

## Overview

### Useful For

Evaluation for patients with a personal or family history suggestive of a hereditary breast or gynecological cancer syndrome

Establishing a diagnosis of a hereditary breast or gynecological cancer syndrome allowing for targeted cancer surveillance based on associated risks

Identifying genetic variants associated with increased risk for breast or gynecological cancers, allowing for predictive testing and appropriate screening of at-risk family members

[Therapeutic eligibility with poly adenosine diphosphate-ribose polymerase \(PARP\) inhibitors based on certain gene alterations \(eg, \*BRCA1\*, \*BRCA2\*\) in selected tumor types](#)

### Genetics Test Information

This test utilizes next-generation sequencing to detect single nucleotide and copy number variants in 20 genes associated with hereditary breast and/or gynecologic cancers: *ATM*, *BARD1*, *BRCA1*, *BRCA2*, *BRIP1*, *CDH1*, *CHEK2*, *EPCAM* (copy number variants only), *MLH1*, *MSH2*, *MSH6*, *NBN*, *NF1*, *PALB2*, *PMS2*, *PTEN* (including promoter), *RAD51C*, *RAD51D*, *STK11*, *TP53*. For more information, see Method Description and [Targeted Genes and Methodology Details for Hereditary Breast/Gynecologic Cancer Panel](#) in Special Instructions.

Identification of a pathogenic variant may assist with diagnosis, prognosis, clinical management, familial screening, and genetic counseling for hereditary breast and gynecologic cancers.

### Special Instructions

- [Molecular Genetics: Inherited Cancer Syndromes Patient Information](#)
- [Informed Consent for Genetic Testing](#)
- [Informed Consent for Genetic Testing \(Spanish\)](#)
- [Targeted Genes and Methodology Details for Hereditary Breast/Gynecologic Cancer Panel](#)

### Method Name

Sequence Capture and Next-Generation Sequencing (NGS), Polymerase Chain Reaction (PCR), Sanger Sequencing and/or Multiplex Ligation-Dependent Probe Amplification (MLPA)

### NY State Available

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Yes

## Specimen

### Specimen Type

Varies

### Ordering Guidance

Customization of this panel and single gene analysis for any gene present on this panel is available. For more information see CGPH / Custom Gene Panel, Hereditary, Next-Generation Sequencing, Varies.

Targeted testing for familial variants (also called site-specific or known mutations testing) is available for the genes on this panel. For more information see FMTT / Familial Mutation, Targeted Testing, Varies.

### Shipping Instructions

Specimen preferred to 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. **Do not** aliquot.

**Specimen Stability Information:** Ambient (preferred) 4 days/Refrigerated

### 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. [Molecular Genetics: Inherited Cancer Syndromes Patient Information \(T519\)](#) in Special Instructions

3. [Targeted Genes and Methodology Details for Hereditary Breast/Gynecologic Cancer Panel](#) in Special Instructions

4. If not ordering electronically, complete, print, and send a [Oncology Test Request \(T729\)](#) with the specimen.

### Reject Due To

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

### Specimen Minimum Volume

See Specimen Required

### Specimen Stability Information

Specimen Type	Temperature	Time	Special Container
Varies	Varies (preferred)		

### Clinical & Interpretive

#### Clinical Information

Breast cancer and gynecologic cancers including ovarian and endometrial carcinoma occur in about 12% and 1% to 3% of the general population, respectively. [\(1\) In some cases, breast and gynecologic cancers may be attributed to a hereditary cancer syndrome.](#) [\(2-5\) Evaluation of the genes on this panel may be useful for families with a history of breast, ovarian, or endometrial cancers to determine cancer risk, surveillance recommendations, and targeted treatments.](#)

Hereditary breast and ovarian cancer syndrome (HBOC), caused by pathogenic variants in the *BRCA1* and *BRCA2* genes, account for the majority of hereditary breast and ovarian cancer. [\(2,4\)](#) HBOC is predominantly characterized by early-onset breast cancer and ovarian cancer. Individuals with HBOC are also at increased risks for prostate, pancreatic, and male breast cancers. [\(2,4\)](#)

Lynch syndrome is one of the most common endometrial and ovarian cancer syndromes, caused by variants in the *MLH1*, *MSH2*, *MSH6*, *PMS2*, mismatch-repair genes, or deletions of the *EPCAM* gene. [\(3,5\)](#) [Lynch syndrome is predominantly characterized by significantly increased risks for colorectal and endometrial cancer.](#) [\(3,5\)](#) [The lifetime risk](#)

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[for cancer is highly variable and dependent on the gene involved. Other malignancies within the tumor spectrum include gastric, ovarian, prostate, hepatobiliary, upper urinary tract, and small bowel cancers.\(3,5\)](#)

There are other genes known to increase risk for breast, ovarian, or uterine cancer that are included on this panel.(2) [The risk for developing cancer associated with these syndromes varies.\(2\) Some individuals with a pathogenic variant in one of these genes develop multiple primary cancers or bilateral cancers.\(2\)](#)

The National Comprehensive Cancer Network and the American Cancer Society provide recommendations regarding the medical management of individuals with hereditary breast and gynecologic cancer syndromes.(2,3,6,7)

### Reference Values

An interpretive report will be provided.

