Gastrointestinal and Colorectal Cancer Panel: Sequencing and CNV Analysis

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 colon 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 polyposis. 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.

**Copy Number Analysis:** Comparative analysis of the NGS read depth (coverage) of the targeted regions of genes on this panel was performed to detect copy number variants (CNV). The accuracy of the detected variants is highly dependent on the size of the event, the sequence context and the coverage obtained for the targeted region. Due to these variables and limitations a minimum validated CNV size cannot be determined; however, single exon deletions and duplications are expected to be below the detection limit of this analysis.

**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. Results of molecular analysis should be interpreted in the context of the patient's clinical/biochemical phenotype.

Analytical sensitivity for sequence variant detection is ~99%.

**Specimen Requirements**

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Submit only 1 of the following specimen types

Type: Whole Blood (EDTA)

Specimen Requirements:
EDTA (Purple Top)
Infants and Young Children (2 years of age to 10 years old): 3-5 ml
Older Children & Adults: 5-10 ml
Autopsy: 2-3 ml unclotted cord or cardiac blood

Specimen Collection and Shipping:
Ship sample at room temperature for receipt at EGL within 72 hours of collection. Do not freeze.

Type: DNA, Isolated

Specimen Requirements:
Microtainer
15µg
Isolation using the Perkin Elmer™ Chemagen™ Chemagen™ Automated Extraction method or Qiagen™ Puregene kit for DNA extraction is recommended.

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

Type: Saliva

Specimen Requirements:
Oragene™ Saliva Collection Kit
Orangene™ Saliva Collection Kit used according to manufacturer instructions. Please contact EGL for a Saliva Collection Kit for patients that cannot provide a blood sample.

Specimen Collection and Shipping:
Please do not refrigerate or freeze saliva sample. Please store and ship at room temperature.

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.