



Medica Central Coverage Policy

Policy Name: Genetic Testing - Oncology Testing: Hereditary Cancer

Effective Date: July 1, 2025

Important Information – Please Read Before Using This Policy

These services may or may not be covered by all Medica Central plans. Coverage is subject to requirements in applicable federal or state laws. Please refer to the member's plan document for other specific coverage information. If there is a difference between this general information and the member's plan document, the member's plan document will be used to determine coverage. With respect to Medicare, Medicaid, and other government programs, this policy will apply unless these programs require different coverage.

Members may contact Medica Customer Service at the phone number listed on their member identification card to discuss their benefits more specifically. Providers with questions may call the Provider Service Center. Please use the Quick Reference Guide on the Provider Communications page for the appropriate phone number. <https://mo-central.medica.com/Providers/SSM-employee-health-plan-for-IL-MO-OK-providers>

Medica Central coverage policies are not medical advice. Members should consult with appropriate health care providers to obtain needed medical advice, care, and treatment.

OVERVIEW

This policy addresses the use of genetic testing for hereditary cancer susceptibility. Pre-test and post-test genetic counseling that facilitates informed decision-making, addresses the possibility of secondary or incidental findings, and a plan for returning results before testing occurs is strongly advised.

For additional information see the [Rationale](#) section.

The tests, CPT codes, and ICD codes referenced in this policy are not comprehensive, and their inclusion does not represent a guarantee of coverage or non-coverage.

POLICY REFERENCE TABLE

COVERAGE CRITERIA SECTION	EXAMPLE TESTS (LABS)	COMMON BILLING CODES	REF
Hereditary Cancer Panels			
Pan-Cancer Hereditary	MyRisk (Myriad Genetics)	81432, 81433, 0134U,	1, 2, 3,

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<u>COVERAGE CRITERIA SECTION</u>	EXAMPLE TESTS (LABS)	COMMON BILLING CODES	<u>REF</u>
<u>Cancer Susceptibility Panels</u>	Common Hereditary Cancers Panel (Invitae)	0474U, C15-26, C50-58, Z17, Z80, Z85.0-85.9	19
	CancerNext (Ambry Genetics)		
	Tempus xG Hereditary Cancer Panel		
	+RNAinsight with CancerNext - 0134U (Ambry Genetics)		
	GeneticsNow Comprehensive Germline Panel - 0474U (GoPath Diagnostics)		
<u>Hereditary Breast and/or Ovarian Cancer Susceptibility Panels</u>	Hereditary BRCA1/2 Panel (Invitae)	81162, 81166, 81167, 81216, 81307, 81321, 81351, 81432, 81433, 0129U, 0131U, 0132U, 0133U, 0134U, 0135U, 0138U, Z85, Z86	1, 18
	BRCA1/2 Seq and Del/Dup (Ambry Genetics)		
	VistaSeq Breast Cancer Panel (Labcorp)		
	Breast Cancer Panel (Invitae)		
	Breast Cancer STAT NGS Panel (Sequencing & Deletion/Duplication) (Fulgent Genetics)		
	Breast Cancer - High Risk Panel (PreventionGenetics, part of Exact Sciences)		
	Breast Cancer High-Risk Panel plus PALB2 (GeneDx)		
	BRCAplus - 0129U (Ambry Genetics)		
	RNAinsight for BreastNext - 0131U RNAinsight for OvaNext -		

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<u>COVERAGE CRITERIA SECTION</u>	EXAMPLE TESTS (LABS)	COMMON BILLING CODES	<u>REF</u>
	0132U RNAinsight for ProstateNext - 0133U RNAinsight for CancerNext - 0134U RNAinsight for GYNPlus - 0135U RNAinsight for BRCA1/2 - 0138U (Ambry Genetics)		
<u>Hereditary GI/Colon Cancer Susceptibility Panels</u>	Colorectal Cancer Panel (Invitae) ColoNext - 0101U (Ambry Genetics) +RNAinsight for ColoNext - 0130U +RNAinsight for CustomNext + RNA: Lynch (MLH1, MSH2, MSH6, PMS2) - 0162U +RNAinsight for CancerNext - 0134U (Ambry Genetics) CustomNext + RNA: MLH1, MSH2, MSH6, and/or PMS2 - 0158U, 0159U, 0160U, 0161U (Ambry Genetics)	81435, 81436, 0101U, 0130U, 0134U, 0158U, 0159U, 0160U, 0161U, 0162U, C15-26, Z80, Z83, Z84, Z85, Z86	2
<u>Hereditary Gastric Cancer Susceptibility Panels</u>	Invitae Gastric Cancer Panel (Invitae) Gastric Cancer Panel (PreventionGenetics, part of Exact Sciences)	81201, 81203, 81292, 81294, 81295, 81297, 81298, 81300, 81317, 81319, 81403, 81404, 81405, 81406, 81408, 81479, C16, Z80, Z85, Z86	6
<u>Hereditary Pancreatic Cancer Susceptibility</u>	Pancreatic Cancer Panel (Invitae)	81162, 81163, 81201, 81292, 81295, 81298,	1

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COVERAGE CRITERIA SECTION	EXAMPLE TESTS (LABS)	COMMON BILLING CODES	REF
Panels	PancNext (Ambry Genetics)	81351, 81433 81479, C25, Z80, Z84, Z85, Z86	
Hereditary Polyposis Susceptibility Panels	Hereditary Polyposis Panel (PreventionGenetics, part of Exact Sciences) Adenomatous Polyposis Panel (Invitae)	81201, 81203, 81406, 81479, D12, K63.5, Z80, Z84, Z85, Z86	2
Hereditary Prostate Cancer Susceptibility Panels	Hereditary Prostate Cancer Panel (Invitae) ProstateNext (Ambry Genetics) +RNAinsight for ProstateNext - 0133U (Ambry Genetics) ProstateNow Prostate Germline Panel - 0475U (GoPath Diagnostics)	81162, 81292, 81295, 81351, 81479, 0133U, 0475U, C61, Z80, Z84, Z85, Z86	1
Hereditary Neuroendocrine Cancer Susceptibility Panels	Hereditary Paraganglioma-Pheochromocytoma Panel (Invitae) PGLNext (Ambry Genetics)	81437, 81438, C74, C75, C7A Z80, Z84, Z85, Z86	5
BRCA1 and BRCA2 Gene Testing			
BRCA1 or BRCA2 Targeted Variant or Known Familial Variant Analysis	BRCA1 or BRCA2 Targeted Variant-Single Test (GeneDx)	81215, 81217, C50, C56, D05, Z17, Z80, Z83, Z84, Z85, Z86, C24.1	1
BRCA1 and BRCA2 Targeted Variant Analysis - Ashkenazi Jewish Founder Variants	BRCA1/2 Ashkenazi Jewish 3-Site Mutation Panel (Ambry Genetics) MultiSite 3 BRCAAnalysis (Myriad Genetics)	81212, C50, C56, D05, Z17, Z80, Z83, Z84, Z85, Z86, C24.1	1
PALB2 Gene Testing			
PALB2 Targeted Variant Analysis	PALB2 Targeted Variant (GeneDx)	81308, C15-26, Z80, Z84, Z85, Z86	1
ATM and/or CHEK2 Gene Testing			

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COVERAGE CRITERIA SECTION	EXAMPLE TESTS (LABS)	COMMON BILLING CODES	REF
ATM or CHEK2 Targeted Variant Analysis	ATM Targeted Variant - Single Test (GeneDx)	81479, C50, D05, Z80, Z84, Z85, Z86	1
	CHEK2 Targeted Variant - Single Test (GeneDx)		
ATM and/or CHEK2 Sequencing and/or Deletion/Duplication Analysis	ATM Full Gene Sequencing and Deletion/Duplication (Invitae)	81408, 81479, 0136U, C50, D05, Z80, Z84, Z85, Z86	1
	Hereditary Breast Cancer via the CHEK2 Gene (PreventionGenetics, part of Exact Sciences)		
	+RNAinsight for ATM - 0136U (Ambry Genetics)		
Lynch Syndrome / Hereditary Nonpolyposis Colorectal Cancer (HNPCC)			
MLH1, MSH2, MSH6, PMS2, or EPCAM Targeted Variant Analysis	MSH6 Targeted Variant; PMS2 Targeted Variant; EPCAM Targeted Variant (GeneDx)	81293, 81296, 81299, 81318, 81479, C15-22, C24-6, C26 C53-57 Z80, Z84, Z85, Z86	2
	Hereditary Nonpolyposis Colorectal Cancer (HNPCC): MLH1 (Known Mutation) (Labcorp)		
	Hereditary Nonpolyposis Colorectal Cancer (HNPCC): MSH2 (Known Mutation) (Labcorp)		
MLH1, MSH2, MSH6, PMS2, and/or EPCAM Sequencing and/or Deletion/Duplication Analysis	HNPCC Concurrent (Ambry Genetics)	81292, 81294, 81295, 81297, 81298, 81300, 81317, 81319, 81403, 0158U, 0159U, 0160U, 0161U, 0162U, 0238U, C15-22, C24-6, C26 C53-57, Z80, Z84, Z85, Z86	2
	Lynch Syndrome Panel (Invitae)		
	Genomic Unity Lynch Syndrome Analysis - 0238U (Variantyx)		
	CustomNext + RNA: MLH1, MSH2, MSH6, and/or		

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	PMS2 - 0158U, 0159U, 0160U, 0161U, or 0162U (Ambry Genetics)		
Adenomatous Polyposis Conditions			
APC or MUTYH Targeted Variant Analysis	APC Targeted Variant - Single Test (GeneDx) MUTYH Targeted Variant - Single Test (GeneDx)	81202, 81403, 81401, C15-21, D12, Z80, Z84, Z85, Z86	2
APC and/or MUTYH Sequencing and/or Deletion/Duplication Analysis	APC Seq and Del/Dup (Ambry Genetics) Familial Adenomatous Polyposis Test (Invitae) +RNAInsight for APC - 0157U (Ambry Genetics) MUTYH Full Gene Sequencing and Deletion/Duplication (Invitae)	81201, 81203, 81406, 81479, 0157U, C15-21, D12, Z80, Z84, Z85, Z86	2, 19
BAP1-Tumor Predisposition Syndrome			
BAP1 Targeted Variant Analysis	BAP1: Site Specific Analysis (familial) (Univ of Pennsylvania School of Medicine-Genetic Diagnostic Laboratory)	81403, C22, C45, C64 C69, D22, D32, Z80, Z84, Z85, Z86	7
BAP1 Sequencing and/or Deletion/Duplication Analysis	BAP1 Full Gene Sequencing and Deletion/Duplication (Invitae)	81479, C22, C45, C64 C69, D22, D32, Z80, Z84, Z85, Z86	4, 7, 10, 11, 12
Birt-Hogg-Dube syndrome (BHDS)			
FLCN Targeted Variant Analysis	FLCN Targeted Variant - Single Test (GeneDx)	81479, C65, D14.3, D23.9, Z84, Z85, Z86	7
FLCN Sequencing and/or Deletion/Duplication	Birt-Hogg-Dube Syndrome Test (Invitae)	81479, C65, D14.3, D23.9, Z84, Z85, Z86	7, 9

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COVERAGE CRITERIA SECTION	EXAMPLE TESTS (LABS)	COMMON BILLING CODES	REF
Analysis			
Cowden Syndrome (CS)/PTEN Hamartoma Tumor Syndrome (PHTS)			
PTEN Targeted Variant Analysis	PTEN Targeted Variant - Single Test (GeneDx)	81322, C15-21, C26, C50, C54, C55, C64, C73, D12, D13, D17, D23, D24, F78, F84.0, Q75.3, Q87.89, Z80, Z84, Z85, Z86	1
PTEN Sequencing and/or Deletion/Duplication Analysis	PTEN Gene Sequencing and Del/Dup (GeneDx)	81321, 81323, C15-21, C26, C50, C54, C55, C64, C73, D12, D13, D17, D23, D24, F78, F84.0, Q75.3, Q87.89, Z80, Z84, Z85, Z86	1
Familial Atypical Multiple Mole Melanoma Syndrome (FAMMM)			
CDKN2A Targeted Variant Analysis	CDKN2A Targeted Variant - Single Test (GeneDx)	81479, C43, Z12.83, Z80, Z84, Z85, Z86	1
CDKN2A Sequencing and/or Deletion/Duplication Analysis	CDKN2A Full Gene Sequencing and Deletion/Duplication (Invitae)	81404, 81479, C43, Z12.83, Z80, Z84, Z85, Z86	1, 4, 17
Hereditary Diffuse Gastric Cancer (aka, Signet Ring Cell Gastric Cancer)			
CDH1 Targeted Variant Analysis	CDH1 Targeted Variant - Single Test (GeneDx)	81479, C16, C50, Q35, Q36, Z80, Z84, Z85, Z86	1, 6
CDH1 Sequencing and/or Deletion/Duplication Analysis	CDH1 Full Gene Sequencing and Deletion/Duplication (Invitae)	81406, 81479, C16, C50, Q35, Q36, Z80, Z84, Z85, Z86	6
Juvenile Polyposis Syndrome (JPS)			
SMAD4 or BMPR1A Targeted Variant Analysis	Targeted Variant: SMAD4 (PreventionGenetics, part of Exact Sciences)	81403, C15-C26, D12, Z80, Z84, Z85, Z86	2
	Targeted Variant: BMPR1A (PreventionGenetics, part of Exact Sciences)		

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<u>COVERAGE CRITERIA SECTION</u>	EXAMPLE TESTS (LABS)	COMMON BILLING CODES	<u>REF</u>
<u>SMAD4 and/or BMPR1A Sequencing and/or Deletion/Duplication Analysis</u>	Juvenile Polyposis Syndrome Panel (Invitae) BMPR1A, SMAD4 Gene Sequencing and Del/Dup (GeneDx)	81405, 81406, 81479, C15-C26, D12, Z80, Z84, Z85, Z86	2
<u>Hereditary Leiomyomatosis and Renal Cell Cancer (HLRCC)</u>			
<u>FH Targeted Variant Analysis</u>	FH Known Familial Mutation Analysis (University Hospitals)	81403, C44, C55, C64, D23, D25, Z84, Z85, Z86	7
<u>FH Sequencing and/or Deletion/Duplication Analysis</u>	Hereditary Leiomyomatosis and Renal Cell Carcinoma (Ambry Genetics)	81405, 81479, C44, C55, C64, D23, D25, Z84, Z85, Z86	7, 16
<u>Li-Fraumeni Syndrome (LFS)</u>			
<u>TP53 Targeted Variant Analysis</u>	TP53 Targeted Variant - Single Test (GeneDx)	81352, C30-41, C15-26, C45, C47-49, C50, C71, C95.9, Z80, Z84, Z85, Z86	1
<u>TP53 Sequencing and/or Deletion/Duplication Analysis</u>	Li-Fraumeni Syndrome, TP53 Sequencing and Deletion/Duplication (Quest Diagnostics)	81351, 81479, C30-41, C15-26, C45, C47-49, C50, C71, C95.9, Z80, Z84, Z85, Z86	1
<u>Multiple Endocrine Neoplasia - Type 1 (MEN1)</u>			
<u>MEN1 Targeted Variant Analysis</u>	MEN1 Targeted Variant - Single Test (GeneDx)	81479, C25, C75.0, D35.2, E31.2, Z80, Z84, Z85, Z86	5
<u>MEN1 Sequencing and/or Deletion/Duplication Analysis</u>	MEN1 Gene Sequencing and Del/Dup (GeneDx) Multiple Endocrine Neoplasia Type 1 Test (Invitae)	81404, 81405, C25, C75.0, D35.2, E31.2, Z80, Z84, Z85, Z86	5
<u>Multiple Endocrine Neoplasia Type 2 (MEN2)</u>			
<u>RET Targeted Variant Analysis</u>	RET Targeted Variant - Single Test (GeneDx)	81404, C73-75, C7A, D3A, Z80, Z84, Z85, Z86	5
<u>RET Sequencing and/or Deletion/Duplication</u>	RET Full Gene Sequencing and Deletion/Duplication	81406, 81479, S3840, C73-75, C7A, D3A, Z80, Z84,	5, 15

