Medical Policy

BlueCross BlueShield Kansas
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Title: Germline Genetic Testing for Hereditary Breast/Ovarian Cancer Syndrome and Other High-Risk Cancers (BRCA1, BRCA2, PALB2)

Prior Authorization of Services may be required by Member's Contract.
http://www.bcbsks.com/CustomerService/Forms/pdf/15-17_predeterm_request_frm.pdf

Related Policies:	▪ *Genetic Cancer Susceptibility Panels Using Next Generation Sequencing* ▪ *Risk-Reducing Mastectomy* ▪ *Germline and Somatic Biomarker Testing (Including Liquid Biopsy) for Targeted Treatment and Immunotherapy in Breast Cancer*

Professional	**Institutional**
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Populations	Interventions	Comparators	Outcomes
Individuals: • With cancer or personal or family cancer history and criteria suggesting risk of hereditary breast/ovarian cancer syndrome	Interventions of interest are: • Genetic testing for a BRCA1 or BRCA2 variant	Comparators of interest are: • Standard of care without genetic testing	Relevant outcomes include: • Overall survival • Disease-specific survival • Test validity • Quality of life
Individuals: • With other high-risk cancers (e.g., cancers of the fallopian tube, pancreas, prostate)	Interventions of interest are: • Genetic testing for a BRCA1 or BRCA2 variant	Comparators of interest are: • Standard of care without genetic testing	Relevant outcomes include: • Overall survival • Disease-specific survival • Test validity • Quality of life
Individuals: • With risk of hereditary breast/ovarian cancer syndrome	Interventions of interest are: • Genetic testing for a *PALB2* variant	Comparators of interest are: • No genetic testing for *PALB2* variants	Relevant outcomes include: • Overall survival • Disease-specific survival • Test validity

DESCRIPTION

Hereditary breast and ovarian cancer syndrome describe the familial cancer syndromes related to variants in the *BRCA* genes (*BRCA1* located on chromosome 17q21, *BRCA2* located on chromosome 13q12-13). The *PALB2* gene is located at 16p12.2 and has 13 exons. PALB2 protein assists *BRCA2* in DNA repair and tumor suppression. Families with hereditary breast and ovarian cancer syndrome have an increased susceptibility to the following types of cancer: breast cancer

occurring at a young age, bilateral breast cancer, male breast cancer, ovarian cancer (at any age), cancer of the fallopian tube, primary peritoneal cancer, prostate cancer, pancreatic cancer, gastrointestinal cancers, melanoma, and laryngeal cancer.

OBJECTIVE

The objective of this evidence review is to determine whether germline genetic testing for *BRCA1*, *BRCA2*, or *PALB2* variants improves the net health outcomes in individuals with cancer or who have a personal or family history of cancer, which might suggest hereditary breast/ovarian cancer syndrome or other high-risk cancers.

BACKGROUND

Hereditary Breast and Ovarian Cancer Syndrome

Several genetic syndromes with an autosomal dominant pattern of inheritance that features breast cancer have been identified. Of these, hereditary breast and ovarian cancer (HBOC)syndrome and some cases of hereditary site-specific breast cancer have in common causative variants in *BRCA* (breast cancer susceptibility) genes. Families suspected of having HBOC syndrome are characterized by an increased susceptibility to breast cancer occurring at a young age, bilateral breast cancer, male breast cancer, ovarian cancer at any age, as well as cancer of the fallopian tube and primary peritoneal cancer. Other cancers, such as prostate cancer, pancreatic cancer, gastrointestinal cancers, melanoma, and laryngeal cancer, occur more frequently in HBOC families. Hereditary site-specific breast cancer families are characterized by early-onset breast cancer with or without male cases, but without ovarian cancer. This evidence review refers collectively to both as *hereditary breast and/or ovarian cancer*.

Germline variants in the *BRCA1* and *BRCA2* genes are responsible for the cancer susceptibility in most HBOC families, especially if ovarian cancer or male breast cancer are features. However, in site-specific cancer, BRCA variants are responsible only for a proportion of affected families. *BRCA* gene variants are inherited in an autosomal dominant fashion through maternal or paternal lineage. It is possible to test for abnormalities in *BRCA1* and *BRCA2* genes to identify the specific variant in cancer cases and to identify family members at increased cancer risk. Family members without existing cancer who are found to have *BRCA* variants can consider preventive interventions for reducing risk and mortality.

Evidence suggests that genetic services are not equitably applied. Chapman-Davis et al (2021) found that non-Hispanic Whites and Asians were more likely to be referred for genetic services based solely on family history than were non-Hispanic Blacks and Hispanics.[1,] In addition, non-Hispanic Black patients and Hispanic patients were more likely to have advanced cancer when referred for genetic services than non-Hispanic Whites and Asians.

Clinical Features Suggestive of *BRCA* Variant

Young age of onset of breast cancer, even in the absence of family history, is a risk factor for *BRCA1* variants. Winchester (1996) estimated that hereditary breast cancers account for 36% to 85% of patients diagnosed before age 30 years.[2,] In several studies, *BRCA* variants were independently predicted by early age at onset, being present in 6% to 10% of breast cancer cases diagnosed at ages younger than various premenopausal age cutoffs (age range, 35 to 50

years).[2,3,4,5,] In cancer-prone families, the mean age of breast cancer diagnosis among women carrying *BRCA1* or *BRCA2* variants is in the 40s.[6,] In the Ashkenazi Jewish population, Frank et al (2002) reported that 13% of 248 cases with no known family history and diagnosed before 50 years of age had *BRCA* variants.[3,] In a similar study by Gershoni-Baruch et al (2000), 31% of Ashkenazi Jewish women, unselected for family history, diagnosed with breast cancer at younger than 42 years of age had *BRCA* variants.[7,] Other studies have indicated that early age of breast cancer diagnosis is a significant predictor of BRCA variants in the absence of family history in this population.[8,9,10,]

As in the general population, a family history of breast or ovarian cancer, particularly of early age onset, is a significant risk factor for a *BRCA* variant in ethnic populations characterized by founder mutations. For example, in unaffected individuals of Ashkenazi Jewish descent, 12% to 31% will have a *BRCA* variant depending on the extent and nature of the family history.[5,] Several other studies have documented the significant influence of family history.[7,8,9,10,11,]

In patients with "triple-negative" breast cancer (ie, negative for expression of estrogen, progesterone, and overexpression of human epidermal growth factor receptor 2 receptors), there is an increased prevalence of *BRCA* variants. Pathophysiologic research has suggested that the physiologic pathway for the development of triple-negative breast cancer is similar to that for *BRCA*-associated breast cancer.[12,] In 200 randomly selected patients with triple-negative breast cancer from a tertiary care center, Kandel et al (2006) reported there was a greater than 3-fold increase in the expected rate of *BRCA* variants.[13,]*BRCA1* variants were found in 39.1% of patients and *BRCA2* variants in 8.7%. Young et al (2009) studied 54 women with high-grade, triple-negative breast cancer with no family history of breast or ovarian cancer, representing a group that previously was not recommended for *BRCA* testing.[14,] Six BRCA variants (5 *BRCA1*, 1 *BRCA2*) were found, for a variant rate of 11%. Finally, Gonzalez-Angulo et al (2011) in a study of 77 patients with triple-negative breast cancer, reported that 15 patients (19.5%) had BRCA variants (12 in *BRCA1*, 3 in *BRCA2*).[15,]

PALB2 **Gene**

The *PALB2* gene (partner and localizer of *BRCA2*) encodes for a protein first described in 2006.[16,] The gene is located at 16p12.2 [Short (p) arm of chromosome 16 at position 12.2.] and has 13 exons. PALB2 protein assists *BRCA2* in DNA repair and tumor suppression. Heterozygous pathogenic *PALB2* variants increase the risk of developing breast and pancreatic cancers; homozygous variants are found in Fanconi anemia. Fanconi anemia is a rare disorder, primarily affecting children, that causes bone marrow failure. Affected individuals also carry a risk of cancers including leukemia. Most pathogenic *PALB2* variants are truncating frameshift or stop codons, and are found throughout the gene. Pathogenic *PALB2* variants are uncommon in unselected populations and prevalence varies by ethnicity and family history. For example, Antoniou et al (2014) assumed a prevalence of 8 per 10,000 in the general population when modeling breast cancer risks.[17,] Variants are more prevalent in ethnic populations where founder mutations have persisted (e.g., Finns, French Canadians, Poles), while infrequently found in others (e.g., Ashkenazi Jews).[18,19,] In women with a family history of breast cancer, the prevalence of pathogenic *PALB2* variants ranges between 0.9% and 3.9%,[17,] or substantially higher than in an unselected general population. Depending on population prevalence, *PALB2* may be responsible for as much as 2.4% of hereditary breast cancers[17,]; and in populations with founder mutations cause 0.5% to 1% of all breast cancers.[20,]

REGULATORY STATUS

Clinical laboratories may develop and validate tests in-house and market them as a laboratory service; laboratory-developed tests must meet the general regulatory standards of the Clinical Laboratory Improvement Amendments. Genetic tests reviewed in this evidence review are available under the auspices of the Clinical Laboratory Improvement Amendments. Laboratories that offer laboratory-developed tests must be licensed by the Clinical Laboratory Improvement Amendments for high-complexity testing. To date, the U.S. Food and Drug Administration (FDA) has chosen not to require any regulatory review of this test.

POLICY

Genetic testing should be performed in a setting that has suitably trained healthcare providers who can give appropriate pre- and post-test counseling and that has access to a Clinical Laboratory Improvement Amendments (CLIA)–licensed laboratory that offers comprehensive variant analysis (see Policy Guidelines: Comprehensive Variant Analysis).

A. **Individuals With Cancer or With a Personal History of Cancer**
Genetic testing for *BRCA1*, *BRCA2,* and *PALB2* variants in cancer-affected individuals may be considered **medically necessary** under any of the following circumstances:

1. Individuals with any close blood relative with a known *BRCA1, BRCA2,* or *PALB2* pathogenic/likely pathogenic variant (see Policy Guidelines for definitions and for testing strategy).

