

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

Physician: Doctor, Example

Patient: Patient, Example

DOB	9/22/1983
Gender:	Female
Patient Identifiers:	01234567890ABCD, 012345
Visit Number (FIN):	01234567890ABCD
Collection Date:	00/00/0000 00:00

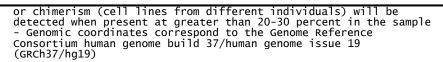
Genomic SNP Microarray, Products of Conception

ARUP test code 2005633

SNP Microarray, Products of Conception	Normal (Ref Inte Test Performed: Genomic SNP Microarray (ARRAY POC) Specimen Type: Products of Conception Indication for Testing: Missed abortion	(Tissue: Fetal)
	 RESULT SUMMARY Normal Microarray Result (Female)	
	RESULT DESCRIPTION No clinically significant copy number homozygosity were detected.	changes or regions of
	INTERPRETATION This analysis showed a normal result.	
	Health care providers with questions m counselor at (800) 242-2787 ext. 2141.	ay contact an ARUP genetic
	Cytogenomic Nomenclature (ISCN) arr(X,1-22)x2	
	Technical Information - This assay was performed using the C (Thermo Fisher Scientific) according to within the Genomic Microarray Laborato - This assay is designed to detect alt, number state (gains and losses) as well alterations (regions of homozygosity; A absence- or loss-of-heterozygosity (AOI alterations to ploidy state due to error early embryonic cell division (i.e. tr - AOH may be present due to molar preg relatedness (consanguinity) or unipare - LOH may be present due to acquired U chromosome) - The detection sensitivity (resolution genomic region may vary dependent upon (markers), probe spacing, and threshold determination - The CytoScan HD array contains 2.67 m genome with average probe spacing of 1 SNP probes and 1.9 million non-polymor - In general, the genome-wide resolutive kb for copy number changes and approxima reporting criteria) - The limit of detection for mosaicism size and type of genomic imbalance. In due to mosaicism (distinct cell lines the second - The State Stat	o validated protocols ry at ARUP Laboratories erations to DNA copy l as copy-neutral ROH) that indicate an H or LOH), and certain ors at fertilization or iploidy, molar pregnancy) nancy, parental ntal disomy (UPD) PD (segmental or whole n) for any particular the number of probes ds for copy number and ROH million markers across the .15 kb, including 750,000 phic probes on is approximately 25-50 mately 3 Mb for ROH (See varies dependent upon the general, genotype mixture

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

Unless otherwise indicated, testing performed at:



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

review

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 nemetrance will be reported

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 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

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

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

Unless otherwise indicated, testing performed at

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

Patient: Patient, Example ARUP Accession: 23-202-114452 Patient Identifiers: 01234567890ABCD, 012345 Visit Number (FIN): 01234567890ABCD Page 2 of 3 | Printed: 8/1/2023 3:02:53 PM 4848

INTERPRETIVE DATA: Genomic SNP Microarray, Products of Conception 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 clinical purposes.

Counseling and informed consent are recommended for genetic testing. Consent forms are available online.

VERIFIED/REPORTED DATES					
Procedure	Accession	Collected	Received	Verified/Reported	
SNP Microarray, Products of Conception	23-202-114452	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:

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

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