Spec

Unknown Origin

Single genotype. A maternal specimen was not submitted for correlation. The fetal sample was tested using STR markers to rule out maternal cell contamination. Only a single genotype was detected. Testing a maternal sample can confirm that this genotype is from the fetus.

This result has been reviewed and approved by [REDACTED]

Maternal Specimen

No

Cytogenomic SNP Microarray - Fetal

Normal (Ref Interval: Normal)

Test Performed: Cytogenomic SNP Microarray- Fetal (ARRAY FE)
Specimen Type: Cultured amniocytes
Indication for Testing: Polyhydramnios; VSD; cardiomegaly; LGA

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.

Health care providers with questions may contact an ARUP genetic counselor at (800) 242-2787 ext. 2141.

Cytogenetic Nomenclature (ISCN)
arr(1-22)x2(X,Y)x1

Technical Information
- This assay was performed using the CytoScan 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), copy-neutral alterations (regions of homozygosity; ROH) that indicate an absence- or loss-of-heterozygosity (AOH or LOH), and certain alterations to ploidy state due to errors at fertilization or early embryonic

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

cell division (i.e. triploidy, molar pregnancy)

- AOH may be present due to molar pregnancy, parental relatedness (consanguinity) or uniparental disomy (UPD)
- LOH may be present due to acquired UPD (segmental or whole chromosome)
- The detection sensitivity (resolution) for any particular genomic region may vary dependent upon 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
- In general, the genome-wide resolution is approximately 25-50 kb for copy number changes and approximately 3 Mb for ROH (See reporting criteria)
- The limit of detection for 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)

Variant Classification and Reporting Criteria

- Copy number variant (CNV) analysis is performed in accordance with recommendations by the American College of Medical Genetics and Genomics (ACMG), using standard 5-tier CNV classification terminology: pathogenic, likely pathogenic, variant of uncertain significance (VUS), likely benign, and benign
- CNVs classified as pathogenic or likely pathogenic are generally reported based on information available at the time of review
- CNVs classified as VUS are generally reported when found to have suspected clinical relevance based on information available at the time of review, or when meeting size criteria
- Known or expected pathogenic CNVs affecting genes with known clinical significance but which are unrelated to the indication for testing will generally be reported
- Variants that do not fall within the standard 5-tier CNV classification categories may be reported with descriptive language specific to that variant
- In general, recessive disease risk and recurrent CNVs with established reduced penetrance will be reported
- For a list of databases used in CNV classification, please refer to ARUP Constitutional CNV Assertion Criteria, which can be found on ARUP's Genetics website at www.aruplab.com/genetics
- CNVs classified as likely benign or benign that are devoid of relevant gene content or reported as common findings in the general population, are generally not reported
- CNV reporting (size) criteria: losses greater than 1 Mb and gains greater than 2 Mb are generally reported, dependent on genomic content
- Regions of homozygosity (ROH) are generally reported when a single terminal ROH is greater than 3 Mb and a single interstitial ROH is greater than 10-20 Mb (dependent upon chromosomal location and likelihood of imprinting disorder) or when total autosomal homozygosity is greater than 5 percent (only autosomal ROH greater than 3 Mb are considered for this estimate)

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

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-
- 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)
 - Most cases of tetraploidy

This result has been reviewed and approved by [REDACTED]

A portion of this analysis was performed at the following location(s):

[REDACTED]

INTERPRETIVE INFORMATION: Cytogenomic SNP Microarray - Fetal

Test developed and characteristics determined by ARUP Laboratories. See Compliance Statement C: aruplab.com/CS

EER Cytogenomic SNP Microarray - Fetal EERUnavailable

Chromosome Analysis, Amniotic Fluid, with Reflex to Genomic Microarray

ARUP test code 2008367

Chromosome Analysis, Amniotic Fluid See Note (Ref Interval: Normal)

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Specimen received

Specimen type: Amniotic Fluid
Reason for referral: Ultrasound abnormality; large for gestational age, polyhydramnios, VSD, cardiomegaly
Test performed: Chromosome Analysis

Laboratory analysis

Number of cells counted: 20
Number of colonies counted: 10
Number of cells analyzed: 20
Number of cells karyotyped: 20
ISCN Band level: 450
Banding Method: G-Banding

Chromosome results: 46,XY

This specimen is being reflexed to genomic microarray.

Diagnostic Impression:
Metaphase cells analyzed from multiple cultures of amniocytes revealed a normal male chromosome complement. The standard cytogenetic methodology used in this analysis may not detect small rearrangements or low level mosaicism, and cannot detect submicroscopic deletions or duplications that are detectable by microarray analysis.

This result has been reviewed and approved by [REDACTED]

A portion of this analysis was performed at the following location(s):

INTERPRETIVE INFORMATION: Chromosome Analysis,
Amniotic Fluid
Test developed and characteristics determined by ARUP Laboratories. See Compliance Statement C: aruplab.com/CS

EER Chrom Analysis AF w/Rflx to Array

See Note

Access ARUP Enhanced Report using either link below:

-Direct access:

-Enter Username, Password:

Username: [REDACTED]
Password: [REDACTED]

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VERIFIED/REPORTED DATES

Procedure	Accession	Collected	Received	Verified/Reported
Maternal Contamination Study Fetal Spec	20-245-401513	00/00/0000 00:00	00/00/0000 00:00	00/00/0000 00:00
Maternal Specimen	20-245-401513	00/00/0000 00:00	00/00/0000 00:00	00/00/0000 00:00
Chromosome Analysis, Amniotic Fluid	20-245-401513	00/00/0000 00:00	00/00/0000 00:00	00/00/0000 00:00
Cytogenomic SNP Microarray - Fetal	20-245-401513	00/00/0000 00:00	00/00/0000 00:00	00/00/0000 00:00
EER Cytogenomic SNP Microarray - Fetal	20-245-401513	00/00/0000 00:00	00/00/0000 00:00	00/00/0000 00:00
EER Chrom Analysis AF w/Rflx to Array	20-245-401513	00/00/0000 00:00	00/00/0000 00:00	00/00/0000 00:00

END OF CHART

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