2. Individuals meeting the criteria below but with previous limited testing (e.g., single gene and/or absent deletion duplication analysis)

3. Personal history of breast cancer and 1 or more of the following:

    a. Diagnosed at age ≤45 years; **OR**

    b. Diagnosed 46 to 50 years with:
        I. One or more close blood relative (see Policy Guidelines) with breast cancer, ovarian, pancreatic, or prostate cancer at any age; **OR**
        II. An unknown or limited family history; **OR**
        III. An additional breast cancer primary at any age

    c. Diagnosed ≤60 years with:
        I. Triple negative breast cancer (see Policy Guidelines)

    d. Diagnosed at any age with:
        I. One or more close blood relative with
            i. Breast cancer diagnosed at ≤50 years; **OR**
            ii. Ovarian, fallopian tube, or primary peritoneal cancer; **OR**
            iii. Metastatic or intraductal/cribriform prostate cancer, or high-risk group or very-high-risk group (see Policy Guidelines) prostate cancer; **OR**
            iv. Pancreatic cancer
        II. ≥3 total diagnoses of breast cancer at any age in individual and/or close blood relatives; **OR**
        III. Ashkenazi Jewish ancestry

    e. Diagnosed at any age with male breast cancer

4. Personal history of epithelial ovarian, fallopian tube, or primary peritoneal cancer at any age

5. Personal history of exocrine pancreatic cancer at any age

6. Personal history of metastatic or intraductal/cribriform histology prostate cancer at any age; or high-risk group or very-high-risk group prostate cancer at any age

7. Personal history of prostate cancer at any age with:
   a. One or more close blood relative with ovarian, fallopian tube, or primary peritoneal cancer, pancreatic cancer, or metastatic or intraductal/cribriform prostate cancer at any age or breast cancer ≤50 years; **OR**
   b. Two or more close blood relatives with breast or prostate cancer (any grade) at any age; **OR**
   c. Ashkenazi Jewish ancestry

8. Personal history of cancer and a mutation identified on tumor genomic testing that has clinical implications if also identified in the germline

B. **Individuals Without Cancer or With Other Personal History of Cancer** (see Policy Guidelines: Testing Unaffected Individuals)

1. Genetic testing for *BRCA1, BRCA2,* and *PALB2* variants of cancer-unaffected individuals and individuals with cancer but not meeting the above criteria (including individuals with cancers unrelated to hereditary breast ovarian cancer syndrome) may be considered **medically necessary** under any of the following circumstances:
   a. An individual with or without cancer not meeting the above criteria but who has a 1st- or 2nd-degree blood relative meeting any criterion listed above for individuals with cancer. If the individual with cancer has pancreatic cancer or prostate cancer (metastatic or intraductal/cribriform or high-risk group or very-high-risk group) then only first-degree relatives should be offered testing unless there are other family history indications for testing.
   b. An individual with any type of cancer who otherwise does not meet the criteria above but has a probability >5% of a *BRCA1/2* or *PALB2* pathogenic variant based on prior probability models (*e.g.*, Tyrer-Cuzick, BRCAPro, PennII)

C. Genetic testing for *BRCA1* and *BRCA2* variants in cancer-affected individuals or of cancer-unaffected individuals with a family history of cancer when criteria above are not met is considered **experimental / investigational**.

D. Testing for *PALB2* variants in individuals who do not meet the criteria outlined above is considered **experimental / investigational**.

E. Genetic testing in minors for *BRCA1, BRCA2,* and *PALB2* variants for hereditary breast ovarian cancer syndrome is considered **experimental / investigational**. (see Policy Guidelines)

POLICY GUIDELINES

A. Testing for *BRCA1, BRCA2,* and/or *PALB2* outside of the above criteria, such as testing all individuals with triple negative breast cancer, may be indicated for guiding cancer therapies.

B. Current U.S. Preventive Services Task Force (USPSTF) guidelines recommend screening women with a personal or family history of breast, ovarian, tubal, or peritoneal cancer or who have an ancestry associated with *BRCA1/2* gene mutation. Women with positive screening result on the risk assessment tool should receive genetic counseling and, if indicated after counseling, genetic testing (B Recommendation).

C. Recommended screening tools designed to identify a family history that may be associated with an increased risk for potentially harmful variants in *BRCA1* or *BRCA2* are:
   1. Ontario Family History Assessment Tool (FHAT)
   2. Manchester Scoring System
   3. Referral Screening Tool (RST)
   4. Pedigree Assessment Tool (PAT)
   5. Family History Screen (FHS-7)
   6. International Breast Cancer Intervention Study instrument (Tyrer-Cuziak)
   7. Brief versions of the BRCAPRO

D. **Close Relatives:** Close relatives are blood related family members including 1st-, 2nd-, and 3rd-degree relatives on the same side of the family (maternal or paternal).
   1. 1st-degree relatives are parents, siblings, and children.
   2. 2nd-degree relatives are grandparents, aunts, uncles, nieces, nephews, grandchildren, and half-siblings.
   3. 3rd-degree relatives are great-grandparents, great-aunts, great-uncles, great-grandchildren, and first cousins.

E. **Prostate Cancer Risk Groups:** Risk groups for prostate cancer in this policy include high-risk groups and very-high-risk groups.
   1. High-risk group: no very-high-risk features and are T3a (American Joint Committee on Cancer staging T3a = tumor has extended outside of the prostate but has not spread to the seminal vesicles); OR Grade Group 4 or 5; OR prostate specific antigen of 20 ng/mL or greater.
   2. Very-high-risk group: T3b-T4 (tumor invades seminal vesicle(s); or tumor is fixed or invades adjacent structures other than seminal vesicles such as external sphincter, rectum, bladder, levator muscles, and/or pelvic wall); OR Primary Gleason Pattern 5; OR 2 or 3 high-risk features; OR greater than 4 cores with Grade Group 4 or 5

F. **Recommended Testing Strategies:** Individuals who meet criteria for genetic testing as outlined in the policy statements above should be tested for variants in *BRCA1, BRCA2,* and *PALB2*. Recommended strategies are listed below.
   1. In individuals with a known familial *BRCA* or *PALB2* variant, targeted testing for the specific variant is recommended.
   2. In individuals with unknown familial *BRCA* or *PALB2* variant:
      a. To identify clinically significant variants, National Comprehensive Cancer Network (NCCN) advises testing a relative who has early-onset disease, bilateral disease, multiple primaries, because that individual has the highest likelihood of obtaining a positive test result. Unless the affected individual is a member of an ethnic group for which particular founder pathogenic or likely pathogenic variants are known, comprehensive genetic testing

(*i.e.,* full sequencing of the genes and detection of large gene rearrangements) should be performed

b. If no living family member with breast or ovarian cancer exists, NCCN suggests testing first- or second-degree family members affected with cancer thought to be related to deleterious *BRCA1* or *BRCA2* variants (e.g., prostate cancer, pancreatic cancer, melanoma).

c. If no familial variant can be identified, 2 possible testing strategies are:
   I. Full sequencing followed by testing for large genomic rearrangements (deletions/duplications) only if sequencing detects no variant (negative result).
      i. More than 90% of *BRCA* variants will be detected by full sequencing.
   II. Alternatively, simultaneous full sequencing and testing for large genomic rearrangements (also known as comprehensive *BRCA* testing; see Comprehensive Variant Analysis, below) may be performed as is recommended by NCCN.
      i. Comprehensive testing can detect 92.5% of *BRCA1* or *BRCA2* variants.
   III. If comprehensive BRCA testing is negative, testing for uncommon large genomic rearrangements (e.g., BART) may be done.
   IV. Testing for *uncommon* large rearrangements should not be done unless both sequencing and testing for *common* large rearrangements have been performed and are negative.
      i. Among patients with negative comprehensive testing, BART identified a deleterious variant (positive result) in less than 1%.

d. Ashkenazi Jewish descent
   I. In individuals of know Ashkenazi Jewish descent, one approach is to test for the 3 known founder mutations (185delAG and 5182insC in BRCA1; 6174delT in BRCA2) first.
   II. If testing is negative for founder mutations and if the individual's ancestry also included non-Ashkenazi ethnicity (or if other BRCA1/2 testing criteria are met), comprehensive genetic testing may should be considered

G. **Comprehensive Variant Analysis:** Comprehensive variant analysis currently includes sequencing the coding regions and intron and exon splice sites, as well as testing to detect large deletions and rearrangements that can be missed with sequence analysis alone. In addition, before August 2006, testing for large deletions and rearrangements was not performed, thus some individuals with familial breast cancer who had negative *BRCA* testing before this time may consider repeat testing for the rearrangements (see Policy section for criteria).

H. **High-Risk Ethnic Groups:** Testing of eligible individuals who belong to ethnic populations in which there are well-characterized founder mutations should begin with tests specifically for these variants. For example, founder mutations account for approximately three-quarters of the *BRCA* variants found in Ashkenazi Jewish populations (see Rationale section). When testing for founder mutations is negative, comprehensive variant analysis should then be performed.

I. **Testing Unaffected Individuals:** In unaffected family members of potential *BRCA* or *PALB2* variant families, most test results will be negative and uninformative. Therefore, it is strongly recommended that an *affected* family member be tested first whenever possible to adequately interpret the test. Should a *BRCA or PALB2* variant be found in an affected family member(s), DNA from an *unaffected* family member can be tested specifically for the same variant of the affected family member without having to sequence the entire gene. Interpreting test results for an unaffected family member without knowing the genetic status of the family may be possible in the case of a positive result for an established disease-associated variant but leads to difficulties in interpreting negative test results (uninformative negative) or variants of uncertain significance because the possibility of a causative *BRCA or PALB2* variant is not ruled out.

J. **Testing Minors:** The use of genetic testing for *BRCA1, BRCA2,* or *PALB2* variants for identifying hereditary breast ovarian cancer syndrome has limited or no clinical utility in minors, because there is no change in management for minors as a result of knowledge of the presence or absence of a deleterious variant. In addition, there are potential harms related to stigmatization and discrimination.

K. **Prostate Cancer:** Individuals with *BRCA* or *PALB2* variants have an increased risk of prostate cancer, and individuals with known *BRCA* or *PALB2* variants may, therefore, consider more aggressive screening approaches for prostate cancer.

L. **Genetics Nomenclature Update:** The Human Genome Variation Society nomenclature is used to report information on variants found in DNA and serves as an international standard in DNA diagnostics. It is being implemented for genetic testing medical evidence review updates starting in 2017 (see Table PG1). The Society's nomenclature is recommended by the Human Variome Project, the Human Genome Organization, and by the Human Genome Variation Society itself.

The American College of Medical Genetics and Genomics and the Association for Molecular Pathology standards and guidelines for interpretation of sequence variants represent expert opinion from both organizations, in addition to the College of American Pathologists. These recommendations primarily apply to genetic tests used in clinical laboratories, including genotyping, single genes, panels, exomes, and genomes. Table PG2 shows the recommended standard terminology- "pathogenic," "likely pathogenic," "uncertain significance," "likely benign," and "benign"- to describe variants identified that cause Mendelian disorders.

