

2.04.08	Genetic Testing for Lynch Syndrome and Other Inherited Colon Cancer Syndromes		
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Section:	2.0 Medicine	Page:	Page 1 of 42

Policy Statement

Note: Starting on July 1, 2022 (per CA law SB 535) for commercial plans regulated by the California Department of Managed Healthcare and California Department of Insurance (PPO and HMO), health care service plans and insurers shall not require prior authorization for biomarker testing, including biomarker testing for cancer progression and recurrence, if a member has stage 3 or 4 cancer. Health care service plans and insurers can still do a medical necessity review of a biomarker test and possibly deny coverage after biomarker testing has been completed and a claim is submitted (post service review).

APC Testing

Genetic testing of the [APC](#) gene may be considered **medically necessary** for a patient with **any** of the following:

- I. At-risk relatives (first or second degree) with familial adenomatous polyposis (FAP) or a [known APC variant](#)
- II. Personal history of 20 or more adenomas
- III. Personal history of between 10 to 20 polyps and 1 or more of the following:
 - A. First or second degree relative with more than 20 polyps
 - B. Other high-risk features as defined by a personal history of desmoid tumor, hepatoblastoma, cribriform-morular variant of papillary thyroid cancer, or multifocal or bilateral congenital hypertrophy of the retinal pigment epithelium (CHRPE)
- IV. When included as part of an approved small genetic [panel](#)

Genetic testing for APC gene variants is considered **not medically necessary** for colorectal cancer (CRC) patients with classical FAP for confirmation of the FAP diagnosis.

Testing for germline APC gene variants for inherited CRC syndromes is considered **investigational** in all other situations.

MUTYH Testing

Genetic testing of the [MUTYH](#) gene may be considered **medically necessary** for a patient with **any** of the following:

- I. [At-risk](#) relatives (first or second degree) with a known MUTYH gene variant (single site analysis only)
- II. A negative result for APC gene variants (when the criteria for approval of APC testing was met)
- III. When included as part of an approved small genetic [panel](#)

Testing for germline MUTYH gene variants for inherited CRC syndromes is considered **investigational** in all other situations.

MisMatch Repair (MMR) Gene and EPCAM Testing

Genetic testing for Lynch Syndrome (LS), also known as Hereditary Nonpolyposis Colorectal Cancer (HNPCC), [MMR](#) genes (*MLH1*, *MSH2*, *MSH6*, *PMS2*); *both initial sequencing and for deletions and duplications*) and the EPCAM gene may be considered **medically necessary** for a patient with **any** of the following:

- I. [Family history](#) of a known LS mutation (Variant single site analysis only)
- II. Personal or family history of colorectal or endometrial cancer diagnosed before 50 years

- III. Patients with CRC or endometrial cancer with tumor testing suggesting germline MMR deficiency (by microsatellite instability-MSI, or loss of mismatch repair protein expression by immunohistochemical-IHC- analysis) or meeting clinical criteria for Lynch syndrome
- IV. Personal or [family history](#) of at least 1 person with colorectal or endometrial cancer and another synchronous or metachronous [Lynch syndrome-related tumor](#) in the same person
- V. Personal (or [family history](#) of at least 2 people) with [LS-related tumors](#) and at least 1 diagnosed before 50 years of age
- VI. Personal or family history of at least 3 people with [LS-related tumors](#), regardless of age
- VII. A 5% or more risk of having an MMR gene mutation based on predictive models (e.g., PREMM5, MMRpro, MMR predict) as documented in the medical record (See policy guidelines for calculators)
- VIII. No diagnosis of colorectal cancer (CRC) but with a [family history](#) meeting the Amsterdam criteria, when no affected family members have been tested for MMR variants (See policy guidelines; Revised Bethesda criteria are included in the above criteria)
- IX. When included as part of an approved small genetic [panel](#)

Testing for germline MMR gene variants for inherited CRC syndromes is considered **investigational** in all other situations.

Testing for germline *EPCAM* gene variants for inherited CRC syndromes is considered **investigational** in all other situations.

***BRAF V600E* or *MLH1* Promoter Methylation**

Somatic (not germline) genetic testing for *BRAF V600E* or *MLH1* promoter methylation may be considered **medically necessary** to exclude a diagnosis of Lynch syndrome when **either** of the following:

- I. The MLH1 protein is not expressed in a colorectal cancer (CRC) tumor on immunohistochemical (IHC) analysis (See Policy Guidelines section)
- II. The included as part of an approved small genetic [panel](#)

Testing for somatic *BRAF V600E* or *MLH1* promoter methylation to exclude a diagnosis of Lynch syndrome is considered **investigational** in all other situations.

***SMAD4* and *BMPR1A* Testing**

Genetic testing of *SMAD4* and *BMPR1A* genes may be considered **medically necessary** when **any** of the following:

- I. Patient with a clinical diagnosis of juvenile polyposis syndrome based on the presence of **any** one of the following:
 - A. At least 3 to 5 juvenile polyps in the colon
 - B. Multiple juvenile polyps found throughout in other parts of the gastrointestinal tract
 - C. Any number of juvenile polyps with a known [family history](#) of juvenile polyps
- II. At-risk relative of a patient suspected of or diagnosed with juvenile polyposis syndrome
- III. When included as part of an approved small genetic [panel](#)

Testing for germline *SMAD4* and *BMPR1A* gene variants for inherited CRC syndromes is considered **investigational** in all other situations.

***STK11* Testing**

Genetic testing for *STK11* gene variants may be considered **medically necessary** in **any** of the following:

- I. Patient with a clinical diagnosis of Peutz-Jeghers syndrome based on the presence of any 2 of the following:
 - A. Presence of 2 or more histologically confirmed Peutz-Jeghers polyps of the gastrointestinal tract
 - B. Characteristic mucocutaneous pigmentation of the mouth, lips, nose, eyes, genitalia, or fingers

- C. Family history of Peutz-Jeghers syndrome
- II. At-risk relative of a patient suspected of or diagnosed with Peutz-Jeghers syndrome
- III. When included as part of an approved small genetic [panel](#)

Testing for germline *STK11* gene variants for inherited CRC syndromes is considered **investigational** in all other situations.

Panel Testing

Limited genetic panels (including at a minimum APC, MUTYH, *MLH1*, *MSH2*, *MSH6*, *PMS2*, EPCAM, SMAD4, BMPR1A, and *STK11* billed as CPT 81435) may be considered **medically necessary** as an alternative to serial testing of individual genes when criteria are met for any genetic testing of hereditary colorectal cancer, as indicated by **one or more** of the following:

- I. Personal history of 20 or more adenomas
- II. Personal history of between 10 to 20 polyps and **one** of the following:
 - A. First or second degree relative with more than 20 polyps
 - B. Other high-risk features as defined by a personal history of desmoid tumor, hepatoblastoma, cribriform-morular variant of papillary thyroid cancer, or multifocal or bilateral congenital hypertrophy of the retinal pigment epithelium (CHRPE)
- III. [Family history](#) of a known LS mutation
- IV. Personal or family history of colorectal or endometrial cancer diagnosed before 50 years
- V. Personal history of colorectal or endometrial cancer at any age with tumor showing evidence of mismatch repair deficiency, either by microsatellite instability (MSI) or loss of mismatch repair protein expression by Immunohistochemical (IHC) analysis
- VI. Personal or [family history](#) of at least 1 person with colorectal or endometrial cancer and another synchronous or metachronous [Lynch syndrome-related tumor](#) in the same person
- VII. Personal (or [family history](#) of at least 2 people) with [LS-related tumors](#) and at least 1 diagnosed before 50 years of age
- VIII. Personal or family history of at least 3 people with [LS-related tumors](#), regardless of age
- IX. A 5% or more risk of having an MMR gene mutation based on predictive models (e.g., PREMM5, MMRpro, MMR predict) as documented in the medical record (See policy guidelines for calculators)
- X. No diagnosis of colorectal cancer (CRC) but with a [family history](#) meeting the Amsterdam criteria, when no affected family members have been tested for MMR variants (See policy guidelines; Revised Bethesda criteria are included in the above criteria)
- XI. Patient with a clinical diagnosis of juvenile polyposis syndrome based on the presence of **any** one of the following:
 - A. At least 3 to 5 juvenile polyps in the colon
 - B. Multiple juvenile polyps in other parts of the gastrointestinal tract
 - C. Any number of juvenile polyps with a known [family history](#) of juvenile polyps
- XII. At-risk relative of a patient suspected of or diagnosed with juvenile polyposis syndrome
- XIII. Patient with a clinical diagnosis of Peutz-Jeghers syndrome based on the presence of any 2 of the following:
 - A. Presence of 2 or more histologically confirmed Peutz-Jeghers polyps of the small intestine
 - B. Characteristic mucocutaneous pigmentation of the mouth, lips, nose, eyes, genitalia, or fingers
 - C. Family history of Peutz-Jeghers syndrome
- XIV. At-risk relative of a patient suspected of or diagnosed with Peutz-Jeghers syndrome
- XV. To exclude a diagnosis of Lynch syndrome when the *MLH1* protein is not expressed in a colorectal cancer (CRC) tumor on immunohistochemical (IHC) analysis

The following are considered **investigational**:

- I. Large multi-gene panels including multiple genes that are not highly associated with hereditary colorectal cancer
- II. Genetic testing of all other genes for an inherited CRC syndrome

NOTE: Refer to [Appendix A](#) to see the policy statement changes (if any) from the previous version.

Policy Guidelines

Note: Initial testing for APC, MUTYH, MMR (MisMatch Repair), or EPCAM genetic variants depends on the clinical situation. Testing for cases in which there are many polyps present (See policy statement and guidelines) usually begins with APC or MUTYH variants while for those with less than 10 lifetime colonic adenomas present, testing usually begins with MMR mutations. While Lynch syndrome can also be associated with colonic adenomas, it is usually much less so than seen with APC/MUTYH mutations (less than 4% of those with Lynch Syndrome [LS] MMR mutations have 10 or more adenomas).

If initial testing is negative, further testing is not automatic, but based on the clinical situation. That is, if initial testing for APC is negative, MMR testing is not automatic; and if initial MMR testing is negative, APC testing is not always needed as a next step.

The Revised Bethesda criteria are included in the reasons for approval

Adenomas are a type of polyp. There are different kinds of both polyps and adenomas. Adenomas are benign, but some can go on to become cancerous.

Panel Testing

When criteria are met, small panel testing using CPT code 81435 is the broadest testing for Lynch syndrome and inherited colon cancer risk allowed and should be used as an alternative to individual gene testing when criteria are met as outlined in the policy statement above. Examples of such limited tests when billed as 81435 may include the myRisk (may also be billed as CPT 81432) or Colaris® panel from Myriad laboratories, the ColoNext panel from Ambry, or a Colorectal Cancer Panel by Invitae). If individual or smaller panel testing meeting criteria is performed initially, any remaining genes (including those in the 81435 panel) that are not included individually in the medically necessary criteria above are considered investigational and are not covered when requested at a later time.

Claims for panel testing should reflect the CPT code closest to the panel being ordered (81435). Claims submitted using individual gene codes rather than the appropriate panel code is considered to be unbundling and improper coding.

Testing related to hereditary breast and ovarian cancer, see Blue Shield of California Medical Policy: Genetic Testing for BRCA1 or BRCA2 for Hereditary Breast/Ovarian Cancer Syndrome and Other High-Risk Cancers.

Panel testing related to non-small-cell lung cancer, see Blue Shield of California Medical Policy: Circulating Tumor DNA for Management of Non-Small-Cell Lung Cancer (Liquid Biopsy).

Panel testing related to cancers other than breast, ovarian, colorectal, and non-small-cell lung cancer, see Blue Shield of California Medical Policy: Genetic Cancer Susceptibility Panels Using Next-Generation Sequencing.

Testing At-risk Relatives

Due to the high lifetime risk of cancer of most genetic syndromes discussed in this policy, "at-risk relatives" primarily refers to first or second degree relatives. However, some judgment must be allowed, e.g., in the case of a small family pedigree, when extended family members may need to be included in the testing strategy.

Targeted Familial Variant Testing

It is recommended that, when possible, initial genetic testing for familial adenomatous polyposis or Lynch syndrome be performed in an affected family member so that testing in unaffected

family members can focus on the variant found in the affected family member (see Benefit Application section). If an affected family member is not available for testing, testing should begin with an unaffected family member most closely related to an affected family member.

In many cases, genetic testing for *MUTYH* gene variants should first target the specific variants *Y165C* and *G382D*, which account for more than 80% of variants in white populations, and subsequently, proceed to sequence only as necessary. However, in other ethnic populations, proceeding directly to sequencing is appropriate. Full gene testing is most commonly requested and can be approved without doing the common variants first.

Known Variant Testing

Known variant testing should be limited to that (site specific) analysis only, rather than the whole gene

High-risk features for *MUTYH* gene variants:

The following may also be considered as high-risk features for *MUTYH* gene variants:

- At least 5 serrated polyps (includes hyperplastic polyps, sessile serrated adenomas or polyps, and traditional serrated adenomas) proximal to the sigmoid colon with 2 or more greater than 10 millimeters (mm)
- 20 or more serrated polyps of any size distributed throughout the colon

Note: A family history of no parents or children with FAP is consistent with *MUTYH*-Associated Polyposis (MAP, which is autosomal recessive).

Lynch Syndrome-Related Tumors

Lynch syndrome-related tumors include colorectal, endometrial, stomach, ovarian, pancreas, ureter and renal pelvis, biliary tract, brain (usually glioblastoma as seen in Turcot syndrome), sebaceous gland adenomas and keratoacanthomas in Muir-Torre syndrome, and carcinoma of the small bowel.

Family History

Family history refers to first- or second-degree relatives.

Hamartomatous and Serrated Polyps

Two or more hamartomatous polyps or five or more serrated polyps may need different genetic testing (see NCCN guidelines).

Evaluation For Lynch Syndrome

For patients with colorectal cancer (CRC) or endometrial cancer being evaluated for Lynch syndrome, the microsatellite instability (MSI) test or the immunohistochemical (IHC) test with or without *BRAF* gene variant testing, or methylation testing, should be used as an initial evaluation of tumor tissue before mismatch repair (MMR) gene analysis. Both tests are not necessary. Proceeding to MMR gene sequencing would depend on results of MSI or IHC testing. In particular, IHC testing may help direct which MMR gene likely contains a variant, if any, and may also provide additional information if MMR genetic testing is inconclusive (See *BRAF V600E* below). MMR testing may still be needed, and can be approved without MSI or IHC test results. For further information on tumor tissue test results, interpretation, and additional testing options, see the [NCCN \[National Comprehensive Cancer Network\] clinical care guidelines on genetic/familial high risk assessment: colorectal](#).

