

## Overview

### Useful For

Evaluation of patients with a personal or family history suggestive of a hereditary prostate cancer syndrome

Establishing a diagnosis of a hereditary prostate cancer syndrome allowing for targeted cancer surveillance based on associated risks

Identifying genetic variants associated with increased risk for prostate cancer, 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*)

### Genetics Test Information

This test utilizes next generation sequencing to detect single nucleotide and copy number variants in 18 genes associated with prostate cancer risk: *ATM*, *BRCA1*, *BRCA2*, *BRIP1*, *CHEK2*, *EPCAM* (copy number variants only), *FANCA*, *HOXB13*, *MLH1*, *MSH2*, *MSH6*, *NBN*, *PALB2*, *PMS2*, *RAD51B*, *RAD51C*, *RAD51D*, *TP53*. See [Targeted Genes and Methodology Details for Hereditary Prostate Cancer Panel](#) in Special Instructions and Method Description for additional details.

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

### 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 Prostate 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

Yes

## Specimen

### Specimen Type

Varies

### Ordering Guidance

Customization of this panel and/or 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 Prostate 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**

Hereditary prostate cancer accounts for approximately 5% to 10% of all prostate cancer cases, and up to half of all early-onset prostate cancer cases.(1-3) Evaluation of the genes on this panel may be useful for families with a history of prostate cancer to determine cancer risk, surveillance recommendations, and targeted treatments (such as poly adenosine diphosphate-ribose polymerase [PARP] inhibitor therapy).(4,5)

The 2 most common hereditary prostate cancer syndromes are hereditary breast and ovarian cancer (HBOC) syndrome and Lynch syndrome.(3-5)

HBOC syndrome is caused by pathogenic variants in the *BRCA1* and *BRCA2* genes. Individuals with HBOC syndrome are also at increased risks for multiple cancer types including prostate cancer.(5)

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Lynch syndrome is caused by variants in the *MLH1*, *MSH2*, *MSH6*, and *PMS2* mismatch-repair genes and deletions of the *EPCAM* gene. A subset of these patients present with prostate cancer.(3-5)

Other genes known to increase risk for prostate cancer are also included this panel.(3-5) The risk for developing cancer associated with these syndromes varies. Some individuals with a pathogenic variant in one of these genes develop multiple primary cancers.(4)

[The National Comprehensive Cancer Network and the American Cancer Society provide recommendations regarding the medical management of individuals with hereditary prostate cancer syndromes.\(4,5\)](#)

### 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.(6) 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 further testing options or for assistance in the interpretation of these results, Mayo Clinic Laboratory genetic counselors can be contacted 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 and detailed information regarding gene specific performance and technical limitations see Method

Description, [Targeted Genes and Methodology Details for Hereditary Prostate Cancer Panel](#) in Special Instructions 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. [Siegel, RL, Miller, KD, Fuchs, H, Jemal, A: Cancer Statistics, 2021. CA Cancer J Clin. 2021;71:7-33](#)
2. Lange EM, Salinas CA, Zuhlke KA, et al: Early onset prostate cancer has a significant genetic component. *Prostate*. 2012 Feb 1;72(2):147-156
3. Pritchard CC, Mateo J, Walsh M, et al: Inherited DNA-repair gene mutations in men with metastatic prostate cancer. *N Engl J Med*. 2016 Aug 4;375(5):443-453
4. Schaeffer E, Srinivas S, Antonarakis ES, et al: NCCN Guidelines Insights: Prostate Cancer, Version 1.2021. *J Natl Compr Canc Netw*. 2021 Feb 2;19(2):134-143
5. Daly MB, Pal T, Berry MP, et al: Genetic/Familial High-Risk Assessment: Breast, Ovarian, and Pancreatic, Version 2.2021, NCCN Clinical Practice Guidelines in Oncology. *J Natl Compr Canc Netw*. 2021 Jan 6;19(1):77-102
6. 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

### 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 are 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 each test see [Targeted Genes and Methodology Details for Hereditary Prostate 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 Prostate Cancer Panel](#) in Special Instructions.

Confirmation of select reportable variants may be performed by alternate methodologies based on internal laboratory criteria. (Unpublished Mayo method)

Genes analyzed: *ATM*, *BRCA1*, *BRCA2*, *BRIP1*, *CHEK2*, *EPCAM* (copy number variants only), *FANCA*, *HOXB13*, *MLH1*, *MSH2*, *MSH6*, *NBN*, *PALB2*, *PMS2*, *RAD51B*, *RAD51C*, *RAD51D*, *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

81408

81162

81403

81292

81295

81298

81307

81319

81351

81479