Table PG1. Nomenclature to Report on Variants Found in DNA

Previous	Updated	Definition
Mutation	Disease-associated variant	Disease-associated change in the DNA sequence
	Variant	Change in the DNA sequence
	Familial variant	Disease-associated variant identified in a proband for use in subsequent targeted genetic testing in first-degree relatives

Table PG2. American College of Medical Genetics and Genomics and the Association for Molecular Pathology Standards and Guidelines for Variant Classification

Variant Classification	Definition
Pathogenic	Disease-causing change in the DNA sequence
Likely pathogenic	Likely disease-causing change in the DNA sequence
Variant of uncertain significance	Change in DNA sequence with uncertain effects on disease
Likely benign	Likely benign change in the DNA sequence
Benign	Benign change in the DNA sequence

M. **Genetic Counseling:** Genetic counseling is primarily aimed at patients who are at risk for inherited disorders, and experts recommend formal genetic counseling in most cases when genetic testing for an inherited condition is considered. The interpretation of the results of genetic tests and the understanding of risk factors can be very difficult and complex. Therefore, genetic counseling will assist individuals in understanding the possible benefits and harms of genetic testing, including the possible impact of the information on the individual's family. Genetic counseling may alter the utilization of genetic testing substantially and may reduce inappropriate testing. Genetic counseling should be performed by an individual with experience and expertise in genetic medicine and genetic testing methods.

Please refer to the member's contract benefits in effect at the time of service to determine coverage or non-coverage of these services as it applies to an individual member.

RATIONALE

This evidence review has been updated regularly with searches of the PubMed database. The most recent literature update was performed through June 22, 2022.

This review was informed by a TEC Assessment (1997).[21,]

Evidence reviews assess whether a medical test is clinically useful. A useful test provides information to make a clinical management decision that improves the net health outcome. That is, the balance of benefits and harms is better when the test is used to manage the condition than when another test or no test is used to manage the condition.

The first step in assessing a medical test is to formulate the clinical context and purpose of the test. The test must be technically reliable, clinically valid, and clinically useful for that purpose. Evidence reviews assess the evidence on whether a test is clinically valid and clinically useful. Technical reliability is outside the scope of these reviews, and credible information on technical reliability is available from other sources.

TESTING FOR *BRCA1* AND *BRCA2* VARIANTS IN INDIVIDUALS AT RISK FOR HEREDITARY BREAST/OVARIAN CANCER SYNDROME OR OTHER HIGH-RISK CANCERS

Clinical Context and Test Purpose

The purpose of testing for *BRCA1* and *BRCA2* variants in individuals at high-risk for hereditary breast and ovarian cancer (HBOC) syndrome is to evaluate whether variants are present and if so, to determine the appropriate surveillance and treatment to decrease the risk of mortality from breast and/or ovarian cancer.

The question addressed in this evidence review is: Does testing for *BRCA1* and *BRCA2* variants improve the net health outcome in individuals with or suspected of having HBOC syndrome or other high-risk cancers?

The following PICO was used to select literature to inform this review.

Populations

The relevant population of interest is patients with cancer (ie, breast cancer, epithelial ovarian, fallopian tube, primary peritoneal cancer), or patients with a personal or family history of cancer and criteria that might suggest they are at risk of HBOC syndrome.

Interventions

The intervention of interest is *BRCA1* and *BRCA2* variant testing.

For patients without a cancer diagnosis who are assessing cancer risk, results may guide potential prophylactic measures such as surveillance, chemoprevention, or prophylactic mastectomy, and/or oophorectomy.

For patients with a cancer diagnosis, results may guide treatment decisions.

Testing for *BRCA1* and *BRCA2* variants is conducted in adults when appropriate treatment and/or prophylactic treatment options are available.

Comparators

The following practice is currently being used to manage HBOC syndrome or other high-risk cancers: standard of care without genetic testing.

Outcomes

The outcomes of interest are overall survival (OS), disease-specific (breast and ovarian cancer) survival, test validity, and quality of life (QOL; e.g., anxiety).

Study Selection Criteria

For the evaluation of clinical validity, studies of variant prevalence and cancer risk were included. For the evaluation of clinical utility, studies that represent the intended clinical use of the technology in the intended population were included. The quality and credibility of the evidence depend on study design and conduct, minimizing bias and confounding that can generate incorrect findings.

Evidence for the 2 indications is presented together because there is overlap in the evidence base for the 2 populations: (1) patients at risk of HBOC syndrome, and (2) patients with other high-risk cancers such as cancers of the fallopian tube, pancreas, and prostate.

Clinically Valid
A test must detect the presence or absence of a condition, the risk of developing a condition in the future, or treatment response (beneficial or adverse).

REVIEW OF EVIDENCE

Prevalence of *BRCA* Variants and Risks of Cancer and Survival

The prevalence of *BRCA* variants is approximately 0.1% to 0.2% in the general population. The prevalence may be much higher for particular ethnic groups with characterized founder mutations (e.g., 2.5% [1/40] in the Ashkenazi Jewish population). Family history of breast and ovarian cancer is an important risk factor for the *BRCA* variant; additionally, age and ethnicity could be independent risk factors.

Systematic Reviews

A systematic review published by Zhu et al (2016) found a significantly lower risk of OS in breast cancer patients with *BRCA1* (pooled hazard ratio [HR], 1.69; 95% confidence interval [CI], 1.35 to 2.12) and with *BRCA2* (pooled HR, 1.50; 95% CI, 1.02 to 2.09; p=.034).[22,] However, in patients with breast cancer, *BRCA1* and *BRCA2* were not associated with a lower breast cancer-specific survival.

Nelson et al (2013) conducted a systematic review that included meta-analytic estimates of the prevalence and penetrance of *BRCA* variants; this review was used to update the U.S. Preventive Services Task Force (USPSTF) recommendation for risk assessment, genetic counseling, and genetic testing for *BRCA*-related cancer.[23,] In high-risk women with positive test results, cumulative risks for developing breast cancer by age 70 years were 46% for *BRCA1* and 50% for *BRCA2* when a single family member was tested, and 70% for *BRCA1* and 71% for *BRCA2* when multiple family members were tested; cumulative risks for developing ovarian cancer by age 70 years were 41% for *BRCA1* and 17% for *BRCA2* when a single family member was tested; and 46% for *BRCA1* and 23% for *BRCA2* when multiple family members were tested. For Ashkenazi Jewish women with positive test results, cumulative risks for developing breast or ovarian cancer by age 75 years were 34% and 21%, respectively. Nelson et al (2013) included meta-analytic estimates of *BRCA* prevalence in their review for USPSTF. In unselected women, *BRCA* variant prevalence estimates were 0.2% to 0.3%; in women with breast cancer, 1.8% for *BRCA1* and 1.3% for *BRCA2*; in women with breast cancer onset at age 40 years or younger, 6%; in women from high-risk families, 13.6% for *BRCA1*, 7.9% for *BRCA2*, and 19.8% for *BRCA1* or *BRCA2*; in unselected Ashkenazi Jewish women, 2.1%; and in Ashkenazi Jewish women from high-risk families, 10.2%.

Estimates of lifetime risk of cancer for *BRCA* variant carriers (penetrance), based on studies of families with an extensive history of the disease, have been as high as 85%. For example, Kuchenbaecker et al (2017) found that the cumulative risk of breast cancer up to age 80 years was 72% in *BRCA1* carriers and 69% in *BRCA2* carriers.[24,] Because other factors that influence risk may be present in families with extensive breast and ovarian cancer histories, early penetrance estimates may have been biased upward.[25,] Studies of founder mutations in ethnic

populations (e.g., Ashkenazi Jewish, Polish, Icelandic populations) unselected for family history have indicated lower penetrance estimates, in the range of 40% to 60% for *BRCA1* and 25% to 40% for *BRCA2*.[8,11,26,27,] However, a genotyping study of Ashkenazi Jewish women with incident invasive breast cancer, selected regardless of family history of cancer and their family members, resulted in an 82% lifetime risk of breast cancer for carriers of any of 3 *BRCA* founder mutations (185delAG, 5382insC, 6174delT).[27,] Importantly, the risk of cancer in variant carriers from families with little history of cancer (»50% of all carriers) did not differ significantly. Lifetime risk estimates of ovarian cancer were 54% for *BRCA1* and 23% for *BRCA2* variant carriers.

Prospective Studies

Women with a history of breast cancer and a *BRCA* variant have a significant risk of contralateral breast cancer. In a prospective study by Metcalfe et al (2004), the 10-year risk was 29.5% for women with initial stage I or II diseases.[28,] In a prospective study, Epidemiological Study of Familial Breast Cancer, Mavaddat et al (2013) reported that the cumulative risk of contralateral breast cancer by age 70 years was 83% in the *BRCA1* variant carriers, and 62% for *BRCA2* variant carriers.[29,] These investigators also reported cumulative risks of breast cancer by age 70 years in women without previous cancer (60% in *BRCA1* carriers, 55% in *BRCA2* carriers). Similarly, the cumulative risk estimates of ovarian cancer by age 70 years in women without previous ovarian cancer were 59% for *BRCA1* carriers and 17% for *BRCA2* carriers.

***BRCA* Variant Rates Associated With Ovarian Cancer**

Women with a personal history of ovarian cancer have an increased rate of *BRCA* variants. In a systematic review of 23 studies, Trainer et al (2010) estimated the rate of *BRCA* variants among women with ovarian cancer to be 3% to 15%.[30,] In this review, 3 U.S. studies tested for both *BRCA1* and *BRCA2*; incidences of *BRCA* variants were 11.3%, 15.3%, and 9.5%. In the systematic review for USPSTF by Nelson et al (2013), meta-analytic estimates of *BRCA* prevalence among women with ovarian cancer were 4.4% for *BRCA1* and 5.6% for *BRCA2*.[23,] Table 1 lists the results from several additional studies measuring the presence of *BRCA* variants among patients with ovarian cancer.[31,32,33,34,35,] One study noted that variant prevalence was higher for women in their 40s (24%) and for women with serous ovarian cancer (18%).[31,] Ethnicity was another risk factor for *BRCA*, with higher rates seen in women of Italian (43.5%), Jewish (30%), and Indo-Pakistani (29.4%) origin.[31,]

Table 1. *BRCA* Variant Rates in Patients With Ovarian Cancer

Study	Population	N	*BRCA* Variant, n (%)	
			BRCA1	*BRCA2*
Harter et al (2017)[35,]	Patients with invasive ovarian cancer across 20 medical centers	523	81 (15.5)	29 (5.5)
Kurian et al (2017)[32,]	Patients with invasive ovarian cancer tested for hereditary cancer risk from a commercial laboratory database	5020[a]	255 (15.5)	199 (5.5)
Langer et al (2016)[33,]	Patients with ovarian cancer tested for hereditary cancer risk from a commercial laboratory database	3088	153 (4.9)	124 (4.0)

Study	Population	N	*BRCA* Variant, n (%)	
			BRCA1	*BRCA2*
Norquist et al (2016)[34,]	Patients with invasive ovarian cancer, from 2 phase 3 clinical trials and a gynecologic oncology tissue bank	1915	182 (9.5)	98 (5.1)
Zhang et al (2011)[31,]	Patients with invasive ovarian cancer	1342	107 (8.0)	67 (5.0)

[a] Total N was reported as 5020, however, the percentage of *BRCA* variants as reported in article is inconsistent with 5020 as the denominator.