MLH1 and MSH2 variants are most common, but testing is usually done in a panel that includes MSH6 and PMS2 and sometimes EPCAM. Standard sequencing methods will not detect large deletions or duplications so testing for large deletions or duplications is appropriate and is usually done at the same time as initial MMR sequence testing.

BRAF V600E or MLH1 Promoter Methylation

Lack of expression of MLH1 (a repair gene) can be due to aberrant (hyper) methylation of the promoter of the MLH1 proteins. This methylation (or hypermethylation) of the promoter silences expression of the MLH1 gene (and occasionally MSH2), and occurs only in tumor tissue (somatic, not germline cancers). But, abnormal IHC testing (low, or lack of the repair proteins) just shows a lack of MLH1 activity in either case. It would not be clear if that was from a genetic (germline, inherited) loss of the protein or because it is silenced by the abnormal promoter methylation in the tumor (somatic). BRAF V600E (and MLH1 promoter methylation) testing can help with whether the lack of expression of MLH1 is from a local tumor issue or inherited problem. Ideally, if IHC testing on the tumor is low, then BRAF V600E or MLH1 promoter methylation testing would be done before moving on to the MMR genetic testing. MMR testing would then be done if there is no methylation found (negative MLH1 methylation). If hypermethylation is found then the abnormal IHC result is more likely due to the somatic (local) tumor issue than due to an inherited problem with the MMR genes.

Amsterdam II Clinical Criteria

The Amsterdam II Clinical Criteria (all criteria must be fulfilled) are the most stringent for defining families at high risk for Lynch syndrome:¹

- 3 or more relatives with an associated cancer (CRC, or cancer of the endometrium, small intestine, ureter, or renal pelvis)
- 1 should be a first-degree relative of the other 2
- 2 or more successive generations affected
- 1 or more relatives diagnosed before the age of 50 years
- Familial adenomatous polyposis (FAP) should be excluded in cases of CRC
- Tumors should be verified by pathologic examination
- Modifications:
 - EITHER: very small families, which cannot be further expanded, can be considered to have hereditary nonpolyposis colorectal cancer (HNPCC) with only 2 CRCs in first-degree relatives if at least 2 generations have the cancer and at least 1 case of CRC was diagnosed by the age of 55 years
 - OR: in families with 2 first-degree relatives affected by CRC, the presence of a third relative with an unusual early-onset neoplasm or endometrial cancer is sufficient

Multiple risk prediction models that provide quantitative estimates of the likelihood of an MMR variant are currently available such MMRpro, PREMM5 (Kastrinos et al, 2017), or MMRpredict. National Comprehensive Cancer Network guidelines recommend (category 2A) testing for Lynch syndrome for individuals with a 5% or higher predicted risk of Lynch syndrome on these risk prediction models. These quantitative estimates of the likelihood of an MMR variant can be ascertained by the use of the following, available calculators:

- **PREMM5:** <http://premm.dfci.harvard.edu/>
- **MMRpro:** <http://www4.utsouthwestern.edu/breasthealth/cagene/>
(Registration for this site is required at the University of Texas Southwestern Medical Center)
- **MMRpredict:** <http://hnpccpredict.hgu.mrc.ac.uk/>

Genetic Counseling

Experts recommend formal genetic counseling for patients who are at risk for inherited disorders and who wish to undergo genetic testing. Interpreting the results of genetic tests and understanding risk factors can be difficult for some patients; genetic counseling helps individuals understand the impact of genetic testing, including the possible effects the test results could have on the individual or their family members. It should be noted that genetic counseling may alter the utilization of genetic testing substantially and may reduce inappropriate testing; further, genetic counseling should be performed by an individual with experience and expertise in genetic medicine and genetic testing methods.

Coding

There is a CPT that represents Genomic Unity® Lynch Syndrome Analysis by Variantyx Inc. Per the manufacturer, this test is for individuals with or suspected of having Lynch syndrome. Genomic DNA isolated from blood or saliva is sequenced, examined for deviations or variants in the Lynch Syndrome related genes and evaluated for potential impact on protein function and pathogenicity based on American College of Medical Genetics guidelines. This service may have been previously billed using CPT codes 81292, 81294, 81295, 81297, 81298, 81300, 81317, 81319, 81479.

- **0238U:** Oncology (Lynch syndrome), genomic DNA sequence analysis of MLH1, MSH2, MSH6, PMS2, and EPCAM, including small sequence changes in exonic and intronic regions, deletions, duplications, mobile element insertions, and variants in non-uniquely mappable regions

The following CPT PLA code represents the Ambry Genetics® APC mRNA sequence analysis panel:

- **0157U:** APC (APC regulator of WNT signaling pathway) (e.g., familial adenomatous polyposis [FAP]) mRNA sequence analysis (List separately in addition to code for primary procedure) (Use in conjunction with CPT code 81201)

The following CPT PLA code represents the Ambry Genetics® MLH1 mRNA sequence analysis panel:

- **0158U:** MLH1 (mutL homolog 1) (e.g., hereditary non-polyposis colorectal cancer, Lynch syndrome) mRNA sequence analysis (List separately in addition to code for primary procedure) (Use in conjunction with CPT code 81292)

The following CPT PLA code represents the Ambry Genetics® MSH2 mRNA sequence analysis panel:

- **0159U:** MSH2 (mutS homolog 2) (e.g., hereditary colon cancer, Lynch syndrome) mRNA sequence analysis (List separately in addition to code for primary procedure) (Use in conjunction with CPT code 81295)

The following CPT PLA code represents the Ambry Genetics® MSH6 mRNA sequence analysis panel:

- **0160U:** MSH6 (mutS homolog 6) (e.g., hereditary colon cancer, Lynch syndrome) mRNA sequence analysis (List separately in addition to code for primary procedure) (Use in conjunction with CPT code 81298)

The following CPT PLA code represents the Ambry Genetics® PMS2 mRNA sequence analysis panel:

- **0161U:** PMS2 (PMS1 homolog 2, mismatch repair system component) (e.g., hereditary non-polyposis colorectal cancer, Lynch syndrome) mRNA sequence analysis (List separately in addition to code for primary procedure) (Use in conjunction with CPT code 81317)

The following CPT PLA code represents the Ambry Genetics® Lynch (MLH1, MSH2, MSH6, PMS2) mRNA sequence analysis panel:

- **0162U:** Hereditary colon cancer (Lynch syndrome), targeted mRNA sequence analysis panel (MLH1, MSH2, MSH6, PMS2) (List separately in addition to code for primary procedure) (Use in conjunction with CPT codes 81292, 81295, 81298, 81317, 81435)

The following CPT PLA code represents the +RNAinsight™ for ColoNext® mRNA sequence analysis panel:

- **0130U:** Hereditary colon cancer disorders (e.g., Lynch syndrome, PTEN hamartoma syndrome, Cowden syndrome, familial adenomatous polyposis), targeted mRNA sequence analysis panel (APC, CDH1, CHEK2, MLH1, MSH2, MSH6, MUTYH, PMS2, PTEN, and TP53) (List separately in addition to code for primary procedure)

There are specific CPT codes for genetic testing of *APC*:

- **81201-81203**: *APC* genetic testing code range

There are specific CPT codes for genetic testing of *MLH1*, *MSH2*, *MSH6*, *PMS2*, and microsatellite instability:

- **81288**: *MLH1* (mutL homolog 1, colon cancer, nonpolyposis type 2) (e.g., hereditary non-polyposis colorectal cancer, Lynch syndrome) gene analysis; promoter methylation analysis
- **81292-81294**: *MLH1* genetic testing code range
- **81295-81297**: *MSH2* genetic testing code range
- **81298-81300**: *MSH6* genetic testing code range
- **81301**: Microsatellite instability analysis (e.g., hereditary non-polyposis colorectal cancer, Lynch syndrome) of markers for mismatch repair deficiency (e.g., *BAT25*, *BAT26*), includes comparison of neoplastic and normal tissue, if performed
- **81317-81319**: *PMS2* genetic testing code range

There is also a specific CPT code for testing of *BRAF* V600 variant(s):

- **81210**: *BRAF* (*B-Raf proto-oncogene, serine/threonine kinase*) (e.g., colon cancer, melanoma), gene analysis, V600 variant(s)

The following CPT code includes testing for *EPCAM*:

- **81403**: Molecular Pathology Procedure Level 4. *EPCAM* (*epithelial cell adhesion molecule*) (e.g., Lynch syndrome), duplication/deletion analysis

The following CPT code may be billed for panel testing:

- **81435**: Hereditary colon cancer disorders (e.g., Lynch syndrome, *PTEN* hamartoma syndrome, Cowden syndrome, familial adenomatous polyposis); genomic sequence analysis panel, must include sequencing of at least 10 genes, including *APC*, *BMP1A*, *CDH1*, *MLH1*, *MSH2*, *MSH6*, *MUTYH*, *PTEN*, *SMAD4*, and *STK11*

Genetic testing for colon cancer is not widely available and is most commonly performed by commercial reference labs or research labs dedicated to genetic testing in general.

Associated genetic counseling performed by a trained genetic counselor would be coded using the following CPT code:

- **96040**: Medical genetics and genetic counseling services, each 30 minutes face-to-face with patient/family

Genetic counseling performed by a physician is coded using the appropriate CPT evaluation and management codes.

Description

Genetic testing is available for both those with and those at risk for various types of hereditary cancer. This review evaluates genetic testing for hereditary colorectal cancer (CRC) and polyposis syndromes, including familial adenomatous polyposis (FAP), Lynch syndrome (formerly known as hereditary nonpolyposis colorectal cancer), *MUTYH*-associated polyposis (MAP), Lynch syndrome-related endometrial cancer, juvenile polyposis syndrome (JPS), and Peutz-Jeghers syndrome (PJS).

Related Policies

- N/A

Benefit Application

Benefit determinations should be based in all cases on the applicable contract language. To the extent there are any conflicts between these guidelines and the contract language, the contract language will control. Please refer to the member's contract benefits in effect at the time of service to determine coverage or non-coverage of these services as it applies to an individual member.

Some state or federal mandates (e.g., Federal Employee Program [FEP]) prohibits plans from denying Food and Drug Administration (FDA)-approved technologies as investigational. In these instances, plans may have to consider the coverage eligibility of FDA-approved technologies on the basis of medical necessity alone.

Regulatory Status

Clinical laboratories may develop and validate tests in-house and market them as a laboratory service; laboratory-developed tests must meet the general regulatory standards of the Clinical Laboratory Improvement Amendments (CLIA). Genetic tests reviewed in this evidence review are available under the auspices of the CLIA. Laboratories that offer laboratory-developed tests must be licensed by the CLIA for high-complexity testing. To date, the U.S. Food and Drug Administration has chosen not to require any regulatory review of this test.

Rationale

Background

Hereditary Colorectal Cancers

Currently, 2 types of hereditary colorectal cancers (CRCs) are well-defined: familial adenomatous polyposis (FAP) and Lynch syndrome (formerly hereditary nonpolyposis CRC). Lynch syndrome has been implicated in some endometrial cancers as well.

Familial Adenomatous Polyposis and Associated Variants

Familial adenomatous polyposis typically develops by age 16 years and can be identified by the appearance of hundreds to thousands of characteristic, precancerous colon polyps. If left untreated, all affected individuals will develop CRC. Mean age of colon cancer diagnosis in untreated individuals is 39 years. The condition accounts for about 1% of CRC and may also be associated with osteomas of the jaw, skull, and limbs; sebaceous cysts; and pigmented spots on the retina referred to as congenital hypertrophy of the retinal pigment epithelium. Familial adenomatous polyposis associated with these collective extraintestinal manifestations is sometimes referred to as Gardner syndrome. This condition may also be related to central nervous system tumors, referred to as Turcot syndrome.

Germline variants in the adenomatous polyposis coli (*APC*) gene, located on chromosome 5, are responsible for FAP and are inherited in an autosomal dominant manner. Variants in the *APC* gene result in altered protein length in about 80% to 85% of cases of FAP. A specific *APC* gene variant (I1307K) has been found in Ashkenazi Jewish descendants, which may explain a portion of the familial CRC occurring in this population.

A subset of FAP patients may have an attenuated form of FAP, typically characterized by fewer than 100 cumulative colorectal adenomas occurring later in life than in classical FAP. In the attenuated form of FAP, CRC occurs at an average age of 50 to 55 years, but lifetime risk of CRC remains high ($\approx 70\%$ by age 80 years). The risk of extraintestinal cancer is also lower but cumulative lifetime risk remains high ($\approx 38\%$) compared with the general population.⁴ Only 30% or fewer of attenuated FAP patients have *APC* variants; some of these patients have variants in the *MUTYH* (formerly *MYH*) gene, and this form of the condition is called *MUTYH*-associated polyposis (MAP). This form of polyposis occurs with a frequency similar to FAP, with some

variability among prevalence estimates for both. While clinical features of MAP are similar to FAP or attenuated FAP, a strong multigenerational family history of polyposis is absent. Biallelic *MUTYH* variants are associated with a cumulative CRC risk of about 80% by age 70, whereas the monoallelic *MUTYH* variant-associated risk of CRC appears to be relatively minimal, although still under debate.⁵ Thus, inheritance for high-risk CRC predisposition is autosomal recessive in contrast to FAP. When relatively few (i.e., between 10 and 99) adenomas are present, and family history is unavailable, the differential diagnosis may include both MAP and Lynch syndrome; genetic testing in this situation could include *APC*, *MUTYH* if *APC* is negative for variants, and screening for variants associated with Lynch syndrome.

It is important to distinguish among classical FAP, attenuated FAP, and MAP (mono- or biallelic) by genetic analysis because recommendations for patient surveillance and cancer prevention vary by syndrome.⁶

Testing

Genetic testing for *APC* variants may be considered in the following situations:

- Patients at high-risk such as those with a family member who tested positive for FAP and have a known *APC* variant.
- Patients undergoing differential diagnosis of attenuated FAP versus MAP versus Lynch syndrome. These patients do not meet the clinical diagnostic criteria for classical FAP and have few adenomatous colonic polyps.
- To confirm FAP in patients with colon cancer with a clinical picture or family history consistent with classical FAP.

