

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

Physician: Doctor, Example

Patient: Patient, Example

DOB: 12/28/1991
Gender: Female
Patient Identifiers: 01234567890ABCD, 012345
Visit Number (FIN): 01234567890ABCD
Collection Date: 00/00/0000 00:00

Duchenne/Becker Muscular Dystrophy (DMD) Sequencing

ARUP test code 2011153

DMD Sequencing Specimen whole Blood

DMD Sequencing Interpretation

Negative

RESULT

No pathogenic variants were detected in DMD gene.

INTERPRETATION

No pathogenic variants were detected in the DMD gene by massively parallel sequencing of the coding regions and exon-intron boundaries. This result decreases the likelihood of, but does not exclude, a diagnosis of Duchenne/Becker muscular dystrophy. Please refer to the background information included in this report for the clinical sensitivity and limitations of this test.

RECOMMENDATIONS

This test does not detect all variants associated with Duchenne/Becker muscular dystrophy, as only a subset of variants are due to sequence variants. If the individual is at risk to be a carrier, consideration may be given to ordering Duchenne/Becker Muscular Dystrophy (DMD), Deletion/Duplication; ARUP test code 2011235. Medical screening and management should rely on clinical findings and family history. Genetic consultation is recommended.

COMMENTS

Reference Sequence: GenBank # NM_004006.2 (DMD)
Likely benign and benign variants are not reported.
Variants in the following region(s) may not be detected by NGS with sufficient confidence in this sample due to technical limitations; reportable variants are confirmed by Sanger sequencing:

NONE

This result has been reviewed and approved by [REDACTED]

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

BACKGROUND INFORMATION: Duchenne/Becker Muscular Dystrophy (DMD) Sequencing

CHARACTERISTICS: Symptoms of Duchenne muscular dystrophy (DMD) usually begin in childhood and include fatigue, learning difficulties, muscle weakness, progressive difficulty walking with eventual wheelchair dependency, breathing difficulties and heart disease. Symptoms of Becker muscular dystrophy (BMD) are similar to DMD but begin at a later age and progress at a slower rate. Dilated cardiomyopathy has been observed in nearly all affected males and many female carriers of DMD and BMD.

EPIDEMIOLOGY: Incidence of DMD: 1 in 3,500 male births, BMD: 1 in 19,000 male births.

INHERITANCE: X-linked; de novo variants occur in 1/3 of cases.

PENETRANCE: Males: 100 percent. Females: Varies with X-chromosome inactivation.

CLINICAL SENSITIVITY: DMD 20-35 percent. BMD: 10-20 percent.

METHODOLOGY: Targeted capture of all coding exons and exon-intron junctions of the DMD gene, followed by massively parallel sequencing. Sanger sequencing was performed as necessary to fill in regions of low coverage and confirm reported variants. Human genome build 19 (Hg 19) was used for data analysis.

ANALYTICAL SENSITIVITY: The analytical sensitivity of this test is approximately 99 percent for single nucleotide variants (SNVs) and greater than 93 percent 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.

LIMITATIONS: A negative result does not exclude a heritable form of muscular dystrophy. This test only detects variants within the coding regions and intron-exon boundaries of the DMD gene. Regulatory region variants and deep intronic variants will not be identified. Deletions/duplications/insertions of any size may not be detected by massive 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 somatic variants associated with disease. Interpretation of this test result may be impacted if this patient has had an allogeneic stem cell transplantation. Non-coding transcripts were not analyzed.

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.

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

VERIFIED/REPORTED DATES				
Procedure	Accession	Collected	Received	Verified/Reported
DMD Sequencing Specimen	22-165-400109	00/00/0000 00:00	00/00/0000 00:00	00/00/0000 00:00
DMD Sequencing Interpretation	22-165-400109	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: 22-165-400109
Patient Identifiers: 01234567890ABCD, 012345
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