Genetic Testing for Hereditary Cancer

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Instructions for Use

Table of Contents Page

Commercial Policy
• Genetic Testing for Hereditary Cancer

Medicare Advantage Coverage Summaries
• Genetic Testing • Laboratory Tests and Services

Application

This Medical Policy does not apply to the states listed below; refer to the state-specific policy/guideline, if noted:

State	Policy/Guideline
Indiana	None
Kentucky	Genetic Testing for Hereditary Cancer (for Kentucky Only)
Louisiana	Genetic Testing for Hereditary Cancer (for Louisiana Only)
Nebraska	None
New Jersey	Genetic Testing for Hereditary Cancer (for New Jersey Only)
Tennessee	Genetic Testing for Hereditary Cancer (for Tennessee Only)

Coverage Rationale

Genetic counseling is strongly recommended prior to these tests in order to inform persons being tested about the advantages and limitations of the test as applied to a unique person.

Hereditary Breast and Ovarian Cancer (*BRCA1/BRCA2*)

Genetic testing for *BRCA1* and *BRCA2* for individuals *with* a personal history of a BRCA-Related Cancer is proven and medically necessary in the following situations:

- A known *BRCA1/BRCA2* mutation in a Close Blood Relative; or
- At least one first- or second-degree relative with a BRCA-Related Cancer; or
- Ashkenazi Jewish ancestry; or
- An unknown or Limited Family History
- A *BRCA 1/2* pathogenic mutation detected in tumor tissue; or
- A personal history of pancreatic cancer; or
- Men with a personal history of Breast Cancer; or

- Men with a personal history of metastatic prostate cancer; or
- Women with a personal history of Ovarian Cancer; or
- Women with a personal history of Breast Cancer in any of the following situations:
  - Metastatic Breast Cancer; or
  - Breast Cancer diagnosed at age 45 or younger; or
  - An additional Breast Cancer primary (prior diagnosis or bilateral cancer); or
  - Triple-Negative Breast Cancer diagnosed at age 60 or younger
- Individual has a Tyrer-Cuzick, BRCAPro or Penn11 Score of 2.5% or greater for a *BRCA1/2* pathogenic variant

Genetic testing for *BRCA1* and *BRCA2* for individuals *without* a personal history of a related cancer is proven and medically necessary in the following situations:
- A known *BRCA1*/*BRCA2* mutation in a Close Blood Relative; or
- At least one first- or second-degree relative with a BRCA-Related Cancer; or
- Ashkenazi Jewish ancestry and at least one Close Blood Relative with a BRCA-Related Cancer; or
- Individual has a Tyrer-Cuzick, BRCAPro or Penn11 Score of 5% or greater for a *BRCA1/2* pathogenic variant

Genetic testing for *BRCA1* and/or *BRCA2* is unproven and not medically necessary for all other indications including:
- Screening for cancer risk for individuals not listed in the proven indications above; or
- Risk assessment of other cancers; or
- Confirmation of direct to consumer genetic testing without meeting any of the proven indications above

Multi-Gene Hereditary Cancer Panel Testing Criteria

Genetic testing with a Multi-Gene hereditary cancer Panel in individuals *with* a personal history of cancer is proven and medically necessary if all of the following criteria are met:
- The suspected hereditary cancer syndromes can be diagnosed by testing of two or more genes included in the specific hereditary cancer panel; and
- At least one of the following:
  - A personal history of at least two different cancers (e.g., Breast and Ovarian); or
  - A personal history of BRCA-related cancer diagnosed at age 40 or younger; or
  - A personal history of BRCA-related cancer and at least one Close Blood Relative with a cancer associated with Lynch Syndrome; or
  - At least one Close Blood Relative diagnosed with a BRCA-Related Cancer at age 40 or younger; or
  - At least three Close Blood Relatives, on the same side of the family, diagnosed with any cancer; or
  - A personal history of cancer associated with Lynch Syndrome; or
  - A personal history of cancer where tumor testing results demonstrate that the cancer was MSI-high or had immunohistochemical staining showing the absence of one or more mismatch repair proteins (*MLH1, MSH2, MSH6* or *PMS2*); or
  - A personal history of colorectal polyposis with at least 10 adenomatous polyps, at least 2 hamartomatous polyps or at least 5 serrated polyps/lesions proximal to the rectum; or
  - The individual has a PREMM5, MMRpro or MMRpredict Score of 2.5% or greater for having a Lynch syndrome gene mutation

Genetic testing with a Multi-Gene hereditary cancer Panel in individuals *without* a personal history of cancer is proven and medically necessary if all of the following criteria are met:
- The suspected hereditary cancer syndromes can be diagnosed by testing of two or more genes included in the specific hereditary cancer Panel; and
- At least one of the following:
  - At least one first- or second-degree relative diagnosed with a BRCA-Related Cancer at age 40 or younger; or
  - At least three Close Blood Relatives, on the same side of the family, diagnosed with any cancer; or
  - At least one first-degree relative with a cancer associated with Lynch Syndrome; or
  - At least one first- or second-degree relative with a cancer associated with Lynch Syndrome diagnosed at age 50 or younger; or
  - At least one first- or second-degree relative with at least two cancers associated with Lynch Syndrome; or
  - Two or more first- or second-degree relatives with a cancer associated with Lynch Syndrome; or

- At least one first- or second-degree relative with a clinical diagnosis of Familial Adenomatous Polyposis, Attenuated Familial Adenomatous Polyposis, Juvenile Polyposis Syndrome or Peutz-Jeghers Syndrome; or
- The individual has a PREMM5, MMRpro or MMRpredict Score of 5% or greater for having a Lynch syndrome gene mutation

Genetic testing with a Multi-Gene hereditary cancer Panel in individuals diagnosed with cancer at age 18 or younger is proven and medically necessary.

Multi-Gene hereditary cancer Panels are unproven and not medically necessary for all other indications.

Genetic testing for *BRCA1* and *BRCA2* or Multi-Gene hereditary cancer Panels with RNA testing are unproven and not medically necessary for all indications.

Definitions

Age Guidelines: For the statements that include Age Guidelines, a person is considered to be 45 years of age up until the day before their 46th birthday, and a person is considered to be 50 years of age up until the day before their 51st birthday.

BRCA-Related Cancers: Breast cancer, Ovarian cancer, pancreatic cancer or metastatic or high-risk (Gleason score >=7) prostate cancer (National Comprehensive Cancer Network [NCCN], 2020a).

Breast Cancer: Either invasive carcinomas or non-invasive (in situ) ductal carcinoma types (NCCN, 2020a).

Close Blood Relatives: Are defined as follows (NCCN, 2020a):
- First degree relatives include parents, siblings, and offspring
- Second degree relatives include half-brothers/sisters, aunts/uncles, grandparents, grandchildren and nieces/nephews affected on the same side of the family
- Third degree relatives include first cousins, great-aunts/uncles, great-grandchildren and great grandparents affected on same side of family.

Founder Mutation: A Founder Mutation is a gene mutation observed with high frequency in a group that is or was geographically or culturally isolated, in which one or more of the ancestors was a carrier of the mutant gene. This phenomenon is often called a Founder effect (National Cancer Institute website [NCI] Dictionary of Genetics; NCCN, 2020a).

Gleason Scoring: Gleason Scoring is a system of grading prostate cancer tissue based on how it looks under a microscope. Gleason Scores range from 2 to 10 and indicate how likely it is that a tumor will spread. A low Gleason Score means the cancer tissue is similar to normal prostate tissue and the tumor is less likely to spread. A high Gleason Score means the cancer tissue is very different from normal and the tumor is more likely to spread (NCI Dictionary of Cancer).

Limited Family History: Defined as having fewer than two known first-degree or second-degree female relatives or female relatives surviving beyond 45 years of age on either or both sides of the family (e.g., individual who is adopted) (NCCN 2020a).

Lynch Syndrome-Associated Cancer: Colorectal, endometrial, gastric, Ovarian, pancreatic, ureter and renal pelvis, brain (usually glioblastoma), biliary tract, small intestinal cancers, sebaceous adenomas, sebaceous carcinomas, and keratoacanthomas as seen in Muire-Torre syndrome (NCCN, 2020b).

Multi-Gene Panel: Genetic tests that use next-generation sequencing to test multiple genes simultaneously. Also called multigene test, multiple-gene Panel test and multiple-gene test (NCI Dictionary of Genetics).

Ovarian Cancer: Includes fallopian tube cancers and primary peritoneal carcinoma (NCCN, 2020a).

Panel: A group of laboratory tests that are performed together to assess a body function or disease (Medicare, 2019; McGraw Hill, 2002).

Penetrance: The probability of a clinical condition developing in the presence of a specific genetic variant/mutation (Daly et al. 2017).

Personal and Family History Documentation: In the form of a pedigree drawing/diagram utilizing standardized nomenclature, should be in the contemporaneous medical records submitted with the testing request (i.e., request form) (NCCN, 2020a).

PREMM: PREdiction Model for gene Mutations. The PREMM model estimates the overall cumulative probability of having an *MLH1, MSH2, MSH6, PMS2*, and *EPCAM* gene mutation.

Triple-Negative Breast Cancer: Refers to any Breast Cancer that does not show expression of estrogen receptors (ER), progesterone receptors (PR) or HER2/neu (NCCN, 2020a).

Applicable Codes

The following list(s) of procedure and/or diagnosis codes is provided for reference purposes only and may not be all inclusive. Listing of a code in this policy does not imply that the service described by the code is a covered or non-covered health service. Benefit coverage for health services is determined by federal, state, or contractual requirements and applicable laws that may require coverage for a specific service. The inclusion of a code does not imply any right to reimbursement or guarantee claim payment. Other Policies and Guidelines may apply.

