Test Definition: IMSNP

Inherited Motor and Sensory Neuropathy Gene Panel, Varies

Overview

Useful For

Establishing a molecular diagnosis for patients with hereditary motor and sensory neuropathy (HMSN) or Charcot-Marie-Tooth (CMT) disease

Identifying variants within genes known to be associated with HMSN or CMT disease, allowing for predictive testing of at-risk family members

Genetics Test Information

This test utilizes-next generation sequencing to detect single nucleotide and copy number variants in 87 genes associated with hereditary motor and sensory neuropathy: *AARS1, ABCD1, AIFM1, ARSA, ATP1A1, ATP7A, BAG3, BSCL2, C1orf194, CHCHD10, CNTNAP1, COX10, COX6A1, CTDP1, DGAT2, DHH, DNM2, DYNC1H1, EGR2, ERCC8, FAM126A, FBLN5, FGD4, FIG4, FMR1, GALC, GAN, GARS1, GBF1, GDAP1, GJB1, GLA, GNB4, HARS1, HINT1, HK1, HSPB1, HSPB8, IGHMBP2, INF2, KARS1, LAMA2, LITAF, LMNA, LRSAM1, MARS1, MCM3AP, MFN2, MORC2, MPV17, MPZ, MTMR2, NDRG1, NEFH, NEFL, PEX7, PHYH, PLEKHG5, PLP1, PMP2, PMP22, PNKP, POLG, PRPS1, PRX, RAB7A, SACS, SBF1, SBF2, SCO2, SH3TC2, SLC12A6, SLC25A46, SORD, SOX10, SURF1, TDP1, TFG, TRIM2, TRPV4, TSFM, TTR, TUBB3, TWNK, TYMP, VPS13D,* and *YARS1*. For more information see Method Description and Targeted Genes and Methodology Details for Inherited Motor and Sensory Neuropathy Gene Panel.

Identification of a disease-causing variant may assist with diagnosis, prognosis, clinical management, recurrence risk assessment, familial screening, and genetic counseling for hereditary motor and sensory neuropathy.

Testing Algorithm

For information see Hereditary Peripheral Neuropathy Diagnostic Algorithm

Special Instructions

- Informed Consent for Genetic Testing
- Hereditary Peripheral Neuropathy Diagnostic Algorithm
- Molecular Genetics: Neurology Patient Information
- Informed Consent for Genetic Testing (Spanish)
- Targeted Genes and Methodology Details for Inherited Motor and Sensory Neuropathy Gene Panel

Method Name

Sequence Capture and Targeted Next-Generation Sequencing (NGS) followed by Polymerase Chain Reaction (PCR) and Sanger Sequencing

NY State Available

Yes

Specimen

Specimen Type

Varies

Ordering Guidance

First tier testing for a diagnosis of Charcot-Marie-Tooth disease type 1 is available; order PMPDD / *PMP22* Gene, Large Deletion/Duplication Analysis, Varies.

Targeted testing for familial variants (also called site-specific or known variants testing) is available for the genes on this panel. See FMTT / Familial Variant, Targeted Testing, Varies. To obtain more information about this testing option, call 800-533-1710.

Customization of this panel and single gene analysis for any gene present on this panel are available. For more information see CGPH / Custom Gene Panel, Hereditary, Next-Generation Sequencing, Varies.

Specimen Required

A previous bone marrow transplant from an allogenic donor will interfere with testing. For information about testing patients who have received a bone marrow transplant, call 800-533-1710.

Submit only 1 of the following specimens:

Specimen Type: Whole blood
Container/Tube: Lavender top (EDTA) or yellow top (ACD)
Specimen Volume: 3 mL
Collection Instructions:
1. Invert several times to mix blood.
2. Send whole blood specimen in original tube. **Do not aliquot**.
3. Whole blood collected postnatal from an umbilical cord is also acceptable. See Additional Information.
Specimen Stability Information: Ambient (preferred) 4 days/Refrigerated 4 days/Frozen 4 days
Additional Information:
1. Specimens are preferred to be received within 4 days of collection. Extraction will be attempted for specimens received after 4 days, and DNA yield will be evaluated to determine if testing may proceed.
2. To ensure minimum volume and concentration of DNA is met, the requested volume must be submitted. Testing may be canceled if DNA requirements are inadequate.
3. For postnatal umbilical cord whole blood specimens, maternal cell contamination studies are recommended to ensure test results reflect that of the patient tested. A maternal blood specimen is required to complete maternal cell contamination studies. Order MATCC / Maternal Cell Contamination, Molecular Analysis, Varies on both the cord blood and maternal blood specimens under separate order numbers.

Specimen Type: Saliva
Patient Preparation: Patient should not eat, drink, smoke, or chew gum 30 minutes prior to collection.
Supplies:
DNA Saliva Kit High Yield (T1007)
Saliva Swab Collection Kit (T786)
Container/Tube:
Preferred: High-yield DNA saliva kit

Acceptable: Saliva swab
Specimen Volume: 1 Tube if using T1007 or 2 swabs if using T786
Collection Instructions: Collect and send specimen per kit instructions.
Specimen Stability Information: Ambient (preferred) 30 days/Refrigerated 30 days
Additional Information: Saliva specimens are acceptable but not recommended. Due to lower quantity/quality of DNA yielded from saliva, some aspects of the test may not perform as well as DNA extracted from a whole blood sample. When applicable, specific gene regions that were unable to be interrogated will be noted in the report. Alternatively, additional specimen may be required to complete testing.

