



1-800-533-1710
Whole Exome Sequencing

WESDX

PATIENT NAME TESTING, WESDX				ORDER NUMBER L623000175
PATIENT ID SA00151670	DATE OF BIRTH 08/18/1984	AGE 37 Y	SEX Male	REQUESTED BY CLIENT CLIENT
COLLECTED 3/23/2022, 7:00 AM	RECEIVED 3/23/2022, 10:35 AM	REPORTED 3/24/2022, 8:23 AM		
The collected, received, and reported dates and times on the report are in the time zone of the performing location. 7028846 MCL RochesterCampus Rochester MN 55901				CLIENT ORDER NUMBER SA00151670 CLIENT MRN SA00151670

SPECIMEN
WB Whole Blood

INTERPRETATION
A full copy of the interpretative report is available as a PDF appended to this cover sheet and is ready to review. To discuss the availability of further testing options or for assistance in the interpretation of these results, Mayo Clinic Laboratory genetic counselors can be contacted at 1-800-533-1710.

RELEASED BY
Nicole J. Boczek, Ph.D.

Code : MCR Laboratory : Mayo Clinic Laboratories - Rochester Main Campus
Lab Director : WILLIAM G MORICE, II MD, PhD CLIA Certificate : 24D0404292

Address : 200 FIRST STREET SW
ROCHESTER MN 55905

TESTING, WESDX

Patient ID: 22-14482 | Family ID: F4565 | Date of birth: 8/18/1984 (37 years old) | Male | Order number: L623000175

Requested by: CLIENT, CLIENT
Requesting Institution: 7028846 | MCL
Rochester Campus | Rochester, MN
55901

Client MRN: SA00151670
Client Order Number: SA00151670

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Clinical Information Summary

Based on information from the ordering provider, the patient's clinical features and history include seizures, developmental regression, and failure to thrive.

Samples were also received from the patient's reportedly unaffected biological mother and father.

Results Summary

A consultation with a genetics professional is recommended. Test results should be interpreted in the context of clinical findings, family history, and other laboratory data. Evaluation for additional features and appropriate screening and/or management measures should be considered.

RESULTS

Likely Causative

No reportable likely causative variants were identified

Possibly Relevant

No reportable possibly relevant variants were identified

Secondary Findings (v3.0)

No reportable secondary findings were identified

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INTERPRETATION

Likely Causative

No variants highly suspected of causing the patient's reported clinical features were identified. However, this does not rule out a genetic cause for the patient's clinical history. A genetic consultation is recommended.

Possibly Relevant

No reportable variants in genes possibly relevant to the patient's reported clinical features were identified.

Secondary Findings (v3.0)

No reportable secondary findings were identified in the medically actionable genes analyzed in accordance with ACMG recommendations. Whole exome sequencing is not specifically designed to rule out all pathogenic variants in this list of genes. If there is clinical suspicion for a condition caused by one of these genes, focused genetic testing may be indicated.

Method

Next generation sequencing (NGS) is performed on DNA extracted from the patient and all submitted comparator samples to test for the presence of variants in coding regions and intron/exon boundaries. The human genome reference GRCh37/hg19 build is used for sequence read alignment. Variants are called using an optimized bioinformatics package (Sentieon). At least 99% of the bases are covered at a read depth over 30X. Sensitivity is estimated at above 99% for single nucleotide variants, above 94% for deletion-insertions (delins) less than 40 base pairs (bp), above 95% for deletions up to 75 bp and insertions up to 47 bp. This assay also detects most copy number variants (deletions/duplications) involving three or more exons. In some instances, resolution of copy number variants less than three exons may be detected, however the reliability of this detection is variable due to isolated reduction in sequence coverage or inherent genomic complexity. Resulting variants are filtered, annotated using public and proprietary resources, and presented for analysis and interpretation using a vended interpretation tool, Franklin by Genoox. Confirmation of select reportable variants in the proband and submitted comparator samples may be performed by alternate methodologies based on internal laboratory criteria.

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There may be regions of genes that cannot be effectively evaluated by sequencing or deletion and duplication analysis as a result of technical limitations of the assay, including regions of homology, high guanine-cytosine (GC) content, and repetitive sequences.

