

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

Physician: Doctor, Example

Patient: Patient, Example

DOB: Unknown
Gender: Male
Patient Identifiers: 01234567890ABCD, 012345
Visit Number (FIN): 01234567890ABCD
Collection Date: 00/00/0000 00:00

Cytogenomic SNP Microarray, Family-Specific Variant

ARUP test code 3005694

Cytogenomic SNP Microarray, Fam Spec Var

Normal

ARRAY FSV NEG
Test Performed: Cytogenomic SNP Microarray, Family Specific Variant (ARRAY FSV)
Specimen Type: Peripheral blood
Indication for Testing: Familial testing

RESULT

16p11.2 Deletion: Not Detected

INTERPRETATION

This targeted analysis was negative for the requested copy number variant (CNV). Genomic coordinates below correspond to the region interrogated in this study.

This result indicates that this individual is not a carrier of the CNV identified in the proband. Variants outside of this targeted region were not evaluated. Balanced rearrangements involving this region have not been ruled out by this analysis.

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

Cytogenomic Nomenclature (ISCN):
arr[GRCh37] 16p11.2(29651576_30191848)x2

This result has been reviewed and approved by [REDACTED]

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

Background Information: Cytogenomic SNP Microarray,
Family-Specific Variant

Technical Information

- This is a targeted microarray test for detection of previously identified familial copy number variants (CNVs). Only requested CNVs that are detectable on this platform will be evaluated.
- Analysis is performed using the CytoScan(TM) HD Suite (Thermo Fisher Scientific) according to validated protocols established within the Genomic Microarray Laboratory at ARUP Laboratories.
- 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 nonpolymorphic probes.
- 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 determination. The general limit of detection for copy number changes across this platform is approximately 25-50 kb.
- 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) will be detected when present at greater than 20 to 30 percent in the sample.
- Genomic coordinates interrogated for targeted CNV analysis correspond to the Genome Reference Consortium human genome build 37/human genome issue 19 (GRCh37/hg19). CNVs reported in other genome builds will be converted to hg19 before interrogation.

Variant Classification and Reporting Criteria

- Interrogated CNV(s) will be reported as "Detected" or "Not Detected."
- In general, requested CNVs will not be classified and an interpretation will not be provided. Reference the original proband report for the interpretation of any interrogated variant.
- Parentage will not be evaluated.
- Inheritance interpretation is based on the familial relationships provided to the laboratory.

Limitations

- This assay only analyzes requested familial CNV(s) and does not rule out alterations outside of the targeted region.
- This analysis cannot provide structural (positional) information associated with genomic imbalance. In some cases, 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 to 30 percent).
- Balanced chromosomal rearrangements (translocations, inversions, and insertions).
- Genomic imbalance in repetitive DNA regions (centromeres, telomeres, segmental duplications, and acrocentric chromosome short arms).

This test was developed and its performance characteristics determined by ARUP Laboratories. It has not been cleared or approved by the U.S. 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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VERIFIED/REPORTED DATES				
Procedure	Accession	Collected	Received	Verified/Reported
Cytogenomic SNP Microarray, Fam Spec Var	24-093-102614	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

Patient: Patient, Example
ARUP Accession: 24-093-102614
Patient Identifiers: 01234567890ABCD, 012345
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