Specimen Type: Extracted DNA
Container/Tube:
Preferred: Screw Cap Micro Tube, 2 mL with skirted conical base
Acceptable: Matrix tube, 1 mL
Collection Instructions:
1. The preferred volume is at least 100 mcL at a concentration of 75 ng/mcL.
2. Include concentration and volume on tube.
Specimen Stability Information: Frozen (preferred) 1 year/Ambient/Refrigerated
Additional Information: DNA must be extracted in a CLIA-certified laboratory or equivalent and must be extracted from a specimen type listed as acceptable for this test (including applicable anticoagulants). Our laboratory has experience with Chemagic, Puregene, Autopure, MagnaPure, and EZ1 extraction platforms and cannot guarantee that all extraction methods are compatible with this test. If testing fails, one repeat will be attempted, and if unsuccessful, the test will be reported as failed and a charge will be applied. If applicable, specific gene regions that were unable to be interrogated due to DNA quality will be noted in the report.

Forms

1. **New York Clients-Informed consent is required.** Document on the request form or electronic order that a copy is on file.
The following documents are available:
-Informed Consent for Genetic Testing (T576)
-Informed Consent for Genetic Testing (Spanish) (T576)
2. Molecular Genetics: Neurology Patient Information
3. If not ordering electronically, complete, print, and send a Neurology Specialty Testing Client Test Request (T732) with the specimen.

Specimen Minimum Volume

See Specimen Required

Reject Due To

All specimens will be evaluated at Mayo Clinic Laboratories for test suitability.

Specimen Stability Information

Specimen Type	Temperature	Time	Special Container
Varies	Varies		

Clinical & Interpretive

Clinical Information

Hereditary motor and sensory neuropathy, or Charcot-Marie-Tooth (CMT) disease, is a major category of inherited peripheral neuropathies and is the most frequently inherited neuromuscular disorder. Individuals with CMT typically present with slowly progressive muscle weakness and atrophy primarily affecting the distal extremities.

Traditionally, the classification of CMT was based on nerve conduction velocity (NCV) and inheritance. The three neuropathy types based on NCV include demyelinating, axonal (non-demyelinating), and dominant intermediate CMT. Demyelinating CMT has a NCV less than 35 m/s and involves slowly progressive muscle weakness and atrophy and sensory loss. Often it can include pes cavus foot deformity and bilateral foot drop. Axonal CMT has a NCV greater than 45 m/s and includes distal muscle weakness and atrophy. Individuals tend to be less disabled and have less sensory loss than those with demyelinating neuropathy. Dominant-intermediate CMT has a NCV of 35 to 45 m/s and is consistent with a typical CMT phenotype.

If a tiered testing approach is preferred, healthcare professionals for individuals with demyelinating polyneuropathy and an autosomal dominant family history of similar features can consider ordering testing for large deletions and duplications in the *PMP22* gene (PMPDD / *PMP22* Gene, Large Deletion/Duplication Analysis, Varies) as a first-tier test. However, copy number variants involving *PMP22* would also be identified by this assay. Duplications in the *PMP22* gene account for as much as 50% of all CMT.

Interpretation

All detected variants are evaluated according to American College of Medical Genetics and Genomics recommendations.(1) Variants are classified based on known, predicted, or possible pathogenicity and reported with interpretive comments detailing their potential or known significance.

Cautions

Clinical Correlations:
Test results should be interpreted in the context of clinical findings, family history, and other laboratory data. Misinterpretation of results may occur if the information provided is inaccurate or incomplete.

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 in an affected family member would allow for more informative testing of at-risk individuals.

To discuss the availability of additional testing options or for assistance in the interpretation of these results, contact the Mayo Clinic Laboratories genetic counselors at 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; 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 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 validated to detect 95% of deletions up to 75 base pairs (bp) and insertions up to 47 bp. Deletions-insertions (delins) of 40 or more bp, including mobile element insertions, may be less reliably detected than smaller delins.

Deletion/Duplication Analysis:
This analysis targets single and multi-exon deletions/duplications; however, in some instances, single exon resolution cannot be achieved due to isolated reduction in sequence coverage or inherent genomic complexity. Balanced structural rearrangements (such as translocations and inversions) may not be detected.

This test is not designed to detect low levels of mosaicism or to differentiate between somatic mutations 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. For detailed information regarding gene specific performance and technical limitations, see Method Description or contact a laboratory genetic counselor.

If the patient has had an allogeneic hematopoietic stem cell transplant or a recent blood transfusion, 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.

Reclassification of Variants:
Currently, it is not standard practice for the laboratory to systematically review previously classified variants on a regular basis. The laboratory encourages healthcare providers to contact the laboratory at any time to learn how the classification of a particular variant may have changed over time. Due to broadening genetic knowledge, it is possible that the laboratory may discover new information of relevance to the patient. Should that occur, the laboratory may issue an amended report.