Lynch Syndrome

Lynch syndrome is an inherited disorder that results in a higher predisposition to CRC and other malignancies including endometrial and gastric cancer. Lynch syndrome is estimated to account for 3% to 5% of all CRC. People with Lynch syndrome have a 70% to 80% lifetime risk of developing any type of cancer.^{7,8} However, the risk varies by genotype. It occurs as a result of germline variant in the mismatch repair (MMR) genes that include *MLH1*, *MSH2*, *MSH6*, and *PMS2*. In approximately 80% of cases, the variants are located in the *MLH1* and *MSH2* genes, while 10% to 12% of variants are located in the *MSH6* gene and 2% to 3% in the *PMS2* gene. Additionally, variants in 3 additional genes (*MLH3*, *PMS1*, *EXO1*) have been implicated with Lynch Syndrome. Notably, in individuals meeting the various clinical criteria for Lynch syndrome, 50% of individuals have a variant in the *MLH1*, *MSH2*, *MSH6*, and *PMS2* genes. The lifetime risk of CRC is nearly 80% in individuals carrying a variant in 1 of these genes.

Testing

Preliminary screening of tumor tissue does not identify MMR gene variants but is used to guide subsequent diagnostic testing via DNA analysis for specific variants. Genetic testing or DNA analysis (gene sequencing, deletion, and duplication testing) for the MMR genes involves assessment for *MLH1*, *MSH2*, *MSH6*, and *PMS2* variants. The following are 3 testing strategies.

- Microsatellite instability (MSI) testing (phenotype): Individuals with high MSI either proceed to genetic testing for *MLH1*, *MSH2*, *MSH6*, and *PMS2* or to immunohistochemical (IHC) testing.
- IHC testing (phenotype): Individuals with negative staining would proceed to genetic testing for *MLH1*, *MSH2*, *MSH6*, and *PMS2*.
- Modification strategy: Tumor tissue of patients with negative staining for *MLH1* on IHC is tested for the *BRAF* V600E variant to determine methylation status. If the *BRAF* variant is not detected, the individual receives *MLH1* DNA analysis.

The phenotype tests used to identify individuals who may be at a high-risk of Lynch syndrome are explained next. The first screening test measures MSI. As a result of variance in the MMR gene family, the MMR protein is either absent or deficient, resulting in an inability to correct DNA replication errors causing MSI. Approximately 80% to 90% of Lynch syndrome CRC tumors have MSI. The National Cancer Institute has recommended screening for 5 markers to detect MSI

(Bethesda markers). Microsatellite instability detection in 2 of these markers is considered a positive result or “high probability of MSI.”⁹

The second phenotype screening test is IHC, which involves the staining of tumor tissue for the presence of 4 MMR proteins (MLH1, MSH2, MSH6, PMS2). The absence of 1 or more of these proteins is considered abnormal.

BRAF testing is an optional screening method that may be used in conjunction with IHC testing for *MLH1* to improve efficiency. A methylation analysis of the *MLH1* gene can largely substitute for *BRAF* testing, or be used in combination to improve efficiency slightly.

Both MSI and IHC have a 5% to 10% false-negative rate. Microsatellite instability testing performance depends on the specific MMR variant. Screening with MSI has a sensitivity of about 89% for *MLH1* and *MSH2* and 77% for *MSH6* and a specificity of about 90% for each. The specificity of MSI testing is low because approximately 10% of sporadic CRCs are MSI-positive due to somatic hypermethylation of the *MLH1* promoter. Additionally, some tumors positive for *MSH6* variants are associated with the MSI-low phenotype rather than MSI-high; thus MSI-low should not be a criterion against proceeding to MMR variant testing.^{10,11} Immunohistochemical screening has sensitivity for *MLH1*, *MSH2*, and *MSH6* of about 83% and a specificity of about 90% for each.

Screening of tumor tissue from patients enables genetic testing for a definitive diagnosis of Lynch syndrome and leads to counseling, cancer surveillance (e.g., through frequent colonoscopic or endometrial screening examinations), and prophylaxis (e.g., risk-reducing colorectal or gynecologic surgeries) for CRC patients, as well as for their family members.

Genetic testing for a MMR gene variant is often limited to *MLH1* and *MSH2* and, if negative, then *MSH6* and *PMS2*. The *BRAF* gene is often mutated in CRC when a particular *BRAF* variant (V600E, a change from valine to glutamic acid at amino acid position 600 in the *BRAF* protein) is present. To date, no *MLH1* gene variants have been reported.¹² Therefore, patients negative for *MLH1* protein expression by IHC, and therefore potentially positive for an *MLH1* variant, could first be screened for a *BRAF* variant. *BRAF*-positive samples need not be further tested by *MLH1* sequencing. *MLH1* gene methylation largely correlates with the presence of *BRAF* V600E and, in combination with *BRAF* testing, can accurately separate Lynch from sporadic CRC in IHC *MLH1*-negative cases.¹³

Novel deletions have been reported to affect the expression of the *MSH2* gene in the absence of a *MSH2* gene variant, and thereby cause Lynch syndrome. In these cases, deletions in *EPCAM*, the gene for the epithelial cell adhesion molecule, are responsible. *EPCAM* testing has been added to many Lynch syndrome profiles and is conducted only when tumor tissue screening results are MSI-high and/or IHC testing shows a lack of *MSH2* expression, but no *MSH2* variant is found by sequencing. *EPCAM* is found just upstream, in a transcriptional sense, of *MSH2*. Deletions of *EPCAM* that encompass the last 2 exons of the *EPCAM* gene, including the polyadenylation signal that normally ends transcription of DNA into messenger RNA, results in transcriptional “read-through” and subsequent hypermethylation of the nearby and downstream *MSH2* promoter. This hypermethylation prevents normal *MSH2* protein expression and leads to Lynch syndrome in a fashion similar to Lynch cases in which a *MSH2* variant prevents *MSH2* gene expression.¹⁴

Distinct from patients with *EPCAM* deletions, rare cases of Lynch syndrome have been reported without detectable germline MMR variants, although IHC testing demonstrated a loss of expression of 1 of the MMR proteins. In at least some of these cases, research has identified germline “epivariants,” i.e., methylation of promoter regions that control the expression of the MMR genes.^{14,15,16} Such methylation may be isolated or be in conjunction with a linked genetic alteration near the affected MMR gene. The germline epivariants may arise de novo or may be heritable in Mendelian or non-Mendelian fashion. This is distinct from some cases of MSI-high

sporadic CRC wherein the tumor tissue may show *MLH1* promoter methylation and IHC nonexpression, but the same is not true of germline cells. Clinical testing for Lynch syndrome-related germline epivariants is not routine but may help in exceptional cases.

Female patients with Lynch syndrome have a predisposition to endometrial cancer. Lynch syndrome is estimated to account for 2% of all endometrial cancers in women and 10% of endometrial cancers in women younger than 50 years of age. Female carriers of the germline variants *MLH1*, *MSH2*, *MSH6*, and *PMS2* have an estimated 40% to 62% lifetime risk of developing endometrial cancer, as well as a 4% to 12% lifetime risk of ovarian cancer.

Population Selection

Various attempts have been made to identify which patients with colon cancer should undergo testing for MMR variants, based primarily on family history and related characteristics using criteria such as the Amsterdam II criteria¹ (low sensitivity but high specificity), Revised Bethesda guidelines² (better sensitivity but poorer specificity), and risk prediction models (e.g., MMRpro; PREMM5; MMRpredict).³ While family history is an important risk factor and should not be discounted in counseling families, it has poor sensitivity and specificity for identifying Lynch syndrome. Based on this and other evidence, the Evaluation of Genomic Applications in Practice and Prevention Working Group recommended testing all newly diagnosed CRC patients for Lynch syndrome, using a screening strategy based on MSI or IHC (with or without *BRAF*) followed by sequencing in screen-positive patients. This recommendation includes genetic testing for the following types of patients:

- Family members of Lynch syndrome patients with a known MMR variant; family members would be tested only for the family variant; those testing positive would benefit from early and increased surveillance to prevent future CRC.
- Patients with a differential diagnosis of Lynch syndrome versus attenuated FAP versus MAP.
- For Lynch syndrome patients, genetic testing of the proband with CRC likely benefits the proband where Lynch syndrome is identified, and appropriate surveillance for associated malignancies can be initiated and maintained, benefiting family members by identifying the family variant.

Juvenile Polyposis Syndrome

Juvenile polyposis syndrome (JPS) is an autosomal dominant genetic disorder characterized by the presence of multiple hamartomatous (benign) polyps in the digestive tract. It is rare, with an estimated incidence of 1 in 100,000 to 160,000. Generalized JPS refers to polyps in the upper and lower gastrointestinal tract, and juvenile polyposis coli refers to polyps of the colon and rectum. Those with JPS are at a higher risk for CRC and gastric cancer.¹⁷ Approximately 60% of patients with JPS have a germline variant in the *BMPR1A* gene or the *SMAD4* gene.^{18,19} Approximately 25% of patients have de novo variants.^{20,21} In most cases, polyps appear in the first decade of life and most patients are symptomatic by age 20 years.²² Rectal bleeding is the most common presenting symptom, occurring in more than half of patients. Other presenting symptoms include prolapsing polyp, melena, pain, iron deficiency anemia, and diarrhea.^{17,21,22}

As noted, individuals with JPS are at increased risk for CRC and gastric cancer. By 35 years of age, the cumulative risk of CRC is 17% to 22%, which increases to 68% by age 60 years.^{23,24} The estimated lifetime risk of gastric cancer is 20% to 30%, with a mean age at diagnosis of 58 years.^{17,21,23} Juvenile polyposis syndrome may also be associated with hereditary hemorrhagic telangiectasia.²⁵ The most common clinical manifestations of hereditary hemorrhagic telangiectasia are telangiectasias of the skin and buccal mucosa, epistaxis, and iron deficiency anemia from bleeding.

Diagnosis

A clinical diagnosis of JPS is made on the basis of the presence of any 1 of the following: at least 3 to 5 juvenile polyps in the colon or multiple juvenile polyps in other parts of the gastrointestinal tract or any number of juvenile polyps in a person with a known family history of juvenile

polyps.²⁶ It is recommended that individuals who meet clinical criteria for JPS undergo genetic testing for a germline variant in the *BMPR1A* and *SMAD4* genes for a confirmatory diagnosis of JPS and to counsel at-risk family members. If there is a known *SMAD4* variant in the family, genetic testing should be performed within the first 6 months of life due to hereditary hemorrhagic telangiectasia risk.²⁷

Peutz-Jeghers Syndrome

Peutz-Jeghers syndrome (PJS) is also an autosomal dominant genetic disorder, similar to JPS, and is characterized by the presence of multiple hamartomatous (benign) polyps in the digestive tract, mucocutaneous pigmentation, and an increased risk of gastrointestinal and non-gastrointestinal cancers. It is rare, with an estimated incidence of 1 in 8000 to 200,000. In most cases, a germline variant in the *STK11 (LKB1)* gene is responsible for PJS, which has a high penetrance of over 90% by the age of 30 years.^{28,29,30} However, 10% to 20% of individuals with PJS have no family history and are presumed to have PJS due to de novo variants.³¹ A variant in *STK11* is detected in only 50% to 80% of families with PJS, suggesting that there is a second PJS gene locus.

The reported lifetime risk for any cancer is between 37% and 93% among those diagnosed with PJS with an average age of cancer diagnosis at 42 years. The most common sites for malignancy are colon and rectum, followed by breast, stomach, small bowel, and pancreas.³² The estimated lifetime risk of gastrointestinal cancer ranges from 38% to 66%.³² Lifetime cancer risk stratified by organ site is colon and rectum (39%), stomach (29%), small bowel (13%), and pancreas (11% to 36%).

Diagnosis

A clinical diagnosis of PJS is made if an individual meets 2 or more of the following criteria: presence of 2 or more histologically confirmed PJ polyps of the small intestine or characteristic mucocutaneous pigmentation of the mouth, lips, nose, eyes, genitalia, fingers, or family history of PJS.²⁶ Individuals who meet clinical criteria for PJS should undergo genetic testing for a germline variant in the *STK11* gene for a confirmatory diagnosis of PJS and counseling at-risk family members.

Literature Review

Evidence reviews assess whether a medical test is clinically useful. A useful test provides information to make a clinical management decision that improves the net health outcome. That is, the balance of benefits and harms is better when the test is used to manage the condition than when another test or no test is used to manage the condition.

The first step in assessing a medical test is to formulate the clinical context and purpose of the test. The test must be technically reliable, clinically valid, and clinically useful for that purpose. Evidence reviews assess the evidence on whether a test is clinically valid and clinically useful. Technical reliability is outside the scope of these reviews, and credible information on technical reliability is available from other sources.

Genetic Testing for Familial Adenomatous Polyposis and *MUTYH*-Associated Polyposis

Clinical Context and Test Purpose

The purpose of genetic testing for familial adenomatous polyposis (FAP) and *MUTYH*-associated polyposis (MAP) is to

- Identify at-risk relatives of patients with FAP and/or a known adenomatous polyposis coli (*APC*) gene variant.
- Make a differential diagnosis of attenuated FAP versus MAP versus Lynch syndrome.

The questions addressed in this evidence review are: (1) Is there evidence that genetic testing for FAP has clinical validity?; and (2) Does genetic testing for attenuated FAP change patient management in a way that improves outcomes as a result of genetic testing?

The following PICO was used to select literature to inform this review.

Populations

The relevant population of interest is at-risk relatives of patients with FAP and/or a known *APC* variant or those who require a differential diagnosis of attenuated FAP versus MAP versus Lynch syndrome.

Interventions

The relevant intervention is genetic testing for *APC* or *MUTYH*. Commercial testing is available from numerous companies.

Comparators

The following practice is currently being used to make decisions about managing FAP and MAP: no genetic testing.

Outcomes

The potential beneficial outcomes of primary interest would be the early detection of colorectal cancer (CRC) and appropriate and timely interventional strategies (e.g., endoscopic resection, colectomy) to prolong life.

The potential harmful outcomes are those resulting from a false test result. False-positive or false-negative test results can lead to the initiation of unnecessary treatment and adverse events from that treatment or undertreatment.

Genetic testing for FAP may be performed at any point during a lifetime. The necessity for genetic testing is guided by the availability of information that alters the risk of an individual of having or developing FAP.

Study Selection Criteria

For the evaluation of the clinical validity of the genetic test, studies that meet the following eligibility criterion were considered:

- Reported on the analytic sensitivity and specificity and/or diagnostic yield of the test.

Clinically Valid

A test must detect the presence or absence of a condition, the risk of developing a condition in the future, or treatment response (beneficial or adverse).