### Interpretation

All detected variants are evaluated according to American College of Medical Genetics and Genomics (ACMG) recommendations.(8) Variants are classified based on known, predicted, or possible pathogenicity and reported with interpretive comments detailing their potential or known significance.

### Cautions

#### Clinical Correlations

Test results should be interpreted in the context of clinical findings, family history, and other laboratory data. Misinterpretation of results may occur if the information provided is inaccurate or incomplete.

If testing was performed because of a clinically significant family history, it is often useful to first test an affected family member. Detection of a reportable variant in an affected family member would allow for more informative testing of at-risk individuals.

To discuss the availability of additional testing options or for assistance in the interpretation of these results, contact the Mayo Clinic Laboratory genetic counselors at [800-533-1710](tel:800-533-1710).

### Technical Limitations

Next-generation sequencing may not detect all types of genomic variants. In rare cases, false-negative or false-positive results may occur. The depth of coverage may be variable for some target regions; assay performance below the minimum acceptable criteria or for failed regions will be noted. Given these limitations, negative results do not rule out the diagnosis of a genetic disorder. If a specific clinical disorder is suspected, evaluation by alternative methods can be

considered.

There may be regions of genes that cannot be effectively evaluated by sequencing or deletion and duplication analysis as a result of technical limitations of the assay, including regions of homology, high guanine-cytosine (GC) content, and repetitive sequences. Confirmation of select reportable variants will be performed by alternate methodologies based on internal laboratory criteria.

This test is validated to detect 95% of deletions up to 75 base pairs (bp) and insertions up to 47 bp. Insertions/deletions (indels) of 40 or more bp, including mobile element insertions, may be less reliably detected than smaller indels.

#### Deletion/Duplication Analysis

This analysis targets single and multi-exon deletions/duplications; however, in some instances single exon resolution cannot be achieved due to isolated reduction in sequence coverage or inherent genomic complexity. Balanced structural rearrangements (such as translocations and inversions) may not be detected.

This test is not designed to detect low levels of mosaicism or to differentiate between somatic and germline variants. If there is a possibility that any detected variant is somatic, additional testing may be necessary to clarify the significance of results.

Genes may be added or removed based on updated clinical relevance. For the most up to date list of genes included in this test, see [Targeted Genes and Methodology Details for Hereditary Breast/Gynecologic Cancer Panel](#) in Special Instructions. For detailed information regarding gene specific performance and technical limitations, see Method Description or contact a laboratory genetic counselor at 800-533-1710.

If the patient has had an allogeneic hematopoietic stem cell transplant or a recent heterologous blood transfusion, results may be inaccurate due to the presence of donor DNA. Call Mayo Clinic Laboratories for instructions for testing patients who have received a bone marrow transplant.

#### Reclassification of Variants Policy

At this time, it is not standard practice for the laboratory to systematically review previously classified variants on a regular basis. The laboratory encourages health care providers to contact the laboratory at any time to learn how the classification of a particular variant may have changed over time.

## Variant Evaluation

Evaluation and categorization of variants is performed using published American College of Medical Genetics and Genomics and the Association for Molecular Pathology recommendations as a guideline. Other gene-specific guidelines may also be considered. Variants are classified based on known, predicted, or possible pathogenicity and reported with interpretive comments detailing their potential or known significance. Variants classified as benign or likely benign are not reported.

Multiple in silico evaluation tools may be used to assist in the interpretation of these results. The accuracy of predictions made by in silico evaluation tools is highly dependent upon the data available for a given gene, and periodic updates to these tools may cause predictions to change over time. Results from in silico evaluation tools should be interpreted with caution and professional clinical judgement.