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COVERAGE CRITERIA SECTION	EXAMPLE TESTS (LABS)	COMMON BILLING CODES	REF
Analysis	(Invitae)	Z85, Z86	
Nevoid Basal Cell Carcinoma Syndrome (NBCCS) (aka Gorlin syndrome)			
PTCH1 or SUFU Targeted Variant Analysis	Targeted Variant: PTCH1 or SUFU (GeneDx)	81479, C44, C71.6, G93, M27.4, Z84, Z85, Z86	13
PTCH1 and/or SUFU Sequencing and/or Deletion/Duplication Analysis	Basal Cell Nevus Syndrome Panel (Invitae)	81479, C44, C71.6, G93, M27.4, Z84, Z85, Z86	13
Hereditary Paraganglioma/Pheochromocytoma Syndrome (PGL/PCC)			
MAX, SDHA, SDHAF2, SDHB, SDHC, SDHD, or TMEM127 Targeted Variant Analysis	SDHB, SDHD, SDHC, MAX, SDHAF2, or TMEM127 Targeted Variant - Single Test (GeneDx)	81479, C7A, C74.1, D35.00, D44.7, Z84, Z85, Z86	7
	Targeted Variants: MAX, SDHAF2, TMEM127 (PreventionGenetics, part of Exact Sciences)		
MAX, SDHA, SDHAF2, SDHB, SDHC, SDHD, and/or TMEM127 Sequencing and/or Deletion/Duplication Analysis	SHDB Full Gene Sequencing and Deletion/Duplication (Invitae)	81404, 81405, 81406, 81479, C7A, C74.1, D35.00, D44.7, Z84, Z85, Z86	5, 14
	SDHA Full Gene Sequencing and Deletion/Duplication (Invitae)		
	SDHC Full Gene Sequencing and Deletion/Duplication (Invitae)		
	SDHD Full Gene Sequencing and Deletion/Duplication (Invitae)		

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	MAX Full Gene Sequencing and Deletion/Duplication (Invitae)		
	SDHAF2 Full Gene Sequencing and Deletion/Duplication (Invitae)		
	TMEM127 Full Gene Sequencing and Deletion/Duplication (Invitae)		
<u>Peutz-Jeghers Syndrome (PJS)</u>			
<u>STK11 Targeted Variant Analysis</u>	STK11 Targeted Variant - Single Test (GeneDx)	81479, C50, Q85.8, Z80, Z84, Z85, Z86	2
<u>STK11 Sequencing and/or Deletion/Duplication Analysis</u>	STK11 Gene Sequencing & Del/Dup (GeneDx)	81404, 81405, C50, Q85.8, Z80, Z84, Z85, Z86	2
<u>Retinoblastoma</u>			
<u>RB1 Targeted Variant Analysis</u>	Retinoblastoma: Site Specific Analysis (Familial) (Univ of Pennsylvania School of Medicine-Genetic Diagnostic Laboratory)	81403, C69, C75.3, Z80, Z84, Z85, Z86	8
<u>RB1 Sequencing and/or Deletion/Duplication Analysis</u>	RB1 Full Gene Sequencing and Deletion/Duplication (Invitae)	81479, S3841, C69, C75.3, Z80, Z84, Z85, Z86	8
<u>Von Hippel-Lindau Syndrome (VHL)</u>			
<u>VHL Targeted Variant Analysis</u>	VHL Known Mutation (Children's Hospital of Philadelphia - Division of Genomic Diagnostics)	81403, C64, C7A, D3A, D35.00, K86.2, N28, N50.3, Q85.8, Z80, Z84, Z85, Z86	7
<u>VHL Sequencing and/or Deletion/Duplication Analysis</u>	VHL Full Gene Sequencing and Deletion/Duplication (Invitae)	81403, 81404, S3842, C64, C7A, D3A, D35.00, K86.2, N28, N50.3, Q85.8, Z80, Z84, Z85, Z86	7
	VHL Gene Sequencing and Del/Dup (GeneDx)		



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RELATED POLICIES

This policy document provides coverage criteria for hereditary cancer susceptibility. Please refer to:

- **Oncology Testing: Algorithmic Assays** for coverage criteria related to gene expression profiling and tumor biomarker tests with algorithmic analyses.
- **Oncology Testing: Cancer Screening and Surveillance** for coverage criteria related to screening and biomarker cancer tests.
- **Oncology Testing: Hematologic Malignancy Molecular Diagnostics** for coverage criteria related to molecular profiling of a known or suspected blood cancer (e.g. broad molecular profiling, including Minimal Residual Disease (MRD) Testing, Tumor Mutational Burden (TMB), and cytogenetic / fusion testing).
- **Oncology Testing: Solid Tumor Molecular Diagnostics** for coverage criteria related to molecular profiling of a known or suspected cancer (e.g. broad molecular profiling, including Minimal Residual Disease (MRD) Testing, Tumor Mutational Burden (TMB), and cytogenetic / fusion testing).
- **Specialty Testing: Hematology** for coverage criteria related to diagnostic tests for benign (non-cancerous) hematologic conditions including sickle cell disease, inherited anemias, and hemophilias.
- **General Approach to Laboratory Testing** for coverage criteria related to hereditary cancer susceptibility, including known familial variant testing, that is not specifically discussed in this or another non-general policy.

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COVERAGE CRITERIA

HEREDITARY CANCER PANELS

Pan-Cancer Hereditary Cancer Susceptibility Panels

A pan-cancer hereditary cancer susceptibility panel includes genes that are associated with inherited susceptibility to several different types of cancer (e.g., breast cancer, colon cancer, stomach cancer, etc.).

- I. Genetic testing using a pan-cancer hereditary cancer susceptibility panel is considered **medically necessary** when the member meets **BOTH** A and B:
 - A. The member has one of the following:
 1. A personal history, or a [close relative](#) with a personal history, of one of the following cancers \leq 50 years of age:
 - a) Breast cancer, **OR**
 - b) Colorectal cancer, **OR**

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- c) Endometrial cancer, **OR**
- 2. The member has a personal history of one of the following:
 - a) Pancreatic cancer at any age, **OR**
 - b) Metastatic prostate cancer at any age, **OR**
- 3. Ovarian, peritoneal, or fallopian tube cancer at any age, **OR**
- 4. The member's personal or family history is suspicious for more than one hereditary cancer syndrome, **AND**
- B. The panel includes, at a minimum, sequencing of the following genes: *BRCA1*, *BRCA2*, *EPCAM*, *MLH1*, *MSH2*, *MSH6*, *PMS2*.
- II. Genetic testing using a pan-cancer hereditary cancer susceptibility panel is considered **investigational** for all other indications.
- III. Hereditary cancer susceptibility panel targeted mRNA sequencing analysis for the interpretation of variants of unknown significance is considered **investigational** because it is typically either considered an existing component of the genetic testing process for quality assurance or follow up testing without proven utility.

NOTE: If a multigene cancer panel is performed, the appropriate panel code should be used.

¹ Targeted testing rather than sequencing has a role in some hereditary cancer syndromes. For example, a single variant in the *HOXB13* gene has been linked to prostate cancer risk.

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Hereditary Breast and/or Ovarian Cancer Susceptibility Panels

A hereditary breast and/or ovarian cancer susceptibility panel includes genes that are associated with an inherited susceptibility to breast cancer, ovarian cancer, or both.

- I. Genetic testing using a hereditary breast and/or ovarian cancer susceptibility panel is considered **medically necessary** when:
 - A. The panel includes, at a minimum, the following genes: *BRCA1*, *BRCA2*, **AND**
 - B. The member has one of the following:
 - 1. The member has a personal history of breast cancer \leq age 65, **OR**
 - 2. The member has a personal history of ovarian cancer (including fallopian tube cancer or peritoneal cancer), **OR**
 - 3. The member has a personal history of breast cancer, **AND**
 - a) One of the following:
 - (1) Ashkenazi Jewish ancestry, **OR**
 - (2) Male (sex assigned at birth), **OR**

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- (3) Triple-negative [breast cancer](#), **OR**
- (4) Pancreatic or ampullary cancer, **OR**
- (5) Metastatic prostate cancer, **OR**
- (6) [High- or very-high-risk group prostate cancer](#), **OR**
- (7) Multiple primary [breast cancers](#) (diagnosed synchronously or metachronously), **OR**
- (8) The member has a [close relative](#) with any one of the following:
 - (a) Breast cancer diagnosed \leq age 50, **OR**
 - (b) Male breast cancer, **OR**
 - (c) Ovarian cancer, **OR**
 - (d) Pancreatic cancer, **OR**
 - (e) Prostate cancer that is either metastatic, [intermediate-risk](#) or [high- or very-high-risk group](#), **OR**
- b) There are ≥ 3 total diagnoses of breast cancer and/or prostate cancer (any grade) on the same side of the family including the member with breast cancer, **OR**
- 4. The member has a personal history of lobular breast cancer, **AND**
 - a) A personal or family history of diffuse gastric cancer, **OR**
- 5. The member is unaffected or the member does not have a personal history of breast cancer that meets the above criteria, **AND**
 - a) The member has a [first- or second-degree relative](#) meeting any of the above criteria, **OR**
 - b) The member's probability of having a *BRCA1* or *BRCA2* pathogenic variant is greater than 2.5% based on prior probability models (e.g., Tyrer-Cuzick, BRCAPro, CanRisk), **OR**
- 6. The member has a personal history of breast cancer, **AND**
 - a) The member has metastatic [breast cancer](#) and is being considered for systemic treatment using PARP inhibitors, **OR**
 - b) The member has HER2-negative [breast cancer](#) and is being considered for adjuvant treatment with olaparib.

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- II. Genetic testing using a STAT hereditary breast cancer panel is considered **medically necessary** when:
 - A. The member meets any of the above criteria, **AND**
 - B. The member requires a rapid turn-around-time for decision making related to surgical interventions or treatment.
- III. *BRCA1/BRCA2* mRNA sequencing analysis in genes associated with breast and/or ovarian cancers for the interpretation of variants of unknown significance is considered **investigational** because it is typically either considered an existing component of the genetic testing process for quality assurance or follow up testing without proven utility.
- IV. Genetic testing using a hereditary breast and/or ovarian cancer susceptibility panel is considered **investigational** for all other indications.

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Hereditary GI/Colon Cancer Susceptibility Panels

- I. Genetic testing using a hereditary colorectal cancer susceptibility panel is considered **medically necessary** when:
 - A. The member meets at least one of the following:
 - 1. The member has a personal history of, or at least one blood relative with any of the following:
 - a) At least 10 adenomatous polyps, **OR**
 - b) At least 2 hamartomatous polyps, **OR**
 - c) At least 5 serrated polyps/lesions proximal to the rectum, **OR**
 - 2. The member meets testing criteria for Lynch syndrome/HNPCC [MLH1, MSH2, MSH6, PMS2, or EPCAM Sequencing and/or Deletion/Duplication Analysis](#), **AND**
 - B. The panel includes, at a minimum, sequencing of the following genes: *APC, MUTYH, MLH1, MSH2, MSH6, PMS2, EPCAM, BMPR1A, SMAD4, PTEN, STK11, and TP53*.
- II. Genetic testing using a hereditary colorectal cancer susceptibility panel is considered **investigational** for all other indications.
- III. Hereditary colorectal cancer susceptibility panel targeted mRNA sequencing analysis for the interpretation of variants of unknown significance is considered **investigational** because it is typically either considered an existing component of the genetic testing process for quality assurance or follow up testing without proven utility.

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NOTE: If a multigene cancer panel is performed, the appropriate panel code should be used.

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Hereditary Gastric Cancer Susceptibility Panels

A hereditary gastric cancer panel includes genes that are associated with inherited susceptibility to gastric (stomach) cancer.

- I. Genetic testing using a hereditary gastric susceptibility panel is considered **medically necessary** when:
 - A. The member is 18 years or older, **AND**
 - B. The member meets sequencing and/or deletion/duplication clinical criteria for at least one of the following:
 1. [Lynch syndrome/Hereditary Nonpolyposis Colorectal Cancer](#), **OR**
 2. [Hereditary Diffuse Gastric Cancer](#), **OR**
 3. [Juvenile Polyposis Syndrome](#), **OR**
 4. [Peutz-Jeghers Syndrome](#), **OR**
 5. [APC and/or MUTYH Sequencing and/or Deletion/Duplication Analysis](#), **AND**
 - C. The panel includes, at a minimum, sequencing of the following genes: *APC*, *BMPR1A*, *CDH1*, *EPCAM*, *MLH1*, *MSH2*, *MSH6*, *PMS2*, *SMAD4*, *STK11*.
- II. Genetic testing using a hereditary gastric cancer susceptibility panel is considered **investigational** for all other indications.

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Hereditary Pancreatic Cancer Susceptibility Panels

A hereditary pancreatic cancer susceptibility panel includes genes that are associated with inherited susceptibility to pancreatic cancer.

- I. Genetic testing using a hereditary pancreatic cancer susceptibility panel is considered **medically necessary** when:
 - A. The member is 18 years or older, **AND**
 - B. The member has one of the following:
 1. Pancreatic cancer, **OR**
 2. A [first-degree relative](#) with pancreatic cancer.
- II. Genetic testing using a hereditary pancreatic cancer susceptibility panel is considered **investigational** for all other indications.

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Hereditary Polyposis Susceptibility Panels

A hereditary polyposis panel is one that includes genes that are associated with inherited susceptibility to colon polyposis.

- I. Genetic testing using a hereditary polyposis panel is considered **medically necessary** when:
 - A. The member meets criteria for sequencing and/or deletion/duplication analysis for [APC and/or MUTYH Sequencing and/or Deletion/Duplication Analysis](#), **AND**
 - B. The panel includes, at a minimum, sequencing of the following genes: *APC* and *MUTYH*.
- II. Genetic testing using a hereditary polyposis panel is considered **investigational** for all other indications.

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Hereditary Prostate Cancer Susceptibility Panels

A hereditary prostate cancer susceptibility panel is one that includes genes that are associated with inherited susceptibility to prostate cancer.

- I. Genetic testing using a hereditary prostate cancer susceptibility panel is considered **medically necessary** when:
 - A. The member is 18 years or older, **AND**
 - B. The member has a personal history of any of the following:
 1. Metastatic or node-positive prostate cancer, **OR**
 2. [High-risk localized prostate cancer](#) or [very-high-risk localized prostate cancer](#), **OR**
 3. Intermediate risk prostate cancer with intraductal/cribriform histology, **OR**
 4. Prostate cancer diagnosed ≤ 55 years of age, **OR**
 - C. The member has a personal history of prostate cancer and any of the following:
 1. One or more [close relative](#) with any of the following:
 - a) [Breast cancer](#) at or under age 50, **OR**
 - b) Triple-negative [breast cancer](#) at any age, **OR**
 - c) Male (sex assigned at birth) [breast cancer](#) at any age, **OR**
 - d) Ovarian cancer at any age, **OR**

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- e) Pancreatic cancer at any age, **OR**
- f) Metastatic, node positive, [very-high-risk prostate cancer](#), or [high-risk prostate cancer](#) at any age, **OR**
- 2. Three or more [close relatives](#) with prostate cancer (any grade) and/or [breast cancer](#) on the same side of the family including the member with prostate cancer, **OR**
- 3. Ashkenazi Jewish ancestry, **OR**
- D. The member has a [first-degree relative](#) meeting any of the criteria above, **OR**
- E. The member's probability of having a *BRCA1* or *BRCA2* pathogenic variant is greater than 2.5% based on prior probability models (e.g., Tyrer-Cuzick, BRCAPro, CanRisk), **AND**
- F. The panel includes, at a minimum, sequencing of the following genes: *BRCA1*, *BRCA2*.
- II. Genetic testing using a hereditary prostate cancer susceptibility panel is considered **investigational** for all other indications.
- III. Hereditary prostate cancer susceptibility panel targeted mRNA sequencing analysis for the interpretation of variants of unknown significance is considered **investigational** because it is typically either considered an existing component of the genetic testing process for quality assurance, or follow up testing without proven utility.