Review of Evidence

The evidence review for FAP genetic testing was initially informed by a Blue Cross Blue Shield Association Technology Evaluation Center (TEC) Assessment (1998).³³ Additional information on attenuated FAP and on MAP diagnostic criteria and genetic testing is based on several publications that build on prior, cited research.^{34,35,36,37}

Clinical sensitivity for classic FAP is about 95%; about 90% of pathogenic variants are detected by sequencing,^{38,39} while 8% to 12% of pathogenic variants are detected by deletion and duplication testing.^{40,41} Among Northern European whites, 98% of pathogenic *MUTYH* variants are detected by full gene sequencing.^{42,43}

A comprehensive review of the *APC* pathogenic variant and its association with classical FAP and attenuated FAP and MAP is beyond the scope of this evidence review. The likelihood of detecting an *APC* pathogenic variant is highly dependent on the severity of colonic polyposis^{40,44,45,46} and family history.⁴⁷ Detection rates are higher in classic polyposis (88%) than in non-classical FAPs such as attenuated colonic phenotypes (57%) or MAP (33%).

Section Summary: Clinically Valid

The analytic and clinical sensitivity and specificity for *APC* and *MUTYH* are high. About 90% of pathogenic variants in classical FAP are detected by sequencing while 8% to 12% of pathogenic variants are detected by deletion and duplication testing. Among Northern European whites, 98% of pathogenic *MUTYH* variants are detected by full gene sequencing. The likelihood of detecting an *APC* pathogenic variant is highly dependent on the severity of colonic polyposis and family history. Detection rates are higher in classic polyposis (88%) than in nonclassical FAPs such as attenuated colonic phenotypes (57%) or MAP (33%).

Clinical Useful

A test is clinically useful if the use of the results informs management decisions that improve the net health outcome of care. The net health outcome can be improved if patients receive correct therapy, more effective therapy, or avoid unnecessary therapy or testing.

Direct Evidence

Direct evidence of clinical utility is provided by studies that have compared health outcomes for patients managed with and without the test. Because these are intervention studies, the preferred evidence would be from randomized controlled trials (RCTs).

No RCTs were identified assessing the clinical utility of genetic testing for FAP and MAP.

Chain of Evidence

Genetic testing of patients requiring a differential diagnosis of attenuated FAP versus MAP versus Lynch syndrome may have clinical utility:

- If the test supports the clinical diagnosis of an attenuated disease, the protocol for endoscopic surveillance is affected and, depending on the situation, may avoid more frequent but unnecessary surveillance or necessitates more frequent surveillance.

Genetic testing of at-risk relatives of patients with FAP and/or a known *APC* variant may have clinical utility:

- If, in the absence of genetic testing, the diagnosis of colorectal polyposis in at-risk relatives of patients with FAP and/or a known *APC* variant can only be established by colonoscopy and subsequent histologic examination of removed polyps, which are burdensome.
- If results are negative, the test results may provide release from the intensified screening program resulting in psychological relief.

A TEC Assessment (1998)³³ offered the following conclusions:

- Genetic testing for FAP may improve health outcomes by identifying which currently unaffected at-risk family members require intense surveillance or prophylactic colectomy.
- At-risk subjects are considered to be those with greater than 10 adenomatous polyps or close relatives of patients with clinically diagnosed FAP or of patients with an identified *APC* variant.
- The optimal testing strategy is to define the specific genetic variant in an affected family member and then test the unaffected family members to see if they have inherited the same variant.

Testing for the *APC* variant has no role in the evaluation, diagnosis, or treatment of patients with classical FAP where the diagnosis and treatment are based on the clinical presentation.

Section Summary: Clinically Useful

Direct evidence of clinical utility for genetic testing of attenuated FAP is not available. Genetic testing of at-risk relatives of patients with FAP and/or a known *APC* variant or those requiring a differential diagnosis of attenuated FAP versus MAP versus Lynch syndrome may have clinical utility by avoiding burdensome and invasive endoscopic examinations, release from an

intensified screening program resulting in psychological relief, and improving health outcomes by identifying currently unaffected at-risk family members who require intense surveillance or prophylactic colectomy.

Lynch Syndrome and Colorectal Cancer Genetic Testing

Clinical Context and Test Purpose

The purpose of genetic testing for Lynch syndrome is to:

- Detect Lynch syndrome in patients diagnosed with CRC or endometrial cancer,
- Identify at-risk relatives of patients with a diagnosed Lynch syndrome and/or a known mismatch repair (MMR) variant and/or positive family history meeting Amsterdam or Revised Bethesda criteria, or documentation of 5% or higher predicted risk of the syndrome on a risk prediction model,
- Make a differential diagnosis of attenuated FAP versus MAP versus Lynch syndrome.

The questions addressed in this evidence review are: (1) Is there evidence that genetic testing for Lynch syndrome has clinical validity?; and (2) Does genetic testing for Lynch syndrome change patient management in a way that improves outcomes as a result of genetic testing?

The following PICO was used to select literature to inform this review.

Populations

The relevant populations of interest are patients diagnosed with CRC or endometrial cancer or at-risk relatives of patients with a diagnosed Lynch syndrome and/or a known MMR variant and/or positive family history meeting Amsterdam or Revised Bethesda criteria, or documentation of 5% or higher predicted risk of the syndrome on a risk prediction model, or those requiring a differential diagnosis of attenuated FAP versus MAP versus Lynch syndrome.

Interventions

The relevant intervention is genetic testing for the *MLH1*, *MSH2*, *MSH6*, *PMS2*, *EPCAM*, and/or *BRAF V600E* genes. Commercial testing is available from numerous companies.

Comparators

The following practice is currently being used to make decisions about managing Lynch syndrome: no genetic testing.

Outcomes

The potential beneficial outcomes of primary interest would be early detection of Lynch syndrome and appropriate and timely interventional strategies (e.g., increased surveillance, endoscopic resection, colectomy) to prolong life.

The potential harmful outcomes are those resulting from a false test result. False-positive or false-negative test results can lead to the initiation of unnecessary treatment and adverse effects from that treatment or undertreatment.

Genetic testing for Lynch syndrome may be performed at any point during a lifetime. The necessity for genetic testing is guided by the availability of information that alters the risk of an individual having or developing Lynch syndrome.

Study Selection Criteria

For the evaluation of the clinical validity of the genetic test, studies that met the following eligibility criterion were considered:

- Reported on the analytic sensitivity and specificity and/or diagnostic yield of the test.

Clinically Valid

A test must detect the presence or absence of a condition, the risk of developing a condition in the future, or treatment response (beneficial or adverse).

Review of Evidence

MMR Genes

Microsatellite instability (MSI) and immunohistochemical (IHC) screening tests for MMR variants have similar sensitivity and specificity. Microsatellite instability screening has a sensitivity of about 89% for *MLH1* and *MSH2* and 77% for *MSH6* and a specificity of about 90% for all.

Immunohistochemical screening has sensitivity for *MLH1*, *MSH2*, and *MSH6* of about 83% and a specificity of about 90% for each.

The evidence for Lynch syndrome genetic testing in patients with CRC is based on an evidence report conducted for the Agency for Healthcare Research and Quality by Bonis et al (2007),⁴⁸ a supplemental assessment to that report contracted by the Evaluation of Genomic Applications in Practice and Prevention (EGAPP) Working Group (2009),¹² and an EGAPP recommendation (2009) for genetic testing in CRC.⁴⁹ Based on the Agency for Healthcare Research and Quality report and supplemental assessment, the EGAPP recommendation concluded the following about genetic testing for MMR variants in patients already diagnosed with CRC:

- Family history, while important information to elicit and consider in each case, has poor sensitivity and specificity as a screening test to determine who should be considered for MMR variant testing and should not be used as a sole determinant or screening test.
- Optional *BRAF* testing can be used to reduce the number of patients, who are negative for *MLH1* expression by IHC, needing *MLH1* gene sequencing, thus improving efficiency without reducing sensitivity for MMR variants.

Vos et al (2020) evaluated the yield to detect Lynch syndrome in a prospective cohort of 3602 newly diagnosed CRC cases below age 70.⁵⁰ The standard testing protocol included IHC or MSI testing, followed by *MLH1* hypermethylation testing. Testing identified *MLH1* hypermethylation in a majority of cases tested (66% of 264). The percentage of MMR deficient CRC explained by hypermethylation increased with age, while the percentage of patients with hereditary CCR decreased with age. Of the 47 patients who underwent genetic testing, 55% (26/47) were determined to have Lynch syndrome. The authors estimated that only 78% of these cases would have been identified by the revised Bethesda guidelines. The percentage by age was 86% (6/7) in those under 40 years, 57% (17/29) in patients aged 40 to 64 years, and 30% (3/10) in patients 65 to 69 years of age and the number needed to test to identify 1 case of Lynch syndrome after prescreening was 1.2 (95% CI: 1.0 to 2.0) in patients under 40 years, 4.1 (95% CI: 3.1 to 5.5) in patients 40 to 64 years of age, and 21 (95% CI: 11 to 43) in CRC patients aged 65 to 69.

EPCAM Testing

Several studies have characterized *EPCAM* deletions, established their correlation with the presence of *EPCAM-MSH2* fusion messenger RNAs (apparently nonfunctional) and with the presence of *MSH2* promoter hypermethylation, and, most importantly, have shown the cosegregation of these *EPCAM* variants with Lynch-like disease in families.^{14,51,52,53,54,55} Because studies differ slightly in how patients were selected, the prevalence of these *EPCAM* variants is difficult to estimate but may be in the range of 20% to 40% of patients/families who meet Lynch syndrome criteria, do not have an MMR variant, but have MSI-high tumor tissue. Kempers et al (2011) reported that carriers of an *EPCAM* deletion had a 75% (95% confidence interval [CI], 65% to 85%) cumulative risk of CRC by age 70 years, which did not differ significantly from that of carriers of an *MSH2* deletion (77%; 95% CI, 64% to 90%). The mean age at diagnosis was 43 years.⁵⁶ However, the cumulative risk of endometrial cancer was low at 12% (95% CI, 0% to 27%) by age 70 compared with carriers of an *MSH2* variant (51%; 95% CI, 33% to 69%; $p < .001$).

BRAF V600 or *MLH1* Promoter Methylation

Jin et al (2013) evaluated MMR proteins in 412 newly diagnosed CRC patients.⁵⁷ *MLH1* and PMS2 protein stains were absent in 65 patients who were subsequently tested for a *BRAF* variant. Thirty-six (55%) of the 65 patients had the *BRAF* V600E variant, thus eliminating the need for further genetic testing or counseling for Lynch syndrome. Capper et al (2013) reported on a technique

of V600E IHC testing for *BRAF* variants on a series of 91 stratified as high MSI CRC patients.⁵⁸ V600E positive lesions were detected in 21% of *MLH1*-negative CRC patients who could be excluded from MMR germline testing for Lynch syndrome. Therefore, V600E IHC testing for *BRAF* could be an alternative to *MLH1* promoter methylation analysis. To summarize, *BRAF* V600E variant or *MLH1* promoter methylation testing are optional screening methods that may be used when IHC testing shows a loss of MLH1 protein expression. The presence of *BRAF* V600E or absence of MLH1 protein expression due to *MLH1* promoter methylation rarely occurs in Lynch syndrome and would eliminate the need for further germline variant analysis for a Lynch syndrome diagnosis.⁵⁹

Clinically Useful

A test is clinically useful if the use of the results informs management decisions that improve the net health outcome of care. The net health outcome can be improved if patients receive correct therapy, more effective therapy, or avoid unnecessary therapy or testing.

Direct Evidence

Direct evidence of clinical utility is provided by studies that have compared health outcomes for patients managed with and without the test. Because these are intervention studies, the preferred evidence would be from RCTs.

No RCTs were identified assessing the clinical utility of genetic testing for Lynch syndrome.

Chain of Evidence

Genetic testing of patients with colon or endometrial cancer to detect Lynch syndrome has clinical utility:

- To make decisions about the preferred approach for treatment (endoscopic resection, colectomy with ileorectal anastomosis or segmental colectomy).

Genetic testing of at-risk relatives of patients with Lynch syndrome and/or a known MMR variant and/or positive family history meeting Amsterdam or Revised Bethesda criteria, or documentation of 5% or higher predicted risk of the syndrome on a risk prediction model, has clinical utility:

- If the individuals diagnosed with Lynch syndrome are recommended for screening for Lynch syndrome-associated cancers.
- If, in the absence of genetic testing, the diagnosis of Lynch syndrome in at-risk relatives of patients can only be established by colonoscopy and subsequent histologic examination of excised polyps, which is burdensome.
- If negative test results prompt release from an intensified screening program, thereby reducing an emotional burden.

Genetic testing of patients requiring a differential diagnosis of attenuated FAP versus MAP versus Lynch syndrome may have clinical utility:

- If the test supports the clinical diagnosis of Lynch syndrome, the protocol for endoscopic surveillance is affected and, depending on the situation, may avoid more frequent but unnecessary surveillance or necessitates more frequent surveillance.

A chain of evidence can be constructed for the clinical utility of testing all patients with CRC for MMR variants. EGAPP conclusions are summarized next.

- Seven studies examined how counseling affected testing and surveillance choices among unaffected family members of Lynch syndrome patients.^{60,61,62,63,64,65,66} About half of the relatives received counseling, and 95% of them chose MMR gene variant testing. Among those positive for MMR gene variants, uptake of colonoscopic surveillance beginning at age 20 to 25 years was high at 53% to 100%.
 - One long-term, nonrandomized controlled study and a cohort study of Lynch syndrome family members found significant reductions in CRC among those who followed recommended colonic surveillance versus those who did not.

- Surveillance and prevention for other Lynch syndrome cancers.
- The chain of evidence from descriptive studies and expert opinion is inadequate (inconclusive) to demonstrate the clinical utility of testing the probands with Lynch syndrome (i.e., the index patient).
 - Although a small body of evidence suggests that MSI-positive tumors are resistant to 5-fluorouracil and more sensitive to irinotecan than MSI-negative tumors, no alteration in therapy according to MSI status has yet been recommended.
 - Surveillance and prevention for other Lynch syndrome cancers:
 - While invasive and not actively recommended, women may choose hysterectomy with salpingo-oophorectomy to prevent gynecologic cancer. In a retrospective study by Schmeler et al (2006), 315 women who chose this option had no gynecologic cancer over 10 years, whereas about one-third of women who did not have surgery developed endometrial cancer, and 5.5% developed ovarian cancer.⁶⁷
 - In a study by Bouzourene et al (2010), surveillance endometrial biopsy detected endometrial cancer and potentially precancerous conditions at earlier stages in those with Lynch syndrome, but results were not statistically significant, and a survival benefit has yet to be shown.¹³ Transvaginal ultrasound is not a highly effective surveillance mechanism for endometrial cancer in patients with Lynch syndrome; however, transvaginal ultrasound in conjunction with endometrial biopsy has been recommended for surveillance.
 - Gastroduodenoscopy for gastric cancer surveillance and urine cytology for urinary tract cancer surveillance are recommended based on expert opinion only, in the absence of adequate supporting evidence.