CPT Code	Description
BRCA1 and BRCA2	
0138U	BRCA1 (BRCA1, DNA repair associated), BRCA2 (BRCA2, DNA repair associated) (e.g., hereditary breast and ovarian cancer) mRNA sequence analysis (List separately in addition to code for primary procedure)
81162	BRCA1 (BRCA1, DNA repair associated), BRCA2 (BRCA2, DNA repair associated) (e.g., hereditary breast and ovarian cancer) gene analysis; full sequence analysis and full duplication/deletion analysis (i.e., detection of large gene rearrangements)
81163	BRCA1 (BRCA1, DNA repair associated), BRCA2 (BRCA2, DNA repair associated) (e.g., hereditary breast and ovarian cancer) gene analysis; full sequence analysis
81164	BRCA1 (BRCA1, DNA repair associated), BRCA2 (BRCA2, DNA repair associated) (e.g., hereditary breast and ovarian cancer) gene analysis; full duplication/deletion analysis (i.e., detection of large gene rearrangements)
81165	BRCA1 (BRCA1, DNA repair associated) (e.g., hereditary breast and ovarian cancer) gene analysis; full sequence analysis
81166	BRCA1 (BRCA1, DNA repair associated) (e.g., hereditary breast and ovarian cancer) gene analysis; full duplication/deletion analysis (i.e., detection of large gene rearrangements)
81167	BRCA2 (BRCA2, DNA repair associated) (e.g., hereditary breast and ovarian cancer) gene analysis; full duplication/deletion analysis (i.e., detection of large gene rearrangements)
81212	BRCA1 (BRCA1, DNA repair associated), BRCA2 (BRCA2, DNA repair associated) (e.g., hereditary breast and ovarian cancer) gene analysis; 185delAG, 5385insC, 6174delT variants)
81215	BRCA1 (BRCA1, DNA repair associated) (e.g., hereditary breast and ovarian cancer) gene analysis; known familial variant
81216	BRCA2 (BRCA2, DNA repair associated) (e.g., hereditary breast and ovarian cancer) gene analysis; full sequence analysis
81217	BRCA2 (BRCA2, DNA repair associated) (e.g., hereditary breast and ovarian cancer) gene analysis; known familial variant

CPT Code	Description
Multi-Gene Panel	
0101U	Hereditary colon cancer disorders (e.g., Lynch syndrome, PTEN hamartoma syndrome, Cowden syndrome, familial adenomatosis polyposis), genomic sequence analysis panel utilizing a combination of NGS, Sanger, MLPA, and array CGH, with MRNA analytics to resolve variants of unknown significance when indicated (15 genes [sequencing and deletion/duplication], EPCAM and GREM1 [deletion/duplication only])
0102U	Hereditary breast cancer-related disorders (e.g., hereditary breast cancer, hereditary ovarian cancer, hereditary endometrial cancer), genomic sequence analysis panel utilizing a combination of NGS, Sanger, MLPA, and array CGH, with MRNA analytics to resolve variants of unknown significance when indicated (17 genes [sequencing and deletion/duplication])
0103U	Hereditary ovarian cancer (e.g., hereditary ovarian cancer, hereditary endometrial cancer), genomic sequence analysis panel utilizing a combination of NGS, Sanger, MLPA, and array CGH, with MRNA analytics to resolve variants of unknown significance when indicated (24 genes [sequencing and deletion/duplication], EPCAM [deletion/duplication only])
0129U	Hereditary breast cancer-related disorders (e.g., hereditary breast cancer, hereditary ovarian cancer, hereditary endometrial cancer), genomic sequence analysis and deletion/duplication analysis panel (ATM, BRCA1, BRCA2, CDH1, CHEK2, PALB2, PTEN, and TP53)
0130U	Hereditary colon cancer disorders (e.g., Lynch syndrome, PTEN hamartoma syndrome, Cowden syndrome, familial adenomatosis polyposis), targeted mRNA sequence analysis panel (APC, CDH1, CHEK2, MLH1, MSH2, MSH6, MUTYH, PMS2, PTEN, and TP53) (List separately in addition to code for primary procedure)
0131U	Hereditary breast cancer-related disorders (e.g., hereditary breast cancer, hereditary ovarian cancer, hereditary endometrial cancer), targeted mRNA sequence analysis panel (13 genes) (List separately in addition to code for primary procedure)
0132U	Hereditary ovarian cancer-related disorders (e.g., hereditary breast cancer, hereditary ovarian cancer, hereditary endometrial cancer), targeted mRNA sequence analysis panel (17 genes) (List separately in addition to code for primary procedure)
0133U	Hereditary prostate cancer-related disorders, targeted mRNA sequence analysis panel (11 genes) (List separately in addition to code for primary procedure)
0134U	Hereditary pan cancer (e.g., hereditary breast and ovarian cancer, hereditary endometrial cancer, hereditary colorectal cancer), targeted mRNA sequence analysis panel (18 genes) (List separately in addition to code for primary procedure)
0135U	Hereditary gynecological cancer (e.g., hereditary breast and ovarian cancer, hereditary endometrial cancer, hereditary colorectal cancer), targeted mRNA sequence analysis panel (12 genes) (List separately in addition to code for primary procedure)
0162U	Hereditary colon cancer (Lynch syndrome), targeted mRNA sequence analysis panel (MLH1, MSH2, MSH6, PMS2) (List separately in addition to code for primary procedure)
0238U	Oncology (Lynch syndrome), genomic DNA sequence analysis of MLH1, MSH2, MSH6, PMS2, and EPCAM, including small sequence changes in exonic and intronic regions, deletions, duplications, mobile element insertions, and variants in non-uniquely mappable regions
81432	Hereditary breast cancer-related disorders (e.g., hereditary breast cancer, hereditary ovarian cancer, hereditary endometrial cancer); genomic sequence analysis panel, must include sequencing of at least 10 genes, always including BRCA1, BRCA2, CDH1, MLH1, MSH2, MSH6, PALB2, PTEN, STK11, and TP53
81433	Hereditary breast cancer-related disorders (e.g., hereditary breast cancer, hereditary ovarian cancer, hereditary endometrial cancer); duplication/deletion analysis panel, must include analyses for BRCA1, BRCA2, MLH1, MSH2, and STK11

CPT Code	Description
Multi-Gene Panel	
81435	Hereditary colon cancer disorders (e.g., Lynch syndrome, PTEN hamartoma syndrome, Cowden syndrome, familial adenomatosis polyposis); genomic sequence analysis panel, must include sequencing of at least 10 genes, including APC, BMPR1A, CDH1, MLH1, MSH2, MSH6, MUTYH, PTEN, SMAD4, and STK11
81436	Hereditary colon cancer disorders (e.g., Lynch syndrome, PTEN hamartoma syndrome, Cowden syndrome, familial adenomatosis polyposis); duplication/deletion analysis panel, must include analysis of at least 5 genes, including MLH1, MSH2, EPCAM, SMAD4, and STK11
81437	Hereditary neuroendocrine tumor disorders (e.g., medullary thyroid carcinoma, parathyroid carcinoma, malignant pheochromocytoma or paraganglioma); genomic sequence analysis panel, must include sequencing of at least 6 genes, including MAX, SDHB, SDHC, SDHD, TMEM127, and VHL
81438	Hereditary neuroendocrine tumor disorders (e.g., medullary thyroid carcinoma, parathyroid carcinoma, malignant pheochromocytoma or paraganglioma); duplication/deletion analysis panel, must include analyses for SDHB, SDHC, SDHD, and VHL

Description of Services

Genetic testing for hereditary cancer susceptibility is used to predict an individual's risk of cancer development in the future. It has been estimated that 5-10% of all cancers are hereditary (Heald et al., 2016).

Hereditary Breast and Ovarian Cancer (*BRCA1/BRCA2*)

Breast Cancer is the second most common cause of cancer-related deaths among women. The inherited tendency to develop Breast and Ovarian Cancer has been termed the Hereditary Breast and Ovarian Cancer syndrome (HBOC). Mutation in either of two genes, BRCA1 and BRCA2, has been associated with an increased risk for Breast Cancer and Ovarian Cancer. A deleterious mutation in either gene may be inherited from either parent; and later an acquired mutation of the other allele can lead to cancer development.

It has been estimated that inherited BRCA1 and BRCA2 mutations account for 5 to 10 percent of Breast Cancers and 10 to 15 percent of Ovarian Cancers among white women in the United States NCI, 2018). Harmful BRCA1 mutation may also increase a woman's risk of developing other cancers. Men with a harmful BRCA1 mutation also have an increased risk of Breast Cancer and, possibly, of pancreatic cancer, testicular cancer and early-onset prostate cancer. However, male Breast Cancer, pancreatic cancer and prostate cancer appear to be more strongly associated with BRCA2 gene mutation (Thompson and Easton, 2002; NCCN, 2020a).

Multi-Gene Hereditary Cancer Panels

Multi-Gene hereditary cancer panels, composed of 5 or more genes, using next-generation sequencing (NGS) technology are currently available, and many different test panels are marketed commercially, most of which also include large deletion/duplication analysis. These panels are intuitively attractive because they can rapidly test for numerous mutations both within a single gene and across multiple genes related to increased cancer risks. It is also possible that these Multi-Gene tests can, in the case of families where more than one hereditary cancer syndrome is suspected, be performed more cost effectively than stepwise individual gene testing. However, many of these panel tests also include low to moderate-risk genes that may result in the identification of gene mutations that are of unclear clinical significance or which would not clearly direct an individual's medical management recommendations. Identification of mutations for which the clinical management is uncertain may lead to unnecessary follow-up testing and procedures, all of which have their own inherent risks (NCCN, 2020a; NCCN, 2020b; LaDuca et al., 2014; Robson et al., 2015; Kurian et al., 2014; Tung et al., 2015; Plon et al., 2011).