BRCA Variant Rates Associated With Fallopian Tube Cancer

A study by Hirst et al (2009) described the high rate of occult fallopian tube cancers in at-risk women having prophylactic bilateral salpingo-oophorectomy.[36,] In this prospective series of 45 women, 4 (9%) had fallopian tube malignancies. Reviewers noted that these findings supported other studies that have demonstrated the fimbrial end of the fallopian tube as an important site of cancer in those with *BRCA1* or *BRCA2* variants.

A long-term study by Powell et al (2013; median follow-up, 7 years; range, 3 to 14 years) followed 32 *BRCA* variant carriers with occult malignancy (4 ovarian, 23 fallopian tube, 5 ovarian and fallopian tube) diagnosed of prophylactic salpingo-oophorectomy.[37,] Among 15 women with invasive carcinoma (median age, 50 years), 7 (47%) experienced recurrence at a median of 33 months, and OS was 73%. Among 17 women with noninvasive neoplasia (median age, 53 years), 4 (24%) received chemotherapy, none of whom experienced recurrence. One (6%) patient who did not receive chemotherapy experienced recurrence at 43 months. OS was 100%. The authors concluded that, in *BRCA* variant carriers, unsuspected invasive carcinoma has a relatively high rate of recurrence, but noninvasive neoplasms rarely recur and may not require adjuvant chemotherapy.

BRCA Variant Rates Associated With Pancreatic Cancer

Unaffected individuals also may be at high-risk due to other patterns of non-breast-cancer malignancies. A personal history of pancreatic cancer is estimated to raise the risk of a *BRCA* variant by 3.5- to 10-fold over the general population.[38,] Table 2 lists the results from several studies measuring the presence of *BRCA* variants among patients with pancreatic adenocarcinoma.[39,40,41,42,43,44,] Patients with pancreatic adenocarcinoma of Jewish descent appear to have a higher prevalence of *BRCA* variants compared with the general population of patients with pancreatic adenocarcinoma.

Table 2. *BRCA* Variant Rates in Patients With Pancreatic Cancer

Study	Population	N	*BRCA* Variant, n (%)	
			BRCA1	*BRCA2*
Hu et al (2018)[44,,a]	Patients with pancreatic adenocarcinoma from a prospective pancreatic cancer registry	3030	18 (0.6)	59 (1.9)
Yurgelun et al (2018)[43,]	Patients with pancreatic adenocarcinoma from 3 medical centers	289	3 (1.0)	4 (1.4)
Shindo et al (2017)[42,]	Patients with pancreatic adenocarcinoma from 1 medical center	854	3 (0.3)	12 (1.4)
Holter et al (2015)[41,]	Patients with pancreatic adenocarcinoma from a large academic health care complex	306	3 (1.0)	11 (3.6)
Ferrone et al (2009)[40,]	Jewish patients with pancreatic adenocarcinoma from 1 hospital	145	2 (1.3)	6 (4.1)
Couch et al (2007)[39,]	Probands from high-risk families identified through pancreatic cancer clinics and a pancreatic tumor registry	180		10 (5.5)

[a] Case-control study; rates for *BRCA1* and *BRCA2* variants in controls were 0.2 and 0.3, respectively.

BRCA Variant Rates Associated With Prostate Cancer

Table 3 lists the results from several studies measuring the presence of *BRCA* variants among patients with prostate cancer.[45,46,47,]

Table 3. *BRCA* Variant Rates in Patients With Prostate Cancer

Study	Population	N	*BRCA* Variant, n (%)	
			BRCA1	***BRCA2***
Abida et al (2017)[47,]	Patients with prostate cancer from 1 clinical practice	221	2 (1)	20 (9)
Pritchard et al (2016)[46,]	Patients with metastatic prostate cancer from 7 case series across multiple centers	692	6 (0.9)	37 (5.3)
Edwards et al (2003)[45,]	Patients with prostate cancer diagnosed before age 56 from 2 cancer study groups	263		6 (2.3)

Testing for Large *BRCA* Rearrangements

A number of studies have shown that a significant percentage of women with a strong family history of breast cancer and negative tests for BRCA variants have large genomic rearrangements (including deletions or duplications) in 1 of these genes. For example, Walsh et al (2006) reported on probands from 300 U.S. families with 4 or more cases of breast or ovarian cancer but with negative (wild-type) commercial genetic tests for *BRCA1* and *BRCA2*.[48,] These patients underwent screening with additional multiple DNA-based and RNA-based methods. Of these 300 patients, 17% carried previously undetected variants, including 35 (12%) with genomic rearrangement of *BRCA1* or *BRCA2*.

A study by Palma et al (2008) evaluated 251 patients with an estimated *BRCA* variant prevalence using the Myriad II model of at least 10%.[49,] In 136 non-Ashkenazi Jewish probands, 36 (26%) had *BRCA* point mutations and 8 (6%) had genomic rearrangements (7 in *BRCA1*, 1 in *BRCA2*). Genomic rearrangements comprised 18% of all identified *BRCA* variants. No genomic rearrangements were identified in the 115 Ashkenazi Jewish probands, but 47 (40%) had point mutations. The authors indicated that the estimated prevalence of a variant did not predict the presence of a genomic rearrangement.

Clinically Useful

A test is clinically useful if the use of the results informs management decisions that improve the net health outcome of care. The net health outcome can be improved if patients receive correct therapy, or more effective therapy, or avoid unnecessary therapy, or avoid unnecessary testing.

Direct Evidence

Direct evidence of clinical utility is provided by studies that have compared health outcomes for patients managed with and without the test. Because these are intervention studies, the preferred evidence would be from randomized controlled trials (RCTs). In their systematic review for the USPSTF, Nelson et al (2019) confirmed that they identified no studies that compared health outcomes for patients managed with and without *BRCA* variant testing.[50,]

Knowledge of variant status in individuals at potentially increased risk of a *BRCA* variant may impact health care decisions to reduce risk.[51,52,53,54,55,56,57,] Risk-reducing options include intensive surveillance, chemoprevention, prophylactic mastectomy, or prophylactic oophorectomy.

Prophylactic mastectomy reduces the risk of breast cancer in high-risk women (based on family history) by 90%.[52,] Prophylactic oophorectomy significantly reduces the risk of ovarian cancer by 80% or more[55,56,58,] and reduces the risk of breast cancer by approximately 50%.[56,] In women who have already had breast cancer, prophylactic oophorectomy reduces the risk of cancer relapse.[42,] Prophylactic oophorectomy or salpingo-oophorectomy in women with *BRCA1* or *BRCA2* reduced the risk of all-cause mortality by 60% to 77%.[58,59,] For patients at risk for both breast and ovarian cancer, a study by Elmi et al (2018), drawing on data from the American College of Surgeon's National Surgical Quality Improvement Program dataset, found that prophylactic mastectomy with concurrent salpingo-oophorectomy was not associated with significant additional morbidity compared with prophylactic mastectomy alone.[60,]

Systematic reviews of observational studies comparing prophylactic surgeries with observation in women who had *BRCA1* and *BRCA2* variants have demonstrated that contralateral prophylactic mastectomy in women with breast cancer is associated with significantly lower all-cause mortality while bilateral prophylactic mastectomy was not associated with all-cause mortality.[61,62,63,] Studies have indicated that the results of genotyping significantly influenced treatment choices.[53,64,57,]

In a systematic review for the USPSTF, Nelson et al (2019) assessed the efficacy of risk-reducing surgery in *BRCA*-positive women.[50,] The literature search was conducted through March 2019. A total of 13 observational studies (n=9938) provided consistent and moderate-strength evidence of the benefits of risk-reducing surgery. For high-risk women and variant carriers, bilateral mastectomy reduced breast cancer incidence by 90% to 100% and breast cancer mortality by 81% to 100%; oophorectomy or salpingo-oophorectomy reduced breast cancer incidence by 37% to 83%, ovarian cancer incidence by 69% to 100%. Some women experienced reduced

anxiety. Limitations of the studies of benefits included lack of comparison groups, variations in methodology and enrollment criteria, and heterogeneous outcome measures. Additionally, a total of 14 observational studies (n=3073) provided low-strength evidence of the harms of risk-reducing surgery. Adverse events included physical complications of the surgery, postsurgical symptoms, and changes in body image. Studies of harms shared the same limitations as the studies of benefits as noted above, with the addition that their findings were inconsistent and the sample sizes were smaller. As reviewers observed, it is still currently unknown whether *BRCA* variant testing reduces cause-specific or all-cause mortality, or if it improves the QOL. Harms associated with false-negative results or variants of uncertain significance also are unknown.

Other studies have looked at the results of prostate cancer screening in men with *BRCA* variants. The Immunotherapy for Prostate Adenocarcinoma Treatment study (2011) evaluated the results of screening in 205 men 40 to 69 years of age who were *BRCA* variant carriers and 95 control patients.[65,] At the baseline screen, biopsies were performed in 7.0% of men with a prostate-specific antigen level greater than 3.0 ng/mL, and prostate cancer was identified in 3.3%. This resulted in a positive predictive value of 47.6%, which is considerably higher than that estimated for men at normal risk. Moreover, the grade of tumor identified was intermediate in 67% of cancers and high in 11%. This differs from the expected distribution of cancer grade in average-risk men, with more than 60% expected to have low-grade cancer.

Section Summary: Testing for *BRCA1* and *BRCA2* Variants in Individuals at Risk for Hereditary Breast and Ovarian Cancer Syndrome or Other High-Risk Cancers
Evidence for the clinical validity of *BRCA1* and *BRCA2* variant testing consists of multiple studies that calculated *BRCA1* and *BRCA2* variant prevalence among samples of patients with HBOC syndrome, fallopian tube cancer, pancreatic cancer, and prostate cancer.

Regarding clinical utility of *BRCA1* and *BRCA2* variant testing, current evidence has not directly evaluated management with and without genetic testing. In terms of prophylactic measures (mastectomy and oophorectomy), RCTs would be difficult to conduct. However, retrospective analyses have shown that prophylactic mastectomy and/or oophorectomy greatly reduced the risk of breast cancer (90%-100%) and ovarian cancer (69%-100%).

PALB2 AND BREAST CANCER RISK ASSESSMENT

Clinical Context and Test Purpose
The purpose of testing for *PALB2* variants in women at high-risk of HBOC is to evaluate whether an abnormal variant is present and, if so, to determine whether the variant conveys a sufficiently high-risk such that changes in surveillance and/or treatment that are likely to decrease the risk of mortality from breast cancer are warranted.