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Hereditary Neuroendocrine Cancer Susceptibility Panels

A hereditary neuroendocrine cancer susceptibility panel is one that includes genes that are associated with inherited susceptibility to a neuroendocrine cancer.

- I. Genetic testing using a hereditary neuroendocrine cancer susceptibility panel is considered **medically necessary** when:
 - A. The member has a diagnosis of at least one of the following:
 - 1. Adrenocortical carcinoma, **OR**
 - 2. Paraganglioma/pheochromocytoma, **OR**
 - 3. Parathyroid adenoma or primary hyperparathyroidism before age 30, **OR**
 - 4. Multiple parathyroid adenomas, **OR**
 - 5. Multigland hyperplasia without obvious secondary cause, **OR**
 - 6. Recurrent primary hyperparathyroidism, **OR**
 - 7. Gastrinoma, **OR**

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8. Duodenal or pancreatic neuroendocrine tumor, **OR**
 9. A [first-degree relative](#) meeting any of the above criteria, but is not available for testing, **OR**
 - B. The member meets criteria for [MEN1 sequencing and/or deletion/duplication analysis](#), **OR**
 - C. The member meets criteria for [RET sequencing and/or deletion duplication analysis](#).
- II. Genetic testing using a hereditary neuroendocrine cancer susceptibility panel is considered **investigational** for all other indications.

NOTE: If a multigene cancer panel is performed, the appropriate panel code should be used [view rationale](#)
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BRCA1 AND BRCA2 GENE TESTING

BRCA1 or BRCA2 Targeted Variant or Known Familial Variant Analysis

- I. *BRCA1* or *BRCA2* targeted variant or known familial variant analysis for hereditary cancer susceptibility is considered **medically necessary** when:
 - A. The member is 18 years or older, **AND**
 - B. One of the following:
 1. The member has a family history of a known *BRCA1* or *BRCA2* pathogenic or likely pathogenic variant, **OR**
 2. A pathogenic or likely pathogenic variant in *BRCA1* or *BRCA2* was identified by tumor profiling in the member and germline analysis has not yet been performed.
- II. *BRCA1* or *BRCA2* targeted variant or known familial variant analysis for hereditary cancer susceptibility is considered **investigational** for all other indications.

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BRCA1 and BRCA2 Targeted Variant Analysis - Ashkenazi Jewish Founder Variants

- I. *BRCA1* and *BRCA2* targeted variant analysis for the 185delAG, 5385insC, 6174delT variants is considered **medically necessary** when:
 - A. The member is 18 years or older, **AND**
 - B. The member is of Ashkenazi Jewish ancestry (at least one grandparent of Ashkenazi Jewish ancestry).

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- II. *BRCA1* and *BRCA2* targeted variant analysis for the 185delAG, 5385insC, 6174delT variants is considered **investigational** for all other indications.

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PALB2 GENE TESTING

PALB2 Targeted Variant Analysis

- I. *PALB2* targeted variant analysis for hereditary breast and/or ovarian cancer susceptibility is considered **medically necessary** when:
 - A. The member is 18 years or older, **AND**
 - B. One of the following:
 - 1. The member has a family history of a known pathogenic or likely pathogenic variant in *PALB2*, **OR**
 - 2. A pathogenic or likely pathogenic variant in *PALB2* was identified by tumor profiling in the member, and germline analysis has not yet been performed.
- II. *PALB2* targeted variant analysis for hereditary breast and/or ovarian cancer susceptibility is considered **investigational** for all other indications.

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ATM AND/OR CHEK2 GENE TESTING

ATM or *CHEK2* Targeted Variant Analysis

- I. *ATM* or *CHEK2* targeted variant analysis for hereditary breast and/or ovarian cancer susceptibility is considered **medically necessary** when:
 - A. The member is 18 years or older, **AND**
 - B. One of the following:
 - 1. The member has a [close relative](#) with a known pathogenic or likely pathogenic variant in *ATM* or *CHEK2*, **OR**
 - 2. A pathogenic or likely pathogenic variant in *ATM* or *CHEK2* was identified by tumor profiling in the member and germline analysis has not yet been performed.
- II. *ATM* or *CHEK2* targeted variant analysis for hereditary breast and/or ovarian cancer susceptibility is considered **investigational** for all other indications.

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ATM and/or CHEK2 Sequencing and/or Deletion/Duplication Analysis

- I. *ATM* and/or *CHEK2* sequencing and/or deletion/duplication analysis for hereditary breast and/or ovarian cancer susceptibility, as a standalone test, is considered **investigational** for all indications.
- II. *ATM* mRNA sequencing analysis for the interpretation of variants of unknown significance is considered **investigational** because it is typically either considered an existing component of the genetic testing process for quality assurance or follow up testing without proven utility.

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LYNCH SYNDROME / HEREDITARY NONPOLYPOSIS COLORECTAL CANCER (HNPCC)

***MLH1, MSH2, MSH6, PMS2, or EPCAM* Targeted Variant Analysis**

- I. *MLH1, MSH2, MSH6, PMS2, or EPCAM* targeted variant analysis for Lynch syndrome/HNPCC is considered **medically necessary** when:
 - A. The member has a blood relative with a known pathogenic or likely pathogenic variant in *MLH1, MSH2, MSH6, PMS2, or EPCAM*, **OR**
 - B. A pathogenic or likely pathogenic variant in *MLH1, MSH2, MSH6, PMS2, or EPCAM* was identified by tumor profiling in the member and germline analysis has not yet been performed.
- II. *MLH1, MSH2, MSH6, PMS2, or EPCAM* targeted variant analysis for Lynch syndrome/HNPCC is considered **investigational** for all other indications.

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***MLH1, MSH2, MSH6, PMS2, and/or EPCAM* Sequencing and/or Deletion/Duplication Analysis**

- I. Lynch syndrome panels, *MLH1, MSH2, MSH6, PMS2, and/or EPCAM* sequencing and/or duplication analysis for Lynch syndrome/HNPCC is considered **medically necessary** when:
 - A. The member has a tumor that shows evidence of mismatch repair (MMR) deficiency (either by microsatellite instability (MSI) or loss of MMR protein expression), **OR**
 - B. The member has a diagnosis of a [Lynch syndrome-related cancer](#) (colorectal, endometrial, gastric, ovarian, pancreatic, ureter and renal pelvic, brain (usually glioblastoma), biliary tract, small intestinal, sebaceous adenoma, sebaceous carcinoma, or keratoacanthoma), **AND** any of the following:
 1. Diagnosed before age 50, **OR**
 2. Diagnosed at any age with an additional Lynch syndrome-related cancer, **OR**

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3. Diagnosed at any age with one or more [first- or second-degree relatives](#) diagnosed before age 50 with a Lynch syndrome-related cancer, **OR**
 4. Diagnosed at any age with two or more [first- or second-degree relatives](#) diagnosed at any age with a Lynch syndrome-related cancer, **OR**
- C. The member has a family history of **any** of the following:
1. One or more [first-degree relatives](#) diagnosed with colorectal or endometrial cancer before age 50, **OR**
 2. One or more [first-degree relatives](#) diagnosed with colorectal or endometrial cancer and an additional Lynch syndrome-related cancer, **OR**
 3. Two or more [first- or second-degree relatives](#) on the same side of the family diagnosed with a Lynch syndrome-related cancer, one of whom was diagnosed before age 50, **OR**
 4. Three or more [first- or second-degree relatives](#) on the same side of the family diagnosed with a Lynch syndrome-related cancer, **OR**
- D. The member has a 5% or greater risk of having Lynch syndrome based on one of the following variant prediction models: MMRpro, PREMM5, MMRpredict, **OR**
- E. The member has a personal history of colorectal and/or endometrial cancer with a PREMM5 score of 2.5% or greater.
- II. Lynch syndrome panel, *MLH1*, *MSH2*, *MSH6*, *PMS2*, and/or *EPCAM* sequencing and/or duplication analysis for Lynch syndrome/HNPCC is considered **investigational** for all other indications.
- III. *MLH1*, *MSH2*, *MSH6*, *PMS2* and *EPCAM* mRNA sequencing analysis for the interpretation of variants of unknown significance is considered **investigational** because it is typically either considered an existing component of the genetic testing process for quality assurance, or follow up testing without proven utility.

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ADENOMATOUS POLYPOSIS CONDITIONS

APC or *MUTYH* Targeted Variant Analysis

- I. *APC* or *MUTYH* targeted variant analysis for [adenomatous polyposis](#) testing is considered **medically necessary** when:
 - A. The member has a family history of a known pathogenic or likely pathogenic variant in *APC* or *MUTYH*, **OR**
 - B. A pathogenic or likely pathogenic variant in *APC* or *MUTYH* was identified by tumor profiling in the member and germline analysis has not yet been performed.

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- II. *APC* or *MUTYH* targeted variant analysis for [adenomatous polyposis](#) conditions is considered **investigational** for all other indications.

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***APC* and/or *MUTYH* Sequencing and/or Deletion/Duplication Analysis**

- I. *APC* sequencing and/or deletion/duplication analysis and/or *MUTYH* sequencing and/or deletion/duplication analysis for [adenomatous polyposis](#) conditions is considered **medically necessary** when:
- A. The member has a history of any of the following:
 - 1. 10 or more cumulative adenomas, **OR**
 - 2. Congenital hypertrophy of the retinal pigment epithelium (CHRPE), **OR**
 - 3. Desmoid tumor, **OR**
 - 4. Hepatoblastoma, **OR**
 - 5. Cribriform-morular variant of papillary thyroid cancer, **OR**
 - 6. A clinical diagnosis of serrated-polypoid syndrome, with at least some adenomas, based on one of the following:
 - a) 5 or more serrated polyps proximal to the rectum, all being 5mm or greater in size and at least 2 being 10mm or greater in size, **OR**
 - b) More than 20 serrated polyps of any size distributed throughout the large bowel, with at least 5 or more being proximal to the rectum, **OR**
 - 7. Duodenal cancer, **OR**
 - 8. Duodenal adenomas.
 - II. *APC* sequencing and/or deletion/duplication analysis and/or *MUTYH* sequencing and/or deletion/duplication analysis for [adenomatous polyposis](#) conditions is considered **investigational** for all other indications.
 - III. *APC* mRNA sequencing analysis for the interpretation of variants of unknown significance is considered **investigational** because it is typically either considered an existing component of the genetic testing process for quality assurance or follow up testing without proven utility.

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BAP1-TUMOR PREDISPOSITION SYNDROME

BAP1 Targeted Variant Analysis

- I. *BAP1* targeted variant analysis for *BAP1*-tumor predisposition syndrome is considered **medically necessary** when:
 - A. The member has a [close relative](#) with a known pathogenic or likely pathogenic variant in *BAP1*, **OR**
 - B. A pathogenic or likely pathogenic variant in *BAP1* was identified by tumor profiling in the member and germline analysis has not yet been performed.
- II. *BAP1* targeted variant analysis for *BAP1*-tumor predisposition syndrome is considered **investigational** for all other indications.

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BAP1 Sequencing and/or Deletion/Duplication Analysis

- I. *BAP1* sequencing and/or deletion/duplication analysis for *BAP1*-tumor predisposition syndrome is considered **medically necessary** when:
 - A. The member has a personal history of:
 1. Two or more of the following:
 - a) *BAP1*-inactivated melanocytic tumors (aka atypical spitz tumor), **OR**
 - b) Uveal melanoma, **OR**
 - c) Malignant mesothelioma, **OR**
 - d) Renal cell carcinoma, **OR**
 - e) Hepatocellular carcinoma, **OR**
 - f) Cholangiocarcinoma, **OR**
 - g) Meningioma, **OR**
 2. One of the tumors/cancers listed in the criteria A.1., **AND**
 - a) A cutaneous melanoma, **OR**
 - b) A basal cell carcinoma, **OR**
 3. One of the tumors/cancers listed in the criteria A.1., **AND**
 - a) A [first- or second-degree relative](#) with any of the following tumors/cancers:

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- (1) *BAP1*-inactivated melanocytic tumors (aka atypical spitz tumor), **OR**
- (2) Uveal melanoma, **OR**
- (3) Malignant mesothelioma, **OR**
- (4) Renal cell carcinoma, **OR**
- (5) Hepatocellular carcinoma, **OR**
- (6) Cholangiocarcinoma, **OR**
- (7) Meningioma, **OR**
- (8) Cutaneous melanoma, **OR**
- (9) Basal cell carcinoma, **OR**

4. Both of the following:

a) A diagnosis of:

- (1) Cutaneous melanoma, **OR**
- (2) Basal cell carcinoma, **AND**

b) A [first- or second-degree relative](#) with any of the following tumors/cancer:

- (1) *BAP1*-inactivated melanocytic tumors (aka atypical spitz tumor), **OR**
- (2) Uveal melanoma, **OR**
- (3) Malignant mesothelioma, **OR**
- (4) Renal cell carcinoma, **OR**
- (5) Hepatocellular carcinoma, **OR**
- (6) Cholangiocarcinoma, **OR**
- (7) Meningioma.

- II. *BAP1* sequencing and/or deletion/duplication analysis for *BAP1*-tumor predisposition syndrome is considered **investigational** for all other indications.

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BIRT-HOGG-DUBE SYNDROME (BHDS)

FLCN Targeted Variant Analysis

- I. *FLCN* targeted variant analysis for Birt-Hogg-Dube syndrome (BHDS) is considered **medically necessary** when:
 - A. The member has a [first- or second-degree relative](#) with a known pathogenic or likely pathogenic variant in *FLCN*, **OR**
 - B. A pathogenic or likely pathogenic variant in *FLCN* was identified by tumor profiling in the member and germline analysis has not yet been performed.
- II. *FLCN* targeted variant analysis for Birt-Hogg-Dube syndrome (BHDS) is considered **investigational** for all other indications.

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FLCN Sequencing and/or Deletion/Duplication Analysis

- I. *FLCN* sequencing and/or deletion/duplication analysis for Birt-Hogg-Dube syndrome (BHDS) is considered **medically necessary** when:
 - A. The member has a personal history of any of the following:
 1. 5 or more fibrofolliculomas/trichodiscomas with at least one confirmed histologically, **OR**
 2. Multiple lung cysts with no apparent cause, with or without pneumothorax, **OR**
 3. Renal cancer diagnosed before 50 years of age, **OR**
 4. Multifocal or bilateral renal cancer, **OR**
 5. Renal cancer of mixed chromophobe and oncocytic, clear cell, or papillary histology, **OR**
 6. Oncocytoma, **OR**
 7. Angiomyolipoma, **OR**
 8. A [first-degree relative](#) with BHDS who has not yet had genetic testing, or the results of genetic testing are unknown.
- II. *FLCN* sequencing and/or deletion/duplication analysis for Birt-Hogg-Dube syndrome (BHDS) is considered **investigational** for all other indications.

