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

Physician: Doctor, Example

Patient: Patient, Example

DOB	Unknown
Gender:	Unknown
Patient Identifiers:	01234567890ABCD, 012345
Visit Number (FIN):	01234567890ABCD
Collection Date:	00/00/0000 00:00

Exome Reanalysis (Originally Tested at ARUP - No Specimen Required)

ARUP test code 3001457

Exome Reanalysis Interpretation	Negative

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

TEST PERFORMED
Exome reanalysis was performed using the original exome sequencing data from report date 10/03/2015, the current bioinformatics pipeline, updated population frequency data, and any new information provided about the patient's clinical findings. The overall result remains unchanged. Variants from the original exome report that are now believed unlikely related to the patient's phenotype have been moved to the end of the report.

RESULT
Primary findings: Negative
Secondary findings: Negative

KEY CLINICAL FINDINGS
Developmental delay, intellectual disability, coarse facial features, feeding difficulties, hypoplastic fifth fingernails.

HPO terms used: HP:0001263 (Global developmental delay), HP:0001249 (Intellectual disability), HP:0000280 (Coarse facial features), HP:0011968 (Feeding difficulties), HP:0008398 (Hypoplastic fifth fingernail).

INTERPRETATION
No variants were identified that are predicted to be causative for the patient's phenotype.

Consent was not provided for reporting of secondary pathogenic variants in the list of genes that the American College of Medical Genetics and Genomics (ACMG) recommends reporting in all individuals undergoing exome sequencing (Miller, 2023).

LIKELY BENIGN VARIANT
Gene: DCHS1 (NM_003737.4)
Variant: c.704G>A; p.Arg235Gln - Heterozygous
Chr11(GRCh37):g.6662141
Frequency: gnomAD: 258 out of 281932 chromosomes, overall MAF 0.000915
Computational prediction programs: Uncertain (REVEL: 0.362)

Due to new information regarding the frequency of this variant in the general population this variant has been reclassified from a variant of uncertain significance to likely benign.

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

REFERENCES
Miller DT, et al. ACMG SF v3.2 list for reporting of secondary findings in clinical exome and genome sequencing: A policy statement of the American College of Medical Genetics and Genomics (ACMG). Genet Med. 2023 Jun 15:100866. PMID: 37347242.

This result has been reviewed and approved by [redacted]

BACKGROUND INFORMATION: Exome Reanalysis (Originally Tested at ARUP - No Specimen Required)

CHARACTERISTICS: Exome reanalysis may be performed when a previous exome analysis fails to determine the etiology for a suspected genetic condition. Rapid progress in the understanding of gene-disease relationships, in addition to improvements in variant-calling pipelines, underscores the utility of performing a bioinformatic-restricted reanalysis.

CLINICAL SENSITIVITY: Approximately 10-28 percent of non-diagnostic clinical exomes receive a definitive diagnosis upon reanalysis.

METHODOLOGY: A FastQ file of massively parallel sequencing (MPS) data from the original exome test was processed through our current variant calling and annotation pipeline. If the original sample(s) was available, Sanger sequencing was performed as necessary to confirm reported variants. Human genome build 19 (Hg19) was used for data analysis.

LIMITATIONS OF ANALYSIS: The human exome cannot be completely analyzed as some genes have not been identified while others, due to technical limitations, cannot either be sequenced or interpreted. Some pathogenic variants reside in regions outside the exome. This test only detects variants within the coding regions and intron-exon boundaries of genes targeted in the original capture. Regulatory region variants and deep intronic variants will not be identified. Mitochondrial DNA is not analyzed. Chromosomal phase of identified variants may not be determined. Deletions/duplications/insertions of any size may not be detected by MPS. Diagnostic errors can occur due to rare sequence variations. 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. Please see Additional Technical Information located at http://ltd.aruplab.com/Tests/Pub/2006332 for more information. A negative result does not exclude a genetic diagnosis.

LIMITATIONS FOR REPORTING AND INTERPRETATION: Only variants in genes suspected to be associated with the patient's symptoms are reported, with the exception of secondary pathogenic findings, if elected. Additionally, de novo and/or rare compound heterozygous variants in genes of unknown clinical relevance maybe reported. Incorrect reporting of biological relationships among family members may affect result interpretation. Mode of inheritance, reduced penetrance, and genetic heterogeneity could reduce clinical sensitivity. Interpretation of this test result may be impacted if this patient has had an allogeneic stem cell transplantation.

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

VERIFIED/REPORTED DATES

Procedure	Accession	Collected	Received	Verified/Reported
Exome Reanalysis Interpretation	24-352-103063	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