Clinical Evidence

Genetic testing for hereditary cancer susceptibility is used to predict an individual's risk of cancer development in the future. It has been estimated that 5-10% of all cancers are hereditary (Heald et al. 2016). Hereditary cancers typically have an earlier age

of onset and have an autosomal dominant pattern of inheritance observable in a family (NCCN, 2020a). A small subset of these inherited cancers, about 15-20%, may be the result of a complex interaction between multiple genes (American Society of Clinical Oncology [ASCO], 2018).

To identify if an individual has an increased risk of having a hereditary cancer, it is important to take a detailed family history that includes first, second and third degree relatives that focuses on cancer diagnoses by age of onset, primary site(s), presence of bilateral disease, and current age or age at time of death. Other conditions that can be a feature of hereditary cancers should be noted, as well as medical and surgical history. The individual should have a thorough physical exam performed by a clinician with familiarity with hereditary cancer syndrome. When applicable, risk assessment tools should be utilized to help identify the risk an individual has a hereditary cancer gene (NCCN, 2020a). Some examples of tools include BRCAPRO, the Breast and Ovarian Cancer Analysis of Disease Incidence and Carrier Estimation Algorithm (BOADICEA) (NCCN, 2020a) and Prediction of MLH1 and MSH2 Model (PREMM) (NCCN, 2020b). Genetic testing is recommended generally when there is a personal or family history consistent with hereditary cancer susceptibility, the test can be adequately interpreted and the results can be used to diagnose or influence the medical management of the individual or at risk family members (Robson et al., 2015).

Table 1: Common cancers that can be hereditary, the associated genes and references that can be utilized to learn about each hereditary cancer syndrome in more detail

Hereditary Cancer Syndrome(s)	Gene(s)	Associated Cancer(s) and References
Hereditary Breast and Ovarian Cancer	*BRCA1, BRCA2, CHEK2, PALB2, BRIP1, RAD51C, RAD51D*[†] *, PTEN, TP53, STK11, NBN, ATM, CDH1*	• Breast (Antoniou et al., 2003; Chen et al., 2006; Hilgart et al., 2012; Shiovitz and Korde, 2015; Daly et al., 2017) • Ovarian (Risch et al., 2001; Chen et al., 2006; Lancaster et al., 2015) • Fallopian tube (Medeiros et al., 2006; Lancaster et al., 2015) • Primary peritoneal (Casey et al., 2005; Finch et al., 2012; Lancaster et al., 2015) • Pancreatic (Breast Cancer Linkage Consortium [BCLC], 1999; van Asperen et al., 2005; Mersch et al., 2015) • Prostate (Risch et al., 2001; Thompson et al., 2002; van Asperen et al., 2005; Mersch et al., 2015) • Melanoma (BCLC, 1999; Mersch et al., 2015) • Gastric/stomach (BCLC, 1999)
Familial adenomatous polyposis (FAP)	*APC*	• Breast (He et al., 2016) • Ovarian (Mostowska et al., 2014) • Colorectal (Feng et al., 2014; Slowik et al., 2015; Leshno et al., 2016) • Pancreatic (Leshno et al., 2016) • Skin (Leshno et al., 2016) • Thyroid (Septer et al., 2013)
Ataxia-telangiectasia	*ATM*	• Breast (Marabelli et al., 2016) • Sarcoma (Ballinger et al., 2016) • Lung (Bhowmik et al., 2015; Huang et al., 2016) • Gastric (Helgason et al., 2015) • Melanoma (Antonopoulou et al., 2015) • Pancreatic (Roberts et al., 2016)
PTEN hamartoma tumor syndrome/ Cowden syndrome	*PTEN*	• Breast (Slattery et al., 2012; Ozturk et al., 2013) • Endometrial (Eng, 2016) • Gastric/digestive (Gao et al., 2013) • Colorectal (Jing et al., 2014) • Thyroid (Eng, 2016)

Hereditary Cancer Syndrome(s)	Gene(s)	Associated Cancer(s) and References
Hereditary nonpolyposis colon cancer (HNPCC)/ Lynch syndrome	*EPCAM, MLH1, MSH2, MSH6, PMS1, PMS2*	• Breast (Smolarz et al., 2015; Kappil et al., 2016; Stoffel et al., 2015; Boland, 2018) • Ovarian (Watson et al., 2008; Bonadona et al., 2011; Auranen and Joutsiniemi, 2011) • Colorectal (Senter et al., 2008; Raskin et al., 2011) • Hepatocellular (Kohlmann and Gruber, 2018) • Endometrial/uterine (Raskin et al., 2011; Castellsagué et al., 2015; Watson et al., 2008; Renkonen-Sinisalo et al., 2007; Auranen and Joutsiniemi, 2011)
Peutz-Jeghers syndrome	*STK11 (LKB1)*	• Breast (Boardman et al.,1998) • Ovarian (McGarrity et al., 2016) • Colorectal (Slattery et al., 2010) • Gastric (Giardiello et al., 1987) • Pancreatic (Klein et al., 2001)
Li-Fraumeni syndrome	*TP53*	• Breast (Sagne et al., 2013; Mai et al., 2016) • Brain/CNS (Mai et al., 2016) • Pancreatic (DaVee et al., 2018) • Prostate (Borges and Ayres, 2015) • Sarcoma (Mai et al., 2016) • Thyroid (Chen et al., 2015)
Hereditary diffuse gastric cancer syndrome	*CDH1*	• Breast (Benusiglio et al., 2013; Hansford et al., 2015) • Gastric (Hansford et al., 2015)
Juvenile polyposis syndrome	*BMPR1A, SMAD4*	• Gupta et al., 2017
Hereditary mixed polyposis	*POLD1, GREM1, POLE*	• Gupta et al., 2017

BRCA1/BRCA2

The BRCA1 and BRCA2 genes are associated with causing HBOC. This syndrome results in an increased risk for Breast Cancer for men and women, and an increased risk for ovarian cancer in women. Other cancers have been associated with HBOC, particularly with BRCA2 variants, including prostate, pancreatic and melanoma. Management of HBOC for those with cancer includes bilateral mastectomy due to the high risk of breast cancer. Treatment of ovarian and other cancers is similar to sporadic cancers. Preventative measures for asymptomatic individuals include prophylactic bilateral mastectomy and oophorectomy, chemoprevention, and increased surveillance (Petrucelli et al., 2016).

Testing for BRCA1 and BRCA2 can include targeted variants for at risk populations, such as for those with Ashkenazi Jewish ancestry, full gene sequencing, and duplication/deletion analysis. BRCA1 accounts for about 66% of HBOC, and sequence analysis can identify variants in about 80% of cases for both BRCA1 and BRCA2. Duplication/deletion testing identifies variants in each gene in an additional 10% of cases (Petrucelli et al., 2016).

The NCCN guidelines present evidence based specific criteria for genetic testing for hereditary breast and/or ovarian cancer syndrome caused by BRCA1/BRCA2 (NCCN, 2020a). In these guidelines, the genetic testing recommendations go beyond BRCA1/BRCA2 and include other high-penetrance breast and/or ovarian cancer susceptibility genes including: CDH1, PALB2, PTEN, and TP53. The guidelines address genetic risk assessment, counseling, testing and management based on test results. Additionally, the guidelines separate the testing into three categories: 1) clinically indicated; 2) may be considered; 3) low probability that testing will have clinical utility. In this third category the scenarios included are having no close blood relative with breast, ovarian, pancreatic, or prostate cancer and men with localized prostate cancer (Gleason score <7) or women with breast cancer diagnsed at age >65 years. The recommended NCCN criteria for testing include:

- Category: Clinically Indicated
  - A known BRCA1/BRCA2 mutation or other pathogenic/likely pathogenic mutation in a cancer susceptibility gene in the family
  - Persons who meet a testing criteria but with limited previous testing and desire multi-gene testing
  - Personal cancer history
  - Diagnosed with ovarian cancer
  - Diagnosed with exocrine pancreatic cancer
  - Diagnosed with male breast cancer
  - Diagnosed with metastatic or intraductal prostate cancer
  - Diagnosed with high-grade prostate cancer (Gleason Score ≥7) with:
    - At least one close blood relative with breast cancer diagnosed age 50 or younger, or ovarian cancer, or pancreatic cancer, or metastatic or intraductal prostate cancer
    - At least two close blood relatives with breast cancer or prostate cancer diagnosed at any age
    - Ashkenazi Jewish ancestry
  - Diagnosed with breast cancer with one of the following conditions:
    - Diagnosed at age <45 years old
    - Diagnosed at age 46–50 with:
      - An additional breast primary
      - At least one close blood relative with breast, ovarian, pancreatic, or high-grade (Gleason Score >7) or intraductal prostate cancer
      - An unknown or limited family history
    - Triple-negative breast cancer diagnosed < age 60
    - Diagnosed at any age with:
      - At least one close blood relative with breast cancer diagnosed age 50 or younger, or ovarian cancer, or pancreatic cancer, or metastatic or intraductal prostate cancer
      - At least two close blood relatives with breast cancer diagnosed at any age
      - Ashkenazi Jewish Ancestry
    - BRCA1/2 pathogenic or likely pathogenic variant or other mutation in a cancer susceptibility gene detected by tumor profiling
  - Family history of cancer
  - Affected or unaffected individual has a first or second degree blood relative meeting above criteria
  - Affected or unaffected individual who does not meet other criteria but has a probabilty (>5%) of a BRCA1/2 pathogenic variant based on probability models
- Category: May Be Considered
  - Bilateral breast cancer, first diagnosed between 50–65 years of age
  - Unaffected individual of Ashkenazi Jewish descent
  - Affected or unaffected individual who does not meet other criteria but has a probabilty (2.5-5%) of a pathogenic variant based on probability models

In addition, NCCN recommends testing an individual in a family with a cancer diagnosis first should be discussed. If there are no living family members with breast or ovarian cancer available for testing, consider testing family members affected with other cancers associated with BRCA1/BRCA2, such as prostate cancer (Gleason Score ≥7 or metastatic), pancreatic cancer or melanoma. Due to potential difficulty in interpreting testing results in an unaffected person, testing of individuals without a cancer diagnosis should only be considered when there is no affected family member available for testing (NCCN, 2020a).