## Clinical Reference

1. Howlander N, Noone AM, Krapcho M: [SEER Cancer Statistics Review, 1975-2018, National Cancer Institute. April 2021. Available at \[https://seer.cancer.gov/csr/1975\\\_2018/\]\(https://seer.cancer.gov/csr/1975\_2018/\)](https://seer.cancer.gov/csr/1975_2018/)
2. Daly MB, Pal T, Berry M, et al: NCCN Guidelines Insights: Genetic/familial high-risk assessment: breast, ovarian, and pancreatic, version 2.2021. *J Natl Compr Canc Netw.* 2021 Jan 6;19(1):77-102
3. Gupta S, Provenzale D, Llor X, et al: NCCN Guidelines Insights: Genetic/familial high-risk assessment: colorectal, version 2.2019. *J Natl Compr Canc Netw.* 2019;17(9):1032-1041
4. Petrucelli N, Daley MB, Pal T: *BRCA1*- and *BRCA2*-associated hereditary breast and ovarian cancer. In: Adams MP, Ardinger HH, Pagon RA, et al, eds. *GeneReviews* [Internet]. University of Washington, Seattle; 1998 Updated December 15, 2016. Accessed May 4, 2021. Available at [www.ncbi.nlm.nih.gov/books/NBK1247/](http://www.ncbi.nlm.nih.gov/books/NBK1247/)
5. Idos G, Valle L. Lynch syndrome. In: Adam MP, Ardinger HH, Pagon RA, et al, eds. *GeneReviews* [Internet]. University of Washington, Seattle; 2004. Updated February 2, 2021. Accessed May 4, 2021 Available at [www.ncbi.nlm.nih.gov/books/NBK1211/](http://www.ncbi.nlm.nih.gov/books/NBK1211/)
6. Saslow D, Boetes C, Burke W, et al: American Cancer Society guidelines for breast screening with MRI as an adjunct to mammography. *CA Cancer J Clin.* 2007 Mar-Apr;57(2):75-89
7. Smith RA, Andrews KS, Brooks D, et al. Cancer screening in the United States, 2019: A review of current American Cancer Society guidelines and current issues in cancer screening. *CA Cancer J Clin.* 2019 May;69(3):184-210
8. Richards S, Aziz N, Bale S, et al: Standards and guidelines for the interpretation of sequence variants: a joint consensus recommendation of the American College of Medical Genetics and Genomics and the Association for Molecular Pathology. *Genet Med.* 2015 May;17(5):405-424

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## Performance

### Method Description

Next-generation sequencing (NGS) and/or Sanger sequencing is performed to test for the presence of variants in coding regions and intron/exon boundaries of the genes analyzed, as well as some other regions that have known pathogenic variants. The human genome reference GRCh37/hg19 build was used for sequence read alignment. At least 99% of the bases are covered at a read depth over 30X. Sensitivity is estimated at above 99% for single nucleotide variants, above 94% for insertions/deletions (indels) less than 40 base pairs (bp), above 95% for deletions up to 75 bp and insertions up to 47 bp. NGS, [multiplex ligation-dependent probe amplification \(MLPA\)](#), and/or a polymerase chain reaction (PCR)-based quantitative method is performed to test for the presence of deletions and duplications in the genes analyzed. [PCR and gel electrophoresis is performed to test for the presence of the 10 megabase inversion of coding exons 1-7 of the MSH2 gene.](#) For details regarding the targeted genes analyzed for this test, see [Targeted Genes and Methodology Details for Hereditary Breast/Gynecologic Cancer Panel](#) in Special Instructions.

There may be regions of genes that cannot be effectively evaluated by sequencing or deletion and duplication analysis as a result of technical limitations of the assay, including regions of homology, high guanine-cytosine (GC) content, and repetitive sequences. For details regarding the specific gene regions not routinely covered, see [Targeted Genes and Methodology Details for Hereditary Breast/Gynecologic Cancer Panel](#) in Special Instructions.(Unpublished Mayo method)

Confirmation of select reportable variants may be performed by alternate methodologies based on internal laboratory criteria.

Genes analyzed: *ATM*, *BARD1*, *BRCA1*, *BRCA2*, *BRIP1*, *CDH1*, *CHEK2*, *EPCAM* (copy number variants only), *MLH1*, *MSH2*, *MSH6*, *NBN*, *NF1*, *PALB2*, *PMS2*, *PTEN* (including promoter), *RAD51C*, *RAD51D*, *STK11*, *TP53*

### PDF Report

Supplemental

### Specimen Retention Time

Whole Blood: 2 weeks (if available); Extracted DNA: 3 months

### Performing Laboratory Location

Rochester

**Fees & Codes**
**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 US Food and Drug Administration.

**CPT Code Information**

81432

81319

81403

**LOINC® Information**

Test ID	Test Order Name	Order LOINC Value
BRGYP	Hereditary Breast/Gyn Cancer Panel	97655-5

Result ID	Reporting Name	LOINC®
614647	Test Description	62364-5
614648	Specimen	31208-2
614649	Source	31208-2
614650	Result Summary	50397-9
614651	Result	82939-0
614652	Interpretation	69047-9
614653	Resources	99622-3
614654	Additional Information	48767-8
614655	Method	85069-3
614656	Genes Analyzed	48018-6
614657	Disclaimer	62364-5
614658	Released By	18771-6