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

Physician: Doctor, Example

Patient: Patient, Example

DOB	4/24/2020
Gender:	Female
Patient Identifiers:	01234567890ABCD, 012345
Visit Number (FIN):	01234567890ABCD
Collection Date:	01/01/2017 12:34

Very Long-Chain Acyl-CoA Dehydrogenase Deficiency (ACADVL) Sequencing and Deletion/Duplication

ARUP test code 2004212

VLCAD FGA Specimen	Whole Blood	
VLCAD (ACADVL) Interpretation	**See Note**	*

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

TEST PERFORMED - 2004212
TEST DESCRIPTION - Very Long-Chain Acyl-CoA Dehydrogenase Deficiency (ACADVL) Sequencing and Deletion/Duplication
INDICATION FOR TEST - Confirm Diagnosis

RESULT
One variant of uncertain significance was detected in the ACADVL gene.

DNA VARIANT
Classification: Uncertain
Gene: ACADVL
Nucleic Acid Change: c.250A>G; Heterozygous
Amino Acid Alteration: p.Thr84Ala

INTERPRETATION
One copy of a variant of uncertain clinical significance, c.250A>G; p.Thr84Ala, was detected in the ACADVL gene by sequencing. No pathogenic variants were detected by deletion/duplication analysis. If the identified variant is later determined to be pathogenic, this individual would be predicted to be at least a carrier of very long-chain acyl-CoA dehydrogenase (VLCAD) deficiency. However, even if the identified variant is confirmed to be pathogenic, by itself, it would not be causative for VLCAD deficiency.

Evidence for variant classification: The ACADVL c.250A>G; p.Thr84Ala variant (rs755575335), to our knowledge, is not reported in the medical literature or gene-specific databases. This variant is found on only four chromosomes (4/251482 alleles) in the Genome Aggregation Database. The threonine at codon 84 is moderately conserved, and computational analyses (SIFT, PolyPhen-2) predict that this variant is tolerated. However, due to limited information, the clinical significance of the p.Thr84Ala variant is uncertain at this time.

RECOMMENDATIONS
The diagnosis and management of VLCAD deficiency should rely on clinical symptoms and biochemical/functional assays. Genetic consultation is recommended. Surveillance of the literature for new information concerning the uncertain variant is recommended.

COMMENTS
Reference Sequence: GenBank # NM_000018.3 (ACADVL)
Nucleotide numbering begins at the "A" of the ATG initiation codon.
Likely benign and benign variants are not included in this report.

This result has been reviewed and approved by [redacted]

BACKGROUND INFORMATION: Very Long-Chain Acyl-CoA Dehydrogenase Deficiency/VLCAD (ACADVL) Deletion/Duplication:

CHARACTERISTICS: Fatty acid beta-oxidation disorder leading to hypoketotic hypoglycemia, dicarboxylic aciduria, hepatic failure, Reye-like symptoms, cardiomyopathy, skeletal myopathy, and sudden death. Clinical presentation varies in severity and age of onset.
INCIDENCE: Approximately 1 in 40,000.
INHERITENCE: Autosomal recessive.
CAUSE: Pathogenic ACADVL gene mutations.
CLINICAL SENSITIVITY: May be as high as 95 percent.
METHODOLOGY: Bidirectional sequencing of the entire coding region and intron-exon boundaries of the ACADVL gene. Multiplex Ligation-dependent Probe Amplification (MLPA) to detect large ACADVL coding region deletions/duplications.
ANALYTICAL SENSITIVITY AND SPECIFICITY: 99 percent.
LIMITATIONS: Diagnostic errors can occur due to rare sequence variations. Regulatory region mutations and deep intronic mutations will not be detected; deletion/duplication breakpoints will not be determined. Deletions/duplications in exon 2 of ACADVL will not be detected.

Test developed and characteristics determined by ARUP Laboratories. See Compliance Statement C: aruplab.com/CS

VERIFIED/REPORTED DATES

Procedure	Accession	Collected	Received	Verified/Reported
VLCAD FGA Specimen	20-141-401252	5/20/2020 9:01:00 AM	5/21/2020 1:19:53 PM	6/4/2020 8 03:00 AM
VLCAD (ACADVL) Interpretation	20-141-401252	5/20/2020 9:01:00 AM	5/21/2020 1:19:53 PM	6/4/2020 8 03:00 AM

END OF CHART

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