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

Physician: Doctor, Example

Patient: Patient, Example

DOB	4/18/1990
Sex:	Male
Patient Identifiers:	01234567890ABCD, 012345
Visit Number (FIN):	01234567890ABCD
Collection Date:	01/01/2017 12:34

Marfan Syndrome (FBN1) Sequencing and Deletion/Duplication

ARUP test code 3004102

Marfan Syndrome (FBN1) Specimen	Whole Blood
Marfan Syndrome (FBN1) Interpretation	Positive

RESULT
One likely pathogenic variant was detected in the FBN1 gene.

LIKELY PATHOGENIC VARIANT
Gene: FBN1 (NM_000138.5)
Nucleic Acid Change: c.6467del; Heterozygous
Amino Acid Alteration: p.Gly2156ValfsTer4
Inheritance: Autosomal Dominant

INTERPRETATION
One likely pathogenic variant, c.6467del; p.Gly2156ValfsTer4, was detected in the FBN1 gene by massively parallel sequencing. Pathogenic FBN1 variants are most commonly causative for Marfan syndrome (MFS); clinical manifestations are variable. Additionally, other phenotypes including mitral valve prolapse syndrome, MASS syndrome, thoracic aortic aneurysms and aortic dissections (TAAD), Shprintzen-Goldberg syndrome, Weill-Marchesani syndrome as well as autosomal dominant ectopia lentis are also associated with pathogenic FBN1 variants. This individual's offspring have a 50 percent chance of inheriting the likely pathogenic variant.

Please refer to the background information included in this report for the methodology and limitations of this test.

Evidence for variant classification:
The FBN1 c.6467del; p.Gly2156ValfsTer4 variant, to our knowledge, is not reported in the medical literature or gene specific databases. This variant is also absent from the Genome Aggregation Database (v2.1.1), indicating it is not a common polymorphism. This variant causes a frameshift by deleting a single nucleotide, so it is predicted to result in a truncated protein or mRNA subject to nonsense-mediated decay. Additionally, several downstream truncating variants have been described in individuals with Marfan syndrome and are considered pathogenic (Growth 2017). Based on available information, this variant is considered to be likely pathogenic.

RECOMMENDATIONS
Genetic consultation is indicated, including a discussion of medical screening and management. At-risk family members should be offered a clinical evaluation for Marfan syndrome. If it is unclear whether or not they are affected, targeted testing for the identified likely pathogenic FBN1 variant should be offered (Familial Targeted Sequencing, ARUP test code 3005867).

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

COMMENTS
Unless otherwise specified, confirmation by Sanger sequencing was not performed for variants with acceptable quality metrics. 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: None

REFERENCES
Groth KA et al. Evaluating the quality of Marfan genotype-phenotype correlations in existing FBN1 databases. Genet Med. 2017 Jul;19(7):772-777. PMID: 27906200.

This result has been reviewed and approved by [redacted]
BACKGROUND INFORMATION: Marfan Syndrome (FBN1) Sequencing and Deletion/Duplication

CHARACTERISTICS: Marfan syndrome is a connective tissue disorder affecting the ocular, skeletal, and cardiovascular systems with a high degree of clinical variability. Common ocular findings include myopia, ectopia lentis, retinal detachment, glaucoma, and early cataracts. Skeletal involvement may include bone overgrowth and joint laxity, disproportionally long extremities, pectus excavatum/carinatum, and scoliosis. Cardiovascular findings include aortic dilatation/dissection, mitral and/or tricuspid valve prolapse, and enlargement of the proximal pulmonary artery. Cardiovascular disease management is necessary to decrease morbidity and early mortality.

EPIDEMIOLOGY: Prevalence is 1 in 5,000 to 1 in 10,000.

CAUSE: Pathogenic germline variants in the FBN1 gene

INHERITANCE: Autosomal dominant. De novo pathogenic variants are causative for 25 percent of cases.

PENETRANCE: Complete, but age dependent.

CLINICAL SENSITIVITY: 95-98 percent.

GENE TESTED: FBN1 (NM_000138)

METHODOLOGY: Probe hybridization-based 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 to confirm reported variants that do not meet acceptable quality metrics. A proprietary bioinformatic algorithm was used to detect large (single exon-level or larger) deletions or duplications in the indicated genes. Large deletions/duplications confirmed using an orthogonal exon-level microarray. Human genome build 19 (Hg 19) was used for data analysis.

ANALYTICAL SENSITIVITY/SPECIFICITY: The analytical sensitivity is approximately 99 percent for single nucleotide variants (SNVs) and greater than 93 percent for insertions/duplications/deletions (indels) from 1-10 base pairs in size. Indels greater than 10 base pairs may be detected, but the analytical sensitivity may be reduced. Deletions of 2 exons or larger are detected with sensitivity greater than 97 percent; single exon deletions are detected with 62 percent sensitivity. Duplications of 3 exons or larger are detected at greater than 83 percent sensitivity. Specificity is greater than 99.9 percent for all variant classes.