The Cancer Genetic Studies Consortium (1997) recommended that if CRC is diagnosed in patients with an identified variant or a strong family history, a subtotal colectomy with ileorectal anastomosis should be considered as an option to segmental resection.⁶⁸ The 2006 joint American Society of Clinical Oncology and Society of Surgical Oncology review assessing risk-reducing surgery in hereditary cancers recommended offering total colectomy plus ileorectal anastomosis or hemicolectomy as options to patients with Lynch syndrome and CRC, especially those who are younger.⁶⁹ The Societies' review also recommended offering Lynch syndrome patients with an index rectal cancer the options of total proctocolectomy with ileal pouch-anal anastomosis or anterior proctosigmoidectomy with primary reconstruction. The rationale for total proctocolectomy is the 17% to 45% rate of metachronous colon cancer in the remaining colon after an index rectal cancer in Lynch syndrome patients.

The risk of endometrial cancer in MMR variant carriers has been estimated at 34% (95% CI, 17% to 60%) by age 70, and at 8% for ovarian cancer (95% CI, 2% to 39%) by age 70.⁷⁰ Risks do not appear to appreciably increase until after age 40. Females with Lynch syndrome who choose risk-reducing surgery are encouraged to consider oophorectomy because of the risk of ovarian cancer in Lynch syndrome. In a retrospective cohort study, Obermair et al (2010) found that hysterectomy improved survival among female colon cancer survivors with Lynch syndrome.⁷¹ This study estimated that, for every 100 women diagnosed with Lynch syndrome-associated CRC, about 23 would be diagnosed with endometrial cancer within 10 years absent a hysterectomy. Surveillance in Lynch syndrome populations for ovarian cancer has not been demonstrated to be successful at improving survival.⁷²

Section Summary: Clinically Useful

Direct evidence of clinical utility for genetic testing for Lynch syndrome is not available. Multiple studies have demonstrated clinical utility in testing unaffected (without cancer) first- and second-degree relatives of patients with Lynch syndrome who have a known MMR variant, in that counseling has been shown to influence testing and surveillance choices among unaffected family members of Lynch syndrome patients. One long-term, nonrandomized controlled study and a cohort study of Lynch syndrome family members found significant reductions in CRC among those who followed and did not follow recommended colonic

surveillance. A positive genetic test for an MMR gene variant can also lead to changes in the management of other Lynch syndrome malignancies.

Genetic Testing for Juvenile Polyposis Syndrome and Peutz-Jeghers Syndrome:

Clinical Context and Test Purpose

The purpose of genetic testing for Juvenile Polyposis syndrome (JPS) and Peutz-Jeghers syndrome (PJS) is:

- To confirm a diagnosis of JPS or PJS in patients suspected of these disorders based on clinical features.
- To identify at-risk relatives of patients with a confirmed diagnosis of JPS or PJS.

The questions addressed in this evidence review are: (1) Is there evidence that genetic testing for patients suspected of JPS and PJS has clinical validity?; and (2) Does genetic testing for JPS and PJS change patient management in a way that improves outcomes as a result of genetic testing?

The following PICO was used to select literature to inform this review.

Populations

The relevant populations of interest are patients with suspected JPS or PJS and individuals who are at-risk relatives of patients suspected of or diagnosed with JPS or PJS.

Interventions

The relevant intervention is genetic testing for *SMAD4* and *BMPR1* (for JPS) and *STK11* (for PJS). Commercial testing is available from numerous companies.

Comparators

The following practice is currently being used to make decisions about managing JPS and PJS: no genetic testing.

Outcomes

The potential beneficial outcomes of primary interest would be early detection of cancer and appropriate and timely interventional strategies (e.g., cancer screening, surgical intervention including polyp resection, gastrectomy, colectomy) to prolong life.

The potential harmful outcomes are those resulting from a false test result. False-positive or false-negative test results can lead to the initiation of unnecessary treatment and adverse events from that treatment or undertreatment.

Genetic testing for *SMAD4* and *BMPR1* (for JPS) and *STK11* (for PJS) may be performed at any point during a lifetime. The necessity for genetic testing is guided by the availability of information that alters the risk of an individual of having or developing JPS and PJS.

Study Selection Criteria

For the evaluation of the clinical validity of the genetic test, studies that met the following eligibility criterion were considered:

- Reported on the diagnostic yield of the test.

Clinically Valid

A test must detect the presence or absence of a condition, the risk of developing a condition in the future, or treatment response (beneficial or adverse).

Review of Evidence

Table 1 summarizes clinical validity studies assessing genetic testing for JPS and PJS.

Table 1. Summary of Clinical Validity Studies Assessing Genetic Testing for JPS and PJS

Study	Study Design and Population	Results
Calva-Cerqueira et al (2009) ⁷³ .	Observational; 102 unrelated JPS probands analyzed all of whom met clinical criteria for JPS	<i>SMAD4</i> and <i>BMPR1A</i> variants detected in 41% (42/102) JPS probands
Aretz et al (2007) ⁷⁴ .	Observational; 80 unrelated patients (65 met clinical criteria for typical JPS; 15 presumed to have JPS) were examined by direct sequencing for <i>SMAD4</i> , <i>BMPR1A</i> , and <i>PTEN</i> variants	<i>SMAD4</i> and <i>BMPR1A</i> variants detected in 60% of typical JPS patients and none in presumed JPS patients; overall diagnostic yield, 49%
Volikos et al (2006) ⁷⁵ .	Observational; 76 clinically diagnosed with PJS	Detection rate of germline variants was about 80% (59/76)
Aretz et al (2005) ⁷⁶ .	Observational; 71 patients (56 met clinical criteria for PJS; 12 presumed to have PJS)	<i>STK11</i> variant detected in 52% (37/71)

JPS: juvenile polyposis syndrome; PJS: Peutz-Jeghers syndrome.

Section Summary: Clinically Valid

The likelihood of detecting a pathogenic variant is highly dependent on the presence of clinical features and family history. Detection rates have been reported to be between 60% and 41% for JPS, and 52% and 80% for PJS.

Clinical Useful

A test is clinically useful if the use of the results informs management decisions that improve the net health outcome of care. The net health outcome can be improved if patients receive correct therapy, more effective therapy, or avoid unnecessary therapy or testing.

Direct Evidence

Direct evidence of clinical utility is provided by studies that have compared health outcomes for patients managed with and without the test. Because these are intervention studies, the preferred evidence would be from RCTs.

No RCTs were identified assessing the clinical utility of genetic testing for JPS and PJS.

Chain of Evidence

Indirect evidence on clinical utility rests on clinical validity. If the evidence is insufficient to demonstrate test performance, no inferences can be made about clinical utility.

Genetic testing of patients with suspected JPS and PJS has clinical utility:

- To make decisions about a preferred approach for treatment (endoscopic resection, colectomy with ileorectal anastomosis, segmental colectomy).

Genetic testing of individuals who are at-risk relatives of patients suspected of or diagnosed with JPS or PJS has clinical utility:

- If the individuals diagnosed with JPS and PJS are recommended for screening for JPS and PJS-associated cancers.
- If, in the absence of genetic testing, the diagnosis of JPS and PJS in at-risk relatives of patients can only be established by colonoscopy and subsequent histologic examination of excised polyps, which is burdensome.
- If negative test results prompt release from an intensified screening program, thereby reducing an emotional burden.

A systematic review of 20 cohort studies with a total of 1644 patients with PJS was published by Lier et al (2010).³² A total of 349 patients developed 384 malignancies at average age of 42 years. Lifetime risk for any cancer varied between 37% and 93% with relative risks (RRs) ranging from 9.9 to 18 versus the general population.

Section Summary: Clinically Useful

Direct evidence of the clinical utility for genetic testing of JPS or PJS is not available. Genetic testing of patients with suspected JPS or PJS or individuals who are at-risk relatives of patients suspected of or diagnosed with a polyposis syndrome or PJS may have clinical utility by avoiding burdensome and invasive endoscopic examinations, release from an intensified screening program resulting in psychological relief, and improving health outcomes by identifying currently unaffected at-risk family members who require intense surveillance or prophylactic colectomy.

Summary of Evidence

For individuals who are suspected of attenuated FAP, MAP, and Lynch syndrome who receive genetic testing for *APC*, or are at-risk relatives of patients with FAP who receive genetic testing for *MUTYH* after a negative *APC* test result, the evidence includes a TEC Assessment. Relevant outcomes are OS, disease-specific survival, and test accuracy and validity. For patients with an *APC* variant, enhanced surveillance and/or prophylactic treatment will reduce the future incidence of colon cancer and improve health outcomes. A related familial polyposis syndrome, MAP syndrome, is associated with variants in the *MUTYH* gene. Testing for this genetic variant is necessary when the differential diagnosis includes both FAP and MAP because distinguishing between the 2 leads to different management strategies. Depending on the presentation, Lynch syndrome may be part of the same differential diagnosis. The evidence is sufficient to determine that the technology results in an improvement in the net health outcome.

For individuals who (1) are suspected of attenuated FAP, MAP, and Lynch syndrome, or (2) have colon cancer, or (3) have endometrial cancer meeting clinical criteria for Lynch syndrome, or (4) are at-risk relatives of patients with Lynch syndrome, or (5) are without colon cancer but with a family history meeting Amsterdam or Revised Bethesda criteria, or documentation of 5% or higher predicted risk of the syndrome on a validated risk prediction model, who receive genetic testing for mismatch repair (MMR) genes, the evidence includes an Agency for Healthcare Research and Quality report, a supplemental assessment to that report by the Evaluation of Genomic Applications in Practice and Prevention Working Group, and an Evaluation of Genomic Applications in Practice and Prevention recommendation for genetic testing in CRC. Relevant outcomes are OS, disease-specific survival, and test accuracy and validity. A chain of evidence from well-designed experimental nonrandomized studies is adequate to demonstrate the clinical utility of testing unaffected (without cancer) first- and second-degree relatives of patients with Lynch syndrome who have a known variant in an MMR gene, in that counseling has been shown to influence testing and surveillance choices among unaffected family members of Lynch syndrome patients. One long-term, nonrandomized controlled study and a cohort study of Lynch syndrome family members found significant reductions in CRC among those who followed recommended colonic surveillance. A positive genetic test for a MMR variant can also lead to changes in the management of other Lynch syndrome malignancies. The evidence is sufficient to determine that the technology results in an improvement in the net health outcome.

For individuals who warrant Lynch testing, screen negative on MMR testing, but positive for MSI and lack MSH2 protein expression who receive genetic testing for *EPCAM* variants, the evidence includes variant prevalence studies and case series. Relevant outcomes are OS, disease-specific survival, and test accuracy and validity. Studies have shown an association between *EPCAM* variants and Lynch-like disease in families, and the cumulative risk for CRC is similar to carriers of an *MSH2* variant. Identification of an *EPCAM* variant could lead to changes in management that improve health outcomes. The evidence is sufficient to determine that the technology results in an improvement in the net health outcome.

For individuals who have CRC in whom MLH1 protein is not expressed on IHC analysis who receive genetic testing for *BRAF* V600E or *MLH1* promoter methylation, the evidence includes case series. Relevant outcomes are OS, disease-specific survival, and test accuracy and validity. Studies have shown, with high sensitivity and specificity, an association between *BRAF* V600E

variant and *MLH1* promoter methylation with sporadic CRC. Therefore, this type of testing could eliminate the need for further genetic testing or counseling for Lynch syndrome. The evidence is sufficient to determine that the technology results in an improvement in the net health outcome.

For individuals who (1) are suspected of JPS or PJS or (2) are at-risk relatives of patients suspected of or diagnosed with JPS or PJS who receive genetic testing for *SMAD4*, *BMPR1A*, or *STK11* genes, respectively, the evidence includes multiple observational studies. Relevant outcomes are OS, disease-specific survival, and test accuracy and validity. Studies have shown, with high sensitivity and specificity, an association between *SMAD4* and *BMPR1A* and *STK11* variants with JPS and PJS, respectively. Direct evidence of clinical utility for genetic testing of JPS or PJS is not available. Genetic testing may have clinical utility by avoiding burdensome and invasive endoscopic examinations, release from intensified screening programs resulting in psychological relief, and improving health outcomes by identifying currently unaffected at-risk family members who require intense surveillance or prophylactic colectomy. The evidence is sufficient to determine that the technology results in an improvement in the net health outcome.

Supplemental Information

The purpose of the following information is to provide reference material. Inclusion does not imply endorsement or alignment with the evidence review conclusions.

Clinical Input From Physician Specialty Societies and Academic Medical Centers

While the various physician specialty societies and academic medical centers may collaborate with and make recommendations during this process, through the provision of appropriate reviewers, input received does not represent an endorsement or position statement by the physician specialty societies or academic medical centers, unless otherwise noted.

In response to requests from Blue Cross Blue Shield Association, input was received from 3 physician specialty societies and 3 academic medical centers in 2009. In general, those providing input agreed with the overall approach described in this policy.

Practice Guidelines and Position Statements

Guidelines or position statements will be considered for inclusion in 'Supplemental Information' if they were issued by, or jointly by, a US professional society, an international society with US representation, or National Institute for Health and Care Excellence (NICE). Priority will be given to guidelines that are informed by a systematic review, include strength of evidence ratings, and include a description of management of conflict of interest.

National Comprehensive Cancer Network

The NCCN guidelines on high-risk colorectal cancer syndromes (v.1.2021) are summarized in Table 2.¹⁷

Table 2. Criteria for Evaluation of Lynch Syndrome

Criteria for the Evaluation of Lynch Syndrome
Known LS variant in the family
An individual with colorectal or endometrial cancer and any of the following: <ul style="list-style-type: none"> • Diagnosed <50 y • Another synchronous or metachronous LS-related cancer^a • 1 first-degree or second-degree relative with LS-related^a cancer diagnosed <50 y • ≥2 first-degree or second-degree relatives with LS-related^a cancers regardless of age
An individual with colorectal or endometrial cancer at any age with tumor showing evidence of MMR deficiency, either by PCR, NGS, or IHC diagnosed at any age. ^{bb}
Family history of any of the following: <ul style="list-style-type: none"> • ≥1 first-degree relative with colorectal or endometrial cancer diagnosed <50 y • ≥1 first-degree relative with colorectal or endometrial cancer and another synchronous or metachronous LS-related cancer^a • ≥2 first-degree or second-degree relatives with LS-related cancer,^a including ≥1 diagnosed <50 y • ≥3 first-degree or second-degree relatives with LS-related cancers,^a regardless of age

An individual with an LS-related cancer^a or unaffected individual with $\geq 5\%$ risk^c of having an MMR gene variant based on predictive models (PREMM5, MMRpro, MMRpredict)

IHC: immunohistochemistry; LS: Lynch syndrome; MMR: mismatch repair; MSI: microsatellite instability; NGS: next generation sequencing; PCR: polymerase chain reaction.

