



Hereditary Colon Cancer Multi-Gene Large Deletion and Duplication Analysis
Test ID: HCCD

USEFUL FOR:

- A second-tier test for patients in whom previous targeted gene mutation analyses for specific hereditary colorectal cancer-related genes were negative
- Dosage analysis is performed to detect large genomic deletions and duplications within the following genes: APC, AXIN2, BMPR1A, CDH1, CHEK2, EPCAM, MLH1, MLH3, MSH2, MSH6, TP53, PMS2, PTEN, SCG5-GREM1, SMAD4, and STK11
- Establishing a diagnosis of a hereditary colon cancer syndrome
- Identifying mutations within genes known to be associated with increased risk for colon cancer allowing for predictive testing of at-risk family members

METHODOLOGY: Gene Dosage Analysis by Array Comparative Genomic Hybridization (aCGH) or Polymerase Chain Reaction (PCR) followed by Multiplex Ligation-Dependent Probe Amplification (MLPA)

REFERENCE VALUES: An interpretive report will be provided.

SPECIMEN REQUIREMENTS: Specimen must arrive within 96 hours of collection.

Specimen Type: Whole blood

Container/Tube:

Preferred: Lavender top (EDTA) or yellow top (ACD)

Acceptable: Any anticoagulant

Specimen Volume: 3 mL

Collection Instructions:

1. Invert several times to mix blood.
2. Send specimen in original tube.

NOTE:

- New York Clients-Informed consent is required. Please document on the request form or electronic order that a copy is on file. An Informed Consent for Genetic Testing (Supply T576) is available in Special Instructions.
- Molecular Genetics-Colon Cancer Patient Information Sheet (Supply T521) in Special Instructions

SPECIMEN STABILITY INFORMATION:

Specimen Type	Temperature	Time
Varies	Ambient (preferred)	
	Frozen	
	Refrigerated	

CAUTIONS:

Clinical Correlations

- Some individuals who have involvement of 1 or more of the genes on the panel may have a mutation that is not identified by the methods performed. The absence of a mutation, therefore, does not eliminate the possibility of a hereditary colorectal cancer syndrome or other heritable risk for colon cancer. For predictive testing of asymptomatic individuals, it is important to first document the presence of a gene mutation in an affected family member.
- Test results should be interpreted in context of clinical findings, family history, and other laboratory data. Misinterpretation of results may occur if the information provided is inaccurate or incomplete.

Technical Limitations

- In some cases, DNA variants of undetermined significance may be identified.
- Rare polymorphisms exist that could lead to false-negative or false-positive results.
- In addition to disease-related probes, the multiplex ligation-dependent probe amplification technique utilizes probes localized to other chromosomal regions as internal controls. In certain circumstances, these control probes may detect other diseases or conditions for which this test was not specifically intended. Results of the control probes are not normally reported. However, in cases where clinically relevant information is identified, the ordering physician will be informed of the result and provided with recommendations for any appropriate follow-up testing.
- A previous bone marrow transplant from an allogenic donor will interfere with testing. Call Mayo Medical Laboratories at 1-800-533-1710 for instructions for testing patients who have received a bone marrow transplant.

Evaluation Tools

- Multiple in-silico evaluation tools were used to assist in the interpretation of these results. These tools are updated regularly; therefore, changes to these algorithms may result in different predictions for a given alteration. Additionally, the predictability of these tools for the determination of pathogenicity is currently unvalidated.

Reclassification Of Variants-Policy

- All detected alterations are evaluated according to American College of Medical Genetics and Genomics recommendations. Variants are classified based on known, predicted, or possible pathogenicity and reported with interpretive comments detailing their potential or known significance. At this time, it is not standard practice for the laboratory to systematically review likely deleterious alterations or variants of uncertain significance that are detected and reported. The laboratory encourages health care providers to contact the laboratory at any time to learn how the status of a particular variant may have changed over time.

CPT CODE:

81228-Cytogenomic constitutional (genome-wide) microarray analysis; interrogation of genomic regions for copy number variants (eg, Bacterial Artificial Chromosome [BAC] or oligo-based comparative genomic hybridization [CGH] microarray analysis)

81319- PMS2 (postmeiotic segregation increased 2 [*S.cerevisiae*] (eg, hereditary non-polyposis colorectal cancer, Lynch syndrome)) gene analysis; duplication/deletion variants

DAY(S) SET UP: Varies, weekly to every other week based on sample volume, will be run twice a month at minimum.

ANALYTIC TIME: 3 weeks

QUESTIONS: Contact your Mayo Medical Laboratories' Regional Manager or Marvin H. Anderson, Jr., MML Laboratory Technologist Resource Coordinator
Telephone: 800-533-1710