Hereditary Neuropathies: Sequencing Panel

**Test Code:** MM350  
**Turnaround time:** 6 weeks  
**CPT Codes:** 28120 x1, 28135 x1, 28140 x1, 28145 x1, 28146 x1, 28147 x1, 28148 x1

### Condition Description

Hereditary neuropathies are a collection of inherited disorders affecting the peripheral nervous system. The hereditary neuropathies are divided into four major subcategories: hereditary motor and sensory neuropathy, hereditary sensory neuropathy, hereditary sensory and autonomic neuropathy, and hereditary motor neuropathy. Charcot-Marie-Tooth disease is of the most common types of the hereditary motor and sensory neuropathy. Clinical presentation typically includes sensory symptoms like pain in the feet and hands, motor symptoms such as weakness in the lower leg and feet muscles. Some hereditary neuropathies can affect the autonomic nerves, resulting in impaired sweating, postural hypotension, or insensitivity to pain.

The estimated prevalence of hereditary neuropathies is about 1 in 2500 individuals. A myriad of genes are associated with hereditary neuropathies.

### Genes

- AARS, ALDH3A2, APTX, ATL1, ATM, ATP7A, BSCL2, CACNB4, COQ8A, CTPD1, DCTN1, DNAJB2, DNM2, DNMT1, DYNC1IH1, EGR2, FAM134B, FGD4, FGF14, FGF4, FXN, GAN, GARS, GDAP1, GJB1, GLA, HOXD10, HSPB1, HSPB8, IGHMBP2, IKBP1, ITPR1, KCNA1, KCNQ3, KIF1A, KIF1B, KIF5A, L1CAM, LITAF, LMNA, LRSAM1, MED28, MFN2, MPZ, MRE11, MTMR2, MTTP, NDRG1, NEFL, NGF, NIP1, NTRK1, PEX7, PHNY, PLEXH5, PLP1, PMP22, PNPLA8, POLG, PRKCG, PRPS1, PRX, RAB7A, REEP1, SAC5, SBF2, SCN9A, SH3TC2, SLC1, SLC1A6, SLC1A7, SLC1B2, SLC2A1, SPC, SPTBN2, SPTLC1, SPTLC2, TDP1, TRPV4, TTBK2, TTPA, TTR, TWNK, WASHC5, WNK1, YARS, ZFYVE26, ZFYVE27

### Indications

This test is indicated for:

- Confirmation of a clinical diagnosis of a neuropathy.

### Methodology

**Next Generation Sequencing:** In-solution hybridization of all coding exons is performed on the patient's genomic DNA. Although some deep intronic regions may also be analyzed, this assay is not meant to interrogate most promoter regions, deep intronic regions, or other regulatory elements, and does not detect single or multi-exon deletions or duplications. Direct sequencing of the captured regions is performed using next generation sequencing. The patient's gene sequences are then compared to a standard reference sequence. Potentially causative variants and areas of low coverage are Sanger-sequenced. Sequence variations are classified as pathogenic, likely pathogenic, benign, likely benign, or variants of unknown significance. Variants of unknown significance may require further studies of the patient and/or family members.

### Detection

**Next Generation Sequencing:** Clinical Sensitivity: Unknown. Pathogenic variants in the promoter region, some pathogenic variants in the introns and other regulatory element pathogenic variants cannot be detected by this analysis. Large deletions will not be detected by this analysis. Results of molecular analysis should be interpreted in the context of the patient's clinical and/or biochemical phenotype.

Analytical Sensitivity: ~99%.

### Specimen Requirements

Submit only 1 of the following specimen types

#### Type: Whole Blood

Specimen Requirements:

In EDTA (purple top) tube:
- Infants (2 years): 3-5 ml
- Older Children & Adults: 5-10 ml.

Specimen Collection and Shipping: Ship sample at room temperature with overnight delivery.

#### Type: Isolated DNA

Disclaimer: This information is confidential and subject to change without notice. It may not be reproduced in whole or part unless authorized in writing by an authorized EGL representative.
Specimen Requirements:

In microtainer: 60 ug

Isolation using the Qiagen™ Puregene kit for DNA extraction is recommended.

Specimen Collection and Shipping: Refrigerate until time of shipment in 100 ng/ul of TE buffer. Ship sample at room temperature with overnight delivery.

Related Tests

- Charcot-Marie-Tooth (PRPS1 Gene Sequencing and Deletion/Duplication Analysis)
- Hereditary Neuropathies: Deletion/Duplication Panel