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

Physician: Doctor, Example

Patient: Patient, Example

DOB	1/23/1984
Gender:	Male
Patient Identifiers:	01234567890ABCD, 012345
Visit Number (FIN):	01234567890ABCD
Collection Date:	00/00/0000 00:00

Cardiomyopathy and Arrhythmia Panel, Sequencing and Deletion/Duplication

ARUP test code 2010183

Cardiomyopathy/Arrhythmia Panel Specimen: Whole Blood

Cardiomyopathy/Arrhythmia Panel Interp: Negative

INDICATION FOR TESTING
Clinical diagnosis of dilated cardiomyopathy.

RESULT
No pathogenic variants were detected in any of the genes tested.

INTERPRETATION
No pathogenic variants were identified by massively parallel sequencing of the coding regions and exon-intron boundaries of the genes tested. No large exonic deletions and duplications were identified in the genes tested. This result decreases the likelihood of, but does not exclude, a heritable form of cardiomyopathy or arrhythmia. Please refer to the background information included in this report for a list of the genes analyzed and limitations of this test.

RECOMMENDATIONS
Medical screening and management should rely on clinical findings and family history. Genetic consultation is recommended.

COMMENTS
Likely benign and benign variants are not reported.

This result has been reviewed and approved by [redacted]

BACKGROUND INFORMATION: Cardiomyopathy and Arrhythmia Panel, Sequencing and Deletion/Duplication

CHARACTERISTICS: Inherited cardiomyopathy and arrhythmia disorders are genetically and phenotypically heterogeneous. Phenotypes include hypertrophic cardiomyopathy (HCM), dilated cardiomyopathy (DCM), arrhythmogenic right ventricular cardiomyopathy (ARVC), left ventricular noncompaction (LVNC), catecholaminergic polymorphic ventricular tachycardia (CPVT), Brugada syndrome (BrS), long QT syndrome (LQTS), and short QT syndrome (SQTS).

EPIDEMIOLOGY: The prevalence of HCM is 1 in 500, DCM is greater than 1 in 500, ARVC is 1 in 1000, LQTS is 1 in 3,000, CPVT is 1 in 10,000, and it is unknown for BrS, LVNC, and SQTS.

CAUSE: Pathogenic germline variants in genes associated with cardiomyopathy and arrhythmia such as nuclear genes encoding

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

sarcomeric or desmosomal proteins, cardiac ion channel components and cytoskeletal proteins, or pathogenic variants within the mitochondrial genome.

INHERITANCE: Is gene dependent and can be autosomal recessive, autosomal dominant, X-linked or mitochondrial.

PENETRANCE: Variable; dependent on gene and variant.

CLINICAL SENSITIVITY: Dependent on clinical phenotype. Estimated at 50 percent for ARVC, 15-30 percent for BrS, 60 percent for CPVT, 30-40 percent for DCM, 50-60 percent for non-syndromic familial HCM, and 60-75 percent for LQTS.

GENES TESTED: ABCC9, ACTC1, ACTN2, ANK2, ANKRD1, BAG3**, CACNA1C, CACNB2, CASQ2, CAV3, CRYAB**, CSRP3, DES, DMD, DSC2, DSG2, DSP, DTNA, EMD**, EYA4, FHL1**, FKRP, FKTN, GAA, GATAD1**, GLA, GPD1L, JPH2, JUP, KCNE1, KCNE2, KCNE3, KCNH2, KCNJ2, KCNQ1, LAMA4, LAMP2, LDB3, LMNA, MYBPC3, MYH6, MYH7, MYL2, MYL3, MYLK2, MYOT, MYOZ2, MYPN, NEXN, PKP2, PLN, PRKAG2, RBM20, RYR2, SCN1B, SCN2B, SCN3B, SCN4B, SCN5A, SGCA, SGCB, SGCD, SGCG, SLC25A4, SNTA1, TAZ**, TCAP, TGFB3, TMEM43, TNNC1, TNNI3, TNNT2, TPM1, TRDN**, TRPM4, TTN*, TTR, VCL

* One or more exons are not covered by sequencing for the indicated gene; see limitations section below.
** Deletion/duplication detection is not available for this gene.

METHODOLOGY: Targeted 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. A custom tiled comparative genomic hybridization array (aCGH) was used to detect large deletions or duplications in the indicated subset of genes. 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 cardiomyopathy or arrhythmia. This test only detects variants within the coding regions and intron-exon boundaries of the targeted genes. Variants in the mitochondrial genome are not detected. Regulatory region variants and deep intronic variants will not be identified and breakpoints of large deletions/duplications will not be determined. Single exon deletions/duplications or deletions/duplications less than 1kb may not be detected. 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.

The following regions are not sequenced due to technical limitations of the assay:
TTN(NM_001267550) exon(s) 172,174,175,176,177,178,179,180,181,182,183,184,185,186,187,188,189,190,191,192,193,194,195,196,197,215
TTN(NM_133378) exon(s) 153,154,155

Single exon deletions/duplications will not be called for the

following exons:
ACTN2(NM_001103) 17; CACNB2(NM_001167945) 7; DMD(NM_000109) 1; DSC2(NM_024422) 1; DTNA(NM_001390) 16,21; KCNH2(NM_000238) 13; KCNQ1(NM_000218) 16; KCNQ1(NM_181798) 1; MYBPC3(NM_000256) 10,24; MYH6(NM_002471) 24,28; MYH7(NM_000257) 29; PKP2(NM_004572) 6; PRKAG2(NM_001304527) 1; PRKAG2(NM_001304531) 2; PRKAG2(NM_016203) 5; SGCB(NM_000232) 1; SGCG(NM_000231) 8; TGFB3(NM_003239) 7; TRPM4(NM_001321285) 4; TRPM4(NM_017636) 7; TTN(NM_001267550) 158,173,176,185,191,194;TTN(NM_133378) 114,148,155,156,167,170

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
Cardiomyopathy/Arrhythmia Panel Specimen	21-085-402602	00/00/0000 00:00	00/00/0000 00:00	00/00/0000 00:00
Cardiomyopathy/Arrhythmia Panel Interp	21-085-402602	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