MAYO CLINIC LABORATORIES

1-800-533-1710

MSUDP

Maple Syrup Urine Disease Gene Panel, Varies

Patient ID	Patient Name		Birth Date	Gender	Age
SA00148272	TESTINGRNV, ATLAS		2000-10-07	F	20
Order Number	**Client Order Number**	**Ordering Physician**	**Report Notes**		
SA00148272	SA00148272	CLIENT,CLIENT			
Account Information		**Collected**			
C7028846 DLMP Rochester		06 Oct 2021 12:00			

MSUD Gene Panel

Interpretation

MCR

BCKDHA, c.1312T>A (p.Y438N), PATHOGENIC
The homozygous c.1312T>A (p.Y438N) variant in the BCKDHA gene (mim: 608348) is an established pathogenic variant. Variants in the BCKDHA gene have been associated with autosomal recessive maple syrup urine disease. This result is supportive of a diagnosis of autosomal recessive maple syrup urine disease. Clinical correlation is recommended.

This result should be interpreted in the context of clinical findings, family history, and other laboratory testing.

Consultation with a genetics professional is recommended for interpretation of this result and to determine whether familial testing may be of benefit to this family. Genetic testing for family members is available by ordering FMTT / Familial Mutation, Targeted Testing for the specific variant(s) detected. Please contact the laboratory at 1–800–533–1710 or the online test catalog at www.mayocliniclabs.com
for information about FMTT.

Result Summary

MCR

Pathogenic Variants Detected

Result

MCR

The following homozygous PATHOGENIC variant was detected:
BCKDHA (NM_000709.4), p.Y438N (p.Tyr438Asn), c.1312T>A, Chr19(GRCh37):g.41930487

No additional reportable variants were detected within all other tested genes. See the Genes Analyzed section for a complete list of genes evaluated by this assay.

Test Description

MCR

Evaluation of 6 genes associated with maple syrup urine disease

Specimen

MCR

WB Whole Blood

Resources

MCR

Disease specific information, including current therapies may be available at:
1. GeneReviews: https://www.ncbi.nlm.nih.gov/books/NBK1116/
2. https://www.fda.gov/drugs

Information regarding clinical trials, if available, can be found at the following sites:
1. ClinicalTrials.gov: http://clinicaltrials.gov/ct2/search/advanced

Method

MCR

Next generation sequencing (NGS) and/or Sanger sequencing was performed to test for the presence of variants in coding regions and intron/exon boundaries of the genes analyzed, as well as select regions that have known pathogenic variants. The human genome reference GRCh37/hg19 build was used for sequence read alignment. At least 99% of the bases are covered at a read depth >30X. Sensitivity is estimated at >99% for single nucleotide variants, >94% for indels up to 39 base pairs, >95% for deletions up to 75 base pairs and insertions up to 47 base pairs. NGS and/or a PCR-based quantitative method was performed to test for the presence of deletions and duplications in the genes analyzed. See the Genes Analyzed field for a list of genes tested.

There may be regions of genes that cannot be effectively evaluated for sequencing or deletion and duplication analysis as a result of technical limitations of the assay, including regions of homology, high GC content, and repetitive sequences. Confirmation of select reportable variants was performed by alternate methodologies based on internal laboratory criteria. See www.mayocliniclabs.com
MSUDP for details regarding genes with regions not routinely covered.

Genes Analyzed

MCR

BCKDHA, BCKDHB, BCKDK, DBT, DLD, and PPM1K

Test Environment
Standard Template

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

MAYO CLINIC LABORATORIES

Patient ID	Patient Name		Birth Date	Gender	Age
SA00148272	TESTINGRNV, ATLAS		2000-10-07	F	20
Order Number	**Client Order Number**	**Ordering Physician**	**Report Notes**		
SA00148272	SA00148272	CLIENT,CLIENT			
Account Information		**Collected**			
C7028846 DLMP Rochester		06 Oct 2021 12:00			

Disclaimer

[1] MCR

Clinical Correlations
An online research opportunity called GenomeConnect (genomeconnect.org), a project of ClinGen, is available for the recipient of this genetic test. This patient registry collects de-identified genetic and health information to advance the knowledge of genetic variants. Mayo Clinic is a collaborator of ClinGen. This may not be applicable for all tests.

If testing was performed because of a clinically significant family history it is often useful to first test an affected family member. Detection of a reportable variant(s) in an affected family member would allow for more informative testing of at risk individuals.

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.

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 target regions, but assay performance below the minimum acceptable criteria or for failed regions will be noted. 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 for sequencing or deletion and duplication analysis as a result of technical limitations of the assay, including regions of homology, high GC content, and repetitive sequences. Confirmation of select reportable variants was performed by alternate methodologies based on internal laboratory criteria.

Additionally, low level mosaic variants may not be detected.

This test is not designed 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.

Genes may be added or removed based on updated clinical relevance. Please refer to the Targeted Genes and Methodology Details for the MSUD Gene Panel in the Special Instructions section of the Test Catalog for the most up to date list of genes included in this test.

Reclassification of Variants Policy
See www.mayocliniclabs.com MSUDP for information regarding the laboratory's policy for reclassification of variants.

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.

Released By

MCR

Devin Oglesbee, Ph.D.

Received: 07 Oct 2021 16:14 **Reported:** 15 Oct 2021 13:32

Environment Test Standard Template

Laboratory Notes

[1] 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.

Performing Site Legend

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MAYO CLINIC

1-800-533-1710

MSUD Gene Panel

MSUDP

PATIENT NAME				ORDER NUMBER
TESTINGRNV, ATLAS				**L107000446**
PATIENT ID SA00148272	DATE OF BIRTH 10/07/2000	AGE 20 Y	SEX Female	REQUESTED BY CLIENT CLIENT
COLLECTED 10/6/2021, 12:00 PM	RECEIVED 10/7/2021, 4:14 PM	REPORTED 10/15/2021, 1:32 PM		
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 SA00148272 CLIENT MRN SA00148272

TEST DESCRIPTION

Evaluation of 6 genes associated with maple syrup urine disease

SPECIMEN

WB Whole Blood

RESULT SUMMARY

Pathogenic Variants Detected

RESULT

The following homozygous PATHOGENIC variant was detected:
BCKDHA (NM_000709.4), p.Y438N (p.Tyr438Asn), c.1312T>A, Chr19(GRCh37):g.41930487

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INTERPRETATION

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RESOURCES

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METHOD

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GENES ANALYZED

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7028846
MCL RochesterCampus
Rochester MN 55901

CLIENT ORDER NUMBER
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SA00148272

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TEST CLASSIFICATION
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RELEASED BY

Devin Oglesbee, Ph.D.

Code : MCR Laboratory : Mayo Clinic Laboratories - Rochester Main Campus Address : 200 FIRST STREET SW
Lab Director : WILLIAM G MORICE, II MD, PhD CLIA Certificate : 24D0404292 ROCHESTER MN 55905