HENRY FORD HEALTH
CENTER FOR PRECISION DIAGNOSTICS

Hereditary Neuroendocrine Tumor Disorders Risk Panel (15 genes)

This Hereditary Neuroendocrine Tumor Disorders Risk Panel is a comprehensive analysis that identifies inherited risks for neuroendocrine cancers from isolated genomic DNA.

Testing Method and Background

This test utilizes Next Generation Sequencing (NGS) technology, which provides coverage of all coding exons and noncoding DNA in exon flanking regions (on average 50 bp) enriched using hybrid capture methodology. This assay can detect >99% of described mutations in the included genes, when present, including single nucleotide variants (point mutations), small insertions/deletions (1-25 bp), larger deletions and duplication (<100 bp), complex insertions/deletions, splice site mutations, whole-gene deletions/duplications and exon-level intragenic deletions/insertions in each gene targeted for analysis. All reportable copy number variants are confirmed by independent methodology.

A proportion of neuroendocrine cancer cases are caused by mutations in cancer predisposition genes. Neuroendocrine tumors from the gastrointestinal and pancreatobiliary tracts are heterogeneous tumors with diverse biologic and clinical behaviors that vary according to the primary tumor origin, type of neuroendocrine cell, and pathologic features. Pheochromocytomas and paragangliomas are genetically heterogeneous neural crest-derived cancers, with almost one third having a germline origin. This panel includes genes responsible for very rare hereditary cancer syndromes, such multiple endocrine neoplasia (MEN1, RET), tuberous sclerosis complex (TSC1, TSC2), neurofibromatosis type I (NF1), Von Hippel-Lindau syndrome (VHL), and hereditary paraganglioma-pheochromocytoma syndromes (MAX, SDHAF2, SDHB, SDHC, SDHD, TMEM127), along with another gene associated with increased risk for developing neuroendocrine tumors (FH).

Highlights of Hereditary Neuroendocrine Tumor Disorders Risk Panel (15 genes)

Targeted Region

Genes: FH, MAX, MEN1, MITF, NF1, RET, SHDA, SDHAF2, SDHB, SDHC, SDHD, TMEM127, TSC1, TSC2, VHL

- **Wide-ranging Coverage of Variants**
  Detects and provides coverage of all coding exons and noncoding DNA in exon flanking regions.
- **Accurate Results Using Clinically Validated Computational Data Analysis**
  A variety of mutation types (point, indels and duplications) are confirmed using computational data analysis for sequence variant calling, filtering and annotation.

Ordering Information

Get started (non-HFHS): Print a Hereditary Cancer Panels requisition form online at www.HenryFord.com/HFCPD

Get started (HFHS): Order through Epic using test “Hereditary Neuroendocrine Tumor Disorders Risk Panel” (DNA210000)

Specimen requirements:

- Peripheral Blood - 1-3ml in lavender top tube (EDTA) **Specimen stability: Ambient - 72 hours; Refrigerated - 1 week**
- Extracted DNA - from a CLIA-certified Laboratory

Cause for Rejection: Clotted, hemolyzed, or frozen specimens, improper anticoagulant, tubes not labeled with dual patient identification, non-dedicated tubes.

TAT: 10-14 business days (after Prior Authorization obtained)

Mail test material to:
Henry Ford Center for Precision Diagnostics
Pathology and Laboratory Medicine
Clinic Building, K6, Core Lab, E-655
2799 W. Grand Blvd., Detroit, MI 48202

CPT Codes: 81437, 81438, G0452

Contact us: Client Services, Account and Billing Set-up, and connect with a Molecular Pathologist at (313) 916-4DNA (4362)

For more information on Comprehensive Molecular Services, visit our website www.HenryFord.com/HFCPD

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