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COWDEN SYNDROME (CS)/PTEN HAMARTOMA TUMOR SYNDROME (PHTS)

PTEN Targeted Variant Analysis

- I. *PTEN* targeted variant analysis for Cowden syndrome (CS)/*PTEN* hamartoma tumor syndrome (PHTS) is considered **medically necessary** when:
 - A. The member has a blood relative with a known pathogenic or likely pathogenic variant in *PTEN*, **OR**
 - B. A pathogenic or likely pathogenic variant in *PTEN* was identified by tumor profiling in the member and germline analysis has not yet been performed.
- II. *PTEN* targeted variant analysis for Cowden syndrome (CS)/*PTEN* hamartoma tumor syndrome (PHTS) is considered **investigational** for all other indications.

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PTEN Sequencing and/or Deletion/Duplication Analysis

- I. *PTEN* sequencing and/or deletion/duplication analysis for Cowden syndrome (CS)/*PTEN* hamartoma tumor syndrome (PHTS) is considered **medically necessary** when:
 - A. The member has a personal history of any of the following:
 1. Bannayan Riley-Ruvalcaba syndrome (BRRS), **OR**
 2. Adult Lhermitte-Duclos disease (LDD) (defined as the presence of a cerebellar dysplastic gangliocytoma), **OR**
 3. Autism-spectrum disorder and macrocephaly, **OR**
 4. At least 2 biopsy-proven trichilemmomas, **OR**
 - B. The member meets clinical criteria for CS/PHTS:
 1. Macrocephaly (greater than or equal to 97 percentile), **OR**
 2. Lhermitte-Duclos disease, **OR**
 3. Gastrointestinal hamartomas or ganglioneuromas, **AND**
 4. At least two of the following:
 - a) [Breast cancer](#), **OR**
 - b) Endometrial cancer, **OR**
 - c) Thyroid cancer (follicular), **OR**
 - d) Macular pigmentation of the glans penis, **OR**

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- e) Mucocutaneous lesions (One biopsy-proven trichilemmoma; multiple palmoplantar keratoses; multifocal or extensive oral mucosal papillomatosis; multiple cutaneous facial papules), **OR**

C. The member has at least two of the following:

1. [Breast cancer](#), **OR**
2. Endometrial cancer, **OR**
3. Thyroid cancer (follicular), **OR**
4. Multiple gastrointestinal hamartomas or ganglioneuromas, **OR**
5. Macrocephaly (greater than or equal to 97 percentile), **OR**
6. Macular pigmentation of the glans penis, **OR**
7. Mucocutaneous lesions (one biopsy-proven trichilemmoma; multiple palmoplantar keratoses; multifocal or extensive oral mucosal papillomatosis; multiple cutaneous facial papules), **AND**
8. At least three of the following:
 - a) Autism spectrum disorder, **OR**
 - b) Colon cancer, **OR**
 - c) Esophageal glycogenic acanthosis (3 or more), **OR**
 - d) Lipomas, **OR**
 - e) Intellectual disability (i.e., IQ less than or equal to 75), **OR**
 - f) Thyroid cancer (papillary or follicular variant of papillary thyroid cancer), **OR**
 - g) Thyroid structural lesions (such as adenoma, multinodular goiter), **OR**
 - h) Renal cell carcinoma, **OR**
 - i) Single GI hamartoma or ganglioneuroma, **OR**
 - j) Testicular lipomatosis, **OR**
 - k) Vascular anomalies (including multiple intracranial developmental venous anomalies), **OR**

D. The member has macrocephaly, **AND**

1. [Breast cancer](#), **OR**
2. Endometrial cancer, **OR**

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3. Thyroid cancer (follicular), **OR**
 4. Multiple gastrointestinal hamartomas or ganglioneuromas, **OR**
 5. Macrocephaly (greater than or equal to 97 percentile), **OR**
 6. Macular pigmentation of the glans penis, **OR**
 7. Mucocutaneous lesions (one biopsy-proven trichilemmoma; multiple palmoplantar keratoses; multifocal or extensive oral mucosal papillomatosis; multiple cutaneous facial papules), **OR**
- E. The member has at least three of the following:
1. [Breast cancer](#), **OR**
 2. Endometrial cancer, **OR**
 3. Thyroid cancer (follicular), **OR**
 4. Multiple gastrointestinal hamartomas or ganglioneuromas, **OR**
 5. Macular pigmentation of the glans penis, **OR**
 6. Mucocutaneous lesions (one biopsy-proven trichilemmoma; multiple palmoplantar keratoses; multifocal or extensive oral mucosal papillomatosis; multiple cutaneous facial papules), **OR**
 7. The member has a [close relative](#) with a clinical diagnosis of CS/PHTS or BRRS for whom testing has not been performed, **OR**
 8. The member has any of the following:
 - a) [Breast cancer](#), **OR**
 - b) Endometrial cancer, **OR**
 - c) Thyroid cancer (follicular), **OR**
 - d) Multiple gastrointestinal hamartomas or ganglioneuromas, **OR**
 - e) Macrocephaly (greater than or equal to 97 percentile), **OR**
 - f) Macular pigmentation of the glans penis, **OR**
 - g) Mucocutaneous lesions (one biopsy-proven trichilemmoma; multiple palmoplantar keratoses; multifocal or extensive oral mucosal papillomatosis; multiple cutaneous facial papules), **AND**
 9. At least three of the following:
 - a) Autism spectrum disorder, **OR**
 - b) Colon cancer, **OR**

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- c) Esophageal glycogenic acanthosis (3 or more), **OR**
- d) Lipomas, **OR**
- e) Intellectual disability (ie, IQ less than or equal to 75), **OR**
- f) Thyroid cancer (papillary or follicular variant of papillary thyroid cancer), **OR**
- g) Thyroid structural lesions (such as adenoma, multinodular goiter), **OR**
- h) Renal cell carcinoma, **OR**
- i) Single GI hamartoma or ganglioneuroma, **OR**
- j) Testicular lipomatosis, **OR**
- k) Vascular anomalies (including multiple intracranial developmental venous anomalies), **OR**

F. The member has at least four of the following:

- 1. Autism spectrum disorder, **OR**
- 2. Colon cancer, **OR**
- 3. Esophageal glycogenic acanthosis (3 or more), **OR**
- 4. Lipomas, **OR**
- 5. Intellectual disability (i.e., IQ less than or equal to 75), **OR**
- 6. Thyroid cancer (papillary or follicular variant of papillary thyroid cancer), **OR**
- 7. Thyroid structural lesions (such as adenoma, multinodular goiter), **OR**
- 8. Renal cell carcinoma, **OR**
- 9. Single GI hamartoma or ganglioneuroma, **OR**
- 10. Testicular lipomatosis, **OR**
- 11. Vascular anomalies (including multiple intracranial developmental venous anomalies), **OR**

G. The member has a [close relative](#) with a clinical diagnosis of CS/PHTS or BRRS for whom testing has not been performed, **AND**

- 1. The member has at least one of the following:
 - a) [Breast cancer](#), **OR**

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- b) Endometrial Cancer, **OR**
 - c) Thyroid Cancer (follicular), **OR**
 - d) Multiple gastrointestinal hamartomas or ganglioneuromas, **OR**
 - e) Macrocephaly (greater than or equal to 97 percentile), **OR**
 - f) Macular pigmentation of the glans penis, **OR**
 - g) Mucocutaneous lesions (one biopsy-proven trichilemmoma; multiple palmoplantar keratoses; multifocal or extensive oral mucosal papillomatosis; multiple cutaneous facial papules), **OR**
2. At least two of the following:
- a) Autism spectrum disorder, **OR**
 - b) Colon cancer, **OR**
 - c) Esophageal glycogenic acanthosis (3 or more), **OR**
 - d) Lipomas, **OR**
 - e) Intellectual disability (i.e., IQ less than or equal to 75), **OR**
 - f) Thyroid cancer (papillary or follicular variant of papillary thyroid cancer), **OR**
 - g) Thyroid structural lesions (such as adenoma, multinodular goiter), **OR**
 - h) Renal cell carcinoma, **OR**
 - i) Single GI hamartoma or ganglioneuroma, **OR**
 - j) Testicular lipomatosis, **OR**
 - k) Vascular anomalies (including multiple intracranial developmental venous anomalies).
- II. *PTEN* sequencing and/or deletion/duplication analysis for Cowden syndrome (CS)/*PTEN* hamartoma tumor syndrome (PHTS) is considered **investigational** for all other indications.

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FAMILIAL ATYPICAL MULTIPLE MOLE MELANOMA SYNDROME (FAMMM)

CDKN2A Targeted Variant Analysis

- I. *CDKN2A* targeted variant analysis for familial atypical multiple mole melanoma (FAMMM) syndrome, also known as melanoma-pancreatic cancer syndrome, is considered **medically necessary** when:
 - A. The member has a [close relative](#) with a known pathogenic or likely pathogenic variant in *CDKN2A*, **OR**
 - B. A *CDKN2A* pathogenic or likely pathogenic variant was identified by tumor profiling in the member and germline analysis has not yet been performed.
- II. *CDKN2A* targeted variant analysis for familial atypical multiple mole melanoma (FAMMM) syndrome, also known as melanoma-pancreatic cancer syndrome is considered **investigational** for all other indications.

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CDKN2A Sequencing and/or Deletion/Duplication Analysis

- I. *CDKN2A* sequencing and/or deletion/duplication analysis for familial atypical multiple mole melanoma (FAMMM) syndrome, also known as melanoma-pancreatic cancer syndrome, is considered **medically necessary** when:
 - A. The member has had 3 or more invasive cutaneous melanomas, **OR**
 - B. The member has had pancreatic adenocarcinoma, **OR**
 - C. The member has had at least one cutaneous melanoma, **AND**
 1. The member has at least two [close relatives](#) with pancreatic cancer or cutaneous melanoma on the same side of the family.
- II. *CDKN2A* sequencing and/or deletion/duplication analysis for familial atypical multiple mole melanoma (FAMMM) syndrome, also known as melanoma-pancreatic cancer syndrome, is considered **investigational** for all other indications.

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HEREDITARY DIFFUSE GASTRIC CANCER (AKA, SIGNET RING CELL GASTRIC CANCER)

CDH1 Targeted Variant Analysis

- I. *CDH1* targeted variant analysis for Hereditary Diffuse Gastric Cancer (aka, Signet Ring Cell Gastric Cancer) is considered **medically necessary** when:
 - A. The member is 18 years or older, **AND**
 - B. One of the following:

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1. The member has a [close relative](#) with a known pathogenic or likely pathogenic variant in *CDH1*, **OR**
 2. A pathogenic or likely pathogenic variant in *CDH1* was identified by tumor profiling in the member and germline analysis has not yet been performed.
- II. *CDH1* targeted variant analysis for Hereditary Diffuse Gastric Cancer (aka, Signet Ring Cell Gastric Cancer) is considered **investigational** for all other indications.

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CDH1 Sequencing and/or Deletion/Duplication Analysis

- I. *CDH1* sequencing and/or deletion/duplication analysis for Hereditary Diffuse Gastric Cancer (aka, Signet Ring Cell Gastric Cancer) is considered **medically necessary** when:
 - A. The member is 18 years or older, **AND**
 - B. The member meets at least one of the following criteria:
 1. Diffuse gastric cancer diagnosed before age 50 years, **OR**
 2. Diffuse gastric cancer diagnosed at any age in a member with [Maori ancestry](#), **OR**
 3. Diffuse gastric cancer diagnosed at any age in a member with a personal or family history of cleft lip/cleft palate, **OR**
 4. Bilateral lobular [breast cancer](#) diagnosed before age 70 years, **OR**
 5. Personal or family history of diffuse gastric cancer and lobular [breast cancer](#), one diagnosed before age 70 years, **OR**
 6. Two cases of gastric cancer in the family, at least one of which is a confirmed case of diffuse gastric cancer, diagnosed at any age, **OR**
 7. Two cases of lobular [breast cancer](#) in family members before 50 years of age.
- II. *CDH1* sequencing and/or deletion/duplication analysis for Hereditary Diffuse Gastric Cancer (aka, Signet Ring Cell Gastric Cancer) is considered **investigational** for all other indications.

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JUVENILE POLYPOSIS SYNDROME (JPS)

SMAD4 or BMPR1A Targeted Variant Analysis

- I. *SMAD4* or *BMPR1A* targeted variant analysis for juvenile polyposis syndrome (JPS) is considered **medically necessary** when:
 - A. The member has a blood relative with a known pathogenic or likely pathogenic variant in *SMAD4* or *BMPR1A*, **OR**
 - B. A pathogenic or likely pathogenic variant in *SMAD4* or *BMPR1A* was identified by tumor profiling in the member and germline analysis has not yet been performed.
- II. *SMAD4* or *BMPR1A* targeted variant analysis for juvenile polyposis syndrome (JPS) is considered **investigational** for all other indications.

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SMAD4 and/or BMPR1A Sequencing and/or Deletion/Duplication Analysis

- I. *SMAD4* and/or *BMPR1A* sequencing and/or deletion/duplication analysis for juvenile polyposis syndrome (JPS) is considered **medically necessary** when:
 - A. The member has 5 or more [juvenile polyps](#) in the colon, **OR**
 - B. The member has multiple [juvenile polyps](#) throughout the gastrointestinal tract, **OR**
 - C. The member has a family history of JPS.
- II. *SMAD4* and/or *BMPR1A* sequencing and/or deletion/duplication analysis for juvenile polyposis syndrome (JPS) is considered **investigational** for all other indications.

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HEREDITARY LEIOMYOMATOSIS AND RENAL CELL CANCER (HLRCC)

FH Targeted Variant Analysis

- I. *FH* targeted variant analysis for hereditary leiomyomatosis and renal cell cancer (HLRCC) is considered **medically necessary** when:
 - A. The member has a [first- or second-degree relative](#) with a known pathogenic or likely pathogenic variant in *FH*, **OR**
 - B. A pathogenic or likely pathogenic variant in *FH* was identified by tumor profiling in the member and germline analysis has not yet been performed.
- II. *FH* targeted variant analysis for hereditary leiomyomatosis and renal cell cancer (HLRCC) is considered **investigational** for all other indications.

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***FH* Sequencing and/or Deletion/Duplication Analysis**

- I. *FH* sequencing and/or deletion/duplication analysis for hereditary leiomyomatosis and renal cell cancer (HLRCC) is considered **medically necessary** when:
 - A. The member is 18 years or older, **AND**
 - B. The member has at least one of the following:
 1. Cutaneous leiomyomata, **OR**
 2. Uterine leiomyomata (uterine fibroids), **OR**
 3. Renal cell carcinoma.
- II. *FH* sequencing and/or deletion/duplication analysis for hereditary leiomyomatosis and renal cell cancer (HLRCC) is considered **investigational** for all other indications.

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LI-FRAUMENI SYNDROME (LFS)

***TP53* Targeted Variant Analysis**

- I. *TP53* targeted variant analysis for Li-Fraumeni syndrome (LFS) is considered **medically necessary** when:
 - A. The member has a [close relative](#) with a known pathogenic or likely pathogenic variant in *TP53*, **OR**
 - B. A pathogenic or likely pathogenic variant in *TP53* was identified by tumor profiling in the member and germline analysis has not yet been performed.
- II. *TP53* targeted variant analysis for Li-Fraumeni syndrome (LFS) is considered **investigational** for all other indications.