The U.S. Preventive Services Task Force (USPSTF) (2019) updated the recommendations on risk assessment, genetic counseling, and genetic testing for BRCA related cancers. The updated document recommends that primary care providers screen women who have a personal or family history of breast, ovarian, tubal or peritoneal cancer or who have an ancestry associated with BRCA1/2 mutations. This screening should be performed with one of several screening tools designed to identify a family history that may be associated with an increased risk for potentially harmful mutations in breast cancer susceptibility genes (BRCA1 or BRCA2). Tools evaluated by the USPSTF include the Ontario Family History Assessment Tool, Manchester Scoring System, Referral Screening Tool, Pedigree Assessment Tool, 7-Question Family History Screening Tool, International Breast Cancer Intervention Study instrument (Tyrer-Cuzick) and brief versions of BRCAPRO. Women with positive screening results should receive genetic counseling and, if indicated after counseling, genetic testing (Grade B recommendation).

In addition, the USPSTF recommends against routine genetic counseling or BRCA testing for women whose personal or family history or ancestry is not associated with an increased risk for potentially harmful mutations in the BRCA1 or BRCA2 genes (Grade D recommendation) (USPSTF, 2019).

Several studies have shown that BRCA1 breast cancer is more likely to be characterized as triple-negative. Studies have reported BRCA1 mutations in 9-28% of patients with triple-negative breast cancer. In addition, it appears that among patients with triple-negative disease, BRCA mutation carriers were diagnosed at a younger age compared with non-carriers (NCCN, 2020a). The triple-negative breast cancer phenotype, which carries an adverse prognosis, accounts for 80% to 90% of BRCA1-associated breast cancers. A study of 54 women with triple-negative breast cancer aged 40 years or younger, who were not considered candidates for BRCA testing because of the lack of a strong family history, showed five with BRCA1 mutations and one with a BRCA2 mutation (11% mutation prevalence) (NCI, 2018a; Young et al., 2009). In a cohort of triple-negative breast cancer patients, Gonzalez-Angulo et al. (2011) found a 19.5% incidence of BRCA mutations. Median age was 51 years (27-83 years). The authors recommend that genetic testing be discussed with patients with triple-negative breast cancer.

Kolor et al. (2017) reviewed medical claims from 2009-2014 for BRCA testing and resulting interventions among women ages 18-64 with employer sponsored health care. They noted that BRCA testing increased 2.3 times in metropolitan and 3.0 times in non-metropolitan areas during the study period. Receipt of preventative services within 90 days of testing also varied between these regions, with the exception of mastectomy (6-10% of testers over the study period). Women were less likely to receive a MRI of the breast in non-metropolitan areas (8.2% vs. 10.3%), as well as mammography (11.5% vs. 13.8%). Receipt of genetic counseling before or after testing was more common in the metropolitan group, but in both groups, an increase was seen over the study period from 5.3-8% in metropolitan areas and 3.8-5.2% in non-metropolitan areas. Overtime, the disparities between the two groups was reduced, and the authors note that the implementation of the USPSTF guidelines and the availability of BRCA counseling and testing under the Affordable Care Act in September of 2010 may have influenced the increase in test and the reduction in differences between the two groups. The highest rate of BRCA testing in the study was 332.5 women per 100,000 women aged 44-54 which is comparable to the estimated prevalence of BRCA mutations in the general US population.

The prevalence of BRCA1/2 large rearrangements (LRs) was investigated in 48,456 patients with diverse clinical histories and ancestries that were referred for clinical molecular testing for suspicion of HBOC. Prevalence data was analyzed for patients from different risk and ethnic groups. Patients were designated as high-risk (n=25,535) if their clinical history predicted a high prior probability. For these patients, LR testing was performed automatically in conjunction with sequencing. Elective patients (n=22,921) did not meet the high-risk criteria, but underwent LR testing if BRCA1/2 sequencing indicated no known mutations. Overall BRCA1/2 mutation prevalence among high-risk patients was 23.8% versus 8.2% for the elective group. The mutation profile for high-risk patients was 90.1% sequencing mutations versus 9.9% LRs, and for elective patients, 94.1% sequencing versus 5.9% LRs. The authors noted that this difference may reflect the bias in high-risk patients to carry mutations in BRCA1, which has a higher penetrance and frequency of LRs compared with BRCA2. Significant differences in the prevalence and types of LRs were found in patients of different ancestries. LR mutations were significantly more common in Latin American/Caribbean patients (Judkins et al., 2012).

Of 211 Ashkenazi Jewish breast cancer probands with a family history of pancreatic cancer, Stadler et al. (2012) found that 30 (14.2%) harbored a BRCA mutation. Fourteen (47%) of the mutations were in BRCA1 and 16 (53%) were in BRCA2. Patients diagnosed with breast cancer at age ≤ 50 years were found to have a higher BRCA1/2 mutation prevalence than probands with breast cancer who were diagnosed at age > 50 years (21.1% vs 6.9%). In patients with a first-, second-, or third-degree relative with pancreatic cancer, mutation prevalence was 15.4%, 15.3% and 8.6%, respectively. The authors found that BRCA1 and BRCA2 mutations are observed with nearly equal distribution in Ashkenazi Jewish breast-pancreas cancer families, suggesting that both genes are associated with pancreatic cancer risk.

Almost 10% of women with breast cancer who are younger than age 50 have BRCA mutations. Most of the BRCA-positive women do not have personal or family histories of breast or ovarian cancer and are not of Ashkenazi Jewish ancestry. Using a simulation model, Kwon et al. (2010) evaluated six populations of women younger than 50 with breast cancer, looking at costs and health benefits. The results led the authors to conclude that testing women with triple-negative breast cancers who were younger than 50 years for BRCA mutations should be adopted into current guidelines for genetic testing.

Ferrone et al. (2009) looked at the prevalence of BRCA1 and BRCA2 in an unselected group of Jewish patients and compared patients with resected BRCA mutation-associated pancreatic adenocarcinoma (PAC) to PAC patients without mutations. Of the 187 Jewish patients who underwent resection for PAC, tissue was available for 145 patients. Founder mutations for BRCA1 and BRCA2 were identified in 5.5% of patients (two with BRCA1 [1.3%] and six with BRCA2 [4.1%]). A previous cancer was reported by 24% (35 of 145) of patients with the most common sites being breast cancer (9 of 35; 74%) and prostate cancer (8 of 35; 23%).

A study (Walsh et al., 2006) found that the only genetic test commercially available in the United States to determine risk for development of hereditary breast cancer failed to detect BRCA1 and BRCA2 mutations in approximately 12% of breast cancer patients (n=300) who were members of a family with at least four cases of breast cancer and/or ovarian cancer. In this study, researchers retested participants for carrier status of genetic mutations known to influence risk for development of breast cancer using a molecular method not currently cleared for market in the United States known as multiplex ligation-dependent probe amplification (MLPA). Prior to enrollment, all participants had received a negative result from the breast cancer genetic test (Myriad Genetics Inc.) used routinely in the United States. The results of MLPA analysis indicated that 17% of study participants were, in fact, carriers of breast cancer-relevant genetic mutation, with 12% found to have alterations of BRCA1 or BRCA2. Inherited alterations of BRCA1 were more frequent among participants who were diagnosed with breast cancer prior to 40 years of age (16%) than among those who were older when diagnosed (6.5%). The clinical implications of these findings cannot be generalized to other populations but results strongly suggest that improved methods for determining breast cancer risk are needed for individuals with strong family histories of breast and/or ovarian cancer.

Unger et al. (2000) assessed the frequency of genomic rearrangements in BRCA1 was in 42 American families with breast and ovarian cancer who were seeking genetic testing and who were subsequently found to be negative for BRCA1 and BRCA2 coding-region mutations. The exon 13 duplication was detected in one family, and four families had other genomic rearrangements. A total of 5 (11. 9%) of the 42 families with breast/ovarian cancer who did not have BRCA1 and BRCA2 coding-region mutations had mutations in BRCA1 that were missed by conformation-sensitive gel electrophoresis or sequencing. Four of five families with BRCA1 genomic rearrangements included at least one individual with both breast and ovarian cancer; therefore, four (30.8%) of 13 families with a case of multiple primary breast and ovarian cancer had a genomic rearrangement in BRCA1. Families with genomic rearrangements had prior probabilities of having a BRCA1 mutation, ranging from 33% to 97% (mean 70%). In contrast, in families without rearrangements, prior probabilities of having a BRCA1 mutation ranged from 7% to 92% (mean 37%).

Clinical Practice Guidelines

American College of Obstetricians and Gynecologists (ACOG)

In 2019, ACOG published a Committee Opinion on Hereditary cancer syndromes and risk assessment (ACOG, 2019). The document included recommendations for genetic testing including:

- A hereditary cancer risk assessment is the key to identifying patients and families who may be at increased risk of developing certain types of cancer. Assessments should be performed by obstetrician–gynecologists or other obstetric–gynecologic care providers and should be updated regularly.
- If a hereditary cancer risk assessment suggests an increased risk of a hereditary cancer syndrome, referral to a specialist in cancer genetics or a health care provider with expertise in genetics is recommended for expanded gathering of family history information, risk assessment, education, and counseling, which may lead to genetic testing and tailored cancer screening or risk reduction measures, or both.
- Genetic testing may be performed using a panel of multiple genes through next-generation sequencing technology. This multigene testing process increases the likelihood of finding variants of unknown significance, and it also allows for testing for pathogenic and likely pathogenic variants in multiple genes that may be associated with a specific cancer syndrome or family cancer phenotype (or multiple phenotypes).

