Overview

Useful For
Establishing a hereditary susceptibility to cancer
Evaluation of families with a history suggestive of a predisposition to both breast and colorectal cancer
Identification of familial BRCA1, BRCA2, TP53, PTEN, CDH1, STK11, MLH1, MSH2, MSH6, PMS2, or EPCAM mutation to allow for predictive testing in family members

Genetics Test Information
This test includes next-generation sequencing, Sanger sequencing, array comparative genomic hybridization, and multiplex ligation-dependent probe amplification to evaluate for mutations and large deletions/duplications in the BRCA1, BRCA2, TP53, PTEN (including the promoter), CDH1, STK11, MLH1, MSH2, MSH6, PMS2, and EPCAM genes. Sanger sequencing may also be performed to confirm detected variants.

Prior Authorization is available for this assay; see Special Instructions.

Special Instructions
- Molecular Genetics: Inherited Cancer Syndromes Patient Information
- Informed Consent for Genetic Testing
- Hereditary Breast and Colorectal Cancer Panel (BRCRC) Prior Authorization Ordering Instructions
- Informed Consent for Genetic Testing (Spanish)

Method Name
Custom Sequence Capture and Targeted Next Generation Sequencing Followed by Polymerase Chain Reaction (PCR) and Sanger Sequencing and Gene Dosage Analysis by Array Comparative Genomic Hybridization (aCGH) or Multiplex Ligation-Dependent Probe Amplification (MLPA)

NY State Available
Yes

Specimen

Specimen Type
Varies

Shipping Instructions
Specimen should arrive within 96 hours of collection.

Specimen Required
Patient Preparation: A previous bone marrow transplant from an allogenic donor will interfere with testing. Call 800-533-1710 for instructions for testing patients who have received a bone marrow transplant.

Specimen Type: Whole blood

Container/Tube:

Preferred: Lavender top (EDTA) or yellow top (ACD)
Acceptable: Any anticoagulant

Specimen Volume: 3 mL

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

Additional Information:
1. To ensure minimum volume and concentration of DNA is met, the preferred volume of blood must be submitted. Testing may be canceled if DNA requirements are inadequate.

2. Prior Authorization is available for this assay; see Special Instructions. Submit the required form with the specimen.

Forms
1. New York Clients-Informed consent is required. Document on the request form or electronic order that a copy is on file. The following documents are available in Special Instructions:
   - Informed Consent for Genetic Testing (T576)
   - Informed Consent for Genetic Testing-Spanish (T826)

2. Hereditary Breast and Colorectal Cancer Panel (BRCRC) Prior Authorization Ordering Instructions in Special Instructions

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

Specimen Minimum Volume
1 mL

Reject Due To
All specimens will be evaluated at Mayo Clinic Laboratories for test suitability.

Specimen Stability Information

<table>
<thead>
<tr>
<th>Specimen Type</th>
<th>Temperature</th>
<th>Time</th>
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<tbody>
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Clinical and Interpretive

Clinical Information
While the risk for breast and colorectal cancer in the general population is 12% and 6%, respectively, these cancers
are rarely attributable to a single abnormal gene that predisposes individuals to increased risks for cancer in a family. Given the prevalence of breast and colon cancer in the general population, it can be challenging to evaluate families with both breast and colon cancer for a possible hereditary predisposition. This panel allows for evaluation of the most common genes associated with both hereditary breast and hereditary colon cancer. Additionally, there is recent evidence to suggest an increased risk for breast cancer associated with the genes that cause Lynch syndrome. Therefore, evaluation for the genes on this panel may be useful for families suspicious of either a hereditary predisposition to breast cancer, colorectal cancer or both.

