Gastrointestinal and Colorectal Cancer: Sequencing Panel

Test Code: MM209  
Turnaround time: 4 weeks  
CPT Codes: 81435 x1

Condition Description

Gastrointestinal cancer affects the gastrointestinal tract and accessory organs of digestion, including the esophagus, stomach, biliary system, pancreas, small intestine, large intestine, rectum and anus. Gastric cancer is a manifestation of a number of inherited cancer predisposition syndromes. The Gastrointestinal and Colorectal Cancer Panel targets genes known to be associated with various cancers that can develop in these organs and along the gastrointestinal tract.

The Gastrointestinal and Colorectal Cancer Panel also includes testing for the well-described hereditary cancer predisposition syndromes; Lynch syndrome, familial adenomatous polyposis (FAP), and MYH-associated polyposis (MAP). Lynch syndrome, FAP, and MutY homolog MAP are three major known types of inherited colorectal cancer, which account for up to 5% of all colorectal cancer cases. Lynch syndrome is most frequently caused by mutations in the mismatch repair genes MLH1, MSH2, MSH6, PMS2, and EPCAM, and is inherited in an autosomal dominant manner.

Familial adenomatous polyposis is manifested as colonic polyposis caused by mutations in the APC gene and is also inherited in an autosomal dominant manner. Finally, MYH-associated polyposis is caused by mutations in the MUTYH gene and is inherited in an autosomal recessive manner but may or may not be associated with polyps. There are variants of both familial adenomatous polyposis (Gardner syndrome—with extracolonic features—and Turcot syndrome, which features medulloblastoma) and Lynch syndrome (Muir-Torre syndrome features sebaceous skin carcinomas, and Turcot syndrome features glioblastomas). Although a clinical diagnosis of familial adenomatous polyposis can be made using colonoscopy, genetic testing is needed to inform at-risk relatives. Because of the overlapping phenotypes between attenuated familial adenomatous polyposis, MYH-associated polyposis, and Lynch syndrome, genetic testing is needed to distinguish among these conditions. This distinction is important, especially for women with Lynch syndrome, who are at increased risk for gynecological cancers.

Reference:

Genes

APC, ATM, BLM, BMPR1A, BRCA1, BRCA2, CDH1, CDKN2A, CHEK2, MLH1, MSH2, MSH6, MUTYH, PMS2, POLD1, PTEN, SMAD4, STK11, TP53

Indications

The test is indicated for:

- Individuals with a clinical or suspected diagnosis of gastrointestinal or colorectal 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.

**Type: Isolated DNA**

Specimen Requirements:

In microtainer: 60 ug

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

**Special Instructions**

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

**Related Tests**

- Hereditary Cancer Syndrome: Sequencing Panel.
- High Risk Colorectal Cancer: Sequencing Panel.
- Pancreatic Cancer: Sequencing Panel.
- Gastrointestinal and Colorectal Cancer: Deletion/Duplication Panel.