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***TP53* Sequencing and/or Deletion/Duplication Analysis**

- I. *TP53* sequencing and/or deletion/duplication analysis for Li-Fraumeni syndrome (LFS) is considered **medically necessary** when:
 - A. The member was diagnosed with [breast cancer](#) before 31 years of age, **OR**
 - B. The member has a personal or family history of pediatric hypodiploid acute lymphoblastic leukemia, **OR**
 - C. The member was diagnosed with a sarcoma before 45 years of age, **AND**
 1. The member has a [first-degree relative](#) diagnosed with any cancer before 45 years of age, **AND**

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2. At least one of the following:
 - a) The member has an additional [first- or second-degree relative](#) diagnosed with any cancer before 45 years of age, **OR**
 - b) The member has an additional [first- or second-degree relative](#) diagnosed with sarcoma at any age, **OR**
- D. The member was diagnosed with any of the following at any age:
 1. Adrenocortical carcinoma, **OR**
 2. Choroid plexus carcinoma, **OR**
 3. Rhabdomyosarcoma of embryonal anaplastic subtype, **OR**
- E. The member was diagnosed with any of the following tumors from the LFS tumor spectrum before 46 years of age:
 1. Soft tissue sarcoma, **OR**
 2. Osteosarcoma, **OR**
 3. Central nervous system tumor, **OR**
 4. [Breast cancer](#), **OR**
 5. Adrenocortical carcinoma, **AND**
 - a) The member has had a second tumor from the LFS tumor spectrum (except [breast cancer](#) if the initial cancer was [breast cancer](#)), **OR**
 - b) The member has a [first- or second-degree relative](#) with a tumor from the LFS tumor spectrum before 56 years of age (except [breast cancer](#) if the member had [breast cancer](#)), **OR**
 - c) The member has a [first- or second-degree relative](#) with a history of multiple primary tumors from the LFS tumor spectrum at any age.
- II. *TP53* sequencing and/or deletion/duplication analysis for Li-Fraumeni syndrome (LFS) is considered **investigational** for all other indications.

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MULTIPLE ENDOCRINE NEOPLASIA - TYPE 1 (MEN1)

MEN1 Targeted Variant Analysis

- I. *MEN1* targeted variant analysis for multiple endocrine neoplasia type 1 (MEN1) is considered **medically necessary** when:

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- A. The member has a [close relative](#) with a known pathogenic or likely pathogenic variant in *MEN1*, **OR**
- B. A pathogenic or likely pathogenic variant in *MEN1* was identified by tumor profiling in the member and germline analysis has not yet been performed.
- II. *MEN1* targeted variant analysis for multiple endocrine neoplasia type 1 (MEN1) is considered **investigational** for all other indications.

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***MEN1* Sequencing and/or Deletion/Duplication Analysis**

- I. *MEN1* sequencing and/or deletion/duplication analysis for multiple endocrine neoplasia type 1 (MEN1) is considered **medically necessary** when:
 - A. The member has a personal history of at least two of the following:
 - 1. Duodenal/pancreatic neuroendocrine tumor, **OR**
 - 2. Primary hyperparathyroidism, **OR**
 - 3. Pituitary adenoma, **OR**
 - 4. Foregut (bronchial, thymic, or gastric) carcinoid, **OR**
 - B. The member has a personal history of one of the above, **AND**
 - 1. The member has a [close relative](#) with at least one of the above.
- II. *MEN1* sequencing and/or deletion/duplication analysis for multiple endocrine neoplasia type 1 (MEN1) is considered **investigational** for all other indications.

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MULTIPLE ENDOCRINE NEOPLASIA TYPE 2 (MEN2)

***RET* Targeted Variant Analysis**

- I. *RET* targeted variant analysis for multiple endocrine neoplasia type 2 (MEN2) is considered **medically necessary** when:
 - A. The member has a [close relative](#) with a known pathogenic or likely pathogenic variant in *RET*, **OR**
 - B. A pathogenic or likely pathogenic variant in *RET* was identified by tumor profiling in the member and germline analysis has not yet been performed.
- II. *RET* targeted variant analysis for multiple endocrine neoplasia type 2 (MEN2) is considered **investigational** for all other indications.

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RET Sequencing and/or Deletion/Duplication Analysis

- I. *RET* sequencing and/or deletion/duplication analysis for multiple endocrine neoplasia type 2 (MEN2) is considered **medically necessary** when:
 - A. The member has a diagnosis of any of the following:
 1. Medullary thyroid cancer, **OR**
 2. Adrenal pheochromocytoma, **OR**
 3. Parathyroid adenoma or hyperplasia, **OR**
 - B. The member has a [first-degree relative](#) that meets at least one of the above criteria, **AND**
 1. The relative has not previously undergone *RET* sequencing and/or deletion/duplication analysis.
- II. *RET* sequencing and/or deletion/duplication analysis for multiple endocrine neoplasia type 2 (MEN2) is considered **investigational** for all other indications.

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NEVOID BASAL CELL CARCINOMA SYNDROME (NBCCS) (AKA GORLIN SYNDROME)

PTCH1 or SUFU Targeted Variant Analysis

- I. *PTCH1* or *SUFU* targeted variant analysis for nevoid basal cell carcinoma syndrome (NBCCS), also known as Gorlin syndrome, is considered **medically necessary** when:
 - A. The member has a [close relative](#) with a known pathogenic or likely pathogenic variant in *PTCH1* or *SUFU*, **OR**
 - B. A pathogenic or likely pathogenic variant in *PTCH1* or *SUFU* was identified by tumor profiling in the member and germline analysis has not yet been performed.
- II. *PTCH1* or *SUFU* targeted variant analysis for nevoid basal cell carcinoma syndrome (NBCCS), also known as Gorlin syndrome, is considered **investigational** for all other indications.

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PTCH1 and/or SUFU Sequencing and/or Deletion/Duplication Analysis

- I. *PTCH1* and/or *SUFU* sequencing and/or deletion duplication analysis for nevoid basal cell carcinoma syndrome (NBCCS), also known as Gorlin syndrome, is considered **medically necessary** when:
 - A. The member has a personal history of:
 1. At least two of the following:

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- a) Lamellar calcification of the falx, **OR**
 - b) Jaw keratocyst, **OR**
 - c) Palmar/plantar pits (2 or more), **OR**
 - d) Multiple basal cell carcinomas (more than 5 in lifetime) or a basal cell carcinoma diagnosed before 30 years of age, **OR**
 - e) A [first-degree relative](#) with NBCCS, **AND**
2. At least one of the following:
- a) Childhood medulloblastoma, **OR**
 - b) Lympho-mesenteric or pleural cysts, **OR**
 - c) Macrocephaly (OFC greater than 97th centile), **OR**
 - d) Cleft lip/palate, **OR**
 - e) Vertebral/rib anomalies (bifid/splayed/extra ribs; bifid vertebrae), **OR**
 - f) Pre- or post-axial polydactyly, **OR**
 - g) Ovarian fibromas, **OR**
 - h) Cardiac fibromas, **OR**
 - i) Ocular anomalies (e.g., cataract, pigmentary changes of the retinal epithelium, developmental defects), **OR**
- B. The member has a personal history of:
1. At least one of the following:
- a) Lamellar calcification of the falx, **OR**
 - b) Jaw keratocyst, **OR**
 - c) Palmar/plantar pits (2 or more), **OR**
 - d) Multiple basal cell carcinomas (more than 5 in lifetime) or a basal cell carcinoma diagnosed before 30 years of age, **OR**
 - e) A [first-degree relative](#) with NBCCS, **AND**
2. At least three of the following:
- a) Childhood medulloblastoma, **OR**
 - b) Lympho-mesenteric or pleural cysts, **OR**

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- c) Macrocephaly (OFC greater than 97th centile), **OR**
 - d) Cleft lip/palate, **OR**
 - e) Vertebral/rib anomalies (bifid/splayed/extra ribs; bifid vertebrae), **OR**
 - f) Pre- or post-axial polydactyly, **OR**
 - g) Ovarian fibromas, **OR**
 - h) Cardiac fibromas, **OR**
 - i) Ocular anomalies (e.g., cataract, pigmentary changes of the retinal epithelium, developmental defects).
- II. *PTCH1* and/or *SUFU* sequencing and/or deletion/duplication analysis is considered **investigational** for all other indications.

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HEREDITARY PARAGANGLIOMA/PHEOCHROMOCYTOMA SYNDROME (PGL/PCC)

MAX, SDHA, SDHAF2, SDHB, SDHC, SDHD, or TMEM127 Targeted Variant Analysis

- I. *MAX, SDHA, SDHAF2, SDHB, SDHC, SDHD, or TMEM127* targeted variant analysis for hereditary paraganglioma/pheochromocytoma syndrome (PGL/PCC) is considered **medically necessary** when:
 - A. The member has a [close relative](#) with a known pathogenic or likely pathogenic variant in *MAX, SDHA, SDHAF2, SDHB, SDHC, SDHD, or TMEM127*, **OR**
 - B. A pathogenic or likely pathogenic variant in *MAX, SDHA, SDHAF2, SDHB, SDHC, SDHD, or TMEM127* was identified by tumor profiling in the member and germline analysis has not yet been performed.
- II. *MAX, SDHA, SDHAF2, SDHB, SDHC, SDHD, or TMEM127* targeted variant analysis for hereditary paraganglioma/pheochromocytoma syndrome (PGL/PCC) is considered **investigational** for all other indications.

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MAX, SDHA, SDHAF2, SDHB, SDHC, SDHD, and/or TMEM127 Sequencing and/or Deletion/Duplication Analysis

- I. *MAX, SDHA, SDHAF2, SDHB, SDHC, SDHD, and/or TMEM127* sequencing and/or deletion/duplication analysis for hereditary paraganglioma/pheochromocytoma syndrome (PGL/PCC) is considered **medically necessary** when:
 - A. The member has a diagnosis of one or more of the following:
 - 1. Pheochromocytoma, **OR**

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2. Paranglioma, **OR**
 3. Clear cell renal cell cancer, **OR**
 4. Gastrointestinal stromal tumor (GIST), **OR**
- B. The member has a [close relative](#) with paraganglioma or pheochromocytoma.
- II. *MAX*, *SDHA*, *SDHAF2*, *SDHB*, *SDHC*, *SDHD*, and/or *TMEM127* sequencing and/or deletion/duplication for hereditary paraganglioma/pheochromocytoma syndrome (PGL/PCC) is considered **investigational** for all other indications.

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PEUTZ-JEGHERS SYNDROME (PJS)

STK11 Targeted Variant Analysis

- I. *STK11* targeted variant analysis for Peutz-Jeghers syndrome (PJS) is considered **medically necessary** when:
 - A. The member has a blood relative with a known pathogenic or likely pathogenic variant in *STK11*, **OR**
 - B. A pathogenic or likely pathogenic variant in *STK11* was identified by tumor profiling in the member and germline analysis has not yet been performed.
- II. *STK11* targeted variant analysis for Peutz-Jeghers syndrome (PJS) is considered **investigational** for all other indications.

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STK11 Sequencing and/or Deletion/Duplication Analysis

- I. *STK11* sequencing and/or deletion/duplication analysis for Peutz-Jeghers syndrome (PJS) is considered **medically necessary** when:
 - A. The member has at least two histologically confirmed Peutz-Jeghers-type hamartomatous polyps of the GI tract, **OR**
 - B. The member has mucocutaneous pigmentation of the mouth, lips, nose, eyes, genitalia, or fingers, **OR**
 - C. The member has a family history of PJS.
- II. *STK11* sequencing and/or deletion/duplication analysis for Peutz-Jeghers syndrome (PJS) is considered **investigational** for all other indications.

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RETINOBLASTOMA

***RB1* Targeted Variant Analysis**

- I. *RB1* targeted variant analysis for retinoblastoma is considered **medically necessary** when:
 - A. The member has a [close relative](#) with a known pathogenic or likely pathogenic variant in *RB1*, **OR**
 - B. A pathogenic or likely pathogenic variant in *RB1* was identified by tumor profiling in the member and germline analysis has not yet been performed.
- II. *RB1* targeted variant analysis for retinoblastoma is considered **investigational** for all other indications.

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***RB1* Sequencing and/or Deletion/Duplication Analysis**

- I. *RB1* sequencing and/or deletion/duplication analysis for retinoblastoma is considered **medically necessary** when:
 - A. The member has a diagnosis of retinoblastoma in one or both eyes, **OR**
 - B. The member has a [close relative](#) with retinoblastoma in one or both eyes.
- II. *RB1* sequencing and/or deletion/duplication analysis for retinoblastoma is considered **investigational** for all other indications.

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VON HIPPEL-LINDAU SYNDROME (VHL)

***VHL* Targeted Variant Analysis**

- I. *VHL* targeted variant analysis for Von Hippel-Lindau syndrome is considered **medically necessary** when:
 - A. The member has a [first- or second-degree relative](#) with a known pathogenic or likely pathogenic variant in *VHL*, **OR**
 - B. A pathogenic or likely pathogenic variant in *VHL* was identified by tumor profiling in the member and germline analysis has not yet been performed.
- II. *VHL* targeted variant analysis for Von Hippel-Lindau syndrome is considered **investigational** for all other indications.

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VHL Sequencing and/or Deletion/Duplication Analysis

- I. VHL sequencing and/or deletion/duplication analysis for Von Hippel-Lindau syndrome is considered **medically necessary** when:
 - A. The member has a diagnosis of one or more of the following:
 1. Hemangioblastoma of the retina, spine, or brain, **OR**
 2. Renal cell carcinoma diagnosed before age 40 years, **OR**
 3. Multiple and/or bilateral renal cell carcinoma diagnosed at any age, **OR**
 4. Pheochromocytoma or paraganglioma (in abdomen, thorax, or neck), **OR**
 5. Retinal angiomas, **OR**
 6. Endolymphatic sac tumor, **OR**
 7. Epididymal or adnexal papillary cystadenoma, **OR**
 8. Pancreatic serous cystadenoma, **OR**
 9. Pancreatic neuroendocrine tumors, **OR**
 10. Multiple renal, pancreatic or hepatic cysts.
- II. VHL sequencing and/or deletion/duplication analysis for Von Hippel-Lindau syndrome is considered **investigational** for all other indications.

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RATIONALE

Pan-Cancer Hereditary Cancer Susceptibility Panels

National Comprehensive Cancer Network (NCCN)

NCCN Breast, Ovarian, and/or Pancreatic, and Prostate Cancer Genetic Assessment guidelines (2.2025) define multi-gene testing as analysis of a set of genes that are associated with one or more cancer phenotypes in a family. NCCN states that in some families, there is suspicion for more than one hereditary cancer syndrome. In those cases, phenotype-directed testing via a “tailored multigene panel” is a more efficient and cost-effective method of testing. They state that “intermediate penetrant (moderate-risk) genes” may also be included in the multigene panels (p. EVAL-A 3 of 11).

These guidelines also recommend consideration of RNA studies, to further define the meaning of variants of unknown significance. Research studies designed to explore the functional impact of variants, such as variant reclassification programs through clinical labs or registries should be considered (p. EVAL-A, 9 of 11).

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NCCN Guidelines for Genetic/Familial High-Risk Assessment Colorectal, Endometrial and Gastric (1.2025) recommend germline multigene panel testing in individuals with a personal history of colorectal cancer who are under age 50 at diagnosis as well as for other Lynch-syndrome related cancers, including ovarian and pancreatic cancer (p. HRS-3). Test selection should include at a minimum selected genes associated with colorectal cancer risk but additional genes can be included based on a patient's personal and family history of cancer (p. HRS-A, 2 of 3).

National Society of Genetic Counselors (NSGC)

The National Society of Genetic Counselors released a position statement (Adopted 2017, reaffirmed 2020 and 2023) endorsing the use of multi-gene panels when clinically warranted and appropriately applied, stating the following:

"These tests can provide a comprehensive and efficient route to identifying the genetic causes of disease. Before ordering a multi-gene panel test, providers should thoroughly evaluate the analytic and clinical validity of the test, as well as its clinical utility. Additional factors to consider include, but are not limited to: clinical and family history information, gene content of the panel, limitations of the sequencing and informatics technologies, and variant interpretation and reporting practices.

Panels magnify the complexities of genetic testing and underscore the value of experts, such as genetic counselors, who can educate stakeholders about appropriate utilization of the technology to mitigate risks of patient harm and unnecessary costs to the healthcare system. NSGC supports straightforward and transparent pricing so that patients, providers, laboratories, and health plans can easily weigh the value of genetic testing in light of its cost."