In a 2017 practice bulletin (reaffirmed 2019), the ACOG recommended criteria for genetic evaluation of HBOC syndrome (ACOG, 2017). These recommendations include:

- Women with the following:
    - A close relative (mother, sister, daughter, grandmother, granddaughter, aunt or niece) with a known BRCA mutation; or a first-degree or several close relatives that meet one or more of the criteria below; or a close relative with male breast cancer
    - Personal history of the following:

- Ovarian cancer
- Breast cancer at age 45 years or less
- Breast cancer and have a close relative with breast cancer at age 50 years or less or close relative with ovarian cancer at any age
- Breast cancer at age 50 years or less with a limited or unknown family history
- Breast cancer and have two or more close relatives with breast cancer at any age or pancreatic cancer or prostate cancer
- Two breast cancer primaries with the first diagnosed before age 50
- Triple-negative breast cancer at age 60 years or less
- Breast cancer and Ashkenazi Jewish ancestry
- Pancreatic cancer and have two or more close relatives with a BRCA related cancer

Additionally, in a 2017 Committee Opinion, ACOG recommends that women with a strong family history of ovarian, breast, or colon cancer may have a BRCA mutation or Lynch Syndrome and should be referred for formal genetic counseling to assess their cancer risk, and if appropriate, be offered testing.

American Society of Breast Surgeons (ASBrS)

An ASBrS consensus guideline (2019) made several recommendations including:

- Breast surgeons, genetic counselors, and other medical professionals knowledgeable in genetic testing can provide patient education and counseling, although when the patient's history and/or test results are complex, referral to a certified genetic counselor or genetics professional may be useful.
- Multi-gene panels are increasingly available for screening purposes. There is a lack of consensus among experts regarding which genes should be tested in different clinical scenarios.
- Genetic testing should be made available to all patients with a personal history of breast cancer.
- Patients who had genetic testing previously may benefit from updated testing.
- Genetic testing should be made available to patients without a history of breast cancer who meet NCCN guidelines. Unaffected patients should be informed that testing an affected relative first, whenever possible, is more informative than undergoing testing themselves.
- Variants of uncertain significance (VUS) are not clinically actionable and are considered inconclusive. Patients should be managed on their risk factors, and not a VUS result.

American Society of Clinical Oncology (ASCO)

ASCO convened an expert panel to determine recommendations for male breast cancer management and recently published the results (Hassett et al., 2020). The panel used 26 studies as the basis of the recommendations. While the majority of recommendations concerned treatment options, the panel did recommend that "genetic counseling and germline genetic testing of cancer predisposition genes should be offered to all men with breast cancer" (Evidence quality: low; Strength of recommendation: strong).

An ASCO policy statement recommends that genetic testing for cancer susceptibility be performed when the following three criteria are met: the individual being tested has a personal or family history suggestive of genetic cancer susceptibility; the test can be adequately interpreted; and the test results have accepted clinical utility (Robson et al., 2015).

National Society of Genetic Counselors (NSGC)

The NSGC recommends that genetic testing be performed in the context of an informed decision-making process (Berliner et al., 2013). The process of cancer risk assessment and genetic counseling for HBOC syndrome requires many steps, including the following:

- Gathering personal medical and family history data
- Psychosocial assessment
- Discussion of cancer and mutation risk and how personalized risk estimates are derived
- Facilitation of the informed consent process through discussion of the risks, benefits, limitations, and likelihood of identifying a mutation with genetic susceptibility testing
- Results disclosure (if applicable)
- Discussion of medical management options
- Review of issues related to genetic discrimination

Society of Gynecologic Oncology (SGO)

The SGO provided a statement on risk assessment and recommended that individuals with a likelihood of inherited predisposition to cancer based on personal or family history should be offered genetic counseling (Lancaster et al., 2015). Beyond this recommendation, there is additional guidance for criteria for patients with an increased likelihood of having an inherited predisposition to breast and ovarian/tubal/peritoneal cancer who should receive genetic counseling and be offered genetic testing including:

- Women affected with:
  - High grade epithelial ovarian/tubal/peritoneal cancer
  - Breast cancer ≤45 years
  - Breast cancer with close relative with breast cancer ≤50 years or close relative with epithelial ovarian/tubal/peritoneal cancer at any age
  - Breast cancer ≤50 years with a limited family history
  - Breast cancer with ≥2 close relatives with breast cancer at any age
  - Breast cancer with ≥2 close relatives with pancreatic cancer, aggressive prostate cancer (Gleason score ≥ 7)
  - Two breast primaries, with the first diagnosed prior to age 50.
  - Triple-negative breast cancer ≤60 years
  - With breast cancer and Ashkenazi Jewish ancestry
  - Pancreatic cancer with ≥2 close relatives with breast, ovarian/tubal/peritoneal, pancreatic, or aggressive prostate cancer (Gleason score ≥ 7)
- Women unaffected with cancer, but with:
  - A first degree or several close relatives that meet one of the above criteria
  - A close relative carrying a known *BRCA1* or *BRCA2* mutation
  - A close relative with male breast cancer

In addition, the statement details criteria for patients with an increased likelihood of Lynch syndrome and for whom genetic assessment is recommended including:

- Patients with endometrial or colorectal cancer with evidence of microsatellite instability or loss of a DNA mismatch repair protein (MLH1, MSH2, MSH6, PMS2) on immunohistochemistry.
- Patients with a first-degree relative affected with endometrial or colorectal cancer who was either diagnosed before age 60 years or who is identified to be at risk for Lynch syndrome by a systematic clinical screen that incorporates a focused personal and medical history.
- Patients with a first or second degree relative with a known mutation in a mismatch repair gene.

Multi-Gene Hereditary Cancer Panels

Multi-gene hereditary cancer panels can be used to investigate various cancers through the use of evaluating multiple genes simultaneously. In some situations, the use of a multi-gene panel test may result in a cost and time efficient approach. This is most useful where multiple high-penetrance genes with actionable results are possible because it is difficult to predict which gene is most likely to be mutated based on personal or family medical history (Robson et al. 2015).

Hereditary Breast and Ovarian Cancer Multi-Gene Panels

Alvarado et al. (2020) evaluated 3,162 women for the prevalence of pathogenic/likely pathogenic variants (PV/LPV) with the same multigene cancer panel with 20 genes. The majority of women (65.4%) were post-breast or ovarian cancer diagnosis. Overall prevalence of any PV/LPV result was 11.7% with nearly 5.4% having BRCA1/2 mutations, while 6.3% had at least one mutation in non-BRCA genes. Breaking the subset down to only those with PV/LPV result, 55% of the total mutations were non-BRCA. The researchers conclused that multigene cancer panel testing may be appropriate in a high-risk cohort.

Corredor et al. (2020) evaluated women with multiple primary breast cancers with panel testing to determine the rate of non-BRCA mutations. Eight-five women were tested with a multigene panel and of those, 33 (38.8%) tested positive for a pathogen mutation:: 9 BRCA1, 5 BRCA2, 5 ATM, 1 BARD1, 4 CHEK2, 1 MSH2, 1 MSH6, 2 PALB2, 1 PMS2, 1 PTEN and 3 TP53. Overall, 17.6% tested positive for a non-BRCA breast cancer predisposition gene.

Daly et al. (2020) provided an overview to NCCN breast and ovarian cancer susceptibility screening guideline updates and described the changes in the appropriate testing algorithms. The guidelines state that there is strong evidence that genes

beyond BRCA1/2 confer markedly increased risk of breast and/or ovarian cancers, such as CDH1, PALB2, PTEN, and TP53. This change is significant enough to modify the "BRCA1/2 Testing Criteria" page to now be titled "Testing Criteria for High-Penetrance Breast and/or Ovarian Cancer Susceptibility Genes." Additionally, the testing criteria is also reorganized into three sections: (1) testing is clinically indicated, (2) testing may be considered, and (3) low probability of testing results having documented clinical utility. The authors also stated that multigene testing may be considered for patients who tested negative for one syndrome but the personal and/or family history is suggestive of an inherited syndrome. The other major updates for the guidelines include revisions to Ashkenazi Jewish ancestry testing criteria and pancreatic cancer screening.

Lee et al. (2018) reviewed several genes on HBOC susceptibility test panels that have not been fully evaluated for strength of association with disease. The researchers used the Clinical Genome Resource (ClinGen) clinical validity framework to calculate the strength of evidence between selected genes and breast or ovarian cancer. For evaluation, 31 genes were selected for evaluation of the relationship between the gene and breast cancer, and 32 were selected for ovarian cancer. The relationship was then classified as: Definitive, Strong, Moderate, Limited, Refuted, Disputed or No Reported Evidence. Of the genes, Definitive clinical validity classifications were made for 10 of 31 and 10 of 32 gene-disease pairs for breast and ovarian cancer, respectively. Only 2 genes had a Moderate classification. In the Limited group, 6 of 31 for breast cancer and 6 of 32 for ovarian cancer were defined. Inconsistent evidence resulted in Disputed or Refuted assertions for 9/31 genes for breast and 4/32 genes for ovarian cancer. No Reported Evidence of disease association was found for 5/31 genes for breast and 11/32 for ovarian cancer. The study demonstrated that there is still some development to be done prior to having standardized panels.

Shimelis et al. (2018) aimed to define the cancer panel genes associated with an increased risk of triple-negative breast cancer (TNBC). A large cohort of patients was assembled and multi-gene panel testing for 21 genes in 8753 patients was performed by a clinical testing laboratory, and testing for 17 genes in 2148 patients was conducted by a Triple-Negative Breast Cancer Consortium (TNBCC) of research studies. The study found that germline pathogenic variants in BARD1, BRCA1, BRCA2, PALB2 and RAD51D were associated with high risk (odds ratio > 5.0) of TNBC and greater than 20% lifetime risk for overall breast cancer among Caucasians. Pathogenic variants in BRIP1, RAD51C, and TP53 were associated with moderate risk (odds ratio > 2) of TNBC. Comparable trends were observed for the African American population. Pathogenic variants in these TNBC genes were detected in 12.0% (3.7% non-BRCA1/2) of all participants. The researchers concluded that multi-gene hereditary cancer panel testing can identify genes that give an elevated risk of TNBC.

