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PATIENT REPORT

Patient Age/Sex: Unknown

Specimen Collected: 11-Sep-23 10:31

SNP Microarray, Products of Conception | **Received: 12-Sep-23 14:13** **Report/Verified: 12-Sep-23 14:15**

Procedure	Result	Units	Reference Interval
SNP Microarray,Products of Conception	**Abnormal** * f1 i1		[Normal]

Result Footnote

f1: SNP Microarray, Products of Conception
Test Performed: Genomic SNP Microarray, Products of Conception (ARRAY POC)
Specimen Type: Products of Conception (Tissue: Fetal)
Indication for Testing: Fetal demise

RESULT SUMMARY
Abnormal Microarray Result (Male)

Trisomy 13

Classification: Pathogenic
Copy number change: 13q11q34 gain
Size: 95.7 Mb

RESULT DESCRIPTION
This analysis showed a gain of all probes on chromosome 13, indicating an additional copy (trisomy) of this chromosome.

INTERPRETATION
This result is consistent with a diagnosis of trisomy 13, which has a reported fetal loss rate of approximately 50 percent between 10-13 weeks gestation and term. Features associated with trisomy 13 in the prenatal period may include heart defects, holoprosencephaly, cleft lip with or without cleft palate, renal malformations, intrauterine growth restriction, polydactyly, clenched fists, and rocker-bottom feet.

Autosomal trisomy is the most frequent type of chromosomal abnormality in pregnancy loss and is usually sporadic.

NOTE: Genomic microarray analysis cannot provide structural information accounting for this gain. As it is uncertain whether this finding represents three independent copies of chromosome 13 or an unbalanced Robertsonian translocation, chromosome analysis should be considered (see recommendations).

Recommendations:
1) Genetic counseling
2) Chromosome analysis. For assistance with ordering testing on this sample, please call ARUP Genetics Processing at (800) 242-2787 ext. 3301 and refer to test code 2002288, Chromosome Analysis, Products of Conception within 7 days.
3) If chromosome analysis on the products of conception sample is not possible, parental chromosome analysis may be considered to determine carrier status for recurrence risk counseling. This test is available, at a charge, through ARUP Laboratories. Please order test code 2002289, Chromosome Analysis, Peripheral Blood and include the accession number for this case (23-172-122236).

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

References:
1) Pont et al. Congenital malformations among liveborn infants with trisomies 18 and 13. Am J Med Genet A. 2006 Aug 15;140(16):1749-56. PMID: 16835915.

*=Abnormal, #=Corrected, C=Critical, f=Result Footnote, H-High, i-Test Information, L-Low, t-Interpretive Text, @=Performing lab

Result Footnote

f1: SNP Microarray, Products of Conception

2) Morris and Savva. The risk of fetal loss following a prenatal diagnosis of trisomy 13 or trisomy 18. Am J Med Genet A. 2008 Apr 1;146A(7):827–32. PMID: 18361449.
3) Gardner and Amor. Gardner and Sutherland's Chromosome Abnormalities and Genetic Counseling. 5th edition. New York, NY: Oxford; 2018.
4) Milunsky. Genetic Disorders and the Fetus: Diagnosis, Prevention and Treatment. 7th edition. West Sussex, UK: John Wiley and Sons; 2016.

Cytogenomic Nomenclature (ISCN):
arr(13)x3

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
- 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

Result Footnote

f1: SNP Microarray, Products of Conception
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 [redacted]

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

Test Information

i1: SNP Microarray, Products of Conception
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.

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

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