American Society of Clinical Oncology (ASCO)

ASCO released guidelines in 2024 regarding appropriate use of multigene panel germline testing for individuals with cancer. As part of the guideline, they recommend germline genetic testing via a multigene panel for patients with cancer who have suspicion for more than one gene related to that cancer type (Table 4, p. 2605). Several genes are listed in Table 1 (p. 2603), which they recommend be included for specific populations of people with cancer (Table 4, p. 2605).

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Hereditary Breast and/or Ovarian Cancer Susceptibility Panels

National Comprehensive Cancer Network (NCCN)

The NCCN guidelines for Genetic/Familial High-Risk Assessment: Breast, Ovarian, Pancreatic, and Prostate Cancers (2.2025) outline clinical criteria for germline genetic testing of high-penetrance breast cancer genes. These guidelines include:

- 1) Personal history of breast cancer at 50 years of age or younger (p. CRIT-2).
- 2) Personal history of breast cancer at any age with specific features (p. CRIT-2):
 - Treatment indications
 - To aid in systemic treatment decisions using PARP inhibitors for metastatic

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- breast cancer
- To aid in adjuvant treatment decisions with olaparib for high-risk, HER2-negative breast cancer, including triple-negative breast cancer
- Pathology/histology
 - Triple-negative breast cancer
 - Multiple primary breast cancers (synchronous or metachronous)
 - Male breast cancer
 - Lobular breast cancer if there is also a personal/family history of diffuse gastric cancer
- Ashkenazi Jewish ancestry
- Family history of at least 1 close blood relative with:
 - Breast cancer at age 50 years or younger
 - Male breast cancer
 - Ovarian cancer
 - Pancreatic cancer
 - Prostate cancer with metastatic, or high- or very-high-risk group
 - 3 or more total diagnoses of breast cancer and/or prostate cancer in patient and/or close blood relatives on the same side of the family

3) Family history-based criteria (p. CRIT-2): Testing is also recommended in select unaffected individuals and those with a personal history that does not meet the above criteria. Qualifying scenarios include the presence of a first- or second-degree blood relative meeting any of the criteria listed above with the exception of relatives who meet criteria only for systemic therapy selection. If the affected relative has pancreatic cancer or prostate cancer, then only first-degree relatives should be offered testing unless indicated based on additional family history.

4) An affected or unaffected individual who otherwise does not meet the criteria above but has a probability of greater than 5% of a *BRCA1/2* pathogenic variant based on prior probability models (eg, Tyrer-Cuzick, BRCAPro, CanRisk) (p. CRIT-2).

These guidelines also recommend consideration of testing for patients with a personal history of breast cancer diagnosed at or before age 65, patients diagnosed with breast cancer at any age with ≥ 1 close blood relative with intermediate-risk prostate cancer with intraductal/criform histology, and for patients affected or unaffected with breast cancer who otherwise do not meet any of the above criteria but with a 2.5%–5% probability of *BRCA1/2* P/LP variant based on prior probability models (eg, Tyrer-Cuzick, BRCAPro, CanRisk) (p. CRIT-3).

The NCCN guidelines further recommend that patients with epithelial ovarian cancer be offered germline genetic testing for genes including *ATM*, *BRCA1*, *BRCA2*, *BRIP1*, *MLH1*, *MSH2*, *MSH6*, *EPCAM*, *PALB2*, *RAD51*, and *RAD51D* (p. CRIT-4). The guideline goes on to list non-epithelial ovarian cancers with a known genetic association, including Peutz-Jeghers (*STK11*), *DICER1*-related disease, and *SMARCA4* (p. CRIT-4).

American Society of Clinical Oncology/Society of Surgical Oncology

Guidelines published by ASCO/SSO (2024) recommend *BRCA1/2* testing to all newly diagnosed patients who are 65 years of age or younger at diagnosis (Type: Formal Consensus; Agreement 87.50%) (p. 590).

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Hereditary GI/Colon Cancer Susceptibility Panels

National Comprehensive Cancer Network (NCCN)

NCCN Genetic/Familial High-Risk Assessment: Colorectal, Endometrial, and Gastric guidelines (1.2025) outline criteria for assessment for hereditary colorectal syndromes as follows:

- Polyposis: Patient with a personal history of, or a single family member with, at least 10 adenomatous polyps, at least 2 hamartomatous polyps, or at least 5 serrated polyps/lesions proximal to the rectum (p. HRS-1)
- Individuals meeting LS testing criteria (p. HRS-1, HRS-3, LS-1) (see [MLH1, MSH2, MSH6, PMS2, EPCAM Sequencing and/or Deletion/Duplication Analysis](#)).

NCCN also states that the CRC-risk associated genes to include in germline multi-gene panel testing are as follows: *APC, BMPR1A, EPCAM, MUTYH, MLH1, MSH2, MSH6, PMS2, PTEN, SMAD4, STK11, and TP53* (p. HRS-A 2 of 3).

Some individuals will have variants of uncertain significance (VUS); post test counseling should include considering referral to research studies for the purpose of learning the functional impact of VUSs such as variant reclassification programs through clinical labs or registries (p. EVAL-A 8 of 9).

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Hereditary Gastric Cancer Susceptibility Panels

National Comprehensive Cancer Network (NCCN)

NCCN Gastric Cancer guidelines (2.2024) outline criteria for further genetic risk assessment for high-risk syndromes associated with gastric cancer, including: hereditary diffuse gastric cancer, Lynch syndrome, Juvenile Polyposis Syndrome, Peutz-Jeghers syndrome, and Familial Adenomatous Polyposis (p. GAST-D 3 of 8 and p. GAST-D 4 of 8).

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Hereditary Pancreatic Cancer Susceptibility Panels

National Comprehensive Cancer Network (NCCN)

NCCN Genetic/Familial High-Risk Assessment: Breast, Ovarian, and Pancreatic guidelines (2.2025) recommend genetic counseling and germline testing for all individuals diagnosed with exocrine pancreatic cancer, as well as individuals with a first-degree relative diagnosed with exocrine pancreatic cancer. These guidelines list the following genes as those that are typically tested for pancreatic cancer risks: *ATM, BRCA1, BRCA2, CDKN2A, MLH1, MSH2, MSH6, EPCAM, PALB2, STK11, TP53* (p. CRIT-5).

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Hereditary Polyposis Susceptibility Panels

National Comprehensive Cancer Network (NCCN)

The NCCN Genetic/Familial High-Risk Assessment: Colorectal guidelines (1.2025) outline recommendations for evaluating individuals with adenomatous polyposis (defined as 10 or more adenomas) (p. HRS-2). Germline multigene testing for all polyposis and colorectal cancer genes is recommended (p. POLYP-1).

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Hereditary Prostate Cancer Susceptibility Panels

National Comprehensive Cancer Network (NCCN)

NCCN Genetic/Familial High-Risk Assessment: Breast, Ovarian, Pancreatic, and Prostate guidelines (2.2025) recommend the following testing criteria for prostate cancer susceptibility genes:

Personal history of prostate cancer with specific clinical features: metastatic disease, high- or very-high risk group, or with 1 or more close relatives with:

- Breast cancer at age 50 years or younger
- Triple-negative breast cancer at any age
- Male breast cancer at any age
- Ovarian cancer any age
- Pancreatic cancer any age
- Metastatic, node positive, high- or very-high risk group at any age
- 3 or more close blood relatives with either breast or prostate cancer (any grade) on the same side of the family including the patient with prostate cancer
- Ashkenazi Jewish ancestry
- Another fulfilling criterion is an individual with or without prostate cancer affected (not meeting testing criteria listed above) with a first-degree blood relative meeting any of the criteria listed above (except unaffected individuals whose relatives meet criteria only for systemic therapy decision-making) (p. CRIT-6).

These guidelines also recommend consideration of testing for:

- An individual with a 2.5%–5% probability of BRCA1/2 P/LP variant based on prior probability models (eg, Tyrer-Cuzick, BRCAPro, CanRisk) (p. CRIT-3)
- Patients with intermediate risk prostate cancer with intraductal/criform histology (p. CRIT-6).

These guidelines also recommend consideration of RNA studies to further define the meaning of variants of unknown significance. Research studies designed to explore the functional impact of variants, such as variant reclassification programs through clinical labs or registries should be considered (p. EVAL-A, 9 of 11).

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Hereditary Neuroendocrine Cancer Susceptibility Panels

National Comprehensive Cancer Network (NCCN)

The NCCN Neuroendocrine and Adrenal Tumors Guideline (4.2024) states that multigene panel testing may be a more efficient and cost-effective solution for evaluating a patient for a hereditary endocrine cancer syndrome, as there is clinical overlap between several genetic conditions that predispose to endocrine neoplasms (p. NE-E 2 of 8).

The guidelines state that genetic testing for hereditary endocrine neoplasia syndromes is recommended for patients with:

- Adrenocortical carcinoma
- Paraganglioma/pheochromocytoma
- Parathyroid adenoma or primary hyperparathyroidism before age 30
- Multiple parathyroid adenomas

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- Multigland hyperplasia without obvious secondary cause
- Recurrent primary hyperparathyroidism
- Clinical suspicion for MEN2
- Clinical suspicion for MEN1.

NCCN also recommends consideration of testing for patients with:

- Gastrinoma
- Duodenal/pancreatic neuroendocrine tumor (p. NE-E, 3 of 8).

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BRCA1 or BRCA2 Targeted Variant or Known Familial Variant Analysis

National Comprehensive Cancer Network (NCCN)

The NCCN guidelines for Genetic/Familial High-Risk Assessment: Breast, Ovarian, Pancreatic, and Prostate (2.2025) states that testing for hereditary cancer susceptibility should be performed in the following situations:

- Individuals with any blood relative with a known pathogenic/likely pathogenic variant in a cancer susceptibility gene
- Individuals with a pathogenic/likely pathogenic (P/LP) variant identified on tumor genomic testing that would impact cancer risk if confirmed to be a germline variant (p.CRIT-1).

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BRCA1 and BRCA2 Targeted Variant Analysis - Ashkenazi Jewish Founder Variants

National Comprehensive Cancer Network (NCCN)

The NCCN guidelines for Genetic/Familial High-Risk Assessment: Breast, Ovarian, Pancreatic, and Prostate (2.2025) recommend consideration of testing for the three known Ashkenazi Jewish founder *BRCA1/2* mutations for individuals who are age 18 years or older and have at least one grandparent who is of Ashkenazi Jewish ancestry (p. CRIT-1 and p. CRIT-1A).

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PALB2 Targeted Variant Analysis

National Comprehensive Cancer Network (NCCN)

The NCCN Genetic/Familial High-Risk Assessment: Genetic/Familial High-Risk Assessment: Breast, Ovarian, Pancreatic, and Prostate guidelines (2.2025) states that testing for hereditary cancer susceptibility should be performed in the following situations:

- Individuals with any blood relative with a known pathogenic/likely pathogenic variant in a cancer susceptibility gene
- Individuals with a pathogenic/likely pathogenic (P/LP) variant identified on tumor genomic testing that would impact cancer risk if confirmed to be a germline variant (p. CRIT-1).

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ATM or CHEK2 Targeted Variant Analysis

National Comprehensive Cancer Network (NCCN)

The NCCN guidelines for Genetic/Familial High-Risk Assessment: Breast, Ovarian, Pancreatic, and Prostate (2.2025) state that testing for hereditary cancer susceptibility should be performed in the following situations:

- Individuals with any blood relative with a known pathogenic/likely pathogenic variant in a cancer susceptibility gene
- Individuals with a pathogenic/likely pathogenic (P/LP) variant identified on tumor genomic testing that would impact cancer risk if confirmed to be a germline variant (p. CRIT-1).

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ATM and/or CHEK2 Sequencing and/or Deletion/Duplication Analysis

National Comprehensive Cancer Network (NCCN)

While the NCCN Genetic/Familial High-Risk Assessment: Breast, Ovarian, Pancreatic, and Prostate guidelines (2.2025) do provide surveillance recommendations for individuals with germline *ATM* and *CHEK2* mutations (p. GENE-A 1 of 11 and p. GENE-A 4 of 10), these genes are not considered high-penetrance breast cancer susceptibility genes, and the guidelines do not include gene-specific clinical criteria for *ATM* and *CHEK2* as they do for the high-penetrance breast cancer susceptibility genes.

In order to help further clarify variants of unknown significance, NCCN recommends consideration of RNA studies as well as a clinical trials referral to help define the functional impact of variants (p. EVAL-A 9 of 10).

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MLH1, MSH2, MSH6, PMS2, or EPCAM Targeted Variant Analysis

National Comprehensive Cancer Network (NCCN)

NCCN Genetic/Familial High-Risk Assessment: Colorectal, Endometrial, and Gastric guidelines (1.2025) outline testing criteria for the evaluation of Lynch syndrome. If there is a known familial pathogenic variant in a Lynch syndrome gene (*MLH1*, *MSH2*, *MSH6*, *PMS2*, or *EPCAM*), genetic testing for the known variant is recommended (p. LS-1). Additionally, it is possible that pathogenic or likely pathogenic variants identified through tumor profiling could be of germline origin. Confirmatory germline testing is indicated for pathogenic/likely pathogenic variants identified via tumor profiling when there is a reasonable clinical suspicion of being of germline origin (p. EVAL-A 5 of 9).

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MLH1, MSH2, MSH6, PMS2, and/or EPCAM Sequencing and/or Deletion/Duplication Analysis

National Comprehensive Cancer Network (NCCN)

NCCN Genetic/Familial High-Risk Assessment: Colorectal, Endometrial, and Gastric guidelines

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(1.2025) outline testing criteria for the evaluation of Lynch syndrome. These criteria include:

- An individual with a Lynch-syndrome (LS)-related cancer (colorectal, endometrial, gastric, ovarian, pancreatic, urothelial, brain (usually glioblastoma), biliary tract, and small intestine, as well as sebaceous adenomas, sebaceous carcinomas, and keratoacanthomas) and any of the following: Diagnosed younger than 50 years; a synchronous or metachronous LS -related cancer regardless of age; 1 first-degree or second-degree relative with an LS-related cancer diagnosed younger than 50 years; or 2 or more first-degree or second-degree relatives with an LS-related cancer regardless of age
- Family history of any of the following: at least 1 first-degree relative with a colorectal or endometrial cancer diagnosed younger than 50 years; at least 1 first-degree relative with a colorectal or endometrial cancer and a synchronous or metachronous LS-related cancer regardless of age; 2 or more first-degree or second-degree relatives with LS-related cancers, one of whom was diagnosed before age 50; 3 or more first-degree or second-degree relatives with LS-related cancers regardless of age
- An individual with a 5% risk or greater of having an MMR gene pathogenic variant based on predictive models (i.e., PREMM5, MMRpro, MMRpredict)
- An individual with a personal history of CRC and/or endometrial cancer with a PREMM5 score of 2.5% or greater.

Some individuals will have variants of uncertain significance (VUS); post test counseling should include considering referral to research studies for the purpose of learning the functional impact of VUSs such as variant reclassification programs through clinical labs or registries (p. HRS-3 and EVAL-A 8 of 9).

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BAP1 Targeted Variant Analysis

National Comprehensive Cancer Network (NCCN)

NCCN guidelines for Kidney Cancer (3.2025) include *BAP1* tumor predisposition syndrome in their overview of hereditary renal cell carcinoma syndromes, and recommend testing for an individual with a close blood relative with a known pathogenic/likely pathogenic variant in a cancer susceptibility gene (p. HERED-RCC-1 and HERED-RCC-2).

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BAP1 Sequencing and/or Deletion/Duplication Analysis

National Comprehensive Cancer Network (NCCN)

NCCN guidelines for Cutaneous Melanoma (1.2025) state that individuals with germline mutations in several genes, including *BAP1*, are at risk to develop single or multiple primary melanomas (p. ME-A 1 of 2).