LIMITATIONS: A negative result does not exclude a diagnosis of Marfan syndrome or other FBN1-related disorders. This test only detects variants within the coding regions and intron-exon boundaries of the FBN1 gene. Deletions/duplications/insertions

of any size may not be detected by massively parallel sequencing. Regulatory region variants and deep intronic variants will not be identified. Precise breakpoints for large deletions or duplications are not determined in this assay and single exon deletions/duplications may not be detected based on the breakpoints of the rearrangement. The actual breakpoints for the deletion or duplication may extend beyond or be within the exon(s) reported. This test is not intended to detect duplications of 2 or fewer exons in size, though these may be identified. Single exon deletions are reported but called at a lower sensitivity. Diagnostic errors can occur due to rare sequence variations. In some cases, variants may not be identified due to technical limitations caused by the presence of pseudogenes, repetitive, or homologous regions. This test is not intended to detect low-level mosaic or somatic variants, gene conversion events, complex inversions, translocations, mitochondrial DNA (mtDNA) mutations, or repeat expansions. Interpretation of this test result may be impacted if this patient has had an allogeneic stem cell transplantation. Noncoding 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.
BACKGROUND INFORMATION: Marfan Syndrome (FBN1) Sequencing and Deletion/Duplication

CHARACTERISTICS: Marfan syndrome is a connective tissue disorder affecting the ocular, skeletal, and cardiovascular systems with a high degree of clinical variability. Common ocular findings include myopia, ectopia lentis, retinal detachment, glaucoma, and early cataracts. Skeletal involvement may include bone overgrowth and joint laxity, disproportionally long extremities, pectus excavatum/carinatum, and scoliosis. Cardiovascular findings include aortic dilatation/dissection, mitral and/or tricuspid valve prolapse, and enlargement of the proximal pulmonary artery. Cardiovascular disease management is necessary to decrease morbidity and early mortality.

EPIDEMIOLOGY: Prevalence is 1 in 5,000 to 1 in 10,000.

CAUSE: Pathogenic germline variants in the FBN1 gene

INHERITANCE: Autosomal dominant. De novo pathogenic variants are causative for 25 percent of cases.

PENETRANCE: Complete, but age dependent.

CLINICAL SENSITIVITY: 95-98 percent.

GENE TESTED: FBN1 (NM_000138)

METHODOLOGY: Probe hybridization-based 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 to confirm reported variants that do not meet acceptable quality metrics. A proprietary bioinformatic algorithm was used to detect large (single exon-level or larger) deletions or duplications in the indicated genes. Large deletions/duplications confirmed using an orthogonal exon-level microarray. Human genome build 19 (Hg 19) was used for data analysis.

ANALYTICAL SENSITIVITY/SPECIFICITY: The analytical sensitivity

is approximately 99 percent for single nucleotide variants (SNVs) and greater than 93 percent for insertions/duplications/deletions (indels) from 1-10 base pairs in size. Indels greater than 10 base pairs may be detected, but the analytical sensitivity may be reduced. Deletions of 2 exons or larger are detected with sensitivity greater than 97 percent; single exon deletions are detected with 62 percent sensitivity. Duplications of 3 exons or larger are detected at greater than 83 percent sensitivity. Specificity is greater than 99.9 percent for all variant classes.

LIMITATIONS: A negative result does not exclude a diagnosis of Marfan syndrome or other FBN1-related disorders. This test only detects variants within the coding regions and intron-exon boundaries of the FBN1 gene. Deletions/duplications/insertions of any size may not be detected by massively parallel sequencing. Regulatory region variants and deep intronic variants will not be identified. Precise breakpoints for large deletions or duplications are not determined in this assay and single exon deletions/duplications may not be detected based on the breakpoints of the rearrangement. The actual breakpoints for the deletion or duplication may extend beyond or be within the exon(s) reported. This test is not intended to detect duplications of 2 or fewer exons in size, though these may be identified. Single exon deletions are reported but called at a lower sensitivity. Diagnostic errors can occur due to rare sequence variations. In some cases, variants may not be identified due to technical limitations caused by the presence of pseudogenes, repetitive, or homologous regions. This test is not intended to detect low-level mosaic or somatic variants, gene conversion events, complex inversions, translocations, mitochondrial DNA (mtDNA) mutations, or repeat expansions. Interpretation of this test result may be impacted if this patient has had an allogeneic stem cell transplantation. Noncoding 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.

VERIFIED/REPORTED DATES

Procedure	Accession	Collected	Received	Verified/Reported
Marfan Syndrome (FBN1) Specimen	25-117-400472	4/27/2025 2:46:00 PM	4/29/2025 8:36:57 AM	5/9/2025 2:35:00 PM
Marfan Syndrome (FBN1) Interpretation	25-117-400472	4/27/2025 2:46:00 PM	4/29/2025 8:36:57 AM	5/9/2025 2:35:00 PM

END OF CHART

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