

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

Physician: Doctor, Example

Patient: Patient, Example

DOB: 11/15/1983
Gender: Female
Patient Identifiers: 01234567890ABCD, 012345
Visit Number (FIN): 01234567890ABCD
Collection Date: 01/01/2017 12:34

Chromosome Analysis, Products of Conception, with Reflex to Genomic Microarray

ARUP test code 2005762

Chromosome Analysis, Prod Concp

See Note (Ref Interval: Normal)

Specimen received

Specimen type: Fetal tissue
Reason for referral: Fetal anomaly
Test performed: Chromosome Analysis

Laboratory analysis

Number of cells counted: 20
Number of cells analyzed: 5
Number of cells karyotyped: 5
ISCN Band level: 400
Banding Method: G-Banding

Chromosome results:46,XY

This specimen is being reflexed to genomic microarray.

Diagnostic Impression:
Metaphase cells examined from multiple cultures of fetal tissue revealed a normal male karyotype. 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]
PhD, FACMG

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

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

EER Chrom Analysis POC w/Rflx to Array

See Note

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

Unless otherwise indicated, testing performed at:

Access ARUP Enhanced Report using the link below:

-Direct access:

Genomic SNP Microarray, Products of Conception

ARUP test code 2005633

SNP Microarray, Products of Conception

Normal (Ref Interval: Normal)

Test Performed: Genomic SNP Microarray, Products of Conception (ARRAY POC)

Specimen Type: Products of Conception (Tissue: Fetal)

Indication for Testing: Fetal anomaly

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(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 an absence- or loss-of-heterozygosity (AOH or LOH), and certain alterations to ploidy state due to errors at fertilization or early embryonic 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

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

Unless otherwise indicated, testing performed at:

ARUP LABORATORIES | 800-522-2787 | aruplab.com
500 Chipeta Way, Salt Lake City, UT 84108-1221
Tracy I. George, MD, Laboratory Director

Patient: Patient, Example
ARUP Accession: 20-024-129633
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- 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, likely pathogenic, or variant of uncertain significance are generally reported, based on information available at the time of review
- 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 Copy Number Variant Assertion Criteria, which can be found on ARUPs Genetics Resources website at www.aruplab.com/genetics/resources
- 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 50 kb and gains greater than 400 kb are generally reported, dependent on genomic content
- ROH are generally reported when a single terminal ROH is greater than 3 Mb and a single interstitial ROH is greater than 10-15 Mb (dependent upon chromosomal location and likelihood of imprinting disorder) or when total autosomal homozygosity is greater than 3 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 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]
Ph.D., FACMG

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

INTERPRETIVE DATA: Genomic SNP Microarray,
Products of Conception

Test developed and characteristics determined by ARUP
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EER SNP Microarray, Products of Concept

EERUnavailable

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VERIFIED/REPORTED DATES

Procedure	Accession	Collected	Received	Verified/Reported
Chromosome Analysis, Prod Concep	20-024-129633	1/24/2020 10:36:00 AM	1/25/2020 1:26:59 PM	2/12/2020 11:33:00 PM
EER Chrom Analysis POC w/Rflx to Array	20-024-129633	1/24/2020 10:36:00 AM	1/25/2020 1:26:59 PM	2/12/2020 11:33:00 PM
SNP Microarray, Products of Conception	20-024-129633	1/24/2020 10:36:00 AM	2/12/2020 11:33:26 PM	2/25/2020 9:09:00 PM
EER SNP Microarray, Products of Conception	20-024-129633	1/24/2020 10:36:00 AM	2/12/2020 11:33:26 PM	2/25/2020 9:09:00 PM

END OF CHART

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