Potential benefit derives from interventions (screening, chemoprevention, risk-reducing surgery) that can prevent first breast cancer, contralateral breast cancer, or cancer in a different organ caused by the same variant. Whether benefit outweighs harms depends on the risk of developing breast cancer (first cancer or a contralateral one) and the effectiveness and the harms of interventions.

Assessing the net health outcome requires:

- That a test accurately identifies variants and pathogenicity can be determined;
- That a variant alters (increasing or decreasing) a woman's risk of developing breast cancer (including contralateral disease in women already diagnosed) sufficient to change decision making, and of a magnitude that
- Management changes informed by testing can lead to improved health outcomes.

The question addressed in this evidence review is: Does genetic testing for *PALB2* variants improve the net health outcome in women at high-risk of HBOC?
The following PICO was used to select literature to inform this review.

Populations
Genetic testing can be considered for women at increased risk of developing hereditary breast cancer based on their family history or in women with breast cancer whose family history or cancer characteristics (e.g., triple-negative disease, young age) increase the likelihood that the breast cancer is hereditary. Testing may also be considered for women from families with known variants.

The relevant population of interest for this review are patients who are undergoing assessment for HBOC syndrome.

Interventions
The intervention of interest is *PALB2* variant testing.

Comparators
The alternative would be to manage women at high-risk of HBOC with no *PALB2* genetic testing.

Outcomes
The outcomes of interest are OS, disease-specific (breast and ovarian cancer) survival, and test validity.

Study Selection Criteria
For the evaluation of the clinical validity of the tests, studies that meet the following eligibility criteria were considered:

- Included a suitable reference standard
- Patient/sample clinical characteristics were described with women at high breast cancer risk
- Patient/sample selection criteria were described.

Clinically Valid
A test must detect the presence or absence of a condition, the risk of developing a condition in the future, or treatment response (beneficial or adverse).

REVIEW OF EVIDENCE

Systematic Reviews
Suszynska et al (2019) reported a systematic review of variants identified in panels of breast and ovarian cancer-related genes.[66,] Results were reported for *PALB2, CHEK2,* and *ATM.*
CHEK2 and *ATM* results will be discussed in the following sections. The systematic review

included studies published through July 2017 reporting on genetic test results of breast and ovarian cancer patients who were referred for evaluation by a multi-gene panel. Given that the Suszynska et al (2019) report included only studies reporting on test results from a panel, it does not substantially overlap with the studies described in the following section including other *PALB2* association studies. The studies of panel results were used to calculate mutation frequencies by the gene. As a control, population mutation frequencies were extracted from the Genome Aggregation Database. Forty-three studies included panels in breast cancer patients. In the breast cancer studies, 95,853 patients were included in the analysis of *PALB2. PALB2* variants were identified in 0.9% of breast cancer patients. The meta-analytic estimate odds ratio (OR) of the association between *PALB2* variants and risk of breast cancer was 4.8 (95% CI, 4.1 to 5.6).

Observational Studies

A number of studies (Tables 4 and 5) reporting relative risks (RR) or ORs for the association between *PALB2* and breast cancer were identified.[18,17,19,20,67,68,69,70,71,72,73,] Study designs included family segregation[67,74,], kin-cohort,[17,] family-based case-control,[19,69,75,] and population-based or multicenter case-control.[18,20,68,70,71,72,73,] The 2 multinational studies included individuals from up to 5 of the single-country studies.[17,71,] The number of pathogenic variants identified varied from 1 (founder mutations examined) to 48 (Table 4). Studies conducted from single-country samples are described first followed by the 2 multinational collaborative efforts.

Single-Country Samples

Woodward et al (2021) assessed the contribution of *PALB2* gene variants to familial breast and ovarian cancer.[73,] A total of 3127 women with a histologically confirmed diagnosis of invasive or in situ breast cancer or an epithelial nonmucinous ovarian cancer who had undergone germline testing of *BRCA1*, *BRCA2*, *PALB2*, and *CHEK2*_c.1100delC were included. Cases were identified from centers in the U.K.

Li et al (2021) assessed the association between 14 known genes associated with HBOC in a sample of 1990 *BRCA 1/2*-negative family members with breast cancer and/or ovarian cancer and 1902 older women (>40 years of age) who were cancer free at the time of the study.[75,] The initial assessment in 3892 women was conducted with targeted gene panel sequencing, followed by assessment of 145 candidate genes and 14 known HBOC genes in a sample of 3780 *BRCA1* and *BRCA2*-negative families and 3839 controls. Index cases were identified from Familial Cancer Centers and a Pathology center in Australia, and controls were identified from the LifePool mammography screening study.

Lu et al (2019) included an analysis of 11,416 patients with breast cancer and/or ovarian cancer who were referred for genetic testing from 1200 U.S. hospitals and clinics and of 3988 controls referred for genetic testing for noncancer conditions between 2014 and 2015.[72,] Whole-exome sequencing was used and suspected pathogenic variants in the breast or ovarian cancer-associated genes were confirmed by Sanger sequencing.

Kurian et al (2017) reported the association between pathogenic variants and breast or ovarian cancer using a commercial laboratory database of 95,561 women tested clinically for hereditary cancer risk using a multi-gene panel that included *PALB2*, *CHEK2*, and *ATM*.[32,] Although the country is not stated, the patients underwent testing between 2013 and 2015 performed at a Clinical Laboratory Improvement Amendments (CLIA) laboratory and, thus, will be assumed to include patients from the U.S. Cases were women with a single diagnosis of breast or ovarian

cancer. Controls were women from the same database (ie, being tested for hereditary cancer) with no cancer history at the time of genetic testing. The multivariable models for breast cancer risk are reported here. Among the breast cancer patients, 244 (0.92%) had a *PALB2* variant. The association between *PALB2* and breast cancer adjusting for age, ancestry, personal and family cancer histories, and Lynch and adenomatous polyposis colon cancer syndromes had an OR of 3.39 (95% CI, 2.79 to 4.12).

Thompson et al (2015) evaluated Australian women with breast cancer (n=1996) referred for genetic evaluation from 1997 to 2014.[70,] A control group was accrued from participants in the LifePool study (n=1998) who were recruited for a mammography screening program. All *PALB2* coding exons were sequenced by next-generation sequencing and novel variants verified by Sanger sequencing. Large deletions or rearrangements were not evaluated. Nineteen distinct pathogenic variants were identified, including 6 not previously described in 26 (1.3%) cases and in 4 (0.2%) controls with an odds for breast cancer of 6.58 (95% CI, 2.3 to 18.9). Moreover, 54 missense variants identified were slightly more common in cases (OR, 1.15; 95% CI, 1.02 to 1.32).

Cybulski et al (2015) examined 2 loss-of-function *PALB2* variants (c.509_510delGA, c.172_175delTTGT) in women with invasive breast cancer diagnosed between 1996 and 2012 in Poland.[20,] From 12,529 genotyped women, a *PALB2* variant was identified in 116 (0.93%) cases (95% CI, 0.76% to 1.09%) versus 10 (0.21%, 95% CI, 0.08% to 0.34%) of 4702 controls (OR, 4.39; 95% CI, 2.30 to 8.37). A *BRCA1* variant was identified in 3.47% of women with breast cancer and in 0.47% of controls (OR, 7.65; 95% CI, 4.98 to 11.75). Authors estimated that a *PALB2* sequence variant conferred a 24% cumulative risk of breast cancer by age 75 years (in the setting of age-adjusted breast cancer rates slightly more than half that in the U.K.[76,] or the U.S.[77,]). A *PALB2* variant was also associated with poorer prognosis: 10-year survival of 48.0% versus 74.7% when the variant was absent (HR adjusted for prognostic factors, 2.27; 95% CI, 1.64 to 3.15).

Catucci et al (2014) performed population-based case-control studies in Italy (Milan or Bergamo) among women at risk for hereditary breast cancer and no *BRCA1* or *BRCA2* variant.[18,] In Milan, 9 different pathogenic *PALB2* variants were detected in 12 of 575 cases and none in 784 controls (blood donor); in Bergamo, *PALB2* c.1027C>T variants were detected in 6 of 113 cases and in 2 of 477 controls (OR, 13.4; 95% CI, 2.7 to 67.4). Performed in 2 distinct populations, the combined sample size was small, and uncertainty existed as indicated by the large effect estimate.

Casadei et al (2011) studied 959 U.S. women (non-Ashkenazi Jewish descent) with a family history of *BRCA1*- or *BRCA2*-negative breast cancer and 83 female relatives using a family-based case-control design.[19,] Using conventional sequencing, pathogenic *PALB2* variants were detected in 31 (3.2%) women with breast cancer and none in controls. Compared with their female relatives without *PALB2* variants, the risk of breast cancer increased 2.3-fold (95% CI, 1.5 to 4.2) by age 55 years and 3.4-fold (95% CI, 2.4 to 5.9) by age 85 years. Mean age at diagnosis was not associated with the presence of a variant (50.0 years with vs. 50.2 years without). Casadei et al (2011) provided few details of their analyses. Additionally, participants reported over 30 ancestries and, given intermarriage in the U.S. population, stratification may have had an impact on results. Generalizability of the risk estimate is therefore unclear.

Heikkinen et al (2009) conducted a population-based case-control study at a Finnish university hospital employing 2 case groups (947 familial and 1274 sporadic breast cancers) and 1079 controls.[68,] The study sample was obtained from 542 patients with familial breast cancer, a series of 884 oncology patients (79% of consecutive new cases), and 986 surgical patients (87% of consecutive new cases); 1706 were genotyped for the *PALB2* c.1592delT variant. All familial cases were *BRCA1*- and *BRCA2*-negative, but among controls, there were 183 *BRCA* carriers. *PALB2* variant prevalence varied with family history: 2.6% when 3 or more family members were affected and 0.7% in all breast cancer patients. Variant prevalence was 0.2% among controls. In women with hereditary disease, a *PALB2* c.1592delT variant was associated with an increased risk of breast cancer (OR, 11.0; 95% CI, 2.65 to 97.78), and was higher in women with the strongest family histories (women with sporadic cancers; OR, 4.19; 95% CI, 1.52 to 12.09). Although data were limited, survival was lower among *PALB2*-associated cases (10-year survival, 66.5%; 95% CI, 44.0% to 89.0% vs. 84.2%; 95% CI, 83.1% to 87.1% in women without a variant; p=.041; HR, 2.94; p=.047). A *PALB2* variant was also associated with triple-negative tumors: 54.5% versus 12.2% with familial disease and 9.4% in sporadic cancers.