Hereditary Breast and Ovarian Cancer

Hereditary breast and ovarian cancer (HBOC) is an autosomal dominant hereditary cancer syndrome associated with germline mutations in the BRCA1 or BRCA2 genes. Mutations within these 2 genes account for the majority of hereditary breast and ovarian cancer families. HBOC is predominantly characterized by young-onset breast cancer and ovarian cancer. However, HBOC is also associated with increased risks for prostate cancer, pancreatic cancer, fallopian tube cancer, and male breast cancer. HBOC is highly penetrant; the risk for developing an invasive breast cancer is about 60% to 65% and the risk for developing ovarian cancer is about 40% by age 70. Some individuals develop multiple primary or bilateral cancers.

Hereditary Breast Cancer

While pathogenic BRCA1 and BRCA2 variants account for the majority of hereditary breast cancer, mutations in other genes may be present in families in which a BRCA1 or BRCA2 gene mutation is not identified. These include TP53, PTEN, CDH1, and STK11. For instance, it has been demonstrated that 8% of women with very early-onset (less than 30 years of age) breast cancer who test negative for a mutation in BRCA1 and BRCA2 have a mutation in TP53.

Mutations in TP53, PTEN, CDH1, and STK11 are associated with hereditary cancer syndromes in which there is an increased risk for breast cancer; however, the risk for developing an invasive breast cancer associated with these syndromes varies. Some individuals with a pathogenic variant in one of these genes develop multiple primary cancers or bilateral cancers. Therefore, testing for mutations in these 4 genes may also be useful when there is a suspicion of a hereditary susceptibility to breast cancer.

Lynch Syndrome

Lynch syndrome (also known as hereditary nonpolyposis colorectal cancer or HNPCC) is an autosomal dominant hereditary cancer syndrome associated with germline mutations in the mismatch repair genes, MLH1, MSH2, MSH6, and PMS2. Deletions within the 3’ end of the EPCAM gene, which lead to inactivation of the MSH2 promotor, have also been associated with Lynch syndrome.

Lynch syndrome is predominantly characterized by significantly increased risks for colorectal and endometrial cancer. The lifetime risk for colorectal cancer is highly variable and dependent on the gene involved. The risk for colorectal cancer-associated MLH1 and MSH2 mutations (approximately 50%-80%) is generally higher than the risks associated with mutations in the other Lynch syndrome-related genes. The lifetime risk for endometrial cancer (approximately 25%-60%) is also highly variable. Other malignancies within the tumor spectrum include gastric cancer, ovarian cancer, hepatobiliary and urinary tract carcinomas, and small bowel cancer. The lifetime risks for these cancers are less than 15%. Of the 4 mismatch repair genes, mutations within the PMS2 gene confer the lowest risk for any of the tumors within the Lynch syndrome spectrum.

The National Comprehensive Cancer Network and the American Cancer Society provide recommendations regarding the medical management of individuals with HBOC and Lynch syndrome.

Reference Values

Reference Values
An interpretive report will be provided.

**Interpretation**

All detected alterations are evaluated according to American College of Medical Genetics and Genomics recommendations.(1) Variants are classified based on known, predicted, or possible pathogenicity and reported with interpretive comments detailing their potential or known significance.

**Cautions**

**Clinical Correlations:**

Some individuals who have a hereditary susceptibility to breast, endometrial, or colon cancer may have a mutation that is not identified by this method (eg, promoter mutations, deep intronic mutations). The absence of a mutation, therefore, does not eliminate the possibility of a hereditary susceptibility to breast cancer in the individual or family. For predictive testing, it is important to first document the presence of a gene mutation in an affected family member.

Test results should be interpreted in the context of clinical findings, family history, and other laboratory data. Errors in our interpretation of results may occur if information given is inaccurate or incomplete. We strongly recommend that patients undergoing predictive testing receive genetic counseling both prior to testing and after results are available.

**Technical Limitations:**

In some cases, DNA variants of undetermined significance may be identified. Due to the limitations of next generation sequencing, we can detect greater than 93% of insertions and deletions up to 20 bases and 43 bases, respectively. If a diagnosis is still suspected, consider full gene sequencing using traditional Sanger methods. Single or multi-exon deletions as well as whole gene deletions will be detected by array comparative genomic hybridization (aCGH) or multiplex ligation-dependent probe amplification (MLPA). Rare polymorphisms exist that could lead to false-negative or false-positive results.