Crawford et al. (2017) tested 300 women who previously tested negative for BRCA1/2. All of the subjects met additional criteria including: a personal history of bilateral breast cancer; or a personal history of Breast Cancer and a first or second degree relative with ovarian cancer; or a personal history of ovarian, fallopian tube, or peritoneal carcinoma. The testing determined that 9% of women had pathogenic mutations and 8% had mutations in genes other than BRCA1/BRCA2. The researchers concluded that individuals with additional criteria may be candidates for additional multi-gene panel testing which has important implications for family testing.

High-Risk Colorectal Cancer Syndromes (including Lynch associated cancers)

The NCCN guidelines present evidence based specific criteria for genetic testing for hereditary high-risk colorectal cancer syndromes caused by a variety of genes (NCCN, 2020b). The guidelines address genetic risk assessment, counseling, testing and management based on test results. The recommended NCCN criteria for genetic testing include:

- Possible Polyposis Syndromes:
  - >10 adenomas; or
  - >2 hamartomatous polyps; or
  - >5 serrated polyps/lesions proximal to the rectum
- Lynch Syndrome:
  - Personal history of a tumor with defective mismatch repair
  - Personal history of colorectal, endometrial, or other Lynch syndrome associated cancer
  - Family history of Lynch syndrome associated cancers in close blood relatives of varying degrees
  - Individual with an increased model-predicted risk for Lynch syndrome associated cancers

For hereditary cancer syndromes associated with colorectal cancer (CRC) and polyposis patients, multigene panel testing has been accepted, however the genes included on the panels are often widely varied. The Collaborative Group of the Americas on Inherited Gastrointestinal Cancer Position Statement Committee performed an evidence review to create on which genes should be included on a multigene panel for a patient with a suspected hereditary CRC or polyposis syndrome (Heald et al., 2020). In addition the group proposed some updated genetic testing criteria. The collaborative group highlighted the following

genes associated with Lynch syndrome: MLH1, MSH2, MSH6, PMS2, EPCAM and the genes associated with polyposis syndromes: APC, BMPRIA, MUTYH, PTEN, and STK11. These genes were noted as the minimum genes that should be included on a multigene panel for these conditions. The group also recommended individual who should undergo multigene panel testing including:

- Colorectal cancer diagnosed age < 50 years
- Multiple Lynch syndrome primary tumors
- Colorectal cancer and at least one first degree relative with colorectal or endometrial cancer
- PREMM5 score ≥ 2.5% or MMRpro or MMRpredict score ≥ 5%
- Mismatch repair-deficient colorectal cancer, not attributed to MLH1 promoter methylation
- Patients meeting any other genetic testing criteria
- ≥ 10 cumulative colorectal adenomas
- ≥ 3 cumulative gastrointestinal hamartomatous polyps

Gupta et al. (2019) published insights regarding the NCCN updated guidelines for susceptibility screening for colorectal cancer syndromes, specifically around multi-gene cancer panels for hereditary colorectal cancer syndromes. For polyposis syndromes that include FAP, attenuated FAP (AFAP), MAP, and other rare genetic causes of multiple adenomatous polyps, data suggested that there are many genes that may contribute to the CRC risk including: AXIN2, GREM1, NTHL1, POLE, POLD1, and MSH3. Likewise, there are many genes that have been associated with Lynch syndrome which yields an increased risk for colon cancer, endometrial and ovarian cancers, as well as gastric, pancreatic, biliary tract, ureter and renal pelvis, small intestine, and brain (usually glioblastoma), as well as sebaceous adenomas, sebaceous carcinomas, and keratoacanthomas, as seen in the Muir-Torre syndrome variant. The use of a multigene panel can help with the identification of Lynch syndrome and manage the future risk of CRC or endometrial cancer. The panel recommends universal screening of all patients with CRC or endometrial cancer at any age with tumor showing evidence of MMR deficiency, either by MSI or loss of MMR protein expression.

Using the ClinGen Clinical Validity framework, Seifert et al. (2018) evaluated gene-disease associations in hereditary colorectal cancer. This study assessed 42 gene-disease pairs. Of all gene-disease pairs evaluated, 14/42 (33.3%) were Definitive, 1/42 (2.4%) were Strong, 6/42 (14.3%) were Moderate, 18/42 (42.9%) were Limited, and 3/42 (7.1%) were either No Reported Evidence, Disputed, or Refuted. The researchers state that providers should recognize that only <60% of genes on available panels have Strong or Definitive evidence of association.

Martin-Morales et al. (2018) used a NGS panel to find genes that were involved in families that fulfill the clinical criteria for Lynch syndrome but lack the germline mutations. For this study, 98 patients from these families were tested with a multi-gene panel targeting 94 genes involved in cancer predisposition. The mutations identified were validated by Sanger sequencing. The study identified 19 likely pathogenic variants in 18 patients and out of these 19, 8 were found in MMR genes (5 in MLH1, 1 in MSH6 and 2 in PMS2). Additionally, 11 mutations were detected in other genes, including high penetrance genes (APC, SMAD4 and TP53) and moderate penetrance genes (BRIP1, CHEK2, MUTYH, HNF1A and XPC). Novel mutations including c.1194G>A in SMAD4, c.714_720dup in PMS2, c.2050T>G in MLH1 and c.1635_1636del in MSH6 were detected. The researchers concluded that the detection of new pathogenic mutations in high and moderate penetrance genes could contribute to the explanation of the heritability of colorectal cancer.

Other Cancers or More than one Hereditary Cancer Syndrome

LaDuca et al. (2020) evaluated 32 cancer predisposition genes in order to study the effect of multigene panel testing for hereditary cancers. The cohort consisted of 165,000 patients referred for multigene panel testing and the researchers assessed phenotype-specific pathogenic variant (PV) frequencies, cancer risk associations, and performance of genetic testing criteria. The study identified extensive genetic heterogeneity with the predisposition to cancer types commonly referred for germline testing (breast, ovarian, colorectal, uterine/endometrial, pancreatic, and melanoma). Patients with ovarian cancer had the highest PV frequencies (13.8%). Fewer than half of PVs identified were in patients that met the testing criteria for only BRCA1/2 (33.1%) or only Lynch syndrome (46.2%). For patients that did not meet the testing criteria, 5.8% had PVs in BRCA1/2 and 26.9% had PVs in Lynch syndrome.

Recently, ASCO convened an expert panel to conduct a literature review on pancreatic cancer (Stoffel et al., 2019). There were several sections regarding genetic testing in Research Question 2 “Which individuals should undergo genetic testing for predisposition to pancreatic cancer?” and the provisional clinical opinion stated that all patients with pancreatic adenocarcinoma should undergo risk assessment for those hereditary cancer syndromes that are associated with pancreatic cancer. Testing and assessment of risk should include a review of family history of cancer. The opinion also stated that

germline genetic testing for cancer susceptibility should be considered in those with pancreatic cancer and unremarkable family history.

In a study by Gardner et al. (2018), 630 individuals were tested with a 27-gene inherited cancer panel and 84% had a family history of cancer. Of these individuals, 65 were determined to have variants classified as pathogenic or likely pathogenic across 14 genes (10.3%). Only 42% of these variants occurred in classic HBOC or Lynch Syndrome-associated genes, while 58% were observed in high or moderate to low risk genes on the panel. The researchers concluded that there is utility to using multi-gene panels over single gene testing particularly in those with an inherited predisposition to cancer.

Giri et al. (2018) reported on a consensus conference for prostate cancer where the goal was to determine the appropriate genetic testing routes. Seventy-one experts participated in the panel and determined that testing of HOXB13 for suspected hereditary prostate cancer was considered to have high grade evidence. Similarly, BRCA1/2 mutations being linked to prostate cancer also provided high grade evidence. The evidence the panel reviewed for DNA mismatch repair genes for suspected Lynch syndrome to prostate cancer risk was considered moderate grade. Both ATM and NBN mutations were considered to be emerging but not quite moderate grade. Other genes on many panels were determined to have low or insufficient data to determine the prostate cancer risk. The authors conclude that additional research is needed to develop more appropriate definitions for hereditary prostate cancer genetic testing.

An analysis of 252,223 individuals by a 25-gene pan-cancer panel was performed by Rosenthal et al. (2017). Of these individuals, the majority (92.8%) met testing criteria for HBOC and/or Lynch syndrome (LS). Pathogenic variants were identified in 6.7% of the tested individuals with BRCA1/2 (42.2%), other breast cancer (BR) genes (32.9%), and the LS genes (13.2%). However, half of the pathogenic variants in individuals who met only HBOC criteria were in non-BRCA1/2 genes. Likewise, in individuals who met LS criteria, half of the pathogenic variants identified were in non-LS genes. These researchers suggest that a pan-cancer panel may provide improved identification of pathogenic variants over single-syndrome testing.

Bholah and Bunchman (2017) published a review of the literature regarding neuroendocrine tumors pheochromocytoma (PCC) and paraganglioma (PGL) in which they demonstrated that the generally accepted concept of 10% of cancers are inherited may not apply to PCC and PGL. They noted that the European-American-Pheochromocytoma-Paraganglioma-Registry (EAPPR) has released data that 80% of individuals in their registry had a germline mutation, and smaller series of reports gave a germline mutation prevalence of 30-40%. Genes that are involved in PCC and PGL include genes responsible for known neuroendocrine syndromes such as von Hippel Lindau (VHL), multiple endocrine neoplasia type II (RET) and neurofibromatosis I (NF1), as well as mitochondrial related genes. These include the subunits for succinate dehydrogenase, SDHA, SDHB, SDHC, SDHD and SDHAF2, and the TMEM, HIPF2A and MAX genes. Variants in these genes can cause rare autosomal dominant PGL-PCC syndromes with varying penetrance.