Variant Evaluation:
Evaluation and categorization of variants are performed using published American College of Medical Genetics and Genomics and the Association for Molecular Pathology recommendations as a guideline.(1) Other gene-specific guidelines may also be considered. Variants are classified based on known, predicted, or possible pathogenicity and reported with interpretive comments detailing their potential or known significance. Variants classified as benign or likely benign are not reported.

Multiple in silico evaluation tools may be used to assist in the interpretation of these results. The accuracy of predictions made by in silico evaluation tools is highly dependent upon the data available for a given gene, and periodic updates to these tools may cause predictions to change over time. Results from in silico evaluation tools should be interpreted with caution and professional clinical judgment.

Rarely, incidental or secondary findings may implicate another predisposition or presence of active disease. These findings will be carefully reviewed to determine whether they will be reported.

Clinical Reference

1. Richards S, Aziz N, Bale S, et al. Standards and guidelines for the interpretation of sequence variants: a joint consensus recommendation of the American College of Medical Genetics and Genomics and the Association for Molecular Pathology. Genet Med. 2015;17(5):405-424
2. Klein CJ. Charcot-Marie-Tooth disease and other hereditary neuropathies. Continuum (Minneap Minn). 2020;26(5):1224-1256
3. Bird TD. Charcot-Marie-Tooth hereditary neuropathy In: Adam MP, Feldman J, Mirzaa GM, et al, eds. GeneReviews [Internet]. University of Washington, Seattle; 1998. Updated January 23, 2025. Accessed March 24, 2025. Available at www.ncbi.nlm.nih.gov/books/NBK1358/
4. Pisciotta C, Bertini A, Tramacere I, et al. Clinical spectrum and frequency of Charcot-Marie-Tooth disease in Italy: Data from the National CMT Registry. Eur J Neurol. 2023;30(8):2461-2470. doi:10.1111/ene.15860

Performance

Method Description

Next-generation sequencing (NGS) and/or Sanger sequencing are performed to test for the presence of variants in coding regions and intron/exon boundaries of the genes analyzed, as well as some other regions that have known disease-causing 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 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. NGS and/or a polymerase chain reaction-based quantitative method is performed to test for the presence of deletions and duplications in the genes analyzed.

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. See Targeted Genes and Methodology Details for Inherited Motor and Sensory Neuropathy Gene Panel for details regarding the targeted genes analyzed for each test and specific gene regions not routinely covered.(Unpublished Mayo method)

Confirmation of select reportable variants may be performed by alternate methodologies based on internal laboratory criteria.

Genes analyzed: *AARS1, ABCD1, AIFM1, ARSA, ATP1A1, ATP7A, BAG3, BSCL2, C1orf194, CHCHD10, CNTNAP1, COX10, COX6A1, CTDP1, DGAT2, DHH, DNM2, DYNC1H1, EGR2, ERCC8, FAM126A, FBLN5, FGD4, FIG4, FMR1, GALC, GAN, GARS1, GBF1, GDAP1, GJB1, GLA, GNB4, HARS1, HINT1, HK1, HSPB1, HSPB8, IGHMBP2, INF2, KARS1, LAMA2, LITAF, LMNA, LRSAM1, MARS1, MCM3AP, MFN2, MORC2, MPV17, MPZ, MTMR2, NDRG1, NEFH, NEFL, PEX7, PHYH, PLEKHG5, PLP1, PMP2, PMP22, PNKP, POLG, PRPS1, PRX, RAB7A, SACS, SBF1, SBF2, SCO2, SH3TC2, SLC12A6, SLC25A46, SORD, SOX10, SURF1, TDP1, TFG, TRIM2, TRPV4, TSFM, TTR, TUBB3, TWNK, TYMP, VPS13D,* and *YARS1*

PDF Report
Supplemental

Day(s) Performed
Varies

Report Available
21 to 28 days

Specimen Retention Time
Whole blood/Saliva 30 days (if available); Extracted DNA: 3 months

Performing Laboratory Location
Mayo Clinic Laboratories - Rochester Main Campus

Fees & Codes

Fees
- Authorized users can sign in to Test Prices for detailed fee information.
- Clients without access to Test Prices can contact Customer Service 24 hours a day, seven days a week.
- Prospective clients should contact their account representative. For assistance, contact Customer Service.

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

CPT Code Information
81448

LOINC® Information

Test ID	Test Order Name	Order LOINC® Value
IMSNP	Motor and Sensory Neuropathy Panel	103728-2

Result ID	Test Result Name	Result LOINC® Value
617585	Test Description	62364-5
617586	Specimen	31208-2
617587	Source	31208-2
617588	Result Summary	50397-9
617589	Result	82939-0
617590	Interpretation	69047-9

618181	Additional Results	82939-0
617591	Resources	99622-3
617592	Additional Information	48767-8
617593	Method	85069-3
617594	Genes Analyzed	48018-6
617595	Disclaimer	62364-5
617596	Released By	18771-6