Multinational Samples

Yang et al (2020) performed a complex segregation analysis to estimate relative and absolute risks of breast cancer from data on 524 families with *PALB2* pathogenic variants from 21 countries, the most frequent being c.3113G>A.[74,] Female breast cancer relative risk (RR) was 7.18 (95% CI, 5.82 to 8.85; $p=6.5x10^{-75}$) when assumed to be constant with age. The age-trend model provided the best fit ($p=2x10^{-3}$) and demonstrated a pattern of decreasing RR with each increased decade in age. The RR was 4.69 (95% CI, 3.28 to 6.70) in those 75 years of age per the age-trend model.

Southey et al (2016) examined the association of 3 *PALB2* variants (2 protein-truncating: c.1592delT and c.3113G>A; 1 missense c.2816T>G) with breast, prostate, and ovarian cancers.[71,] The association with breast cancer was examined among participants in the Breast Cancer Association Consortium (BCAC; 42,671 cases and 42,164 controls). The BCAC (part of the larger Collaborative Oncological Gene-environment Study) included 48 separate studies with participants of multiple ethnicities, but mainly European, Asian, and African American. Most studies were population- or hospital-based case-controls with some oversampling cases with family histories or bilateral disease. A custom array was used for genotyping at 4 centers, with 2% duplicate samples. The ORs were estimated adjusting for study among all participants, and excluding those studies selecting patients based on family history or bilateral disease (37,039 cases, 38,260 controls). The c.1592delT variant was identified in 35 cases and 6 controls (from 4 studies in the U.K., Australia, U.S., Canada; OR, 4.52; 95% CI, 1.90 to 10.8; p<.001); in those with no family history or bilateral disease (OR, 3.44; 95% CI, 1.39 to 8.52; p=.003). The c3113G>A variant was identified in 44 cases and 8 controls (9 studies from Finland and Sweden; OR, 5.93; 95% CI, 2.77 to 12.7; p<.001) and in those with no family history or bilateral disease (OR, 4.21; 95% CI, 1.84 to 9.60; p<.001). There was no association between the c2816T>G missense variant and breast cancer (found in 150 cases and 145 controls). These results, derived from a large sample, used a different analytic approach than Antoniou et al (2014), described next, and examined only 2 pathogenic variants. The magnitude of the estimated RR approaches that of a high penetrance gene but is accompanied by wide CIs owing to the study design and low carrier prevalence. The lower estimates obtained following exclusion of those selected based

on family history or bilateral disease are consistent with the importance of carefully considering the risk of hereditary disease prior to genetic testing.

Antoniou et al (2014) analyzed data from 362 members of 154 families with deleterious *PALB2* variants.[17,] Individuals with benign variants or variants of uncertain significance were excluded. Families were recruited at 14 centers in 8 countries (U.S., U.K., Finland, Greece, Australia, Canada, Belgium, Italy) and had at least 1 member with a *BRCA1*- or *BRCA2*-negative *PALB2*-positive breast cancer. There were 311 women with *PALB2* variants: 229 had breast cancer; 51 men also had *PALB2* variants (7 had breast cancer). Of the 48 pathogenic (loss-of-function) variants identified, 2 were most common (c.1592delT in 44 families, c.3113G>A in 25 families); 39 of the 48 pathogenic variants were found in just 1 or 2 families. Carriers of *PALB2* variants (men and women) had a 9.47-fold increased risk for breast cancer (95% CI, 7.16 to 12.57) compared with the U.K. population under a single-gene model and age-constant RR; 30% of tumors were triple-negative. For a woman aged 50 to 54 years, the estimated RR was 6.55 (95% CI, 4.60 to 9.18). The RR of breast cancer for males with *PALB2* variants, compared with the male breast cancer incidence in the general population, was 8.3 (95% CI, 0.77 to 88.5; p=.08). The cumulative risk at age 50 years of breast cancer for female *PALB2* carriers without considering family history was 14% (95% CI, 9% to 20%); by age 70 years, it was 35% (95% CI, 26% to 46%). A family history of breast cancer increased the cumulative risk. If a woman with a *PALB2* variant has a sister and mother who had breast cancer at age 50 years, by age 50 years she would have a 27% (95% CI, 21% to 33%) estimated risk of developing breast cancer; and by age 70 years, a 58% (95% CI, 50% to 66%) risk. These results emphasize that family history affects penetrance. Authors noted that the study "includes most of the reported families with *PALB2* variant carriers, as well as many not previously reported".

Table 4. Included Association Studies of Pathogenic *PALB2* Variants

Study	Year	Country	Design	N	Families	*PALB2* Variants		Totals		Pathogenic Variants Identified	
						Cases	Controls	Cases	Controls	N	Prevalence Cases, %
Woodward et al[73,]	2021	U.K.	Single-center CC	4694		35	3	3127	1567	NR	1.12
Li et al (BEACCON)[75,]	2021	Australia	Family-based CC	3892		144	98	1990	1902	NR	2.49
Yang et al[74,]	2020	Multinational	Multicenter family segregation	17,906	524	976	NR	NR	NR	976	5.5
Lu et al[72,]	2019	U.S.	Multicenter CC	15,404		61	NR	15,532	3988	NR	0.4

Study	Year	Country	Design	N	Families	*PALB2* Variants		Totals		Pathogenic Variants Identified	
Thompson et al[70,]	2015	Australia	Population-based CC	3994		26	4	1996	1998	19	1.3
Cybulski et al[20,]	2015	Poland	Population-based CC[f]	17,231		116	10	12,529	4702	2	0.9
Catucci et al[18,a,b]	2014	Italy	Population-based CC	590[e]		6	2	113	477	1 (c.1027C>T)	5.3
Heikkinen et al[68,,a,b]	2009	Finland	Population-based CC	2026		19	2	947	1079	1 (c.1592delT)	2.0
Casadei et al[19,a]	2011	U.S.	Family-based CC[d]	1042		31	0	959	83	13	3.2
Rahman et al[69,a,b]	2007	U.K.	Family-based CC	2007	923	10	0	923	1084	5	1.1
Erkko et al[67,a,b]	2008	Finland	Family segregation	213	17[c]	17	?			1 (c.1592delT)	
Antoniou et al[17,]	2014	Multinational	Kin-cohort	2980	154	229	82	542	2438	48	
Southey et al[71,]	2016	Multinational	Mutlicenter CC	84,835		35	6	42,671	42,164	1 (c.1592delT)	
						44	8			1 (c.3113G>A)	
Kurian et al[32,]	2017	U.S.	CC	95,561		257	NR	26,384	Unclear	NR	0.97

BEACCON: Hereditary BrEAst Case CONtrol study; CC: case-control; NR: not reported.
[a] All or selected families included in Antoniou et al (2014).
[b] Participants included in Southey et al (2016).
[c] 10 with a family history.
[d] Non-Ashkenazi Jewish descent, males excluded.
[e] Bergamo sample, Milan sample 0 controls with *PALB2* variants.
[f] Study primary survival outcome was obtained as part of a prospective cohort. The analysis and sampling to assess breast cancer risk were as a case-control study.

Table 5. Measures of Association and Penetrance for Breast Cancer and *PALB2*

Study	Year	Analysis	RR or (95% CI)	Penetrance at Age 70 years (95% CI), %	Mean (Median) Age Onset, y	Triple-Negative Tumors, %	
						***PALB2*+**	***PALB2*-**
Woodward et al[73],	2021	Standard CC	5.90 (1.92 to 18.36)				
Li et al (BEACCON)[75],	2021	Standard CC	3.47 (1.92 to 6.65)			27.6	
Yang et al[74],	2019	Segregation	7.18 (5.82 to 8.85)	52.8 (43.7 to 62.7)[d]	NR	NR	NR
Lu et al[72],	2019	Standard CC	5.5 (2.2 to 17.7)				
Antoniou et al[17],	2014	Segregation[b]	6.6 (4.6 to 9.2)[c]	47.5 (38.6 to 57.4)[e]		30	
Erkko et al[67],	2008	Segregation	6.1 (2.2 to 17.2)[a]	40 (17 to 77)	54.3 (+FH); 59.3 (FH unavailable)		
Rahman et al[69],	2007	Segregation[b]	2.3 (1.4 to 3.9)[f]		46 (IQR, 40 to 51)		
Casadei et al[19],	2011	Relative risk	2.3 (1.5 to 4.2)[g]		50.0 (SD, 11.9)		
Thompson et al[70],	2015	Standard CC	6.6 (2.3 to 18.9)				
Cybulski et al[20],	2015	Standard CC	4.4 (2.3 to 8.4)		53.3	34.4	14.4
Catucci et al[18],	2014	Standard CC	13.4 (2.7 to 67.4)				
Heikkinen et al[68],	2009	Standard CC	11.0 (2.6 to 97.8)		53.1 (95% CI, 33.4 to 79.9)	54.5	9.4, 12.2[h]
Southey et al[71],	2016	Standard CC	4.5 (1.9 to 10.8) (c.1592delT)				
			5.9 (2.8 to 12.7) (c.3113G>A)				
Kurian et al[32],	2017	Standard CC	3.39 (2.79 to 4.12)				

BEACCON: Hereditary BrEAst Case CONtrol study; CC: case-control; CI: confidence interval; FH: family history; IQR: interquartile range; NR: not reported; OR: odds ratio; RR: relative risk; SD: standard deviation.

[a] Using an "augmented" dataset assuming no cases among families without recorded histories. Analyses limited to those with recorded histories yielded a RR of 14.3 (95% CI, 6.6 to 31.2).
[b] Modified.
[c] Estimate for women age 50.
[d] Estimate for women age 80.
[e] Estimates varied according to family history. For women with a mother and sister with breast cancer at age 50, cumulative risk was estimated at 58% (95% CI, 50% to 66%); for women with no family history, 33% (95% CI, 26% to 46%).
[f] For women <50 years, RR of 3.0 (95% CI, 1.4 to 3.9); for women >50 years, RR of 1.9 (95% CI, 0.8 to 3.7).
[g] At age 85 years, RR of 3.4 (95% CI, 2.4 to 5.9).
[h] In sporadic and familial cancers without *PALB2* variants.

Notable limitations identified in each study are shown in Tables 6 and 7.