A retrospective study by Babic et al. (2017) analyzed pediatric pheochromocytomas and paragangliomas to determine the role of genetic testing. Of 55 patients, 44 (80%) had a germline mutation with the majority found to have either VHL (38%) or SDHB (25%) mutation. The authors concluded that the majority of pediatric patients with pheochromocytomas and paragangliomas likely have detectable germline mutations and thus, genetic testing may be helpful to guide treatment.

Pilié et al. (2017) used a multi-gene panel to sequence germline DNA from 102 men with prostate cancer and at least one additional primary cancer who also met one of three additional criteria. The researchers identified over 3500 variants including deleterious or likely pathogenic germline mutations in 11 of the 102 men (10.8%) of men. Eight of the men had germline variants in 1 of 6 cancer predisposition genes including BRCA2 (three cases), ATM (two cases) and one case in MLH1. The researchers concluded that men with prostate cancer and at least 1 additional primary cancer may have a germline deleterious mutation.

In October of 2016, the American Association of Cancer Research (AACR) held the Childhood Cancer Predisposition Workshop. International experts in care of children with a hereditary risk of cancer met to define surveillance strategies and management of children with cancer predisposition syndromes. Several consensus publications resulted. Achatz et al. (2017) focused on inherited polyposis gastrointestinal syndrome cancers of childhood, and published consensus guidelines established by their expert panel from the workshop, which included recommendations on genetic testing strategies. They noted that children at risk for an inherited polyposis syndrome are typically identified in two ways; through family history, because a close family member has been diagnosed and second, because the child has symptoms. In the first clinical scenario, the expert panel recommends first testing the affected blood relative in order to ensure that highly accurate and actionable

results are available for the family. Genetic testing in the child should be only for the familial pathogenic variant, and not take place until 1 year before the age at which the first surveillance action would occur. This allows time for coordination of genetic counseling and testing. In the second scenario, when the child presents with symptoms, genetic testing should be targeted for the gene most likely to be causative, when possible. For example, if the presenting symptom is congenital hypertrophy of the retinal pigment epithelia (CHRPE) associated with familial adenomatous polyposis (FAP), testing should be for the APC gene. This will help assure high specificity with fewer variants of unknown significant or unanticipated findings. The expert panel noted, however, that many of these disorders have broad, overlapping clinical presentations and in some cases, when clinical features can't identify the most likely syndrome, a multi-gene hereditary cancer panel may be time efficient and cost effective in identifying a causative variant. The expert panel cautions that the larger the panel, the more likely it is that a variant of unknown significance will be found, and the chance of identifying an incidental, adult onset disorder goes up. Genetic counseling is highly recommended.

Druker et al. (2017) reported on genetic counselor recommendations for testing and surveillance for pediatric cancers from the 2016 AACR Childhood Cancer Predisposition Workshop. The authors note that with the advent of NGS technology, it is increasingly common for patients with childhood cancer to undergo somatic genetic testing of their tumor, or undergo germline testing using large gene sequencing panels, genome-wide chromosomal microarrays, and/or whole exome/genome sequencing. Given the lack of guidelines for genetic counseling and testing in the pediatric cancer population, the authors provide expert consensus recommendations for when to refer to pediatric cancer genetics clinics, pretest counseling and informed consent and assent for cancer genetic testing of children, test selection and timing of testing, posttest counseling, and psychosocial aspects of cancer surveillance for children with hereditary cancer syndromes. It is recommended that the child and family be referred to genetic counseling at the time that the tumor is diagnosed or germline genetic testing is being considered. When considering a genetic testing, the clinician should consider the clinical presentation and family history to determine whether to order a test for a familial variant or a broader panel. The authors recommend that when a family pathogenic variant is known, the test ordered should be only for that variant. They note that this is the least expensive and most efficient approach, and if possible the same lab the identified the mutation in the initial family member should be use. When the patient's presentation clearly fits a specific syndrome, only the gene(s) for that specific syndrome should be tested. This ensures the greatest specificity and reduces the risk of a variant of unknown significance. When a patient presents with symptoms that can be explained by multiple syndromes, a multi-gene hereditary cancer panel can be considered. This increases the chance that a causative variant will be identified. However, it also increases the chance that a variant of unknown significance will be identified, as well as variants in moderate-risk genes for which limited surveillance or clinical management recommendations may be available. Finally, whole exome or genome sequencing should be considered for those with multi-system phenotypes, those with negative multi-gene panel results, and for those wanting to participate in research. The limitations noted with whole exome or genome sequencing include, but are not limited to, inconsistent coverage of genes of interest, inconsistent coverage of copy number variants, the greatest chance of finding variants of unknown significance or incidental findings, and challenges in storing and reinterpreting data. Finally, the clinician should ensure that the test ordered includes the gene(s) of interest, the testing methodology and variant interpretation have been well validated, should understand the labs reinterpretation practices, cost, turnaround time, and the laboratory's policies regarding data sharing.

Hermel et al. (2017) described the experience of a rural Familial Cancer Program implementing multi-gene panel testing. They conducted a retrospective review of patients undergoing panel testing between May 2011 and August 2015. A total of 236 patients were identified. Seven were denied testing by insurance, and two cancelled, leaving 227 patients who completed the process. Patients were at risk for hereditary cancer syndromes based on personal or family history. Most, 84%, had a personal history of cancer, and 25% had multiple primary tumors. Breast Cancer was most common in 80% of patients with single primary tumors, followed by 16% with a history of polyps with 8% had a concomitant history of cancer. About 20% of patients had already had either BRCA1/2 or MSH2 testing prior to the multi-gene panel. Sixty seven patients had reportable finding. Twenty eight, 12%, had a pathogenic variant identified in one of the following genes: PLAB2, ATM, BARD1, CDKN2A, CHEK2, GALNT12, NBN, PMS2, APC, BRCA1, BRCA, or MUTYH. Forty four patients, 19%, had a variant of unknown significance (VUS), and five had both a pathogenic variant and a VUS. An additional three patients had two VUS. Of the patients with a pathogenic variant, 36%, representing 4% of the overall cohort had a variant in a highly penetrant gene with an odds ratio over 5 for organ specific cancer.

Nguyen et al. (2017) published a retrospective review of the use of a 19 gene hereditary cancer panel in patients diagnosed with kidney cancer. Patients were tested at a commercial laboratory from August 2013 to June 2016. Clinical characteristics such as age, gender, age of diagnosis, ordering institution, kidney cancer histology, personal history and cancer history were obtained from test requisitions. In total, 1235 patients with renal cell carcinoma had testing. The majority of the cohort was

Caucasian (64%) and male (54%). The average age of diagnosis was 46. Histology was available on 942 patients and common tumor histology such as clear cell, papillary and chromophobe kidney tumors was present in 67% of these individuals. The remainder reported less common and mixed histology. Overall, 859 had only kidney cancer, and 283 had an additional primary cancer, and 93 had more than two primary cancers. A positive family history for cancer was reported in 1007 patients, and of these, 369 reported a family history of kidney cancer. Half of all cases were referred by university based hospitals, 44% from non-university hospitals, 4.5% from private practice clinicians. Genetics providers referred 81% of cases, oncologists 14%, non-oncology physicians 1%, and other healthcare providers referred the remainder. Overall, 6.1% had a pathogenic variant identified, 18% had a variant of unknown significance, and the remainder had a negative result. Mutations were found in 15 of the 19 genes in the panel. The genes with the highest rate of mutations were FLCN, FH, MITF and SDHB. The authors note that their study was limited by the retrospective review and the reliance on submitted histology information and not a centralized pathology review. It was additionally noted that panel tests are relatively new, and the larger the panel, the more likely that variants of unknown significance (VUS) are found. The outcomes and decisions by treating physicians were not available, but it has been hypothesized that clinicians may act and medically intervene for VUS where it may not be warranted. However, this is the first publication to report on the results for a large cohort for kidney cancer patients undergoing multi-gene hereditary cancer panel testing.

Parsons et al. (2016) conducted a study to determine the prevalence of somatic and germline mutations in children with solid tumors. From August 2012 through June 2014, children with newly diagnosed and previously untreated central nervous system (CNS) and non-CNS solid tumors were prospectively enrolled in the study at a large academic children's hospital. Blood and tumor samples underwent whole exome sequencing (WES) in a certified clinical laboratory with genetic results categorized by clinical relevance. A total of 150 children participated, with a mean age of 7 years, with 80 boys and 70 girls. Tumor samples were available for WES in 121 patients. In this group, somatic mutations with established clinical utility were found in 4 patients, and mutations with possible clinical utility were found in 29. CTNNB1 had the most mutations, followed by KIT, TSC2, BRAF, KRAS, and NRAS. Diagnostic germline mutations related to the child's clinical presentation was found in 150 patients and included 13 dominant mutations in known cancer susceptibility genes, including TP53, VHL, and BRCA1. One recessive liver disorder with liver cancer was identified in TJP2 and one renal cancer, CLCN5. Incidental findings were found in 8 patients. Nearly all patients (98%) had variants of unknown significance in known cancer genes, drug response genes, and genes known to be associated with recessive disorders.