NCCN guidelines for Uveal Melanoma (1.2024) include germline *BAP1* mutations as a risk factor for developing uveal melanoma (p. UM-A 1 of 2).

NCCN guidelines for Malignant Pleural Mesothelioma (2.2025) state that approximately 12-16% of patients with pleural or peritoneal mesothelioma have a germline mutation, including in *BAP1* (p. PM-A 5 of 8).

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NCCN guidelines for Kidney Cancer (3.2025) include *BAP1* tumor predisposition syndrome in their overview of hereditary renal cell carcinoma syndromes (p. HERED-RCC-2).

GeneReviews: BAP1 Tumor Predisposition Syndrome (BAP1-TPDS)

GeneReviews is an expert-authored review of current literature on a genetic disease, and goes through a rigorous editing and peer review process before being published online. The clinical description and testing indications for *BAP1* Tumor Predisposition syndrome are as follows:

BAP1-TPDS should be suspected in an individual who has EITHER of the following:

- Two or more confirmed BAP1-TPDS tumors*
- One BAP1-TPDS tumor and a first- or second-degree relative with a confirmed BAP1-TPDS tumor*

*Excluding two basal cell cancers and/or cutaneous melanomas, given their high frequency in the general population

In addition to *BAP1*-inactivated melanocytic tumors, uveal melanoma, malignant mesothelioma, cutaneous melanoma, renal cell carcinoma, and basal cell carcinoma, individuals with germline mutations in *BAP1* may have an increased risk for hepatocellular carcinoma, cholangiocarcinoma, and meningioma.

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FLCN Targeted Variant Analysis

National Comprehensive Cancer Network (NCCN)

NCCN guidelines for Kidney Cancer (3.2025) includes Birt-Hogg-Dube syndrome in their overview of hereditary renal cell carcinoma syndromes, and recommend testing for an individual with a close blood relative with a known pathogenic/likely pathogenic variant in a cancer predisposition gene (p. HERED-RCC-1 and HERED-RCC-2).

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FLCN Sequencing and/or Deletion/Duplication Analysis

National Comprehensive Cancer Network (NCCN)

NCCN guidelines for Kidney Cancer (3.2025) include Birt-Hogg-Dube syndrome in their overview of hereditary renal cell carcinoma syndromes. Commonly seen histologies include chromophobe, hybrid oncocytic tumors, clear cell, oncocytomas, angiomyolipomas, and papillary RCC (p. HERED-RCC-2).

GeneReviews: Birt-Hogg-Dube Syndrome (BHDS)

GeneReviews is an expert-authored review of current literature on a genetic disease, and goes through a rigorous editing and peer review process before being published online. The clinical description and testing indications for Birt-Hogg-Dube syndrome (BHDS) are as follows:

BHDS should be suspected in individuals with any of the following major or minor criteria.

Major criteria

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- Five or more fibrofolliculomas/trichodiscomas with at least one confirmed histologically
- Identification of a heterozygous pathogenic variant in *FLCN*

Minor criteria

- Multiple lung cysts. Bilateral basally located lung cysts with no other apparent cause, with or without spontaneous primary pneumothorax
- Early-onset renal cancer (age <50 years)
- Multifocal or bilateral renal cancer
- Renal cancer of mixed chromophobe and oncocytic histology
- First-degree relative with BHDS

The diagnosis of BHDS is established in a proband with:

- One major criteria (Note: Identification of a heterozygous pathogenic variant in *FLCN* is one of the major criteria); **OR**
- Two minor criteria

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***PTEN* Targeted Variant Analysis**

National Comprehensive Cancer Network (NCCN)

The NCCN Genetic/Familial High-Risk Assessment: Breast, Ovarian, and Pancreatic guidelines (2.2025) states that testing should be performed in the following situations:

- Individuals with any blood relative with a known pathogenic/likely pathogenic variant in a cancer susceptibility gene
- Individuals with a pathogenic/likely pathogenic (P/LP) variant identified on tumor genomic testing that has clinical implications if also identified in the germline (p. CRIT-1).

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***PTEN* Sequencing and/or Deletion/Duplication Analysis**

National Comprehensive Cancer Network (NCCN)

NCCN Genetic/Familial High-Risk Assessment: Breast, Ovarian, and Pancreatic guidelines (1.2025) outline clinical criteria for the genetic testing for Cowden syndrome (CS)/*PTEN* hamartoma tumor syndrome (PHTS) These include:

- Individual from a family with a known *PTEN* pathogenic or likely pathogenic variant
- Individual with a personal history of Bannayan-Riley-Ruvalcaba syndrome (BRRS)
- Individual meeting clinical diagnostic criteria* for CS/PHTS [Cowden syndrome/*PTEN* hamartoma tumor syndrome]
- Individual not meeting clinical diagnostic criteria for CS/PHTS with a personal history of: Adult Lhermitte-Duclos disease (cerebellar tumors); Autism spectrum disorder and macrocephaly; Two or more biopsy-proven trichilemmomas; Two or more major criteria (one must be macrocephaly); Three major criteria, without macrocephaly; One major

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- and 3 or more minor criteria; 4 or more minor criteria
- At-risk individual with a relative with a clinical diagnosis of CS/PHTS or BRRS for whom testing has not been performed. The at-risk individual must have the following: Any one major criterion or two minor criteria (p. CRIT-8 and CRIT-8A).

*These NCCN guidelines also include Revised Clinical Diagnostic Criteria for PTEN Hamartoma Tumor Syndrome. This includes an operational diagnosis in an individual with either of the following:

1. Three or more major criteria, but one must include macrocephaly, Lhermitte-Duclos disease, or GI hamartomas; or
2. Two major and three minor criteria (p. CRIT-8A).

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APC or *MUTYH* Targeted Variant Analysis

National Comprehensive Cancer Network (NCCN)

NCCN Genetic/Familial High-Risk Assessment: Colorectal guidelines (1.2025) outline clinical criteria for the genetic testing, which includes a known pathogenic variant in an adenomatous polyposis gene in the family (p. POLYP-1). and recommend targeted APC or *MUTYH* gene testing when the familial pathogenic variant is known (p. FAP-2, MAP-1).

Additionally, it is possible that pathogenic or likely pathogenic variants identified through tumor profiling could be of germline origin. Confirmatory germline testing is indicated for pathogenic/likely pathogenic variants identified via tumor profiling when there is a reasonable clinical suspicion of being of germline origin (p. HRS-B, 5 of 9).

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APC and/or *MUTYH* Sequencing and/or Deletion/Duplication Analysis

National Comprehensive Cancer Network (NCCN)

NCCN Genetic/Familial High-Risk Assessment: Colorectal guidelines (1.2025) outline Adenomatous Polyposis testing criteria. These include: Personal history of greater than or equal to 20 cumulative adenomas, or multifocal/bilateral congenital hypertrophy of retinal pigment epithelium (CHRPE). NCCN recommends consideration of testing when there is a personal history of 10 or more cumulative adenomas, desmoid tumor, hepatoblastoma, cribriform-morular variant of papillary thyroid cancer, and unilateral CHRPE (p. POLYP-1). For *MUTYH*-Associated polyposis specifically, NCCN lists additional common features including duodenal cancer and duodenal adenomas (p. MAP-1).

The guidelines also note that biallelic *MUTYH* mutations have also been implicated in rare cases of serrated polyposis syndrome (defined as 5 or more serrated polyps proximal to the rectum all being 5mm or larger with 2 or more being 10 or more mm in size, or more than 20 serrated polyps of any size distributed throughout the colon, with 5 or more being proximal to the rectum) (p. SPS-1).

Some individuals will have variants of uncertain significance (VUS); post test counseling should include considering referral to research studies for the purpose of learning the functional impact of VUSs such as variant reclassification programs through clinical labs or registries (p. EVAL-A,

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American Society of Clinical Oncology (ASCO)

ASCO released guidelines in 2024 regarding appropriate use of multigene panel germline testing for individuals with cancer. As part of the guideline, they recommend germline genetic testing via a multigene panel for patients with cancer who have suspicion for more than one gene related to that cancer type (Table 4, p. 2605). Several genes are listed in Table 1 (p. 2603). ASCO recognizes that it may be appropriate not to include all polyposis syndrome-related genes in testing if the patient's personal and/or family history is not consistent with the phenotype.

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CDKN2A Targeted Variant Analysis

The NCCN Genetic/Familial High-Risk Assessment: Breast, Ovarian, and Pancreatic guidelines (2.2025) state that testing for hereditary cancer susceptibility should be performed in the following situations:

- Individuals with any blood relative with a known pathogenic/likely pathogenic variant in a cancer susceptibility gene
- Individuals with a pathogenic/likely pathogenic (P/LP) variant identified on tumor genomic testing that would impact cancer risk if confirmed to be a germline variant (p.CRIT-1).

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CDKN2A Sequencing and/or Deletion/Duplication Analysis

National Comprehensive Cancer Network (NCCN)

NCCN Cutaneous Melanoma guidelines (1.2025) recommend consideration of a genetic counseling referral for *p16/CDKN2A* mutation testing (and possibly other genes) when a patient has 3 or more invasive cutaneous melanomas, or a personal or family history of invasive melanoma, pancreatic cancer, and/or astrocytoma diagnoses (p. ME-12).

NCCN Genetic/Familial High-Risk Assessment: Breast, Ovarian, and Pancreatic guidelines (1.2025) recognize CDKN2A as a pancreatic cancer susceptibility gene; testing is recommended in an individual with exocrine pancreatic cancer or a first degree relative with exocrine pancreatic cancer (p. CRIT-5).

American Academy of Dermatology

Guidelines published in 2018 by the American Academy of Dermatology (Swetter, et al) recommend genetic risk assessment for patients with cutaneous melanoma who have two or more relatives with cutaneous melanoma and/or pancreatic cancer, especially when a first degree relative is involved (p. 237).

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CDH1 Targeted Variant Analysis

National Comprehensive Cancer Network (NCCN)

NCCN Gastric Cancer guidelines (2.2024) outline criteria for further risk assessment for high risk gastric cancer syndromes, which recommend risk evaluation when there is a known mutation in a gastric cancer susceptibility gene in a close relative (p. GAST-D 1 of 8).

The NCCN Genetic/Familial High-Risk Assessment: Breast, Ovarian, and Pancreatic guidelines (1.2025) state that testing for hereditary cancer susceptibility should be performed in the following situations:

- Individuals with any blood relative with a known pathogenic/likely pathogenic variant in a cancer susceptibility gene
- Individuals with a pathogenic/likely pathogenic (P/LP) variant identified on tumor genomic testing that would impact cancer risk if confirmed to be a germline variant (p. CRIT-1).

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CDH1 Sequencing and/or Deletion/Duplication Analysis

National Comprehensive Cancer Network (NCCN)

NCCN Gastric Cancer guidelines (2.2024) outline testing criteria for germline *CDH1* testing which incorporates both personal and family history of gastric cancer and lobular breast cancer. These include:

- Two gastric cancer cases in a family, one confirmed diffuse gastric cancer (DGC) regardless of age
- DGC diagnosed before age 50 years without a family history
- Personal or family history of DGC and lobular breast cancer, one diagnosed before age 70 years
- Two cases of lobular breast cancer in family members before 50 years of age
- DGC at any age in individuals of Māori ethnicity, or with a personal or family history of cleft lip/cleft palate
- Bilateral lobular breast cancer before age 70 years (p. GAST-D 3 of 8).

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SMAD4 or BMPR1A Targeted Variant Analysis

National Comprehensive Cancer Network (NCCN)

NCCN Genetic/Familial High-Risk Assessment: Colorectal guidelines (1.2025) outline clinical criteria for genetic testing for Juvenile Polyposis syndrome. Testing is recommended when there is a known *BMPR1A* or *SMAD4* pathogenic variant in the family (p. JPS-1).

Additionally, it is possible that pathogenic or likely pathogenic variants identified through tumor profiling could be of germline origin. Confirmatory germline testing is indicated for pathogenic/likely pathogenic variants identified via tumor profiling when there is a reasonable clinical suspicion of being of germline origin (p. HRS-B, 5 of 9).

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SMAD4 and/or BMPR1A Sequencing and/or Deletion/Duplication Analysis

National Comprehensive Cancer Network (NCCN)

NCCN Genetic/Familial High-Risk Assessment: Colorectal guidelines (1.2025) outline clinical criteria for genetic testing for juvenile polyposis syndrome (JPS) in individuals with a personal and/or family history suggestive of JPS. Genetic testing is recommended when criteria are met or when there is a family history of JPS.

These criteria include 5 or more colonic juvenile polyps, multiple juvenile polyps throughout the gastrointestinal tract, and any number of juvenile polyps in someone with a family history of JPS (p. JPS-1).

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FH Targeted Variant Analysis

National Comprehensive Cancer Network (NCCN)

NCCN guidelines for Kidney Cancer (3.2025) include hereditary leiomyomatosis and renal cell carcinoma (HLRCC) in their overview of hereditary renal cell carcinoma syndromes, and state that testing is indicated for an individual with a close blood relative with a known pathogenic/likely pathogenic variant in a cancer predisposition gene (p. HERED-RCC-1 and HERED-RCC-2).

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FH Sequencing and/or Deletion/Duplication Analysis

National Comprehensive Cancer Network (NCCN)

NCCN guidelines for Kidney Cancer (3.2025) outline criteria for further genetic risk evaluation for hereditary renal cell carcinoma syndromes, including HLRCC-associated renal cell carcinoma. Testing is recommended for an individual whose tumor is HLRCC-associated renal cell carcinoma, FH deficient renal cell carcinoma, or has other histologic features of HLRCC (p. HERED-RCC-1).

GeneReviews: FH Tumor Predisposition Syndrome

GeneReviews is an expert-authored review of current literature on a genetic disease, and goes through a rigorous editing and peer review process before being published online. The recommended testing for FH tumor predisposition syndrome (HLRCC) is as follows:

FH tumor predisposition syndrome should be suspected in individuals with the following features:

Cutaneous leiomyomata (~50%):

- Skin-colored to light brown/reddish papules or nodules distributed over the trunk, extremities, and occasionally on the face and neck
- May be single, grouped/clustered, segmental, or disseminated

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- Histopathology shows bundles of smooth muscle fibers with central, long blunt-edged nuclei.

Uterine leiomyomata (uterine fibroids) (~90% of females):

- Fibroids tend to be numerous and large
- Fibroids often demonstrate loss of FH staining and positive cytoplasmic staining for S-(2-succino) cysteine.

Renal tumors (~15%) are usually solitary, highly aggressive renal cell carcinoma (RCC) that metastasizes early.

The spectrum of renal tumors includes type 2 papillary, undefined papillary, unclassified, tubulocystic, and collecting-duct carcinoma.

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TP53 Targeted Variant Analysis

National Comprehensive Cancer Network (NCCN)

The NCCN Genetic/Familial High-Risk Assessment: Breast, Ovarian, and Pancreatic guidelines (2.2025) states that testing for hereditary cancer susceptibility should be performed in the following situations:

- Individuals with any blood relative with a known pathogenic/likely pathogenic variant in a cancer susceptibility gene
- Individuals with a pathogenic/likely pathogenic (P/LP) variant identified on tumor genomic testing that would impact cancer risk if confirmed to be a germline variant (p. CRIT-1).

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TP53 Sequencing and/or Deletion/Duplication Analysis

National Comprehensive Cancer Network (NCCN)

NCCN Genetic/Familial High-Risk Assessment: Breast, Ovarian, and Pancreatic guidelines (2.2025) outline clinical testing criteria for the genetic testing for Li-Fraumeni syndrome. This includes classic Li-Fraumeni syndrome criteria and Chompret criteria and considerations for family history:

Classic Li-Fraumeni syndrome (LFS) criteria:

- Combination of an individual diagnosed at age younger than 45 years with a sarcoma **AND**
- A first-degree relative diagnosed at age younger than 45 years with cancer **AND**
- An additional first- or second-degree relative in the same lineage with cancer diagnosed at age younger than 45 years, or a sarcoma at any age.

