MAYO CLINIC LABORATORIES

Test Definition: PANCP

Hereditary Pancreatic Cancer Panel, Varies

Overview

Useful For

Evaluating patients with a personal or family history suggestive of a hereditary pancreatic cancer syndrome

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

Identifying genetic variants associated with increased risk for pancreatic 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 12 genes associated with pancreatic cancer: *ATM, BRCA1, BRCA2, CDKN2A, EPCAM* (copy number variants only)*, MLH1, MSH2, MSH6, PALB2, PMS2, STK11,* and *TP53*. For more information see Method Description and Targeted Genes and Methodology Details for Hereditary Pancreatic Cancer Panel.

Identification of a disease-causing variant may assist with diagnosis, prognosis, clinical management, familial screening, and genetic counseling for hereditary pancreatic 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 Pancreatic 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

This test assesses for hereditary forms of pancreatic adenocarcinoma and not other pancreatic lesions such as pancreatic neuroendocrine tumors. For genetic testing for pancreatic neuroendocrine tumors, see ENDCP / Hereditary Endocrine Cancer Panel, Varies.

This test does not analyze genes associated with hereditary pancreatitis. For genetic testing for pancreatitis, see HPANP / Hereditary Pancreatitis Gene Panel, Varies.

Customization of this panel and single gene analysis for any gene present on this panel are 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. See FMTT / Familial Variant, Targeted Testing, Varies. To obtain more information about this testing option, call 800-533-1710.

Testing minors for adult-onset predisposition syndromes is discouraged by the American Academy of Pediatrics, the American College of Medical Genetics and Genomics, and the National Society of Genetic Counselors.

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. For instructions for testing patients who have received a bone marrow transplant, call 800-533-1710.
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 whole blood specimen in original tube. **Do not aliquot.**
Specimen Stability Information: Ambient (preferred) 4 days/Refrigerated
Additional Information: 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.

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:
-Informed Consent for Genetic Testing (T576)
-Informed Consent for Genetic Testing (Spanish) (T826)
2. Molecular Genetics: Inherited Cancer Syndromes Patient Information (T519)
3. If not ordering electronically, complete, print, and send one of the following with the specimen:
-Oncology Test Request (T729)
-Gastroenterology and Hepatology Test Request (T728)

Specimen Minimum Volume
1 mL

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

Specimen Stability Information

Specimen Type	Temperature	Time	Special Container
Varies	Varies		

Clinical & Interpretive

Clinical Information
Pancreatic cancer occurs in approximately 1.6% of individuals.(1) About 10% of these pancreatic cancers are caused by a hereditary predisposition that may also increase risk for other types of cancer.(2) In rare cases, individuals with a personal or family history of pancreatic cancer may be at increased risk of cancer due to a hereditary cancer syndrome. Evaluation of the genes on this panel may be useful to determine cancer risk, surveillance recommendations, and targeted treatments.(2,3)

A few of the most common hereditary pancreatic cancer syndromes are hereditary breast and ovarian cancer (HBOC) syndrome caused by variants in the *BRCA1* and *BRCA2* genes,(2,4) Lynch syndrome caused by variants in the *MLH1*, *MSH2*, *MSH6*, *PMS2* mismatch-repair genes and deletions of the *EPCAM* gene, and familial atypical multiple mole melanoma syndrome (FAMMM) caused by variants in the *CDKN2A* gene.(2-5) Individuals with Peutz-Jeghers syndrome, caused by alterations within the *STK11* gene, also have an increased risk of developing pancreatic cancer.(6)

Other genes are also known to cause hereditary pancreatic cancer. The risk of developing cancer associated with these syndromes varies. Some individuals with a disease-causing variant in one of these genes develop multiple primary cancers.(2)

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

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 Laboratories genetic counselors at 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. Deletions-insertions (delins) of 40 or more bp, including mobile element insertions, may be less reliably detected than smaller delins.

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 detailed information regarding gene-specific performance, and technical limitations, see Method Description or contact a laboratory genetic counselor.

If the patient has had an allogeneic hematopoietic stem cell transplant or a recent 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:
Currently, it is not standard practice for the laboratory to systematically review previously classified variants on a regular basis. The laboratory encourages healthcare 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 are performed using published American College of Medical Genetics and Genomics and the Association for Molecular Pathology recommendations as a guideline.(6) 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 judgment.

Rarely, incidental or secondary findings may implicate another predisposition or presence of active disease. Incidental findings may include, but are not limited to, results related to the sex chromosomes. These findings will be carefully reviewed to determine whether they will be reported.

Clinical Reference

1. Howlader N, Noone AM, Krapcho M, et al. SEER Cancer Statistics Review. 1975-2018. National Cancer Institute. Updated April 2021. Accessed April 26, 2024. Available at: https://seer.cancer.gov/csr/1975_2018
2. Daly MB, Pal T, Berry M, 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;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, Daly MB, Pal T, et al. *BRCA1*- and *BRCA2*-associated hereditary breast and ovarian cancer. In: Adams MP, Everman DB, Mirzaa GM, et al, eds. GeneReviews [Internet]. University of Washington, Seattle; 1998. Updated September 21, 2023. Accessed April 26, 2024. Available at www.ncbi.nlm.nih.gov/books/NBK1247/
5. Idos G, Valle L. Lynch syndrome. In: Adam MP, Everman DB, Mirzaa GM, et al, eds. GeneReviews [Internet]. University of Washington, Seattle; 2004. Updated February 4, 2021. Accessed April 26, 2024. Available at www.ncbi.nlm.nih.gov/books/NBK1211/
6. McGarrity TJ, Amos CI, Baker MJ. Peutz-Jeghers syndrome. In: Adam MP, Everman DB, Mirzaa GM, et al, eds. GeneReviews [Internet]. University of Washington, Seattle; 2001. Updated September 2, 2021. Accessed April 26, 2024. Available at www.ncbi.nlm.nih.gov/books/NBK1266/
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;17(5):405-424

Performance

Method Description

Next-generation sequencing (NGS) and/or Sanger sequencing are 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 disease-causing 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 deletion/insertions (delins) 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.

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 targeted genes analyzed or specific gene regions not routinely covered, see Targeted Genes and Methodology Details for Hereditary Pancreatic Cancer Panel.(Unpublished Mayo method)

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

Genes analyzed: *ATM, BRCA1, BRCA2, CDKN2A, EPCAM* (copy number variants only)*, MLH1, MSH2, MSH6, PALB2, PMS2, STK11,* and *TP53*

PDF Report
Supplemental

Day(s) Performed
Varies

Report Available
14 to 21 days

Specimen Retention Time
Whole blood: 2 weeks (if available); Extracted DNA: 3 months

Performing Laboratory Location
Rochester

Fees & 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 account representative. 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. It has not been cleared or approved by the US Food and Drug Administration.

CPT Code Information

81162
81292
81295
81298
81307
81317
81319
81351
81403
81404
81405
81408
81479 (if appropriate for government payers)

LOINC® Information

Test ID	Test Order Name	Order LOINC® Value
PANCP	Hereditary Pancreatic Cancer Panel	In Process

Result ID	Test Result Name	Result LOINC® Value
614779	Test Description	62364-5
614780	Specimen	31208-2
614781	Source	31208-2
614782	Result Summary	50397-9
614783	Result	82939-0
614784	Interpretation	69047-9
614785	Resources	99622-3
614786	Additional Information	48767-8
614787	Method	85069-3
614788	Genes Analyzed	48018-6
614789	Disclaimer	62364-5
614790	Released By	18771-6