

500 Chipeta Way, Salt Lake City, Utah 84108-1221

phone: 801-583-2787, toll free: 800-522-2787

Tracy I. George, MD, Chief Medical Officer

Patient Age/Gender: 24 years Female

Specimen Collected: 10-Mar-21 14:02

Hypertrophic Cardiomyopathy by NGS | Received: 10-Mar-21 14:02 Report/Verified: 10-Mar-21 14:05

Procedure	Result	Units	Reference Interval
Hypertrophic Cardiomyopathy Specimen	Whole Blood		
Hypertrophic Cardiomyopathy Interp	Negative <sup>f1 i1</sup>		

**Result Footnote**

f1: Hypertrophic Cardiomyopathy Interp  
INDICATION FOR TESTING  
Left ventricular hypertrophy

**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. This result decreases the likelihood of, but does not exclude, a heritable form of hypertrophic cardiomyopathy. 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 of this individual should rely on clinical findings and family history. Cardiology and genetic consultations are recommended.

**COMMENTS**

Likely benign and benign variants are not included in this report [remove the following phrase for non-NY cases], but are available upon request.

**Test Information**

i1: Hypertrophic Cardiomyopathy Interp  
BACKGROUND INFORMATION: Hypertrophic Cardiomyopathy Panel,  
Sequencing

**CHARACTERISTICS:** Familial hypertrophic cardiomyopathy (HCM) is a genetically heterogeneous disorder characterized by unexplained left ventricular hypertrophy (LVH). Common symptoms include shortness of breath, chest pain, palpitations, orthostasis, and syncope. Individuals with HCM may remain asymptomatic. Affected individuals are at risk for arrhythmias, outflow tract obstruction, thromboembolic complications, heart failure, and sudden cardiac death. Onset of familial HCM is often in adolescence or early adulthood. Syndromic forms of HCM, which include extracardiac manifestations, can present as isolated LVH.

**EPIDEMIOLOGY:** Prevalence of HCM is 1:500.

**CAUSE:** Pathogenic germline variants in sarcomeric genes and other genes associated with HCM.

\*=Abnormal, #=Corrected, C=Critical, f=Result Footnote, H=High, i=Test Information, L=Low, t=Interpretive Text, @=Performing lab

**Unless otherwise indicated, testing performed at:**

**ARUP Laboratories**

500 Chipeta Way, Salt Lake City, UT 84108

Laboratory Director: Tracy I. George, MD

**ARUP Accession:** n/a**Report Request ID:** 14708243**Printed:** 10-Mar-21 14:07

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**Test Information**

i1: Hypertrophic Cardiomyopathy Interp

INHERITANCE: Typically autosomal dominant for familial HCM. Genes with X-linked, autosomal recessive, and mitochondrial inheritance are also associated. De novo variation, compound heterozygous, or digenic heterozygous variants have been reported.

PENETRANCE: Variable.

CLINICAL SENSITIVITY: 50-60 percent for familial HCM, 20-30 percent for isolated HCM.

GENES TESTED: ACTC1, ACTN2, AGL, ALPK3, BRAF\*, CACNA1C, CSRP3, DES, FHL1, FLNC\*, GAA, GLA, HRAS, JPH2, KRAS, LAMP2, MAP2K1, MAP2K2, MYBPC3, MYH7, MYL2, MYL3, NRAS, PLN, PRKAG2\*, PTPN11, RAF1, RIT1, SOS1, TNNC1, TNNI3, TNNT2, TPM1, TTR

\* 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. Human genome build 19 (Hg 19) was used for data analysis.

ANALYTICAL SENSITIVITY/SPECIFICITY: 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 hypertrophic cardiomyopathy. This test only detects variants within the coding regions and intron-exon boundaries of the targeted genes. Mitochondrial genes are not interrogated. Regulatory region variants, large deletions/duplications/inversions, 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 mosaic or 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 are not analyzed.

The following regions are not sequenced due to technical limitations of the assay:

BRAF (NM\_004333) exon(s) 5,18

FLNC (NM\_001458) exon(s) 47,48

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**Test Information**

i1: Hypertrophic Cardiomyopathy Interp  
PRKAG2 (NM\_016203) exon(s) 10,13

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.

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