



1-800-533-1710

Hemiplegic Migraine Gene Panel

HMEP

PATIENT NAME TESTRNV, IMPLEMENTATION				ORDER NUMBER L624000482
PATIENT ID X100383796	DATE OF BIRTH 02/19/1968	AGE 54 Y	SEX Male	REQUESTED BY PROVIDER UNKNOWN
COLLECTED 3/24/2022, 11:00 AM	RECEIVED 3/25/2022, 10:14 AM	REPORTED 4/12/2022, 2:32 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 X100383796 CLIENT MRN 321

TEST DESCRIPTION

Evaluation of 9 genes associated with hemiplegic migraine

SPECIMEN

WB Whole Blood

RESULT SUMMARY

Likely Pathogenic Variant Detected

RESULT

The following heterozygous **LIKELY PATHOGENIC** variant was detected:
ATP1A2 (NM_000702.3), chr1(GRCh37):g.160098814C>T, c.1261C>T, p.Arg421* (p.R421*)

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.

INTERPRETATION

ATP1A2 c.1261C>T (p.R421*): The heterozygous c.1261C>T (p.R421*) nonsense variant in the ATP1A2 gene (MIM:182340) is classified as likely pathogenic. Pathogenic variants in the ATP1A2 gene are associated with autosomal dominant familial hemiplegic migraine and autosomal dominant alternating hemiplegia of childhood. This variant is predicted to cause premature protein truncation and is expected to result in loss-of-function. To our knowledge, this variant has not been reported in affected individuals. This variant has been observed at a very low frequency in exome and/or genome sequencing data gathered from large, multi-ethnic cohorts, suggesting it is a rare variant (1,2). This result is supportive of a diagnosis of an ATP1A2-related disorder for this individual. Clinical correlation is recommended.

Individuals may have a pathogenic variant in one of the interrogated genes that is not detectable by the methods utilized. Additionally, the clinical phenotype that is observed in this individual and/or family may be due to a pathogenic variant or variants in another gene not targeted by this test.

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 reproductive risk assessment and 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.

REFERENCES:

- 1) dbSNP: www.ncbi.nlm.nih.gov/snp; Sherry ST, Ward M and Sirotkin K. dbSNP-Database for Single Nucleotide Polymorphisms and Other Classes of Minor Genetic Variation. Genome Res. 1999;9:677-679 (PMID 10447503)
- 2) gnomAD Browser: gnomad.broadinstitute.org/; Karczewski K, Francioli LC, MacArthur DG, et al. The mutational



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constraint spectrum quantified from variation in 141,456 humans. Nature. 2020; 581(7809):434-443 (PMID 32461654)

RESOURCES

Disease specific information, including current therapies may be available at:

1. GeneReviews: <https://www.ncbi.nlm.nih.gov/books/NBK1388/>
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

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 (TEST ID HMEP) for details regarding genes with regions not routinely covered.

GENES ANALYZED

ATP1A2, ATP1A3, CACNA1A, COL4A1, NOTCH3, POLG, PRRT2, SCN1A and SLC2A1

DISCLAIMER

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



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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 Hemiplegic Migraine with or without Epilepsy 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 (TEST ID HMEP) 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.

TEST CLASSIFICATION

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

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