Test Definition: ML1HM

MLH1 Hypermethylation Analys, Tumor

Overview

Useful For

An adjunct to MSI / Microsatellite Instability (MSI), Tumor and Mismatch Repair (MMR) Protein Immunohistochemistry Only, Tumor when colon or endometrial tumor demonstrates microsatellite instability (MSI-H) and loss of MLH1 protein expression, to help distinguish a somatic versus germline event prior to performing expensive germline testing

An adjunct to negative *MLH1* germline testing in cases where colon or endometrial tumor demonstrates MSI-H and loss of MLH1 protein expression

Additional Tests

Test ID	Reporting Name	Available Separately	Always Performed
SLIRV	Slide Review in MG	No, (Bill Only)	Yes

Testing Algorithm

When this test is ordered, slide review will always be performed at an additional charge.

See Lynch Syndrome Testing Algorithm in Special Instructions.

Special Instructions

- Molecular Genetics: Inherited Cancer Syndromes Patient Information
- Lynch Syndrome Testing Algorithm

Method Name

Polymerase Chain Reaction (PCR) Analysis

NY State Available

Yes

Specimen

Specimen Type

Varies

Advisory Information

This test is **not** recommended as a first-tier screening measure for hereditary nonpolyposis colon cancer (HNPCC). Refer to MSI / Microsatellite Instability (MSI), Tumor and Mismatch Repair (MMR) Protein Immunohistochemistry Only, Tumor.

Testing will only be performed on colon or endometrial tumors demonstrating loss of *MLH1* protein expression by immunohistochemistry.

Mayo's preferred screening test (BRMLH / *MLH1* Hypermethylation and *BRAF* Mutation Analysis, Tumor) includes both *MLH1* promoter hypermethylation and *BRAF* V600E testing.

Extracted DNA from tissues is **not** an acceptable specimen type.

Necessary Information

Pathology report **must** accompany specimen in order for testing to be performed.

Specimen Required

Specimen Type: Tissue block or slide

Collection Instructions:

1. Submit formalin-fixed, paraffin-embedded tissue block (preferred) or 1 slide stained with hematoxylin and eosin and 10 unstained, nonbaked slides (5-micron thick sections) of the tumor tissue.

2. Sections should contain tumor tissue.

Forms

1. Molecular Genetics: Inherited Cancer Syndromes Patient Information(T519) in Special Instructions

2. If not ordering electronically, complete, print, and send 1 of the following forms with the specimen:

-Gastroenterology and Hepatology Client Test Request (T728)

-Oncology Test Request (T729)

Reject Due To

Hemolysis	NA
Lipemia	NA
Icterus	NA
Other	Specimens that have been decalcified (all methods); specimens that have not been formalin-fixed, paraffin-embedded; bone marrow in EDTA, extracted DNA

Specimen Stability Information

Specimen Type	Temperature	Time	Special Container
Varies	Ambient (preferred)		
	Frozen		
	Refrigerated		

Clinical and Interpretive

Clinical Information

Hereditary nonpolyposis colon cancer (HNPCC), also known as Lynch syndrome, is an inherited cancer syndrome caused by a germline mutation in one of several genes involved in DNA mismatch repair (MMR), including *MLH1*, *MSH2, MSH6,* and *PMS2.* There are several laboratory-based strategies that help establish the diagnosis of HNPCC/Lynch syndrome, including testing tumor tissue for the presence of microsatellite instability (MSI-H) and loss of protein expression for any one of the MMR proteins by immunohistochemistry (IHC). It is important to note,

however, that the MSI-H tumor phenotype is not restricted to inherited cancer cases; approximately 20% of sporadic colon cancers are MSI-H. Thus, MSI-H does not distinguish between a somatic (sporadic) and a germline (inherited) mutation, nor does it identify which gene is involved. Although IHC analysis is helpful in identifying the responsible gene, it also does not distinguish between somatic and germline defects.

Defective MMR in sporadic colon cancer is most often due to an abnormality in *MLH1*, and the most common cause of gene inactivation is promoter hypermethylation (epigenetic silencing). A specific mutation in the *BRAF* gene (V600E) has been shown to be present in approximately 70% of tumors with hypermethylation of the *MLH1* promoter. Importantly, the V600E mutation is rarely identified in cases with germline *MLH1* mutations. Thus, direct assessment of *MLH1* promoter methylation status and testing for the *BRAF* V600E mutation can be used to help distinguish between a germline mutation and epigenetic/somatic inactivation of *MLH1*. Tumors that have the *BRAF* V600E mutation and demonstrate *MLH1* promoter hypermethylation are almost certainly sporadic, whereas tumors that show neither are most often caused by an inherited mutation.