^a LS-related cancers include colorectal, endometrial, gastric, ovarian, pancreas, ureter and renal pelvis, brain (usually glioblastoma), biliary tract, small intestinal cancers, as well as sebaceous carcinomas, and keratoacanthomas as seen in Muir-Torre syndrome.

^b Tumor screening for MMR deficiency is appropriate for all colorectal and endometrial cancers regardless of age at diagnosis, however, germline genetic testing is generally reserved for patients with early age at diagnosis; positive family history; or abnormal tumor testing results; MSI or loss of MMR protein expression.

^c There are recent data that resulted in a lower threshold of $\geq 2.5\%$ for the PREMM5 predictive model risk for having an MMR gene variant. Based on these data, it is reasonable for testing to be done based on the $\geq 2.5\%$ score result and clinical judgment. Of note, with the lower threshold, there is an increase in sensitivity, but a decrease in specificity. It is not known how this applies to the general population of unaffected individuals.

Genetic Testing Recommendations for Lynch Syndrome

Screening of the tumor for defective DNA mismatch repair (MMR) using immunohistochemistry (IHC) and/or microsatellite instability (MSI) is used to identify which patients should undergo mutation testing for Lynch syndrome.²⁷ The NCCN guidelines also indicate *BRAF* V600E testing or *MLH1* promoter methylation testing may be used when *MLH1* is not expressed in the tumor on IHC analysis to exclude a diagnosis of Lynch syndrome.

The NCCN guidelines for colon cancer (v.2.2021) recommend that all newly diagnosed patients with colon cancer be tested for MMR or MSI.²⁶

The NCCN guidelines for uterine neoplasm (v.3.2021) also recommend universal screening for MMR genes.²⁷ Additionally, the NCCN guidelines recommend screening for Lynch syndrome in all endometrial cancer patients younger than 50 years.

The NCCN guidelines for genetic/familial high-risk assessment: colorectal (v1.2021) recommend genetic testing for at-risk family members of patients with positive variants in *MLH1*, *MSH2*, *MSH6*, *PMS2*, and *EPCAM*.²⁷ These guidelines also address familial adenomatous polyposis (classical and attenuated) and *MUTYH*-associated polyposis and are consistent with the information provided in this evidence review.

Surveillance Recommendations for Lynch Syndrome

The NCCN guidelines for colon cancer (v.2.2021)²⁶ and for colorectal cancer (CRC) screening (v.2.2021)²⁸ recommend CRC patients treated with curative-intent surgery undergo surveillance colonoscopy at 1 year postsurgery and, if normal, again in 3 years, then every 5 years based on findings.

The NCCN guidelines on genetic/familial high-risk assessment for CRC indicate for *MLH1*, *MSH2*, and *EPCAM* variant carriers that surveillance with colonoscopy should begin "at age 20 to 25 years or 2 to 5 years before the earliest colon cancer if it is diagnosed before age 25 years and repeat every 1 to 2 years."²⁷

MSH6 and *PMS2* variant carriers should begin surveillance with colonoscopy "at age 30 to 35 years or 2 to 5 years before the earliest colon cancer if it is diagnosed before age 30 years and repeat every 1 to 2 years"²⁷.

Peutz-Jeghers Syndrome and Juvenile Polyposis Syndrome

There are limited data on the efficacy of various screening modalities in juvenile polyposis syndrome (JPS) and Peutz-Jeghers syndrome (PJS). The NCCN cancer risk and surveillance 2 category 2A recommendations for these indications are summarized in Tables 3 and 4.²⁷

Table 3. Risk and Surveillance Guidelines for Peutz-Jeghers Syndrome

Site	Lifetime Risk, %	Screening Procedure and Interval	Initiation Age, y
Breast	32 to 54	<ul style="list-style-type: none"> Mammogram and breast MRI annually Clinical breast exam every 6 mo 	≈30 y
Colon	39	Colonoscopy every 2 to 3 y	Late teens
Stomach	29	Upper endoscopy every 2 to 3 y	Late teens
Small intestine	13	Small bowel visualization (CT or MRI enterography or video capsule endoscopy baseline at 8 to 10 y with follow-up interval based on findings but at least by age 18, then every 2 to 3 y, though this may be individualized, or with symptoms)	≈8 to 10 y
Pancreas	11 to 36	Magnetic resonance cholangiopancreatography with contrast or endoscopic ultrasound every 1 to 2 h	≈30 to 35 y
Ovary; Cervix (typically cervical adenoma malignum)	18 to 21	<ul style="list-style-type: none"> Pelvic examination and Pap smear annually 	≈18 to 20 y
Uterus	10		
Ovary (typically benign sex cord/Sertoli cell tumors)	9	<ul style="list-style-type: none"> Pelvic examination and Pap smear annually 	≈18 to 20 y
Lung	7 to 17	<ul style="list-style-type: none"> Provide education about symptoms and smoking cessation No other specific recommendations have been made 	

CT: computed tomography; MRI: magnetic resonance imaging.

Table 4. Risk and Surveillance Guidelines for Juvenile Polyposis Syndrome

Site	Lifetime Risk, %	Screening Procedure and Interval	Initiation Age, y
Colon	up to 50	Colonoscopy: Repeat every 2 to 3 years. If polyps are found, repeat at shorter intervals based on polyp size, number, and pathology. ^a	≈ 18 y
Stomach	up to 21 especially if multiple polyps present	Upper endoscopy: Repeat every 2 to 3 years. If polyps are found, repeat at shorter intervals based on polyp size, number, and pathology. ^a	≈ 18 y
Small intestine	Rare, undefined	No recommendations made	

^a In families where a SMAD4 or BMPR1A mutation is not identified, consider extending colonoscopy/upper endoscopy intervals in at-risk individuals who have no polyps from 2 to 3 years to 5 years beginning at age 20, and then every 10 years beginning at age 40s,

American College of Gastroenterology

The American College of Gastroenterology (2015) issued practice guidelines for the management of patients with hereditary gastrointestinal cancer syndromes.²¹

For Lynch syndrome, the College recommended:

“All newly diagnosed colorectal cancers (CRCs) should be evaluated for mismatch repair deficiency.

Analysis may be done by immunohistochemical testing for the *MLH1/MSH2/MSH6/PMS2* proteins and/or testing for microsatellite instability. Tumors that demonstrate loss of *MLH1* should undergo BRAF testing or analysis for *MLH1* promoter hypermethylation.

Individuals who have a personal history of a tumor showing evidence of mismatch repair deficiency (and no demonstrated BRAF variant or hypermethylation of *MLH1*), a known family variant associated with LS [Lynch syndrome], or a risk of ≥5% chance of LS based on risk prediction models should undergo genetic evaluation for LS.⁷⁹

Genetic testing of patients with suspected LS should include germline variant genetic testing for the *MLH1*, *MSH2*, *MSH6*, *PMS2*, and/or *EPCAM* genes or the altered gene(s) indicated by IHC testing.”

For adenomatous polyposis syndromes, the College recommended:

“Familial adenomatous polyposis (FAP)/*MUTYH*-associated polyposis/attenuated polyposis Individuals who have a personal history of >10 cumulative colorectal adenomas, a family history of one of the adenomatous polyposis syndromes, or a history of adenomas and FAP-type extracolonic manifestations (duodenal/ampullary adenomas, desmoid tumors, papillary thyroid cancer, congenital hypertrophy of the retinal pigment epithelium, epidermal cysts, osteomas) should undergo assessment for the adenomatous polyposis syndromes.

Genetic testing of patients with suspected adenomatous polyposis syndromes should include *APC* and *MUTYH* gene variant analysis.”

For juvenile polyposis syndrome, the College recommended:

“Genetic evaluation of a patient with possible JPS [juvenile polyposis syndrome] should include testing for *SMAD4* and *BMPR1A* mutations”

“Surveillance of the gastrointestinal (GI) tract in affected or at-risk JPS patients should include screening for colon, stomach, and small bowel cancers (strong recommendation, very low quality of evidence).

Colectomy and ileorectal anastomosis or proctocolectomy and ileal pouch-anal anastomosis is indicated for polyp-related symptoms, or when the polyps cannot be managed endoscopically (strong recommendation, low quality of evidence).

Cardiovascular examination for and evaluation for hereditary hemorrhagic telangiectasia should be considered for *SMAD4* mutation carriers (conditional recommendation, very low quality of evidence).”

For Peutz-Jeghers syndrome, the College recommended:

“Genetic evaluation of a patient with possible PJS [Peutz-Jeghers syndrome] should include testing for *STK11* mutations.”

“Surveillance in affected or at-risk PJS patients should include monitoring for colon, stomach, small bowel, pancreas, breast, ovary, uterus, cervix, and testes cancers. Risk for lung cancer is increased, but no specific screening has been recommended. It would seem wise to consider annual chest radiograph or chest computed tomography (CT) in smokers (conditional recommendation, low quality of evidence).”

American Society of Clinical Oncology and Society of Surgical Oncology

The American Society of Clinical Oncology (2015) concluded the European Society for Medical Oncology clinical guidelines published in 2013 were based on the most relevant scientific evidence and therefore endorsed them with minor qualifying statements (in bold italics).⁸⁰ The recommendations as related to genetic testing hereditary CRC syndromes are summarized below:

- “Tumor testing **for DNA mismatch repair (MMR) deficiency** with immunohistochemistry for MMR proteins and/or MSI should be **assessed** in all CRC patients. As an alternate strategy, tumor testing should be carried out in individuals with CRC younger than 70 years, or those older than 70 years who fulfill any of the revised Bethesda guidelines.
- If loss of *MLH1*/*PMS2* **protein expression** is observed in the tumor, analysis of *BRAF* V600E mutation or analysis of methylation of the *MLH1* promoter should be carried out first to rule out a sporadic case. **If tumor is MMR deficient and somatic *BRAF* mutation is not detected or *MLH1* promoter methylation is not identified, testing for germline mutations is indicated.**

- If loss of any of the other proteins (MSH2, MSH6, PMS2) is observed, germline genetic testing should be carried out **for the genes corresponding to the absent proteins (e.g., MSH2, MSH6, EPCAM, PMS2, or MLH1).**
- Full germline genetic testing **for Lynch syndrome** should include DNA sequencing and large rearrangement analysis.
- Patients with multiple colorectal adenomas should be considered for full germline genetic testing of *APC* and/or *MUTYH*.
- Germline testing of *MUTYH* can be initiated by screening for the most common mutations (*G396D*, *Y179C*) in the white population followed by analysis of the entire gene in heterozygotes. Founder mutations among ethnic groups should be taken into account. **For nonwhite individuals, full sequencing of *MUTYH* should be considered.**

U.S. Preventive Services Task Force Recommendations

No U.S. Preventive Services Task Force recommendations for genetic testing of Lynch syndrome and other inherited colon cancer syndromes have been identified.

Medicare National Coverage

Under Medicare, genetic tests for cancer are a covered benefit only for a beneficiary with a personal history of an illness, injury, or signs/symptoms thereof (i.e., clinically affected). A person with a personal history of a relevant cancer is a clinically affected person, even if the cancer is considered cured. Predictive or presymptomatic genetic tests and services, in the absence of past or present illness in the beneficiary, are not covered under national Medicare rules. The Centers for Medicare & Medicaid Services recognizes Lynch syndrome as “an autosomal dominant syndrome that accounts for about 3% to 5% of colorectal cancer cases. [Lynch] syndrome variants occur in the following genes: *hMLH1*, *hMSH2*, *hMSH6*, *PMS2*, and *EPCAM*.” The Centers for Medicare & Medicaid Services also recognize familial adenomatous polyposis and *MUTYH*-associated polyposis syndromes and their associated variants.

Ongoing and Unpublished Clinical Trials

Some currently ongoing and unpublished trials that might influence this review are listed in Table 5.

Table 5. Summary of Key Trials

NCT No.	Trial Name	Planned Enrollment	Completion Date
Ongoing			
NCT02494791	Universal Screening for Lynch Syndrome in Women With Endometrial and Non-Serous Ovarian Cancer	886	July 2025
NCT04494945	Approaches to Identify and Care for Individuals With Inherited Cancer Syndromes	27500	Jun 2030
Unpublished			
NCT01850654	Ohio Colorectal Cancer Prevention Initiative: Universal Screening for Lynch Syndrome	3470	Jan 2018 (completed)

NCT: national clinical trial.

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Documentation for Clinical Review

Please provide the following documentation:

- History and physical and/or consultation notes including:
 - Laboratory invoice/order indicating specific test(s)/panel(s) and associated procedure codes
 - Personal and/or family history of cancer (if applicable) including: family relationship, cancer site(s), age at diagnosis
 - Preliminary diagnosis and prognosis
 - Specific test(s) requested and clinical reason/justification for testing
 - Treatment plan
 - Genetic counseling/professional results (if available)
 - Laboratory and/or Pathology report(s) (e.g., APC gene mutations, MSH2, MMR mutations, tumor MSI status)

Post Service (in addition to the above, please include the following):

- Results/reports of tests performed
- Procedure report(s)

Coding

This Policy relates only to the services or supplies described herein. Benefits may vary according to product design; therefore, contract language should be reviewed before applying the terms of the Policy.

The following codes are included below for informational purposes. Inclusion or exclusion of a code(s) does not constitute or imply member coverage or provider reimbursement policy. Policy Statements are intended to provide member coverage information and may include the use of some codes for clarity. The Policy Guidelines section may also provide additional information for how to interpret the Policy Statements and to provide coding guidance in some cases.

