Patient ID	Patient Name		Birth Date	Sex	Age
SA00178384	TESTING VALIDATION, MCCRC NORMAL		1973-05-01	F	52
Order Number	**Client Order Number**	**Ordering Physician**	**Report Notes**		
SA00178384	SA00178384	CLIENT,CLIENT			
Account Information		**Collected**			
C7028846 DLMP Rochester		01 Dec 2025 13:00			

MayoComplete CRC Panel

Result

MCR

Provided diagnosis: adenocarcinoma involving omentum

Microsatellite Instability (MSI) status: Stable (MSS)

No reportable sequence variants were detected within the analyzed regions of the tested genes listed in the method description.

Interpretation

MCR

Current data suggests that the efficacy of EGFR-targeted therapies in colorectal cancer is confined to patients with tumors lacking KRAS, HRAS, NRAS and BRAF mutations. Thus, the absence of a detectable mutation in these genes suggests that this patient may respond to such therapies [PMID 23666916, PMID 28275037].

Additional studies are needed to assess the therapeutic significance in tumor types other than colorectal.

MSI: Stable (MSS)
NO evidence of microsatellite instability was detected suggesting the presence of normal DNA mismatch repair function within the tumor. Current data suggest that advanced stage solid tumors with intact mismatch repair (MSS) are less likely to be responsive to treatment with immunotherapies such as anti-PD-1 therapies [PMID 28596308, PMID 29355075].

Additional Information

MCR

CLINICAL TRIALS

Possible clinical trials of benefit for this patient can be found at the following sites:
1) ClinicalTrials.gov:
www.clinicaltrials.gov/ct2/search/advanced
2) Mayo Clinic: www.mayo.edu/research/clinical-trials/ 3) National Cancer Institute: www.cancer.gov/clinicaltrials/search

Specimen

MCR

Tissue, Tumor

Tissue ID

MCR

13415

Method

MCR

Microscopic examination is performed by a pathologist to identify areas of tumor for enrichment by macrodissection.

Next generation sequencing is performed to test for the presence of microsatellite instability and a mutation within all coding regions and exon/intron boundaries of the following 13 targeted genes: APC, BRAF, HRAS, KRAS, MLH1, MSH2, MSH6, NRAS, PIK3CA, PIK3R1, PMS2, POLE and PTEN.

Variant nomenclature is based on build GRCh37 (hg19). For details about gene transcripts (RefSeq accession numbers), specific targeted regions of each gene, and additional information on this test, see www.mayocliniclabs.com (Test ID MCCRC).

Disclaimer

1 MCR

This test cannot differentiate between somatic and germline alterations. Additional testing may be necessary to clarify the significance of results if there is a potential hereditary risk.

DNA variants of uncertain significance may be identified.

A negative result does not rule out the presence of a variant that may be present but below the limits of detection of this assay. The analytical sensitivity of this assay for sequence reportable alterations is 5% mutant allele frequency with a minimum coverage of 500X in a sample with at least 20% tumor content.

Point mutations and small insertion/deletion mutations will be detected in the APC, BRAF, HRAS, KRAS, MLH1, MSH2, MSH6, NRAS, PIK3CA, PIK3R1, PMS2, POLE and PTEN genes only. This test may detect single exon deletions but does not detect

Performing Site Legend

Code	Laboratory	Address	Lab Director	CLIA Certificate
MCR	Mayo Clinic Laboratories - Rochester Main Campus	200 First Street SW, Rochester, MN 55905	Nikola Baumann Ph.D.	24D0404292

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SA00178384	TESTING VALIDATION, MCCRC NORMAL		1973-05-01	F	52
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multi-exon deletions, duplications, larger-scale genomic copy number variants, copy neutral loss of heterozygosity (LOH), or epigenetic modifications such as promoter methylation. DELINS of 1,000 bp or less are detectable with at least 50 or more supporting reads.

This test cannot reliably determine if a variant identified in PMS2 exons 11–15 originated from PMS2 or the highly homologous pseudogene PMS2CL. In the instance that a reportable variant is detected in PMS2 exons 11–15, additional testing will be recommended in the patient report.

Variant allele frequency (VAF) is the percentage of sequencing reads supporting a specific variant divided by the total sequencing reads at that position. In somatic testing, VAF should be interpreted in the context of several factors including, but not limited to: tumor purity/heterogeneity/copy number status (ploidy, gains/losses, loss of heterozygosity) and sequencing artifact/misalignment [PMID: 27144058, PMID: 29769535].

Rare polymorphisms may be present that could lead to false-negative or false-positive results.

The presence or absence of a variant may not be predictive of response to therapy in all patients.

Test results should be interpreted in the context of clinical, tumor sampling, histopathological, and other laboratory data. If results obtained do not match other clinical or laboratory findings, contact the laboratory for discussion. Misinterpretation of results may occur if the information provided is inaccurate and/or incomplete.

Reliable results are dependent on adequate specimen collection and processing. This test has been validated on cytology slides and formalin-fixed, paraffin-embedded tissues; other types of fixatives are discouraged. Improper treatment of tissues, such as decalcification, may cause PCR failure.

Released By MCR

Benjamin R. Kipp, Ph.D.

Received: 02 Dec 2025 09:26 **Reported:** 03 Dec 2025 13:33

Laboratory Notes

1 This test was developed and its performance characteristics determined by Mayo Clinic in a manner consistent with CLIA requirements. This test has not been cleared or approved by the U.S. Food and Drug Administration.

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