Although testing for the *BRAF* V600E mutation and *MLH1* promoter hypermethylation are best interpreted together, they are also available separately to accommodate various clinical situations and tumor types. These tests can provide helpful diagnostic information when evaluating an individual suspected of having HNPCC/Lynch syndrome, especially when testing is performed in conjunction with MSI / Microsatellite Instability (MSI), Tumor and Mismatch Repair (MMR) Protein Immunohistochemistry Only, Tumor studies. It should be noted that these tests are not genetic tests, but rather stratify the risk of having an inherited cancer predisposition and identify patients who might benefit from subsequent genetic testing.

See Lynch Syndrome Testing Algorithm in Special Instructions.

Reference Values

An interpretative report will be provided.

Interpretation

An interpretive report will be provided. The likelihood of a germline (inherited) mutation is very low in those cases where the tumor demonstrates *MLH1* promoter hypermethylation and the normal tissue is unmethylated. The likelihood of a germline mutation is high in those cases where the tumor and normal tissue lack *MLH1* promoter hypermethylation. In cases where the tumor and normal tissue demonstrate *MLH1* promoter hypermethylation, this result will be interpreted as equivocal and a blood sample will be requested to confirm potential germline hypermethylation.

Cautions

Testing tumors other than colon or endometrial for *MLH1* hypermethylation has not been fully evaluated, and these specimens are not accepted for testing.

Colon cancer is relatively common and it is possible for a sporadic colon cancer to occur in an HNPCC family. Therefore, evaluation of other family members should still be considered in cases with *MLH1* promoter hypermethylation if there is high clinical suspicion of HNPCC.

Clinical Reference

1. Cunningham JM, Kim CY, Christensen ER, et al: The frequency of hereditary defective mismatch repair in a prospective series of unselected colorectal carcinomas. Am J Hum Genet 2001;69:780-790

2. Wang L, Cunningham JM, Winters JL, et al: *BRAF* mutations in colon cancer are not likely attributable to defective DNA mismatch repair. Cancer Res 2003;63:5209-5212

3. Domingo E, Laiho P, Ollikainen M, et al: *BRAF* screening as a low-cost effective strategy for simplifying HNPCC genetic testing. J Med Genet 2004;41:664-668

4. Bettstetter M, Dechant S, Ruemmele P, et al: Distinction of hereditary nonpolyposis colorectal cancer and sporadic microsatellite-unstable colorectal cancer through quantification of *MLH1* methylation by real-time PCR. Clin Cancer Res 2007;13:3221-3228

Performance

Method Description

A PCR-based assay is used to test tumor DNA for the presence of hypermethylation of the *MLH1* promoter. This is a modification of the method described by Grady et al.(Grady WM, Rajput A, Lutterbaugh JD, Markowitz S: Detection of aberrantly methylated *hMLH1* promoter DNA in the serum of patients with microsatellite unstable colon cancer. Cancer Res 2001;61:900)

PDF Report

No

Day(s) and Time(s) Test Performed

Weekly; Varies

Analytic Time

7 days

Maximum Laboratory Time

14 days

Specimen Retention Time

Extracted DNA: 3 months

Performing Laboratory Location

Rochester

Fees and Codes

Fees

- Authorized users can sign in to Test Prices for detailed fee information.
- Clients without access to Test Prices can contact Customer Service 24 hours a day, seven days a week.
- Prospective clients should contact their Regional Manager. For assistance, contact Customer Service.

Test Classification

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.

CPT Code Information

81288

88381

LOINC® Information

Test Definition: ML1HM

MLH1 Hypermethylation Analys, Tumor

Test ID	Test Order Name	Order LOINC Value
ML1HM	MLH1 Hypermethylation Analys, Tumor	In Process

Result ID	Test Result Name	Result LOINC Value
53299	Result Summary	50397-9
53300	Result	82939-0
53301	Interpretation	69047-9
53302	Reason for Referral	42349-1
53303	Specimen	31208-2
53304	Source	85298-8
54447	Tissue ID	80398-1
53305	Released By	18771-6