Type	Code	Description
CPT®	0101U	Hereditary colon cancer disorders (e.g., Lynch syndrome, PTEN hamartoma syndrome, Cowden syndrome, familial adenomatosis polyposis); genomic sequence analysis panel utilizing a combination of NGS, Sanger, MLPA and array CGH, with mRNA analytics to resolve variants of unknown significance when indicated [15 genes (sequencing and deletion/duplication), EPCAM and GREM1 (deletion/duplication only)]
	0130U	Hereditary colon cancer disorders (e.g., Lynch syndrome, PTEN hamartoma syndrome, Cowden syndrome, familial adenomatosis polyposis), targeted mRNA sequence analysis panel (APC, CDH1, CHEK2, MLH1, MSH2, MSH6, MUTYH, PMS2, PTEN, and TP53) (List separately in addition to code for primary procedure)
	0157U	APC (APC regulator of WNT signaling pathway) (e.g., familial adenomatosis polyposis [FAP]) mRNA sequence analysis (List separately in addition to code for primary procedure)
	0158U	MLH1 (mutL homolog 1) (e.g., hereditary non-polyposis colorectal cancer, Lynch syndrome) mRNA sequence analysis (List separately in addition to code for primary procedure)
	0159U	MSH2 (mutS homolog 2) (e.g., hereditary colon cancer, Lynch syndrome) mRNA sequence analysis (List separately in addition to code for primary procedure)

Type	Code	Description
	0160U	<i>MSH6</i> (mutS homolog 6) (e.g., hereditary colon cancer, Lynch syndrome) mRNA sequence analysis (List separately in addition to code for primary procedure)
	0161U	<i>PMS2</i> (PMS1 homolog 2, mismatch repair system component) (e.g., hereditary non-polyposis colorectal cancer, Lynch syndrome) mRNA sequence analysis (List separately in addition to code for primary procedure)
	0162U	Hereditary colon cancer (Lynch syndrome), targeted mRNA sequence analysis panel (<i>MLH1</i> , <i>MSH2</i> , <i>MSH6</i> , <i>PMS2</i>) (List separately in addition to code for primary procedure)
	0238U	Oncology (Lynch syndrome), genomic DNA sequence analysis of <i>MLH1</i> , <i>MSH2</i> , <i>MSH6</i> , <i>PMS2</i> , and <i>EPCAM</i> , including small sequence changes in exonic and intronic regions, deletions, duplications, mobile element insertions, and variants in non-uniquely mappable regions
	81201	<i>APC</i> (adenomatous polyposis coli) (e.g., familial adenomatous polyposis [FAP], attenuated FAP) gene analysis; full gene sequence
	81202	<i>APC</i> (adenomatous polyposis coli) (e.g., familial adenomatous polyposis [FAP], attenuated FAP) gene analysis; known familial variants
	81203	<i>APC</i> (adenomatous polyposis coli) (e.g., familial adenomatous polyposis [FAP], attenuated FAP) gene analysis; duplication/deletion variants
	81210	<i>BRAF</i> (B-Raf proto-oncogene, serine/threonine kinase) (e.g., colon cancer, melanoma), gene analysis, V600 variant(s)
	81288	<i>MLH1</i> (mutL homolog 1, colon cancer, nonpolyposis type 2) (e.g., hereditary non-polyposis colorectal cancer, Lynch syndrome) gene analysis; promoter methylation analysis
	81292	<i>MLH1</i> (mutL homolog 1, colon cancer, nonpolyposis type 2) (e.g., hereditary non-polyposis colorectal cancer, Lynch syndrome) gene analysis; full sequence analysis
	81293	<i>MLH1</i> (mutL homolog 1, colon cancer, nonpolyposis type 2) (e.g., hereditary non-polyposis colorectal cancer, Lynch syndrome) gene analysis; known familial variants
	81294	<i>MLH1</i> (mutL homolog 1, colon cancer, nonpolyposis type 2) (e.g., hereditary non-polyposis colorectal cancer, Lynch syndrome) gene analysis; duplication/deletion variants
	81295	<i>MSH2</i> (mutS homolog 2, colon cancer, nonpolyposis type 1) (e.g., hereditary non-polyposis colorectal cancer, Lynch syndrome) gene analysis; full sequence analysis
	81296	<i>MSH2</i> (mutS homolog 2, colon cancer, nonpolyposis type 1) (e.g., hereditary non-polyposis colorectal cancer, Lynch syndrome) gene analysis; known familial variants
	81297	<i>MSH2</i> (mutS homolog 2, colon cancer, nonpolyposis type 1) (e.g., hereditary non-polyposis colorectal cancer, Lynch syndrome) gene analysis; duplication/deletion variants
	81298	<i>MSH6</i> (mutS homolog 6 [<i>E. coli</i>]) (e.g., hereditary non-polyposis colorectal cancer, Lynch syndrome) gene analysis; full sequence analysis
	81299	<i>MSH6</i> (mutS homolog 6 [<i>E. coli</i>]) (e.g., hereditary non-polyposis colorectal cancer, Lynch syndrome) gene analysis; known familial variants

Type	Code	Description
	81300	<i>MSH6</i> (mutS homolog 6 [<i>E. coli</i>]) (e.g., hereditary non-polyposis colorectal cancer, Lynch syndrome) gene analysis; duplication/deletion variants
	81301	Microsatellite instability analysis (e.g., hereditary non-polyposis colorectal cancer, Lynch syndrome) of markers for mismatch repair deficiency (e.g., BAT25, BAT26), includes comparison of neoplastic and normal tissue, if performed
	81317	<i>PMS2</i> (postmeiotic segregation increased 2 [<i>S. cerevisiae</i>]) (e.g., hereditary non-polyposis colorectal cancer, Lynch syndrome) gene analysis; full sequence analysis
	81318	<i>PMS2</i> (postmeiotic segregation increased 2 [<i>S. cerevisiae</i>]) (e.g., hereditary non-polyposis colorectal cancer, Lynch syndrome) gene analysis; known familial variants
	81319	<i>PMS2</i> (postmeiotic segregation increased 2 [<i>S. cerevisiae</i>]) (e.g., hereditary non-polyposis colorectal cancer, Lynch syndrome) gene analysis; duplication/deletion variants
	81401	Molecular Pathology Procedure Level 2
	81403	Molecular Pathology Procedure Level 4
	81406	Molecular Pathology Procedure Level 7
	81435	Hereditary colon cancer disorders (e.g., Lynch syndrome, PTEN hamartoma syndrome, Cowden syndrome, familial adenomatous polyposis); genomic sequence analysis panel, must include sequencing of at least 10 genes, including <i>APC</i> , <i>BMPR1A</i> , <i>CDH1</i> , <i>MLH1</i> , <i>MSH2</i> , <i>MSH6</i> , <i>MUTYH</i> , <i>PTEN</i> , <i>SMAD4</i> , and <i>STK11</i>
	81436	Hereditary colon cancer disorders (e.g., Lynch syndrome, PTEN hamartoma syndrome, Cowden syndrome, familial adenomatous polyposis); duplication/deletion analysis panel, must include analysis of at least 5 genes, including <i>MLH1</i> , <i>MSH2</i> , <i>EPCAM</i> , <i>SMAD4</i> , and <i>STK11</i>
	96040	Medical genetics and genetic counseling services, each 30 minutes face-to-face with patient/family
HCPCS	None	

Policy History

This section provides a chronological history of the activities, updates and changes that have occurred with this Medical Policy.

Effective Date	Action
10/14/1998	New Policy Adoption
05/01/2001	Policy Review
02/02/2010	Policy revision with position change
06/28/2010	Policy revision with position change Coding update
07/02/2010	Policy revision with position change Coding update
04/12/2012	Policy revision with position change
02/22/2013	Coding Update
03/28/2014	Policy revision with position change
10/31/2014	Policy title change from Genetic Testing for Colorectal Cancer Policy revision without position change
01/30/2015	Coding Update
02/01/2016	Coding update
06/01/2016	Policy revision without position change
08/01/2017	Policy revision without position change

Effective Date	Action
11/01/2017	Policy revision without position change
09/01/2018	Policy revision without position change
11/01/2018	Policy revision without position change
01/01/2019	Policy statement clarification
05/01/2019	Policy revision without position change Coding update
08/01/2019	Administrative Update
11/01/2019	Coding update
12/01/2019	Policy revision without position change
03/01/2020	Coding update
05/01/2020	Administrative update. Policy statement and guidelines updated.
12/01/2020	Annual review. Policy statement, guidelines and literature updated.
12/01/2021	Annual review. Policy statement, guidelines and literature updated.
05/01/2022	Administrative update.

Definitions of Decision Determinations

Medically Necessary: Services that are Medically Necessary include only those which have been established as safe and effective, are furnished under generally accepted professional standards to treat illness, injury or medical condition, and which, as determined by Blue Shield, are: (a) consistent with Blue Shield medical policy; (b) consistent with the symptoms or diagnosis; (c) not furnished primarily for the convenience of the patient, the attending Physician or other provider; (d) furnished at the most appropriate level which can be provided safely and effectively to the patient; and (e) not more costly than an alternative service or sequence of services at least as likely to produce equivalent therapeutic or diagnostic results as to the diagnosis or treatment of the Member’s illness, injury, or disease.

Investigational/Experimental: A treatment, procedure, or drug is investigational when it has not been recognized as safe and effective for use in treating the particular condition in accordance with generally accepted professional medical standards. This includes services where approval by the federal or state governmental is required prior to use, but has not yet been granted.

Split Evaluation: Blue Shield of California/Blue Shield of California Life & Health Insurance Company (Blue Shield) policy review can result in a split evaluation, where a treatment, procedure, or drug will be considered to be investigational for certain indications or conditions, but will be deemed safe and effective for other indications or conditions, and therefore potentially medically necessary in those instances.

Prior Authorization Requirements (as applicable to your plan)

Within five days before the actual date of service, the provider must confirm with Blue Shield that the member's health plan coverage is still in effect. Blue Shield reserves the right to revoke an authorization prior to services being rendered based on cancellation of the member's eligibility. Final determination of benefits will be made after review of the claim for limitations or exclusions.

Questions regarding the applicability of this policy should be directed to the Prior Authorization Department at (800) 541-6652, or the Transplant Case Management Department at (800) 637-2066 ext. 3507708 or visit the provider portal at www.blueshieldca.com/provider.

Disclaimer: This medical policy is a guide in evaluating the medical necessity of a particular service or treatment. Blue Shield of California may consider published peer-reviewed scientific literature, national guidelines, and local standards of practice in developing its medical policy. Federal and state law, as well as contract language, including definitions and specific contract provisions/exclusions, take precedence

2.04.08 Genetic Testing for Lynch Syndrome and Other Inherited Colon Cancer Syndromes

Page 36 of 42

over medical policy and must be considered first in determining covered services. Member contracts may differ in their benefits. Blue Shield reserves the right to review and update policies as appropriate.

Appendix A

POLICY STATEMENT	
BEFORE	AFTER <i>Blue font: Verbiage Changes/Additions</i>
<p>Genetic Testing for Lynch Syndrome and Other Inherited Colon Cancer Syndromes 2.04.08</p> <p>Policy Statement:</p> <p>APC Testing Genetic testing of the APC gene may be considered medically necessary for a patient with any of the following:</p> <ol style="list-style-type: none"> I. At-risk relatives (first or second degree) with familial adenomatous polyposis (FAP) or a known APC variant II. Personal history of 20 or more adenomas III. Personal history of between 10 to 20 polyps and 1 or more of the following: <ol style="list-style-type: none"> A. First or second degree relative with more than 20 polyps B. Other high-risk features as defined by a personal history of desmoid tumor, hepatoblastoma, cribriform-morular variant of papillary thyroid cancer, or multifocal or bilateral congenital hypertrophy of the retinal pigment epithelium (CHRPE) IV. When included as part of an approved small genetic panel <p>Genetic testing for APC gene variants is considered not medically necessary for colorectal cancer (CRC) patients with classical FAP for confirmation of the FAP diagnosis.</p>	<p>Genetic Testing for Lynch Syndrome and Other Inherited Colon Cancer Syndromes 2.04.08</p> <p>Policy Statement: <i>Note: Starting on July 1, 2022 (per CA law SB 535) for commercial plans regulated by the California Department of Managed Healthcare and California Department of Insurance (PPO and HMO), health care service plans and insurers shall not require prior authorization for biomarker testing, including biomarker testing for cancer progression and recurrence, if a member has stage 3 or 4 cancer. Health care service plans and insurers can still do a medical necessity review of a biomarker test and possibly deny coverage after biomarker testing has been completed and a claim is submitted (post service review).</i></p> <p>APC Testing Genetic testing of the APC gene may be considered medically necessary for a patient with any of the following:</p> <ol style="list-style-type: none"> I. At-risk relatives (first or second degree) with familial adenomatous polyposis (FAP) or a known APC variant II. Personal history of 20 or more adenomas III. Personal history of between 10 to 20 polyps and 1 or more of the following: <ol style="list-style-type: none"> A. First or second degree relative with more than 20 polyps B. Other high-risk features as defined by a personal history of desmoid tumor, hepatoblastoma, cribriform-morular variant of papillary thyroid cancer, or multifocal or bilateral congenital hypertrophy of the retinal pigment epithelium (CHRPE) IV. When included as part of an approved small genetic panel <p>Genetic testing for APC gene variants is considered not medically necessary for colorectal cancer (CRC) patients with classical FAP for confirmation of the FAP diagnosis.</p>

POLICY STATEMENT

BEFORE	AFTER Blue font: Verbiage Changes/Additions
<p>Testing for germline <i>APC</i> gene variants for inherited CRC syndromes is considered investigational in all other situations.</p> <p>MUTYH Testing Genetic testing of the MUTYH gene may be considered medically necessary for a patient with any of the following:</p> <ol style="list-style-type: none"> I. At-risk relatives (first or second degree) with a known MUTYH gene variant (single site analysis only) II. A negative result for APC gene variants (when the criteria for approval of APC testing was met) III. When included as part of an approved small genetic panel <p>Testing for germline <i>MUTYH</i> gene variants for inherited CRC syndromes is considered investigational in all other situations.</p> <p>MisMatch Repair (MMR) Gene and EPCAM Testing Genetic testing for Lynch Syndrome (LS), also known as Hereditary Nonpolyposis Colorectal Cancer (HNPCC), MMR genes (<i>MLH1, MSH2, MSH6, PMS2</i>); <i>both initial sequencing and for deletions and duplications</i>) and the EPCAM gene may be considered medically necessary for a patient with any of the following:</p> <ol style="list-style-type: none"> I. Family history of a known LS mutation (Variant single site analysis only) II. Personal or family history of colorectal or endometrial cancer diagnosed before 50 years III. Patients with CRC or endometrial cancer with tumor testing suggesting germline MMR deficiency (by microsatellite instability-MSI, or loss of mismatch repair protein expression by immunohistochemical-IHC- analysis) or meeting clinical criteria for Lynch syndrome IV. Personal or family history of at least 1 person with colorectal or endometrial cancer and another synchronous or metachronous Lynch syndrome-related tumor in the same person V. Personal (or family history of at least 2 people) with LS-related tumors and at least 1 diagnosed before 50 years of age VI. Personal or family history of at least 3 people with LS-related tumors, regardless of age 	<p>Testing for germline <i>APC</i> gene variants for inherited CRC syndromes is considered investigational in all other situations.</p> <p>MUTYH Testing Genetic testing of the MUTYH gene may be considered medically necessary for a patient with any of the following:</p> <ol style="list-style-type: none"> I. At-risk relatives (first or second degree) with a known MUTYH gene variant (single site analysis only) II. A negative result for APC gene variants (when the criteria for approval of APC testing was met) III. When included as part of an approved small genetic panel <p>Testing for germline <i>MUTYH</i> gene variants for inherited CRC syndromes is considered investigational in all other situations.</p> <p>MisMatch Repair (MMR) Gene and EPCAM Testing Genetic testing for Lynch Syndrome (LS), also known as Hereditary Nonpolyposis Colorectal Cancer (HNPCC), MMR genes (<i>MLH1, MSH2, MSH6, PMS2</i>); <i>both initial sequencing and for deletions and duplications</i>) and the EPCAM gene may be considered medically necessary for a patient with any of the following:</p> <ol style="list-style-type: none"> I. Family history of a known LS mutation (Variant single site analysis only) II. Personal or family history of colorectal or endometrial cancer diagnosed before 50 years III. Patients with CRC or endometrial cancer with tumor testing suggesting germline MMR deficiency (by microsatellite instability-MSI, or loss of mismatch repair protein expression by immunohistochemical-IHC- analysis) or meeting clinical criteria for Lynch syndrome IV. Personal or family history of at least 1 person with colorectal or endometrial cancer and another synchronous or metachronous Lynch syndrome-related tumor in the same person V. Personal (or family history of at least 2 people) with LS-related tumors and at least 1 diagnosed before 50 years of age VI. Personal or family history of at least 3 people with LS-related tumors, regardless of age

