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

Physician: Doctor, Example

Patient: Patient, Example

DOB	12/31/1752
Sex:	Female
Patient Identifiers:	01234567890ABCD, 012345
Visit Number (FIN):	01234567890ABCD
Collection Date:	00/00/0000 00:00

Genome Sequencing

ARUP test code 3019943

WGS PRO Interp

Negative

TEST PERFORMED
Genome Sequencing
Specimens tested: Proband and both parents

INDICATION FOR TESTING
Abnormality of eye movement, abnormal cerebellar vermis morphology, abnormal head movements, cerebellar dysplasia, neurodevelopmental delay

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RESULT SUMMARY
Primary findings- Related to Phenotype: Negative

Primary Findings- Possibly Related to Phenotype: Negative

Secondary Findings: Negative

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

The following were not identified in the genome data:
-Clinically relevant sequence variants in the nuclear and mitochondrial genome related to the patient's reported phenotype.
-Clinically relevant copy number variants (CNVs) in the nuclear genome related to the patient's reported phenotype.
-Homozygous loss of SMN1 exon 7, causative for spinal muscular atrophy.

No secondary findings variants were detected. The American College of Medical Genetics and Genomics (ACMG) recommends analysis of specific, medically actionable secondary findings (SF) genes in all consented individuals undergoing genome sequencing even though these variants may not be related to the indication for testing (1). Although no secondary findings variants involving genes from the ACMG SF v3.3 list (2) were identified in this individual, this result does not exclude the possibility this individual may carry a pathogenic variant involving one of these genes, or another gene that is not included on this list. If there is clinical suspicion or family

history of a genetic condition associated with one of the ACMG SF genes, additional targeted testing should be considered as genome sequencing will not identify all pathogenic variants involving these genes. Note that single pathogenic variants in autosomal recessive ACMG SF genes are not generally reported.

RECOMMENDATIONS
- Genetic counseling.
- If after one year from the date of this report, clinical suspicion remains high for a genetic etiology, or upon encounter of new significant clinical findings, a reanalysis may be ordered, for a fee, using these original sequencing data. Please order ARUP test code 3005939, Whole Genome Reanalysis.

NOTES
97.1% of bases in the targeted genome were covered by more than 20 sequencing reads.

Health care providers with questions may contact an ARUP genetic counselor at (800) 242-2787 ext. 2141.

Reference
1: Miller DT, Lee K, Gordon AS, et al. Recommendations for reporting of secondary findings in clinical exome and genome sequencing, 2021 update: a policy statement of the American College of Medical Genetics and Genomics (ACMG). Genet Med. 2021. PMID: 34012069.
2: Lee K, Abul-Husn NS, Amendola LM et al. ACMG SF v3.3 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 2025. PMID:40568962.

This result has been reviewed and approved by [redacted]

BACKGROUND INFORMATION: Genome Sequencing

CHARACTERISTICS: The purpose of whole genome sequencing (WGS) is to establish a diagnosis when a genetic condition is suspected but a patients clinical features are not suggestive of a single disorder. WGS utilizes next generation sequencing (NGS) to interrogate more than 92 percent of the genome (excluding telomeric and centromeric regions), including the mitochondrial genome. The inclusion of parental samples is strongly recommended for accurate variant interpretation.

CLINICAL SENSITIVITY: Varies based on clinical symptoms, family history, inheritance pattern, and previous clinical evaluations.

METHODOLOGY: Genomic DNA is extracted from whole blood or saliva, prepared into libraries, then sequenced by NGS. Variant calling is performed using the Illumina DRAGEN Bio-IT Platform incorporated with a custom bioinformatics pipeline. Human genome build 19 (Hg 19) is used for data analysis. The analytical procedure identifies single nucleotide variants (SNVs), small insertions/deletions, and copy number variants (CNVs) known, or suspected to be, disease-causing.

ANALYTICAL SENSITIVITY: The analytical sensitivity of this assay is 99.2 percent for SNVs, 99.2 percent for insertions/duplications/deletions (indels) ranging in size from 1-15 base pairs (bp), and 96.9 percent for indels 16-50 bp in size. For mitochondrial SNVs with heteroplasmy greater than or

equal to 3 percent, analytical sensitivity is 98.4 percent. Analytical sensitivity for CNVs is greater than 99.9 percent for variants 10 kb or larger in size, and 84.6 percent for those 1-10 kb in size.

LIMITATIONS OF ANALYSIS: A negative result does not exclude a genetic diagnosis. Due to technical limitations, some regions of the genome cannot be sequenced or interpreted. SNVs in intergenic or deep intronic regions will only be evaluated if an effect on gene expression is predicted based on annotation software. Diagnostic errors can occur due to rare sequence variations. In some cases, variants may not be identified due to technical limitations related to pseudogenes or repetitive or homologous regions. This assay is not designed to detect somatic variants, mosaic variants, trinucleotide repeats, uniparental disomy, absence of heterozygosity (AOH), or mitochondrial CNVs. This assay is not designed to detect CNVs greater than 50 bp but less than 1 kb in size. See Additional Technical Information located at http://ltd.aruplab.com/Tests/Pub/3019943 for more information on whole genome sequencing.

REPORTING CONSIDERATIONS: Variant interpretation and reporting is limited to variants known or predicted to have an impact on gene expression. Mitochondrial variant reporting is limited to SNVs with heteroplasmy greater than or equal to 10 percent. Heteroplasmy may vary across tissue types; therefore, reported levels reflect only the tested sample. Variable penetrance and genetic heterogeneity may impact clinical sensitivity. Reported variants are limited to those known or suspected to be causative of the patient's phenotype. Patients may opt in for reporting of secondary pathogenic/likely pathogenic findings, including those involving medically actionable genes on the ACMG Secondary Findings Gene List located at http://ltd.aruplab.com/Tests/Pub/3019943. This gene list is updated periodically and is only accurate for this sample at the time of reporting. Absence of parental data, whether through non-submission, technical failure, or misattributed parentage, will impact interpretation of proband results. Likewise, interpretation of test results may be impacted if any of the tested individuals have undergone allogeneic stem cell transplantation.

This test was developed and its performance characteristics determined by ARUP Laboratories. It has not been cleared or approved by the U.S. 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.

EER WGS PRO — EERUnavailable

VERIFIED/REPORTED DATES

Procedure	Accession	Collected	Received	Verified/Reported
WGS PRO Interp	25-323-105558	00/00/0000 00:00	00/00/0000 00:00	00/00/0000 00:00
EER WGS PRO	25-323-105558	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