Disclaimer**CLINICAL CORRELATIONS**

This report contains variants in genes related to the patient's reported clinical features. The interpretation is based upon the clinical information reported by the ordering health care provider(s) at the time of testing. Misinterpretation of results may occur if the clinical information provided is inaccurate or incomplete.

Familial segregation analysis may help inform the clinical significance of reported variants. To discuss the availability of further testing options, or for assistance in the interpretation of these results, Mayo Clinic Laboratory genetic counselors can be contacted at 1-800-533-1710.

Previously reported variants in this patient may not be re-reported or detected for any of the following reasons: insufficient phenotypic overlap, minor allele frequency greater than 1%, outside of the capture region for this assay, genotype quality filters, and/or the variant is currently classified as likely benign or benign.

It is possible that a variant may not be recognized as the underlying cause of disease due to incomplete scientific knowledge about the function of all genes in the human genome and/or the impact of variants in those genes. Deidentified variant information may be shared in public genetic databases, such as GeneMatcher or ClinVar.

TECHNICAL LIMITATIONS

Next-generation sequencing may not detect all types of genomic variants. In rare cases, false-negative or false-positive results may occur. The depth of coverage may be variable for some regions. Given these limitations, negative results do not rule out the diagnosis of a genetic disorder. If a specific clinical disorder is suspected, evaluation by alternative methods can be considered.

There may be regions of genes that cannot be effectively evaluated by sequencing or deletion and duplication analysis as a result of technical limitations of the assay, including regions of homology, high guanine-cytosine (GC) content, and repetitive sequences. Confirmation of select reportable variants will be performed by alternate methodologies based on internal laboratory criteria.

This test is not designed to detect deep intronic variants, trinucleotide repeat variants, balanced structural rearrangements (such as translocations and inversions), or variants in the mitochondrial genome. If separate mitochondrial genome testing is desired, please order Mitochondrial Full Genome Analysis by Next-Generation Sequencing (MITOP).

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This test is not designed to detect low levels of mosaicism or to differentiate between somatic and germline variants. If there is a possibility that any detected variant is somatic, additional testing may be necessary to clarify the significance of results.

If the patient has had an allogeneic marrow transplant or a recent heterologous blood transfusion, these results may be inaccurate due to the presence of donor DNA. Call Mayo Clinic Laboratories for instructions for testing patients who have received a bone marrow transplant.

SECONDARY FINDINGS

Patients are evaluated for medically actionable secondary findings as recommended by the published ACMG guidelines unless they opt-out. Refer to the results and interpretation sections of the report for the ACMG secondary findings gene list version used at the time of testing. Reportable variants include pathogenic variants and likely pathogenic variants. Variants of uncertain significance (VUS) in these genes are not reported unless they overlap with the patient's phenotype. Presence of the variant in comparator samples is stated, unless they opt-out of secondary findings. Variants that are present in a family member but absent from the proband are not evaluated.

The absence of a reportable secondary finding does not guarantee that there are no known or expected pathogenic variants in these genes, as portions of the genes may not be adequately covered by this testing methodology. If a patient opts-out of receiving these results, these variants will not be reported unless they occur in a gene that is clinically related to the patient's presenting phenotype.

VARIANT EVALUATION

Variant curation is performed using published ACMG-AMP recommendations as a guideline. Other gene-specific guidelines may also be considered. Variants classified as benign or likely benign are not reported.

Results from in silico evaluation tools may change over time and should be interpreted with caution and professional clinical judgment.

RECLASSIFICATION OF VARIANTS

See www.mayocliniclabs.com (Test ID WESDX) for information regarding the laboratory's policy for reclassification of variants.

EXOME REANALYSIS

Healthcare providers may contact the laboratory at 800-533-1710 any time to request reanalysis of the patient's exome; a charge may apply for reanalysis.

TEST CLASSIFICATION

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This test was developed and its performance characteristics determined by Mayo Clinic in a manner consistent with CLIA requirements. This test has not been cleared or approved by the U.S. Food and Drug Administration.

Released By

Nicole J. Boczek, PhD on 3/24/2022

Performing Site Legend

Code	Laboratory	Address	Lab Director	CLIA Certificate
MCR	Mayo Clinic Laboratories – Rochester Main Campus	200 First Street SW, Rochester, MN 55905	William G. Morice M.D. Ph.D	24D0404292