HENRY FORD HEALTH
CENTER FOR PRECISION DIAGNOSTICS

Colorectal Solid Tumor Gene Sequencing Panel

The Colorectal Solid Tumor Gene Sequencing Panel is a comprehensive genomic profile (CGP) test utilizing integrated DNA and RNA analysis of a wide range of oncogenes and tumor suppressor genes associated with colorectal cancer. The genes and types of variant analysis were carefully selected to include content cited by professional organizations such as the National Comprehensive Cancer Network (NCCN) and the European Society for Medical Oncology (ESMO). This test is used for diagnostic, prognostic, and predictive purposes.

Testing Method and Background

This panel test utilizes **Next Generation Sequencing (NGS) technology** to **simultaneously** interrogate 10 target genes associated with colorectal cancer to identify single nucleotide variants (SNVs), small insertions/deletions (Indels), gene amplifications and other copy number variants (CNVs), gene fusions, oncogenic splicing isoforms, Tumor Mutation Burden (TMB) and Microsatellite Instability (MSI) status. This assay utilizes tumor-only workflow with low quantity of input DNA and RNA (40 ng) and accurate detection of variants down to 5% mutant allele frequency from low-quality formalin fixed paraffin-embedded (FFPE) tissue blocks. The report includes information about clinically relevant biomarkers and genomic alterations to **help match patients to approved targeted therapies, immunotherapies, and consideration for enrollment in clinical trials.**

Highlights of the Colorectal Solid Tumor Gene Sequencing Panel (10 genes + TMB and MSI)

Genes Targeted

SNVs / Indels / CNVs: *BRAF, ERBB2, KRAS, NRAS, POLD1, POLE*

Gene Fusions / Splicing Isoforms: *NTRK1, NTRK2, NTRK3, RET*

Other Biomarkers: Tumor Mutation Burden (**TMB**) and Microsatellite Instability (**MSI**) status

- **Wide-ranging Coverage of Cancer-Related Variants and Biomarkers**
  Assessment of single-nucleotide variants, insertions/deletions, amplifications and other copy number variants, oncogenic gene fusions and splice variants, TMB and MSI status in one assay using DNA and RNA
- **Accurate Results from Low-Quality Samples**
  Sensitive variant detection with as little as 40 ng of input DNA and RNA, and as low as 5% mutant allele frequency, maximizes the results from low input sample types such as formalin fixed, paraffin embedded (FFPE) sections
- **Integrated, Streamlined Workflow**
  DNA and RNA are prepared in parallel with an integrated workflow following DNA shearing/cDNA synthesis

Ordering Information

Get started (non-HFHS): Print a Solid Tumor test requisition form online at www.HenryFord.com/HFCPD

Get started (HFHS): Order through Epic using test " Colorectal Solid Tumor Gene Sequencing Panel" (MOL8002 / HFHMO3)

Specimen requirements: The presence of adequate tumor materials submitted for analysis should be confirmed by a surgical pathologist. Sections should be confirmed to contain >50% tumor. If the submitted material for analysis contains <50% of tumor, areas of predominant tumor will be micro-dissected to enrich for neoplastic cells, if possible.

- Formalin-fixed, paraffin-embedded tissue, preferably no older than 2 years
- 5-6 tissue sections at 5-6 micron thickness (please include H&E slide and a copy of pathology report)
- Cytology slides (cell block with 500+ tumor cells, submit block or 5-6 tissue sections at 5-10 micron thickness depending on cellularity)

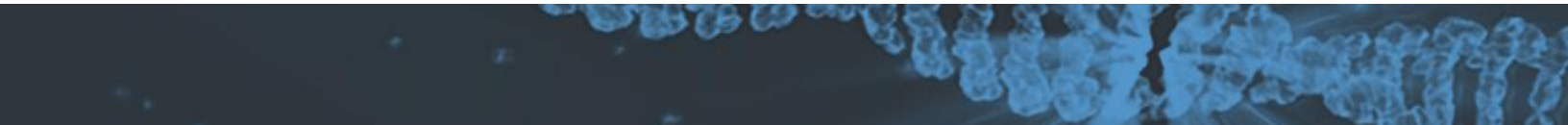
Causes For Rejection: Insufficient tumor cell content or quantity, and decalcified specimens

TAT: 5-10 business days

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: 81459, G0452 (88363 or 88381 may apply)

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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