Table 6. Study Relevance Limitations of Individuals Studies of Pathogenic *PALB2* Variants

Study	Population[a]	Intervention[b]	Comparator[c]	Outcomes[d]	Duration of FU[e]
Woodward et al (2021)[73,]	4. Case-control population of breast cancer patients referred for genetic testing (and controls), likely overestimated risk				
Li et al (2021) (BEACCON)[75,]	4. Case-control population of familial BRCA 1/2 negative breast cancer patients (and controls)				
Yang et al (2019)[74,]	4. No case-control group	1. Not clear which variants were included			
Lu et al (2019)[72,]	4. Case-control population of breast cancer patients (and controls), likely overestimated risk	1. Not clear which variants were included			
Kurian et al (2017)[32,]	4. Case-control population of breast cancer patients (and controls), likely overestimated risk	1. Not clear which variants were included			1: Control chosen from patients being tested for hereditary cancer; unclear how many developed cancer
Southey et al (2016)[71,]	4. Case-control population of breast cancer patients (and controls), likely overestimated risk				

Study	Population[a]	Intervention[b]	Comparator[c]	Outcomes[d]	Duration of FU[e]
Thompson et al (2015)[70,]	4. Case-control population of breast cancer patients (and controls), likely overestimated risk				
Cybulski et al (2015)[20,]	4. Case-control population of breast cancer patients (and controls), likely overestimated risk				
Catucci et al (2014)[18,]	4. Case-control population of breast cancer patients referred for genetic testing (and controls), likely overestimated risk				
Antoniou et al (2014)[17,]	4. Case-control population of breast cancer patients (and controls), likely overestimated risk; only kin-cohort included				
Casadei et al (2011)[19,]	4. Case-control population of breast cancer patients (and controls), likely overestimated risk				
Heikkinen et al (2009)[68,]	4. Case-control population of breast cancer patients referred for genetic testing (and controls), likely overestimated risk				
Erkko et al (2008)[67,]	4. No case-control group				
Rahman et al (2007)[69,]	4. Case-control population of breast cancer patients (and controls), likely overestimated risk				

The study limitations stated in this table are those notable in the current review; this is not a comprehensive gaps assessment.
BEACCON: Hereditary BrEAst Case CONtrol study; FU: follow-up.
[a] Population key: 1. Intended use population unclear; 2. Clinical context is unclear; 3. Study population is unclear; 4. Study population not representative of intended use.
[b] Intervention key: 1. Classification thresholds not defined; 2. Version used unclear; 3. Not intervention of interest.
[c] Comparator key: 1. Classification thresholds not defined; 2. Not compared to credible reference standard; 3. Not compared to other tests in use for same purpose.

[d] Outcomes key: 1. Study does not directly assess a key health outcome; 2. Evidence chain or decision model not explicated; 3. Key clinical validity outcomes not reported (sensitivity, specificity and predictive values); 4. Reclassification of diagnostic or risk categories not reported; 5. Adverse events of the test not described (excluding minor discomforts and inconvenience of venipuncture or noninvasive tests).
[e] Follow-Up key: 1. Follow-up duration not sufficient with respect to natural history of disease (true-positives, true-negatives, false-positives, false-negatives cannot be determined).

Table 7. Study Design and Conduct Limitations of Individuals Studies of Pathogenic *PALB2* Variants

Study	Selection[a]	Blinding[b]	Delivery of Test[c]	Selective Reporting[d]	Data Completeness[e]	Statistical[f]
Woodward et al (2021)[73,]	1. Incomplete description of how controls selected					
Li et al (2021) (BEACCON)[75,]				1. Registration not reported	1. No description of disposition of eligible patients/samples	
Yang et al (2019)[74,]	1. Incomplete descriptions of how family groups selected			1. Registration not reported	1. No description of disposition of eligible patients/samples	
Lu et al (2019)[72,]	1. Incomplete description of how controls selected			1. Registration not reported	1. No description of disposition of eligible patients/samples	
Kurian et al (2017)[32,]				1. Registration not reported	1. No description of disposition of eligible patients/samples	
Southey et al (2016)[71,]				1. Registration not reported		
Thompson et al (2015)[70,]	1. Incomplete description of how controls selected			1. Registration not reported	1. No description of disposition of eligible patients/samples	
Cybulski et al (2015)[20,]	1. Incomplete description of how controls selected			1. Registration not reported		
Catucci et al (2015)[18,]	1. Incomplete description of how controls selected			1. Registration not reported	1. No description of disposition of eligible patients/samples	

Study	Selection[a]	Blinding[b]	Delivery of Test[c]	Selective Reporting[d]	Data Completeness[e]	Statistical[f]
Antoniou et al (2014)[17,]	2. Kin-cohort-controls not randomized					
Casadei et al (2011)[19,]	2. Family groups: controls not randomized			1. Registration not reported		
Heikkinen et al (2009)[68,]	1. Incomplete description of how controls selected			1. Registration not reported		
Erkko et al (2008)[67,]	2. Family groups: selection not randomized			1. Registration not reported; number of controls unknown		
Rahman et al (2007)[69,]	2. Family groups: controls not randomized			1. Registration not reported		

The study limitations stated in this table are those notable in the current review; this is not a comprehensive gaps assessment.
BEACCON: Hereditary BrEAst Case CONtrol study.
[a] Selection key: 1. Selection not described; 2. Selection not random or consecutive (ie, convenience).
[b] Blinding key: 1. Not blinded to results of reference or other comparator tests.
[c] Test Delivery key: 1. Timing of delivery of index or reference test not described; 2. Timing of index and comparator tests not same; 3. Procedure for interpreting tests not described; 4. Expertise of evaluators not described.
[d] Selective Reporting key: 1. Not registered; 2. Evidence of selective reporting; 3. Evidence of selective publication.
[e] Data Completeness key: 1. Inadequate description of indeterminate and missing samples; 2. High number of samples excluded; 3. High loss to follow-up or missing data.
[f] Statistical key: 1. Confidence intervals and/or p values not reported; 2. Comparison with other tests not reported.

Clinically Useful

A test is clinically useful if the use of the results informs management decisions that improve the net health outcome of care. The net health outcome can be improved if patients receive correct therapy, more effective therapy, or avoid unnecessary therapy or testing.

Direct Evidence

Direct evidence of clinical utility is provided by studies that have compared health outcomes for patients managed with and without the test. Because these are intervention studies, the preferred evidence would be from RCTs.

Evidence of clinical utility limited to women with *PALB2* variants was not identified.

Chain of Evidence

Indirect evidence on clinical utility rests on clinical validity. If the evidence is insufficient to demonstrate test performance, no inferences can be made about clinical utility.
Rosenthal et al (2017) reported an analysis of the impact of testing for genes other than *BRCA1/2* and by calculating whether carriers of these gene variants would have been

identified as candidates for enhanced screening based on family history alone.[78,] The database included 194,107 women who were tested using a hereditary cancer panel between 2013 and 2016. The women were referred by their health care providers for clinical suspicion of hereditary cancer. It is unclear what proportion of the women met professional society criteria for genetic testing for breast cancer risk; baseline information regarding family history was not reported. Of the women in the database, 893 had *PALB2* variants and were eligible for Claus assessment to estimate the risk of breast cancer. Approximately 27% of women with *PALB2* variants would have had an estimated risk of breast cancer of 20% or higher based on the Claus model. The report did not include health outcomes and it is unclear whether enhanced screening in women who had a moderate penetrance variant but did not have an estimated risk of breast cancer of 20% or greater based on the Claus model would have improved health outcomes from enhanced surveillance.

Studies of women at high-risk based on family history alone or in those with *BRCA1* and *BRCA2* variants are relevant to the clinical utility of *PALB2* testing given the penetrance estimates for *PALB2* and related molecular mechanism ("BRCA-ness"). Interventions to decrease breast cancer risk in asymptomatic high-risk women include screening[79,] (e.g., starting at an early age, the addition of magnetic resonance imaging to mammography, and screening annually), chemoprevention,[80,] and prophylactic mastectomy.[81,] In women with breast cancer, contralateral prophylactic mastectomy is of interest; other treatment decisions are dictated by clinical, pathologic, and other prognostic factors.

In women at high-risk of hereditary breast cancer, including *BRCA1* and *BRCA2* carriers, evidence supports a reduction in subsequent breast cancer after bilateral or contralateral prophylactic mastectomy. Decision analyses have also concluded the impact on breast cancer incidence extends life in high, but not average risk,[82,] women. For example, Schrag et al (1997, 2000) modeled the impact of preventive interventions in women with *BRCA1* or *BRCA2* variants and examined penetrance magnitudes similar to those estimated for a *PALB2* variant.[83,84,] Compared with surveillance, a 30-year-old *BRCA* carrier with an expected 40% risk of breast cancer and 5% risk of ovarian cancer by age 70 years would gain an expected 2.9 years following a prophylactic mastectomy alone and an additional 0.3 years with a prophylactic oophorectomy (Table 8).[83,] A 50-year-old female *BRCA* carrier with node-negative breast cancer and a 24% risk of contralateral breast cancer at age 70 years would anticipate 0.9 years in improved life expectancy (0.6 years for node-negative disease) following a prophylactic contralateral mastectomy.[84,]

Table 8. Model Results of the Effects of Bilateral Risk-Reducing Mastectomy versus Surveillance on Life Expectancy in *BRCA* Carriers According to Penetrance

Risk Level and Strategy	**Age of Carrier, years**			
	30	**40**	**50**	**60**
40% risk of breast cancer				
Mastectomy	2.9	2.0	1.0	0.2
Mastectomy delayed 10 years	1.8	0.8	0.1	0.0
60% risk of breast cancer				
Mastectomy	4.1	2.9	1.6	0.3

Risk Level and Strategy	Age of Carrier, years			
	30	40	50	60
Mastectomy delayed 10 years	2.4	1.1	0.1	0.0
85% risk of breast cancer				
Mastectomy	5.3	3.7	2.3	0.5
Mastectomy delayed 10 years	2.6	1.1	0.1	0.1

Adapted from Schrag et al (1997).[83,]

Section Summary: *PALB2* and Breast Cancer Risk Assessment
Identified studies differed by populations, designs, sample sizes, analyses, and variants examined. While estimates of the magnitude of the association between *PALB2* and breast cancer risk varied across studies, their magnitudes are of moderate to high penetrance.

Of interest is how variant detection affects penetrance estimates compared with family history alone. As with *BRCA* variants, model-based estimates allow estimating risks for individual patient and family characteristics. To illustrate using the Breast and Ovarian Analysis of Disease Incidence and Carrier Estimation Algorithm model, a woman age 30 years whose mother had breast cancer at age 35 years has an estimated 14.4% risk of breast cancer at age 70 years. If she carries a *PALB2* variant, the risk increases to 51.1%. A woman, age 50 years, with breast cancer whose mother had breast cancer at age 50 years, has an estimated 11.7% risk of contralateral cancer by age 70 years, increasing to 28.7% if she carries a *PALB2* variant.

Evidence concerning preventive interventions in women with *PALB2* variants is indirect, relying on studies of high-risk women and *BRCA* carriers. In women at high-risk of hereditary breast cancer who would consider preventive interventions, identifying a *PALB2* variant provides a more accurate estimated risk of developing breast cancer compared with family history alone and can offer a better understanding of benefits and potential harms of interventions.

