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Patient Report

Patient Age/Gender: 40 years Female

Specimen Collected: 21-Jun-21 15:01

Distal Arthrogryposis Panel by NGS | **Received: 21-Jun-21 15:01** | **Report/Verified: 23-Jun-21 13:59**

Procedure	Result	Units	Reference Interval
Distal Arthrogryposis Specimen	Whole Blood		
Distal Arthrogryposis Interp	Positive [f1] [i1]		

Result Footnote

f1: Distal Arthrogryposis Interp

Section 79-1 of New York State Civil Rights Law requires informed consent be obtained from patients (or their legal guardians) prior to pursuing genetic testing. These forms must be kept on file by the ordering physician. Consent forms for genetic testing are available at www.aruplab.com. Incidental findings are not reported unless clinically significant but are available upon request.

Test Information

i1: Distal Arthrogryposis Interp

BACKGROUND INFORMATION: Distal Arthrogryposis Panel, Sequencing

CHARACTERISTICS: Distal arthrogryposes (DA) are a subset of arthrogryposis disorders that involve contractures of the distal parts of the limbs. The contractures are congenital but typically do not have primary neurologic and/or muscle disease; the shared findings among DA include a consistent pattern of hand and foot involvement, limited involvement of the proximal joints, and variable expressivity. There are multiple types of DA caused by different genes (genetic heterogeneity). PREVALENCE: 1 in ~3,000.

CAUSE: Pathogenic germline variants in genes associated with decreased fetal movement leading to contractures.

INHERITANCE: Autosomal dominant and autosomal recessive.

GENES TESTED: ECEL1, FBN2, MYBPC1, MYH3, MYH8*, NALCN*, PIEZO2*, TNNI2, TNNT3, TPM2

*One or more exons are not covered by sequencing for the indicated gene; see Limitations section below.

METHODOLOGY: Capture of all coding exons and exon-intron junctions of the targeted genes, followed by massively parallel sequencing. Sanger sequencing was performed as necessary to fill in regions of low coverage and confirm reported variants.

ANALYTICAL SENSITIVITY/SPECIFICITY: The analytical sensitivity of this test is approximately 99% for single nucleotide variants (SNVs) and greater than 93% for insertions/duplications/deletions from 1-10 base pairs in size. Variants greater than 10 base pairs may be detected, but the analytical sensitivity may be reduced.

Test Information

i1: Distal Arthrogryposis Interp

LIMITATIONS: A negative result does not exclude a heritable form of arthrogryposis. This test only detects variants within the coding regions and intron-exon boundaries of the targeted genes. Regulatory region variants and deep intronic variants will not be identified. Deletions/duplications/insertions of any size may not be detected by massively parallel sequencing. Diagnostic errors can occur due to rare sequence variations. In some cases, variants may not be identified due to technical limitations in the presence of pseudogenes, repetitive, or homologous regions. This assay may not detect low-level mosaic or somatic variants associated with disease. Interpretation of this test result may be impacted if this patient had an allogeneic stem cell transplantation. Noncoding transcripts were not analyzed.

The following regions are not sequenced due to technical limitations of the assay:
MYH8 (NM_002472) exon 5
NALCN (NM_001350748) exon 19
PIEZO2 (NM_022068) exon 4

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.