Client: ARUP Example Report Only
500 Chipeta Way
Salt Lake City, UT 84108
UNITED STATES

Physician: arup, arup

Patient: Genomics, VLCAD NGS 1

DOB	
Sex:	Female
Patient Identifiers:	36445
Visit Number (FIN):	36764
Collection Date:	2/23/2022 11:00

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

ARUP test code 3004419

VLCAD Specimen	Whole Blood
VLCAD Interp	Negative

RESULT
No pathogenic variants were detected in the ACADVL gene.

INTERPRETATION
No pathogenic variants were identified by massively parallel sequencing of the coding regions and exon-intron boundaries of the ACADVL gene. No large exonic deletions and duplications were identified in the ACADVL gene. This result decreases the likelihood that this individual is affected with, or a carrier of, very long-chain acyl-CoA dehydrogenase (VLCAD) deficiency. Please refer to the background information included in this report for limitations of this test.

RECOMMENDATIONS
The diagnosis and management of VLCAD deficiency should rely on clinical symptoms and biochemical/functional assays. Genetic consultation is recommended.

COMMENTS
Likely benign and benign variants are not reported.

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

CHARACTERISTICS: VLCAD deficiency is a long-chain fatty acid oxidation disorder associated with three phenotypes that vary in age of onset and severity. Clinical symptoms may include cardiomyopathy, pericardial effusion, hypotonia, hepatomegaly, hypoketotic hypoglycemia, skeletal myopathy, exercise intolerance, and rhabdomyolysis induced by exercise.

EPIDEMIOLOGY: Approximately 1 in 40,000

CAUSE: Pathogenic germline variants in the ACADVL gene

INHERITANCE: Autosomal recessive

CLINICAL SENSITIVITY: 95-97 percent

GENE TESTED: ACADVL (NM_000018)

METHODOLOGY: Probe hybridization-based capture of all coding exons and exon-intron junctions of the ACADVL gene, followed by

massively parallel sequencing. Sanger sequencing was performed as necessary to fill in regions of low coverage and confirm reported variants. A proprietary bioinformatic algorithm was used to detect large (single exon-level or larger) deletions or duplications in the indicated genes. Large deletions/duplications were 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 VLCAD deficiency. This test only detects variants within the coding regions and intron-exon boundaries of the ACADVL 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. 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.

VERIFIED/REPORTED DATES

Procedure	Accession	Collected	Received	Verified/Reported
VLCAD Specimen	22-054-104287	2/23/2022 11:00:00 AM	2/23/2022 11:02:02 AM	2/23/2022 12:18:00 PM
VLCAD Interp	22-054-104287	2/23/2022 11:00:00 AM	2/23/2022 11:02:02 AM	2/23/2022 12:18:00 PM

END OF CHART

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