Chompret criteria:

- Individual with a tumor from LFS tumor spectrum (e.g., soft tissue sarcoma,

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osteosarcoma, CNS tumor, breast cancer, adrenocortical carcinoma), before 46 years of age, **AND**

- At least one first- or second-degree relative with any of the aforementioned cancers (other than breast cancer if the proband has breast cancer) before the age of 56 years or with multiple primaries at any age, **OR**
- Individual with multiple tumors (except multiple breast tumors), two of which belong to LFS tumor spectrum with the initial cancer occurring before the age of 46 years, **OR**
- Individual with adrenocortical carcinoma, or choroid plexus carcinoma or rhabdomyosarcoma of embryonal anaplastic subtype, at any age of onset, regardless of family history, **OR**
- Breast cancer before 31 years of age.

Personal/Family history criteria:

- Personal or family history of pediatric hypodiploid acute lymphoblastic leukemia.

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MEN1 Targeted Variant Analysis

National Comprehensive Cancer Network (NCCN)

NCCN Neuroendocrine and Adrenal Tumors guidelines (4.2024) recommend that targeted genetic testing for *MEN1* be performed for individuals with a close blood relative with a known pathogenic variant/likely pathogenic variant in a cancer susceptibility gene (p. NE-E 3 of 8).

Additionally, NCCN recommends genetic risk evaluation and genetic testing for Hereditary Endocrine Neoplasia Syndromes when a mutation is identified on tumor genomic testing that has clinical implications if also identified in the germline (p. NE-E 3 of 8).

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MEN1 Sequencing and/or Deletion/Duplication Analysis

National Comprehensive Cancer Network (NCCN)

NCCN Neuroendocrine and Adrenal Tumors guidelines (4.2024) recommend that patients with two or more of the following, or one AND a family history of one or more of the following, be evaluated for *MEN1* germline mutations:

- Foregut carcinoid (bronchial, thymic, or gastric)
- Pituitary adenoma
- Duodenal or pancreatic neuroendocrine tumor
- Primary hyperparathyroidism (p. NE-E 3 of 8).

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RET Targeted Variant Analysis

National Comprehensive Cancer Network (NCCN)

NCCN Neuroendocrine and Adrenal Tumors guidelines (4.2024) recommend that targeted genetic testing for *MEN2* be performed for individuals with a close blood relative with a known

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pathogenic variant/likely pathogenic variant in a cancer susceptibility gene (p. NE-E 3 of 8).

Additionally, NCCN states that testing is recommended when a mutation is identified on tumor genomic testing that has clinical implications if also identified in the germline (p. NE-E 3 of 8).

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RET Sequencing and/or Deletion/Duplication Analysis

GeneReviews: Multiple Endocrine Neoplasia Type 2

GeneReviews is an expert-authored review of current literature on a genetic disease, and goes through a rigorous editing and peer review process before being published online. The clinical description and testing indications for multiple endocrine neoplasia type 2 are as follows:

Multiple endocrine neoplasia type 2A (MEN2A) should be suspected in any individual with medullary thyroid carcinoma, pheochromocytoma (usually adrenal) or parathyroid adenoma/hyperplasia. Familial Medullary Thyroid Carcinoma should be suspected in families with more than one individual diagnosed with MTC in the absence of pheochromocytoma or parathyroid adenoma/hyperplasia. Multiple endocrine neoplasia type 2B (MEN2B) should be suspected in individuals with distinctive facies including lip mucosal neuromas resulting in thick vermilion of the upper and lower lip, mucosal neuromas of the lips and tongue, medullated corneal nerve fibers, marfanoid habitus, and MTC.

National Comprehensive Cancer Network (NCCN)

NCCN Neuroendocrine and Adrenal Tumors guidelines (4.2024) also recommends MEN2 testing when there is clinical suspicion of MEN2 due to the presence of medullary thyroid cancer or other combination of MEN2-related features. Genetic testing is recommended for a first degree relative meeting this criteria, where the relative is not available for testing (p. NE-E 3 of 8).

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PTCH1 or SUFU Targeted Variant Analysis

GeneReviews: Nevoid Basal Cell Carcinoma Syndrome

GeneReviews is an expert-authored review of current literature on a genetic disease, and goes through a rigorous editing and peer review process before being published online.

GeneReviews states that it is appropriate to evaluate apparently asymptomatic older and younger at-risk relatives (including children) of an affected individual in order to identify as early as possible those who would benefit from surveillance for complications of NBCCS (most notably medulloblastoma in children and jaw cysts and BCCs in adults) and avoidance of x-rays and sun exposure. Evaluations can include molecular genetic testing if the pathogenic variant in the family is known.

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PTCH1 and/or SUFU Sequencing and/or Deletion/Duplication Analysis

GeneReviews: Nevoid Basal Cell Carcinoma Syndrome

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GeneReviews is an expert-authored review of current literature on a genetic disease, and goes through a rigorous editing and peer review process before being published online.

Nevoid basal cell carcinoma syndrome (NBCCS) should be suspected in individuals with the following findings, which constitute major or minor diagnostic criteria. The diagnosis of NBCCS is established in a proband with either:

- Two major diagnostic criteria and one minor diagnostic criterion, or
- One major and three minor diagnostic criteria

Major criteria

- Lamellar (sheet-like) calcification of the falx or clear evidence of calcification in an individual younger than age 20 years. Falx calcification is nearly always present and is visible on anteroposterior (AP) x-rays of the skull after age 20 years (see Notes regarding radiographs)
- Jaw keratocyst. Odontogenic keratocyst histologically; seen on orthopantomogram as an area of translucency
- Palmar/plantar pits (at least 2); particularly useful in diagnosis and more pronounced when the hands and feet are soaked in warm water for up to ten minutes. Pits may appear as white "punched-out" or pink "pin-prick" lesions
- Multiple basal cell carcinomas (BCCs) (more than 5 in a lifetime) or a BCC before age 30 years. Provision needs to be made for decreased risk of BCC in individuals with dark skin and increased risk in those with light skin living in hot sunny climates, particularly those with type 1 Celtic skin and red hair, and of this group, particularly those with the common *MC1R* variant (rs1805007), which can modify age of onset for NBCCS
- First-degree relative with NBCCS.

Minor criteria

- Childhood medulloblastoma (also called primitive neuroectodermal tumor)
- Lympho-mesenteric or pleural cysts
- Macrocephaly (OFC greater than 97th centile)
- Cleft lip/palate
- Vertebral/rib anomalies observed on chest x-ray and/or spinal x-ray: bifid/splayed/extra ribs; bifid vertebrae
- Preaxial or postaxial polydactyly
- Ovarian/cardiac fibromas
- Ocular anomalies (e.g., cataract, developmental defects, and pigmentary changes of the retinal epithelium).

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MAX, SDHA, SDHAF2, SDHB, SDHC, SDHD, or TMEM127 Targeted Variant Analysis

National Comprehensive Cancer Network (NCCN)

NCCN guidelines for Kidney Cancer (3.2025) include Hereditary paraganglioma/pheochromocytoma (PGL/PCC) syndrome in their overview of hereditary renal cell carcinoma syndromes. Genetic testing is recommended for an individual with a close blood

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relative with a known pathogenic/likely pathogenic variant in a cancer susceptibility gene (p. HERED-RCC-1 and HERED-RCC-2).

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MAX, SDHA, SDHAF2, SDHB, SDHC, SDHD, and/or TMEM127 Sequencing and/or Deletion/Duplication Analysis

National Comprehensive Cancer Network (NCCN)

NCCN guidelines for Neuroendocrine and Adrenal Tumors (4.2024) recommend genetic testing for hereditary endocrine neoplasia syndromes such as Hereditary Paranglioma/Pheochromocytoma Syndrome for patients with either a paraganglioma or pheochromocytoma or with a first degree relative with either of these tumors who is unavailable for testing (p. NE-E, 3 of 8). Other manifestations of this syndrome include gastrointestinal stromal tumor and renal cell cancer (p. NE-E, 4 of 8).

GeneReviews: Hereditary Paranglioma-Pheochromocytoma Syndromes

GeneReviews is an expert-authored review of current literature on a genetic disease, and goes through a rigorous editing and peer review process before being published online. The clinical description and testing indications for hereditary paranglioma-pheochromocytoma syndromes are as follows:

Hereditary paraganglioma-pheochromocytoma (PGL/PCC) syndromes should be suspected in any individual with a paraganglioma or pheochromocytoma. Other tumors associated with these conditions are gastrointestinal stromal tumors (GIST) and renal clear cell carcinoma. In addition, individuals with a family history of paraganglioma or pheochromocytoma should also be suspected to have hereditary paraganglioma-pheochromocytoma syndromes.

The diagnosis of hereditary PGL/PCC should be strongly suspected in an individual with multiple, multifocal, recurrent, or early-onset paraganglioma or pheochromocytoma and/or a family history of paraganglioma or pheochromocytoma.

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STK11 Targeted Variant Analysis

National Comprehensive Cancer Network (NCCN)

NCCN Genetic/Familial High-Risk Assessment: Colorectal guidelines (1.2025) outline testing criteria for the evaluation of Peutz-Jeghers Syndrome (PJS) and recommend clinical genetic testing when there is a family history of confirmed PJS. NCCN states that pathogenic mutations in *STK11* cause the majority of PJS cases (p. PJS-1).

Additionally, it is possible that pathogenic or likely pathogenic variants identified through tumor profiling could be of germline origin. Confirmatory germline testing is indicated for pathogenic/likely pathogenic variants identified via tumor profiling when there is a reasonable clinical suspicion of being of germline origin (p. HRS-B, 5 of 9).

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STK11 Sequencing and/or Deletion/Duplication Analysis

National Comprehensive Cancer Network (NCCN)

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NCCN Genetic/Familial High-Risk Assessment: Colorectal guidelines (1.2025) outline clinical criteria for PJS genetic testing in individuals with a personal and/or family history suggestive of PJS, as a majority of cases occur due to pathogenic variants in the *STK11* (*LKB1*) gene. These criteria include: two or more PJS-type hamartomas in the GI tract, hyperpigmentation in mucocutaneous membranes (such as the mouth, lips, nose, eyes, genitals, or fingers) and a family history of PJS (p. PJS-1).

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RB1 Targeted Variant Analysis

American Association of Ophthalmic Oncologists and Pathologists (AAOOP)

The AAOOP with support of the American Association for Pediatric Ophthalmology and Strabismus and the American Academy of Pediatrics (AAP) developed expert consensus guidelines for children at risk for development of retinoblastoma (2018). These guidelines indicate that identification of a germline mutation in RB1 in a patient with retinoblastoma should lead to testing relatives for the familial mutation to determine whether ophthalmic screening is required. In addition, identification of RB1 mutation in the tumor, followed by blood testing for the mutation, allows for recommendations for screening and genetic testing for family members (p. 455).

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RB1 Sequencing and/or Deletion/Duplication Analysis

American Association of Ophthalmic Oncologists and Pathologists (AAOOP)

The AAOOP with support of the American Association for Pediatric Ophthalmology and Strabismus and the American Academy of Pediatrics (AAP) developed expert consensus guidelines for children at risk for development of retinoblastoma (2018). The guidelines included the following recommendations:

Genetic counseling and testing clarify the risk for retinoblastoma in children with a family history of the disease and improve outcomes at reduced cost, justifying making testing available to all patients with a personal or family history of retinoblastoma. Genetic evaluation should be initiated whether the affected relative demonstrated unilateral or bilateral disease because both have a substantial risk of being heritable (grade C) (p. 456).

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VHL Targeted Variant Analysis

National Comprehensive Cancer Network (NCCN)

NCCN guidelines for Kidney Cancer (3.2025) include von Hippel-Lindau (VHL) syndrome in their overview of hereditary renal cell carcinoma syndromes, and state that this testing is indicated for an individual with a close blood relative with a known pathogenic/likely pathogenic variant in a cancer susceptibility gene (p. HERED-RCC-1 and HERED-RCC-2).

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VHL Sequencing and/or Deletion/Duplication Analysis

National Comprehensive Cancer Network (NCCN)

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NCCN Kidney Cancer guidelines (3.2025) outline clinical features seen in Von Hippel-Lindau syndrome including: hemangioblastomas (in the retina, spine, or brain), clear cell RCC (diagnosed before age 40 years or multiple/bilateral RCC diagnosed at any age), pheochromocytomas, paragangliomas (in the abdomen, thorax, or neck), retinal angiomas, endolymphatic sac tumors, epididymal or broad ligament papillary cystadenomas, multiple pancreatic serous cystadenomas, pancreatic neuroendocrine tumors, or multiple cysts in the pancreas. While these clinical features are categorized within the categories “major” and “minor,” the NCCN guidelines do not provide a scoring system required for patients to meet testing criteria (p. HERED-RCC-A).

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DEFINITIONS

1. **Adenomatous polyposis** are conditions that cause multiple adenomas (i.e., benign polyps) in the gastrointestinal tract.
2. **Breast cancer** is a term that applies to patients with invasive cancer or ductal carcinoma in situ (DCIS).
3. **Close relatives** include first, second, and third degree blood relatives:
 - a. **First-degree relatives** are parents, siblings, and children
 - b. **Second-degree relatives** are grandparents, aunts, uncles, nieces, nephews, grandchildren, and half siblings
 - c. **Third-degree relatives** are great grandparents, great aunts, great uncles, great grandchildren, and first cousins
4. **High-risk breast cancer for olaparib therapy** is defined as
 - a. Triple negative breast cancer treated with either:
 - i. Adjuvant chemotherapy with axillary node-positive disease or an invasive primary tumor greater than or equal to 2 cm on pathology analysis, **OR**
 - ii. Neoadjuvant chemotherapy with residual invasive breast cancer in the breast or resected lymph nodes, **OR**
 - b. Hormone receptor positive disease treated with either:
 - i. Adjuvant chemotherapy with four or more positive pathologically confirmed lymph nodes, **OR**
 - ii. Neoadjuvant chemotherapy which did not have a complete pathologic response, with a CPS+CG score [pre-treatment clinical (CS) and post-treatment pathological stage (PS), estrogen-receptor status (E) and grade (G)] of 3 or higher.

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5. **High-risk prostate cancer** is defined by the NCCN Prostate Cancer Guidelines (1.2025) as an individual who has one or more of the following high-risk features, but does not meet criteria for very-high-risk prostate cancer.
 - a. cT3-cT4a
 - b. Grade Group 4
 - c. PSA > 20ng/ml
6. **Juvenile polyps** are associated with Juvenile Polyposis Syndrome. These polyps are exophytic and eroded. They typically contain the following: marked edema and inflammation within the lamina propria, cystic glands filled with thick mucin, and some degree of smooth muscle proliferation.
7. **Lynch syndrome-related cancer** is defined as any of the following cancer types: colorectal, endometrial, gastric, ovarian, pancreatic, ureter and renal pelvic, brain (usually glioblastoma), biliary tract, small intestinal, sebaceous adenoma, sebaceous carcinoma, or keratoacanthoma.
8. **Maori ancestry** describes individuals who are of indigenous New Zealand ethnic background.
9. **Very-high-risk prostate cancer** is defined by NCCN Prostate Cancer Guidelines (1.2025) as an individual who has at least two of the following:
 - a. cT3-cT4
 - b. PSA >40 ng/mL
 - c. Grade Group 4 or 5

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Note: The Health Plan uses the genetic testing clinical criteria developed by Concert Genetics, an industry-leader in genetic testing technology assessment and policy development.

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