Lincoln et al. (2015) tested 1105 individuals using a 29-gene NGS panel. The 1105 cases included 1062 clinical cases (735 patients prospectively accrued following NCCN guidelines for HBOC, 118 patients with known familial mutations, 209 patients retrospectively collected with high-risk criteria). Of the 1062 clinical cases, 975 had previously received BRCA1/2 testing and the results showed a concordance of 99.8%. Overall, 260 variants were determined. The 735 prospective patients had 66 patients (9.0%) with a BRCA1 or BRCA2 variant. Twenty-six patients (3.9%) were BRCA-negative but had variants in other genes with known associated to breast/ovarian cancer or those associated with Lynch syndrome. Most common non-BRCA findings were ATM (five cases), PALB2 (five cases), CHEK2 (three cases), and the Lynch syndrome genes (eight cases). Another 2.7% of these BRCA-negative patients were carriers of MUTYH. The high-risk patients (n=2009) were determined to have BRCA1 or BRCA2 in 40% of the patients and of the BRCA-negative individuals, 6.1% were positive of another variant. The researchers found that variants of uncertain significance (VUS) increased as the number of genes was tested. Of the 1062 clinical cases, 41.0% had at least one VUS and of those 11.4% had two or more. Additionally, 68% of the VUS detected were rare, missense variants that were not identified in the 1000Genomes Project. They concluded that NGS testing of panels can offer results that may be missed by traditional testing, but the issue with understanding and addressing VUS remains a challenge.

Zhang et al. (2015) studied the prevalence of cancer pre-disposition germline mutations in children and adolescents with cancer in 1,120 patients under the age of 20. Whole exomes were sequenced in 456 patients and whole genomes were sequenced in 595, or both in 69. Results were analyzed in 565 genes, including 60 that are associated with autosomal dominant cancer syndromes. Genetic variant pathogenicity was determined by a team of experts who relied on peer reviewed literature, cancer and locus specific databases, computational predictions, and second hits identified in the participant tumor genome. This same variant calling approach was used to analyze data on 966 controls from the 1000 Genomes Projects who were not known to have cancer, and data from 733 children from an autism study. Overall, germline mutations were found in 95 children with cancer (8.5%), as compared to only 1.1% of 1000 Genome Project and 0.6% of autism study controls. The mutations were most commonly found in TP53, APC, BRCA2, NF1, PMS2, RB1 and RUNX3. Eighteen patients also have variants in tumor suppressor genes. Of the 58 patients who had family history information available and a mutation in a predisposing dominant cancer gene, 40% had a significant family history of cancer.

Clinical Practice Guidelines

American College of Gastroenterology (ACG)

The ACG published recommendations for the management of patients with hereditary gastrointestinal cancer syndromes, including genetic testing recommendations (Syngal et al., 2015). The authors note that genetic testing is widely available and should be part of standard of care of patients at increased risk for a hereditary cancer syndrome. The guidelines recommend targeted gene analysis for the syndrome most likely to be responsible for an individual's symptoms. The authors address multigene panels and NGS technology, noting that genetic specialists are increasingly using NGS panels for patients with more than one genetic syndrome on the differential diagnosis list, as testing for multiple conditions at once can decrease costs and be time efficient when compared to sequentially screening the possible list of genes. It is additionally noted, however, that even though there might be time efficiency compared to sequential screening, the time to results is typically longer for large panels. The larger the panel, the more likely it is that variants of unknown significance will be found. In addition, the authors caution that these panels often include genes for which there is little data on how to manage cancer risks, and sometimes the degree of cancer risk is unknown. The clinician is no better off and must manage the patient based on family and medical history, which can cause confusion for the patient. At the time of publication, the authors do not recommend multiple gene sequencing, but note that in the future it may be likely that at risk patients may be screened simultaneously for all hereditary cancer syndrome genes.

American Society of Clinical Oncology (ASCO)

Genetic testing for cancer susceptibility may be efficient in circumstances where the medical and family history of a patient require evaluation of multiple high-penetrance genes that have established clinical utility. Because such panels might include genes with low to moderate penetrance, and results could include variants of unknown significant, it is recommended that providers with particular expertise in cancer risk assessment should be involved in the ordering and interpretation of multigene panels, especially those that include genes of uncertain clinical utility and genes not suggested by the patient's personal and/or family history (Robson et al., 2015).

Endocrine Society

An algorithm for genetic testing when a PGL-PCC syndrome is suspected was developed by the Endocrine Society task force, comprised of members from the Endocrine Society, European Society of Endocrinology, and American Association for Clinical Chemistry (Lenders et al., 2014). Identifying which gene is responsible for a suspected PGL-PCC syndrome can aid in determining a therapeutic approach. When a PCC or PGL is present, the patient's family and medical history should be examined for known syndrome of NF1, MEN II and VHL, and if appropriate, targeted genetic testing should take place. In the presence of metastatic disease, the succinate dehydrogenase subunit genes should be evaluated. In non-metastatic disease, and the absence of a clear syndrome, genetic testing should be targeted on the basis of other laboratory results for adrenal and extra-adrenal adrenergic results:

- Extra-adrenal:
  - Dopaminergic – SDHB, SDHD, SDHC
  - Noradrenergic – SDHB, SDHD, SDHC, VHL, MAX
- Adrenal:
  - Dopaminergic – *SDHB, SDHD, SDHC*
  - Noradrenergic – *VHL, if negative, SDHB, SDHD, SDHC, MAX*
  - Adrenergic – *RET, if negative, TMEM127, MAX*

Genetic Testing of BRCA1/2 or Multi-Gene Hereditary Cancer Panels with RNA Testing

There is insufficient evidence to support the use of RNA testing as part of genetic testing of BRCA1/2 or multi-gene hereditary cancer panels. The quality of the studies was low due to small study populations, short follow-up, and lack of randomization and appropriate control groups.

A recent study by Landrith et al. (2020) reported on a collaboration of Ambry Genetics with 19 other clinical institutions. The researchers evaluated 18 tumor suppressor genes in 345 samples from healthy donors to develop splicing profiles. The study then assessed the utility of this splicing profile on 1000 patients with suspected hereditary cancer syndromes. The RNA testing coupled with DNA testing was performed and the RNA testing identified seven patients with pathogenic mutations that would have been negative or inconclusive with DNA testing alone. For six of the seven, medical management changes would likely be recommended. This analysis showed a 9.1% relatively increase in diagnostic yield when RNA testing is performed.

Karam et al. (2019) evaluated patients with inconclusive variants after DNA testing to determine if RNA testing improved the data. The study included patients and/or families with hereditary breast and ovarian cancer, Lynch syndrome, and hereditary diffuse gastric cancer. Only 93 of 909 eligible familes sent in additional tests. The RNA testing results clarified the interpretation of 49 of 56 inconclusive cases (88%) studied. However only 26 (47%) were reclassified as clinically actionable and the remaining 23 (41%) were clarified as benign. An additional section of this study evaluated 307,812 patient results that had only undergone DNA testing and the researchers determined that 7,265 of these had inconclusive variants that affect splicing. Overall, taking into account the previous study, approximately 1 in 43 individuals may benefit from RNA testing.

U.S. Food and Drug Administration (FDA)

This section is to be used for informational purposes only. FDA approval alone is not a basis for coverage.

Laboratories that perform genetic tests are regulated under the Clinical Laboratory Improvement Amendments (CLIA) Act of 1988. More information is available at:
https://www.fda.gov/medicaldevices/deviceregulationandguidance/ivdregulatoryassistance/ucm124105.htm.
(Accessed August 28, 2020)

Centers for Medicare and Medicaid Services (CMS)

Medicare does cover Next Generation Sequencing when criteria are met. See the National Coverage Determination (NCD) for Next Generation Sequencing (NGS) (90.2). Local Coverage Determinations (LCDs)/Local Coverage Articles (LCAs) exist. Refer to the following LCDs/LCAs at https://www.cms.gov/medicare-coverage-database/overview-and-quick-search.aspx?kq=true:

- BRCA1 and BRCA2 Genetic Testing
- Biomarkers for Oncology
- MolDX: BRCA1 and BRCA2 Genetic Testing
- Genetic Testing for Lynch Syndrome
- MolDX: APC and MUTYH Gene Testing
- MolDX: Genetic Testing for Lynch Syndrome
- MolDX: Molecular Diagnostic Tests (MDT)
- MolDX: Myriad's BRACAnalysis CDx®
- MolDX: Repeat Germline Testing
- MolDX: Testing of Multiple Genes
- Molecular Diagnostic Tests (MDT)
- Molecular Pathology Procedures

(Accessed September 4, 2020)

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Policy History/Revision Information

Date	Summary of Changes
05/01/2021	**Template Update** • Replaced content sub-heading titled "Professional Societies" with "Clinical Practice Guidelines" in *Clinical Evidence* section • Removed *CMS* section • Replaced reference to "MCG™ Care Guidelines" with "InterQual® criteria" in *Instructions for Use* **Application** • Added language to indicate this policy does not apply to the state of Indiana; refer to the state-specific policy version
02/01/2021	**Application** • Reformatted content • Added language to indicate this policy does not apply to the state of Kentucky; refer to the state-specific policy version
01/01/2021	**Applicable Codes** • Updated list of applicable CPT codes for Multi-Gene Panel to reflect annual edits; added 0238U **Supporting Information** • Archived previous policy version CS049.N

Instructions for Use

This Medical Policy provides assistance in interpreting UnitedHealthcare standard benefit plans. When deciding coverage, the federal, state or contractual requirements for benefit plan coverage must be referenced as the terms of the federal, state or contractual requirements for benefit plan coverage may differ from the standard benefit plan. In the event of a conflict, the federal, state or contractual requirements for benefit plan coverage govern. Before using this policy, please check the federal, state or contractual requirements for benefit plan coverage. UnitedHealthcare reserves the right to modify its Policies and Guidelines as necessary. This Medical Policy is provided for informational purposes. It does not constitute medical advice.

UnitedHealthcare may also use tools developed by third parties, such as the InterQual® criteria, to assist us in administering health benefits. The UnitedHealthcare Medical Policies are intended to be used in connection with the independent professional medical judgment of a qualified health care provider and do not constitute the practice of medicine or medical advice.