Hereditary Cancer Syndrome: Sequencing Panel

**Test Code:** MM200  
**Turnaround time:** 6 weeks  
**CPT Codes:** 81163 x1, 81201 x1, 81292 x1, 81295 x1, 81298 x1, 81317 x1, 81321 x1, 81403 x1, 81404 x2, 81405 x3, 81406 x6, 81408 x1

### Condition Description

Approximately 5-10% of all cancers are inherited, meaning that pathogenic variants in a single cancer susceptibility gene can predispose an individual to develop cancer and these pathogenic variants can be passed down in families. The risk for developing cancer can vary dramatically from syndrome to syndrome, from about a 55% risk of developing breast cancer in Peutz-Jeghers syndrome to as high as a 100% risk for colon cancer for familial adenomatous polyposis syndrome. Accurate and timely diagnoses are necessary to provide proper medical surveillance and treatment to affected and at-risk individuals.

Many of the inherited cancers syndromes and cancer susceptibility genes are phenotypically heterogeneous, making molecular testing necessary to confirm a clinical diagnosis. The traditional tiered, single gene approach to genetic testing for inherited cancer syndromes can be costly and time consuming. The Hereditary Cancer Syndrome Panel is designed to detect germline pathogenic variants in individuals with a suspected inherited cancer syndrome. This panel includes sequencing analysis for syndromes such as, Lynch syndrome, Cowden syndrome, Multiple Endocrine Neoplasia syndrome, Birt-Hogg Dube syndrome, and Li-Fraumeni syndrome. Additional syndromes are also tested for by this panel.

### Reference:


### Genes

- AIP, ALK, APC, ATM, BAP1, BARD1, BLM, BMPR1A, BRCA1, BRCA2, BRIP1, BUB1B, CDC73, CDH1, CDK4, CDKN1B, CDKN1C, CDKN2A, CHEK2, FH, FLCN, GPC3, MAX, MEN1, MET, MGMT, MLH1, MRE11, MSH2, MSH6, MUTYH, NBN, NF2, PALB2, PHOX2B, PMS2, POLD1, PParkinA1, PTCH1, PTEN, RAD50, RAD51C, RAD51D, RET, SDHAF2, SDHB, SDHC, SDHD, SMAD4, SMARCA4, SMARCB1, STK11, SUFU, TMEM127, TP53, TSC1, TSC2, VHL, WT1, XRCG2

### Indications

- Individuals with a clinical or suspected diagnosis of an inherited cancer syndrome based on personal or family history of cancer.

### 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. Mutations in the promoter region, some mutations in the introns and other regulatory element mutations cannot be detected by this analysis. Large deletions/duplications will not be detected by this analysis. Results of molecular analysis should be interpreted in the context of the patient's clinical/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

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.

**Special Instructions**

This test is for germline mutation analysis. DNA isolated from FFPE tumor samples is not suitable for this test.

**Related Tests**

- Endocrine Cancer: Sequencing Panel and Deletion/Duplication Panels.
- Pheochromocytoma-Paraganglioma: Sequencing and Deletion/Duplication Panels.
- Brain, CNS, and PNS Cancer: Sequencing and Deletion/Duplication Panels.
- High Risk Colorectal Cancer: Sequencing and Deletion/Duplication Panels.
- Renal Cancer: Sequencing and Deletion/Duplication Panels.
- Wilms Tumor: Sequencing and Deletion/Duplication Panels.
- Breast and Ovarian Cancer: Sequencing and Deletion/Duplication Panel.
- Melanoma: Sequencing and Deletion/Duplication Panels.
- Pancreatic Cancer: Sequencing and Deletion/Duplication Panels.
- Gastrointestinal and Colorectal Cancer: Sequencing and Deletion/Duplication Panels.