If results obtained do not match the clinical findings, additional testing should be considered.

**Evaluation Tools:**

Multiple in-silico evaluation tools were used to assist in the interpretation of these results. These tools are updated regularly; therefore, changes to these algorithms may result in different predictions for a given alteration. Additionally, the predictability of these tools for the determination of pathogenicity is currently not validated.

Unless reported or predicted to cause disease, alterations found deep in the intron or alterations that do not result in an amino acid substitution are not reported. These and common polymorphisms identified for this patient are available upon request.

**Reclassification of Variants-Policy:**

All detected alterations are evaluated according to American College of Medical Genetics and Genomics recommendations.(1) Variants are classified based on known, predicted, or possible pathogenicity and reported with interpretive comments detailing their potential or known significance. At this time, it is not standard practice for the laboratory to systematically re-review likely deleterious alterations or variants of uncertain significance that are detected and reported. The laboratory encourages health care providers to contact the laboratory at any time to learn how the status of a particular variant may have changed over time.

**Clinical Reference**

Performance

Method Description

Next-generation sequencing is performed to test for the presence of a mutation in the \textit{BRCA1}, \textit{BRCA2}, \textit{TP53}, \textit{PTEN} (including analysis of the promoter: c.-1344\_c.-745), \textit{CDH1}, \textit{STK11}, \textit{MLH1}, \textit{MSH2}, and \textit{MSH6} genes. (Pritchard CC, Smith C, Salipante SJ, et al: ColoSeq provides comprehensive Lynch and polyposis syndrome mutational analysis

Gene dosage analysis by multiplex ligation-dependent probe amplification (MLPA) is used to test for the presence of large deletions and duplications in the BRCA1 and BRCA2 genes. (Unpublished Mayo method)

Gene dosage analysis by array comparative genomic hybridization (aCGH) is used to test for the presence of large deletions and duplications in the TP53, PTEN, CDH1, STK11, MLH1, MSH2, MSH6, and EPCAM genes. (Swaroop A, Lewis R, Bonaga T, et al: Exon-level array CGH in a large clinical cohort demonstrates increased sensitivity of diagnostic testing for Mendelian disorders. Genet Med 2012;14[6]:594-603)


Reported variants detected by next-generation sequencing will be confirmed by Sanger sequencing.

**PDF Report**

No

**Day(s) and Time(s) Test Performed**

Performed weekly; Varies

**Analytic Time**

3 weeks

**Maximum Laboratory Time**

4 weeks

**Specimen Retention Time**

Whole Blood: 2 weeks (if available) Extracted DNA: Indefinitely

**Performing Laboratory Location**

Rochester

**Fees and Codes**

**Fees**

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

**Test Classification**

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

**CPT Code Information**

81162-BRCA-1-BRCA2
81321-PTEN
81405-STK11
81405-TP53
81406-CDH1
81292-MLH1
81295-MSH2
81298-MSH6
81317-PMS2
81319-PMS2 (postmeiotic segregation increased 2 [S. cerevisiae]) (eg, hereditary non-polyposis colorectal cancer, Lynch syndrome) gene analysis; duplication/deletion variants
81403-EPCAM
81228-Cytogenomic constitutional (genome-wide) microarray analysis; interrogation of genomic regions for copy number variants (eg, Bacterial Artificial Chromosome [BAC] or oligo-based comparative genomic hybridization [CGH] microarray analysis)

**LOINC® Information**

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**Prior Authorization**

Insurance preauthorization is available for this testing; forms are available in Special Instructions.

Patient financial assistance may be available to those who qualify. Patients who receive a bill from Mayo Clinic Laboratories will receive information on eligibility and how to apply.