Test Definition: XCP

Hereditary Expanded Cancer Panel

Overview

Useful For

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

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

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

Therapeutic eligibility with poly adenosine diphospate-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 87 genes associated with a variety of hereditary cancer syndromes: AIP, ALK, APC (including promoters 1A and 1B), ATM, AXIN2, BAP1, BARD1, BLM, BMPR1A, BRCA1, BRCA2, BRIP1, BUB1B, CDC73, CDH1, CDK4, CDKN1B, CDKN2A, CHEK2, CTTNA1, DICER1, DIS3L2, EGFR, ELP1, EPCAM (copy number variants only), EXT1, EXT2, FANCA, FH, FLCN, GPC3, GREM1 (upstream enhancer region duplication only), HOXB13, KIT, LZTR1, MAX, MC1R, MEN1, MET, MITF (c.952G>A p.E318K variant only), MLH1, MLH3, MSH2, MSH3, MSH6, MUTYH, NBN, NF1, NF2, NTHL1, PALB2, PDGFRA, PHOX2B, PMS2, POLD1, POLE, POT1, PRKAR1A, PTCH1, PTEN (including promoter), RAD51B, RAD51C, RAD51D, RB1, RECQL4, REST, RET, RNF43, SDHA, SDHAF2, SDHB, SDHC, SDHD, SMAD4, SMARCA4, SMARCB1, SMARCE1, STK11, SUFU, TMEM127, TP53, TRIP13, TSC1, TSC2, VHL, WRN, WT1. For additional details see Method Description, Targeted Genes and Methodology Details for Hereditary Expanded Cancer Panel in Special Instructions.

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

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 Expanded 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 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 Sheet (T519) in Special Instructions

3. Targeted Genes and Methodology Details for Hereditary Expanded 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 cancer syndromes explain about 5% to 10% of cancer cases.(1,2) Determining if there is a genetic risk factor contributing to cancer in an individual or family can be useful for tailoring surveillance plans, consideration of prophylactic risk reducing interventions, targeted cancer treatments, and determining risk for family members.(3)

This panel evaluates for 87 genes associated with an increased risk of cancer including breast cancer, colon cancer, gastric cancer, paragangliomas, pheochromocytomas, ovarian cancer, pancreatic cancer, prostate cancer, renal cancer, skin cancer, thyroid cancer, endometrial cancer, and Wilms tumor.

The risk for developing cancer associated with these syndromes varies. Several of the of the genes on this panel have established cancer risk and National Comprehensive Cancer Network (NCCN) or expert group guidelines and recommendations for management.(4-9)

Indications for testing include but are not limited to:

-Individuals with multiple primary cancers

-Individuals with cancer diagnosed at young age

-Individuals with a family history of multiple relatives with cancer

-Individuals whose family history of cancer may seem to overlap with more than one hereditary cancer syndrome

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.(10) 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.

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 or for detailed information regarding gene specific performance and technical limitations, see Method Description, Targeted Genes and Methodology Details for Hereditary Expanded Cancer Panel in Special Instructions or contact a laboratory genetic counselor.

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. Howlader N, Noone AM, Krapcho M, et al: SEER Cancer Statistics Review. 1975-2018. National Cancer Institute. Updated April 2021. Accessed July 7, 2021. Available at: https://seer.cancer.gov/csr/1975_2018/

2. Nagy R, Sweet K, Eng C: Highly penetrant hereditary cancer syndromes. Oncogene. 2004 Aug 23;23(38):6445-6470

3. Samadder NJ, Rigert-Johnson D, Boardman L, et al: Comparison of Universal Genetic Testing vs Guideline-Directed Targeted Testing or Patients With Hereditary Cancer Syndrome. JAMA Oncol. 2021 Feb 1;7(2):230-237

4. 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

5. 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 Sep 1;17(9):1032-1041

6. Coit DG, Thompson JA, Albertini MR, et al: Cutaneous Melanoma, Version 2.2019, NCCN Clinical Practice Guidelines in Oncology. J Natl Compr Canc Netw. 2019 Apr 1;17(4):367-402

7. Haddad RI, Nasr C, Bischoff L, et al: NCCN Guidelines Insights: Thyroid Carcinoma, Version 2.2018. J Natl Compr Canc Netw. 2018 Dec;16(12):1429-1440

8. 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

9. 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

10. 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 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 each test see Targeted Genes and Methodology Details for Hereditary Expanded 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 Expanded 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: *AIP, ALK, APC* (including promoters 1A & 1B)*, ATM, AXIN2, BAP1, BARD1, BLM, BMPR1A, BRCA1, BRCA2, BRIP1, BUB1B, CDC73, CDH1, CDK4, CDKN1B, CDKN2A, CHEK2, CTTNA1, DICER1, DIS3L2, EGFR, ELP1, EPCAM* (copy number variants only)*, EXT1, EXT2, FANCA, FH, FLCN, GPC3, GREM1* (upstream enhancer region duplication only)*, HOXB13, KIT, LZTR1, MAX, MC1R, MEN1, MET, MITF* (c.952G>A p.E318K variant only)*, MLH1, MLH3, MSH2, MSH3, MSH6, MUTYH, NBN, NF1, NF2, NTHL1, PALB2, PDGFRA, PHOX2B, PMS2, POLD1, POLE, POT1, PRKAR1A, PTCH1, PTEN* (including promoter)*, RAD51B, RAD51C, RAD51D, RB1, RECQL4, REST, RET, RNF43, SDHA, SDHAF2, SDHB, SDHC, SDHD, SMAD4, SMARCA4, SMARCB1, SMARCE1, STK11, SUFU, TMEM127, TP53, TRIP13, TSC1, TSC2, VHL, WRN, WT1*

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

81319

81403

81292

81295

81298

81162

81201

81307

81321

81351

81404 x 4

81405 x 6

81406 x 7

81407

81408 x 2

81479

LOINC® Information

Test ID	Test Order Name	Order LOINC Value
XCP	Hereditary Expanded Cancer Panel	In Process

Result ID	Reporting Name	LOINC®
614899	Test Description	62364-5
614900	Specimen	31208-2
614901	Source	31208-2
614902	Result Summary	50397-9
614903	Result	82939-0
614904	Interpretation	69047-9
614905	Resources	99622-3
614906	Additional Information	48767-8
614907	Method	85069-3
614908	Genes Analyzed	48018-6
614909	Disclaimer	62364-5
614910	Released By	18771-6