POLICY STATEMENT

BEFORE	AFTER Blue font: Verbiage Changes/Additions
<p>VII. A 5% or more risk of having an MMR gene mutation based on predictive models (e.g., PREMM5, MMRpro, MMR predict) as documented in the medical record (See policy guidelines for calculators)</p> <p>VIII. No diagnosis of colorectal cancer (CRC) but with a family history meeting the Amsterdam criteria, when no affected family members have been tested for MMR variants (See policy guidelines; Revised Bethesda criteria are included in the above criteria)</p> <p>IX. When included as part of an approved small genetic panel</p> <p>Testing for germline MMR gene variants for inherited CRC syndromes is considered investigational in all other situations.</p> <p>Testing for germline <i>EPCAM</i> gene variants for inherited CRC syndromes is considered investigational in all other situations.</p> <p>BRAF V600E or MLH1 Promoter Methylation Somatic (not germline) genetic testing for <i>BRAF V600E</i> or <i>MLH1</i> promoter methylation may be considered medically necessary to exclude a diagnosis of Lynch syndrome when either of the following:</p> <ol style="list-style-type: none"> I. The MLH1 protein is not expressed in a colorectal cancer (CRC) tumor on immunohistochemical (IHC) analysis (See Policy Guidelines section) II. The included as part of an approved small genetic panel <p>Testing for somatic <i>BRAF V600E</i> or <i>MLH1</i> promoter methylation to exclude a diagnosis of Lynch syndrome is considered investigational in all other situations.</p> <p>SMAD4 and BMPR1A Testing Genetic testing of <i>SMAD4</i> and <i>BMPR1A</i> genes may be considered medically necessary when any of the following:</p> <ol style="list-style-type: none"> I. Patient with a clinical diagnosis of juvenile polyposis syndrome based on the presence of any one of the following: <ol style="list-style-type: none"> A. At least 3 to 5 juvenile polyps in the colon 	<p>VII. A 5% or more risk of having an MMR gene mutation based on predictive models (e.g., PREMM5, MMRpro, MMR predict) as documented in the medical record (See policy guidelines for calculators)</p> <p>VIII. No diagnosis of colorectal cancer (CRC) but with a family history meeting the Amsterdam criteria, when no affected family members have been tested for MMR variants (See policy guidelines; Revised Bethesda criteria are included in the above criteria)</p> <p>IX. When included as part of an approved small genetic panel</p> <p>Testing for germline MMR gene variants for inherited CRC syndromes is considered investigational in all other situations.</p> <p>Testing for germline <i>EPCAM</i> gene variants for inherited CRC syndromes is considered investigational in all other situations.</p> <p>BRAF V600E or MLH1 Promoter Methylation Somatic (not germline) genetic testing for <i>BRAF V600E</i> or <i>MLH1</i> promoter methylation may be considered medically necessary to exclude a diagnosis of Lynch syndrome when either of the following:</p> <ol style="list-style-type: none"> I. The MLH1 protein is not expressed in a colorectal cancer (CRC) tumor on immunohistochemical (IHC) analysis (See Policy Guidelines section) II. The included as part of an approved small genetic panel <p>Testing for somatic <i>BRAF V600E</i> or <i>MLH1</i> promoter methylation to exclude a diagnosis of Lynch syndrome is considered investigational in all other situations.</p> <p>SMAD4 and BMPR1A Testing Genetic testing of <i>SMAD4</i> and <i>BMPR1A</i> genes may be considered medically necessary when any of the following:</p> <ol style="list-style-type: none"> I. Patient with a clinical diagnosis of juvenile polyposis syndrome based on the presence of any one of the following: <ol style="list-style-type: none"> A. At least 3 to 5 juvenile polyps in the colon

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<p>B. Multiple juvenile polyps found throughout in other parts of the gastrointestinal tract</p> <p>C. Any number of juvenile polyps with a known family history of juvenile polyps</p> <p>II. At-risk relative of a patient suspected of or diagnosed with juvenile polyposis syndrome</p> <p>III. When included as part of an approved small genetic panel</p> <p>Testing for germline <i>SMAD4</i> and <i>BMPR1A</i> gene variants for inherited CRC syndromes is considered investigational in all other situations.</p> <p>STK11 Testing Genetic testing for <i>STK11</i> gene variants may be considered medically necessary in any of the following:</p> <p>I. Patient with a clinical diagnosis of Peutz-Jeghers syndrome based on the presence of any 2 of the following:</p> <p>A. Presence of 2 or more histologically confirmed Peutz-Jeghers polyps of the gastrointestinal tract</p> <p>B. Characteristic mucocutaneous pigmentation of the mouth, lips, nose, eyes, genitalia, or fingers</p> <p>C. Family history of Peutz-Jeghers syndrome</p> <p>II. At-risk relative of a patient suspected of or diagnosed with Peutz-Jeghers syndrome</p> <p>III. When included as part of an approved small genetic panel</p> <p>Testing for germline <i>STK11</i> gene variants for inherited CRC syndromes is considered investigational in all other situations.</p> <p>Panel Testing Limited genetic panels (including at a minimum APC, MUTYH, <i>MLH1</i>, <i>MSH2</i>, <i>MSH6</i>, <i>PMS2</i>, EPCAM, <i>SMAD4</i>, <i>BMPR1A</i>, and <i>STK11</i> billed as CPT 81435) may be considered medically necessary as an alternative to serial testing of individual genes when criteria are met for any genetic testing of hereditary colorectal cancer, as indicated by one or more of the following:</p> <p>I. Personal history of 20 or more adenomas</p> <p>II. Personal history of between 10 to 20 polyps and one of the following:</p>	<p>B. Multiple juvenile polyps found throughout in other parts of the gastrointestinal tract</p> <p>C. Any number of juvenile polyps with a known family history of juvenile polyps</p> <p>II. At-risk relative of a patient suspected of or diagnosed with juvenile polyposis syndrome</p> <p>III. When included as part of an approved small genetic panel</p> <p>Testing for germline <i>SMAD4</i> and <i>BMPR1A</i> gene variants for inherited CRC syndromes is considered investigational in all other situations.</p> <p>STK11 Testing Genetic testing for <i>STK11</i> gene variants may be considered medically necessary in any of the following:</p> <p>I. Patient with a clinical diagnosis of Peutz-Jeghers syndrome based on the presence of any 2 of the following:</p> <p>A. Presence of 2 or more histologically confirmed Peutz-Jeghers polyps of the gastrointestinal tract</p> <p>B. Characteristic mucocutaneous pigmentation of the mouth, lips, nose, eyes, genitalia, or fingers</p> <p>C. Family history of Peutz-Jeghers syndrome</p> <p>II. At-risk relative of a patient suspected of or diagnosed with Peutz-Jeghers syndrome</p> <p>III. When included as part of an approved small genetic panel</p> <p>Testing for germline <i>STK11</i> gene variants for inherited CRC syndromes is considered investigational in all other situations.</p> <p>Panel Testing Limited genetic panels (including at a minimum APC, MUTYH, <i>MLH1</i>, <i>MSH2</i>, <i>MSH6</i>, <i>PMS2</i>, EPCAM, <i>SMAD4</i>, <i>BMPR1A</i>, and <i>STK11</i> billed as CPT 81435) may be considered medically necessary as an alternative to serial testing of individual genes when criteria are met for any genetic testing of hereditary colorectal cancer, as indicated by one or more of the following:</p> <p>I. Personal history of 20 or more adenomas</p> <p>II. Personal history of between 10 to 20 polyps and one of the following:</p>

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<p>A. First or second degree relative with more than 20 polyps</p> <p>B. Other high-risk features as defined by a personal history of desmoid tumor, hepatoblastoma, cribriform-morular variant of papillary thyroid cancer, or multifocal or bilateral congenital hypertrophy of the retinal pigment epithelium (CHRPE)</p> <p>III. <u>Family history</u> of a known LS mutation</p> <p>IV. Personal or family history of colorectal or endometrial cancer diagnosed before 50 years</p> <p>V. Personal history of colorectal or endometrial cancer at any age with tumor showing evidence of mismatch repair deficiency, either by microsatellite instability (MSI) or loss of mismatch repair protein expression by Immunohistochemical (IHC) analysis</p> <p>VI. Personal or <u>family history</u> of at least 1 person with colorectal or endometrial cancer and another synchronous or metachronous <u>Lynch syndrome-related tumor</u> in the same person</p> <p>VII. Personal (or <u>family history</u> of at least 2 people) with <u>LS-related tumors</u> and at least 1 diagnosed before 50 years of age</p> <p>VIII. Personal or family history of at least 3 people with <u>LS-related tumors</u>, regardless of age</p> <p>IX. A 5% or more risk of having an MMR gene mutation based on predictive models (e.g., PREMM5, MMRpro, MMR predict) as documented in the medical record (See policy guidelines for calculators)</p> <p>X. No diagnosis of colorectal cancer (CRC) but with a <u>family history</u> meeting the Amsterdam criteria, when no affected family members have been tested for MMR variants (See policy guidelines; Revised Bethesda criteria are included in the above criteria)</p> <p>XI. Patient with a clinical diagnosis of juvenile polyposis syndrome based on the presence of any one of the following:</p> <p>A. At least 3 to 5 juvenile polyps in the colon</p> <p>B. Multiple juvenile polyps in other parts of the gastrointestinal tract</p> <p>C. Any number of juvenile polyps with a known <u>family history</u> of juvenile polyps</p> <p>XII. At-risk relative of a patient suspected of or diagnosed with juvenile polyposis syndrome</p>	<p>A. First or second degree relative with more than 20 polyps</p> <p>B. Other high-risk features as defined by a personal history of desmoid tumor, hepatoblastoma, cribriform-morular variant of papillary thyroid cancer, or multifocal or bilateral congenital hypertrophy of the retinal pigment epithelium (CHRPE)</p> <p>III. <u>Family history</u> of a known LS mutation</p> <p>IV. Personal or family history of colorectal or endometrial cancer diagnosed before 50 years</p> <p>V. Personal history of colorectal or endometrial cancer at any age with tumor showing evidence of mismatch repair deficiency, either by microsatellite instability (MSI) or loss of mismatch repair protein expression by Immunohistochemical (IHC) analysis</p> <p>VI. Personal or <u>family history</u> of at least 1 person with colorectal or endometrial cancer and another synchronous or metachronous <u>Lynch syndrome-related tumor</u> in the same person</p> <p>VII. Personal (or <u>family history</u> of at least 2 people) with <u>LS-related tumors</u> and at least 1 diagnosed before 50 years of age</p> <p>VIII. Personal or family history of at least 3 people with <u>LS-related tumors</u>, regardless of age</p> <p>IX. A 5% or more risk of having an MMR gene mutation based on predictive models (e.g., PREMM5, MMRpro, MMR predict) as documented in the medical record (See policy guidelines for calculators)</p> <p>X. No diagnosis of colorectal cancer (CRC) but with a <u>family history</u> meeting the Amsterdam criteria, when no affected family members have been tested for MMR variants (See policy guidelines; Revised Bethesda criteria are included in the above criteria)</p> <p>XI. Patient with a clinical diagnosis of juvenile polyposis syndrome based on the presence of any one of the following:</p> <p>A. At least 3 to 5 juvenile polyps in the colon</p> <p>B. Multiple juvenile polyps in other parts of the gastrointestinal tract</p> <p>C. Any number of juvenile polyps with a known <u>family history</u> of juvenile polyps</p> <p>XII. At-risk relative of a patient suspected of or diagnosed with juvenile polyposis syndrome</p>

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<p>XIII. Patient with a clinical diagnosis of Peutz-Jeghers syndrome based on the presence of any 2 of the following:</p> <ul style="list-style-type: none"> A. Presence of 2 or more histologically confirmed Peutz-Jeghers polyps of the small intestine B. Characteristic mucocutaneous pigmentation of the mouth, lips, nose, eyes, genitalia, or fingers C. Family history of Peutz-Jeghers syndrome <p>XIV. At-risk relative of a patient suspected of or diagnosed with Peutz-Jeghers syndrome</p> <p>XV. To exclude a diagnosis of Lynch syndrome when the MLH1 protein is not expressed in a colorectal cancer (CRC) tumor on immunohistochemical (IHC) analysis</p> <p>The following are considered investigational:</p> <ul style="list-style-type: none"> I. Large multi-gene panels including multiple genes that are not highly associated with hereditary colorectal cancer II. Genetic testing of all other genes for an inherited CRC syndrome 	<p>XIII. Patient with a clinical diagnosis of Peutz-Jeghers syndrome based on the presence of any 2 of the following:</p> <ul style="list-style-type: none"> A. Presence of 2 or more histologically confirmed Peutz-Jeghers polyps of the small intestine B. Characteristic mucocutaneous pigmentation of the mouth, lips, nose, eyes, genitalia, or fingers C. Family history of Peutz-Jeghers syndrome <p>XIV. At-risk relative of a patient suspected of or diagnosed with Peutz-Jeghers syndrome</p> <p>XV. To exclude a diagnosis of Lynch syndrome when the MLH1 protein is not expressed in a colorectal cancer (CRC) tumor on immunohistochemical (IHC) analysis</p> <p>The following are considered investigational:</p> <ul style="list-style-type: none"> I. Large multi-gene panels including multiple genes that are not highly associated with hereditary colorectal cancer II. Genetic testing of all other genes for an inherited CRC syndrome