Summary of Evidence
For individuals who have cancer or a personal or family cancer history and meet criteria suggesting a risk of HBOC syndrome who receive genetic testing for a *BRCA1* or *BRCA2* variant, the evidence includes a TEC Assessment and studies of variant prevalence and cancer risk. Relevant outcomes are OS , disease-specific survival, test validity, and QOL. The accuracy of variant testing has been shown to be high. Studies of lifetime risk of cancer for carriers of a *BRCA* variant have shown a risk as high as 85%. Knowledge of *BRCA* variant status in individuals at risk of a *BRCA* variant may impact health care decisions to reduce risk, including intensive surveillance, chemoprevention, and/or prophylactic intervention. In individuals with *BRCA1* or *BRCA2* variants, prophylactic mastectomy and oophorectomy have been found to significantly increase disease-specific survival and OS. Knowledge of *BRCA* variant status in individuals diagnosed with breast cancer may impact treatment decisions. The evidence is sufficient to determine that the technology results in an improvement in the net health outcome.

For individuals who have other high-risk cancers (e.g., cancers of the fallopian tube, pancreas, prostate) who receive genetic testing for a *BRCA1* or *BRCA2* variant, the evidence includes studies of variant prevalence and cancer risk. Relevant outcomes are OS, disease-specific survival, test validity, and QOL. The accuracy of variant testing has been shown to be high.

Knowledge of *BRCA* variant status in individuals with other high-risk cancers can inform decisions regarding genetic counseling, chemotherapy, and enrollment in clinical trials. The evidence is sufficient to determine that the technology results in an improvement in the net health outcome.

For individuals with a risk of HBOC syndrome who receive genetic testing for a *PALB2* variant, the evidence includes studies of clinical validity and studies of breast cancer risk, including a meta-analysis. Relevant outcomes are OS, disease-specific survival, and test validity. Evidence supporting clinical validity was obtained from numerous studies reporting RRs or ORs. Study designs included family segregation, kin-cohort, family-based case-control, and population-based case-control. The number of pathogenic variants identified in studies varied from 1 (founder mutations) to 48. The RR for breast cancer associated with a *PALB2* variant ranged from 2.3 to 13.4, with the 2 family-based studies reporting the lowest values. Evidence of preventive interventions in women with *PALB2* variants is indirect, relying on studies of high-risk women and *BRCA* carriers. These interventions include screening with magnetic resonance imaging, chemoprevention, and risk-reducing mastectomy. Given the penetrance of *PALB2* variants, the outcomes following bilateral and contralateral risk-reducing mastectomy examined in women with a family history consistent with hereditary breast cancer (including *BRCA1* and *BRCA2* carriers) can be applied to women with *PALB2* variants, with the benefit-to-risk balance affected by penetrance. In women at high-risk of hereditary breast cancer who would consider risk-reducing interventions, identifying a *PALB2* variant provides a more precise estimated risk of developing breast cancer compared with family history alone and can offer women a more accurate understanding of benefits and potential harms of any intervention. The evidence is sufficient to determine that the technology results in an improvement in the net health outcome.

SUPPLEMENTAL INFORMATION

The purpose of the following information is to provide reference material. Inclusion does not imply endorsement or alignment with the evidence review conclusions.

Clinical Input From Physician Specialty Societies and Academic Medical Centers

While the various physician specialty societies and academic medical centers may collaborate with and make recommendations during this process, through the provision of appropriate reviewers, input received does not represent an endorsement or position statement by the physician specialty societies or academic medical centers, unless otherwise noted.

2010 Input

In response to requests, input was received for 3 physician specialty societies (5 reviewers) and 3 academic medical centers (5 reviewers) while this policy was under review in 2010. Those providing input were in general agreement with the Policy statements considering testing for genomic rearrangements of *BRCA1* and *BRCA2* as medically necessary and with adding fallopian tube and primary peritoneal cancer as *BRCA*-associated malignancies to assess when obtaining the family history.

Practice Guidelines and Position Statements

Guidelines or position statements will be considered for inclusion in 'Supplemental Information' if they were issued by, or jointly by, a US professional society, an international society with US representation, or National Institute for Health and Care Excellence (NICE). Priority will be given to guidelines that are informed by a systematic review, include strength of evidence ratings, and include a description of management of conflict of interest.

NATIONAL COMPREHENSIVE CANCER NETWORK

Breast Cancer and Ovarian Cancer

Current NCCN (v.2.2022) guidelines on the genetic and familial high-risk assessment of breast and ovarian cancers include criteria for identifying individuals who should be referred for further risk assessment and separate criteria for genetic testing.[85,] Patients who satisfy any of the testing criteria listed in CRIT-1 through CRIT-4 should undergo "further personalized risk assessment, genetic counseling, and often genetic testing and management." For these criteria, both invasive and in situ breast cancers were included. Maternal and paternal sides of the family should be considered independently for familial patterns of cancer. Testing of unaffected individuals should be considered "only when an appropriate affected family member is unavailable for testing."

The recommendations are for testing high penetrance breast cancer susceptibility genes, specifically *BRCA1*, *BRCA2*, *CDH1*, *PALB2*, *PTEN,* and *TP53*. Use of "tailored panels that are disease-focused and include clinically actionable cancer susceptibility genes is preferred over large panels that include genes of uncertain clinical relevance".

BRCA1 and *BRCA2* somatic variants are uncommon. The NCCN recommends if a somatic variant is identified through tumor profiling, then *BRCA1* and *BRCA2* germline testing is recommended.

Additionally, the NCCN Ovarian Cancer guidelines (v.1.2022) recommend tumor molecular testing for persistent/recurrent disease (OV-6) and describe in multiple algorithms that testing should include at least *BRCA1/2,* homologous recombination, microsatellite instability, tumor mutational burden, and neurotrophic tyrosine receptor kinase , (OV-6, OV-7, OV-B Principles of Pathology, OV-C Principles of Systemic Therapy).[86,]

Pancreatic Adenocarcinoma

Current NCCN guidelines for pancreatic adenocarcinoma (v.1.2022) refers to the NCCN guidelines on genetic/familial high-risk assessment of breast and ovarian detailed above, and state: "Germline testing is recommended for any patient with confirmed pancreatic cancer, using comprehensive gene panels for hereditary cancer syndromes."[87,]

Prostate Cancer

The current NCCN guidelines for prostate cancer are version 4.2022.[88,] The Principles of Genetics section (PROS-B) provides appropriate scenarios for germline genetic testing in individuals with a personal history of prostate cancer.

American Society of Breast Surgeons

A consensus guideline on genetic testing for hereditary breast cancer was updated in February 2019.[89,] The guideline states that genetic testing should be made available to all patients with a personal history of breast cancer and that such testing should include *BRCA1/BRCA2* and *PALB2*, with other genes as appropriate for the clinical scenario and patient family history. Furthermore, patients who had previous genetic testing may benefit from updated testing. Finally, genetic testing should be made available to patients without a personal history of breast cancer when they meet National Comprehensive Cancer Network (NCCN) guideline criteria. The guidelines also note that variants of uncertain significance are not clinically actionable.

Society of Gynecologic Oncology
In 2015, the Society of Gynecologic Oncology (SGO) published an evidence-based consensus statement on risk assessment for inherited gynecologic cancer.[90,] The statement included criteria for recommending genetic assessment (counseling with or without testing) to patients who may be genetically predisposed to breast or ovarian cancer. Overall, the SGO and the NCCN recommendations are very similar; the main differences are the exclusion of women with breast cancer onset at age 50 years or younger who have 1 or more first-, second-, or third-degree relatives with breast cancer at any age; women with breast cancer or history of breast cancer who have a first-, second-, or third-degree male relative with breast cancer; and men with a personal history of breast cancer. Additionally, SGO recommended genetic assessment for unaffected women who have a male relative with breast cancer. Moreover, SGO indicated that some patients who do not satisfy criteria may still benefit from genetic assessment (e.g., few female relatives, hysterectomy, or oophorectomy at a young age in multiple family members, or adoption in the lineage).

American College of Obstetricians and Gynecologists
The American College of Obstetricians and Gynecologists (2017, reaffirmed 2019) published a Practice Bulletin on hereditary breast and ovarian cancer syndrome.[91,] The following recommendation was based primarily on consensus and expert opinion (level C): "Genetic testing is recommended when the results of a detailed risk assessment that is performed as part of genetic counseling suggest the presence of an inherited cancer syndrome for which specific genes have been identified and when the results of testing are likely to influence medical management."

U.S. Preventive Services Task Force
Current U.S. Preventative Services Task Force (USPSTF) recommendations (2019)[92,] for genetic testing of *BRCA1* and *BRCA2* variants in women state:

"The USPSTF recommends that primary care clinicians assess women with a personal or family history of breast, ovarian, tubal, or peritoneal cancer or who have an ancestry associated with *BRCA1/2* gene mutation with an appropriate brief familial risk assessment tool. Women with a positive result on the risk assessment tool should receive genetic counseling and, if indicated after counseling, genetic testing (B recommendation). The USPSTF recommends against routine risk assessment, genetic counseling, or genetic testing for women whose personal or family history or ancestry is not associated with potentially harmful *BRCA1/2* gene mutations. (D recommendation)"

Recommended screening tools included 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-Cuziak), and brief versions of the BRCAPRO.

Ongoing and Unpublished Clinical Trials
Some currently unpublished trials that might influence this review are listed in Table 9.

Table 9. Summary of Key Trials

NCT No.	Trial Name	Planned Enrollment	Completion Date (status if beyond Completion Date)
Ongoing			
NCT04009148	Cascade Testing in Families With Newly Diagnosed Hereditary Breast and Ovarian Cancer Syndrome	300	Mar 2023
NCT03246841	Investigation of Tumour Spectrum, Penetrance and Clinical Utility of Germline Mutations in New Breast and Ovarian Cancer Susceptibility Genes (TUMOSPEC)	500	Dec 2023
NCT02321228	Early Salpingectomy (Tubectomy) With Delayed Oophorectomy to Improve Quality of Life as Alternative for Risk Reducing Salpingo-oophorectomy in BRCA1/2 Gene Mutation Carriers (TUBA)	510	Jan 2035

NCT: national clinical trial.
[a] Denotes industry-sponsored or cosponsored trial.

CODING

The following codes for treatment and procedures applicable to this policy are included below for informational purposes. This may not be a comprehensive list of procedure codes applicable to this policy.

Inclusion or exclusion of a procedure, diagnosis or device code(s) does not constitute or imply member coverage or provider reimbursement. Please refer to the member's contract benefits in effect at the time of service to determine coverage or non-coverage of these services as it applies to an individual member.

The code(s) listed below are medically necessary ONLY if the procedure is performed according to the "Policy" section of this document.

CPT/HCPCS	
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	BRCA 1 (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
81307	PALB2 (partner and localizer of BRCA2) (e.g., breast and pancreatic cancer) gene analysis; full gene sequence
81308	PALB2 (partner and localizer of BRCA2) (e.g., breast and pancreatic cancer) gene analysis; known familial variant
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

CPT/HCPCS	
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
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)
0131U	Hereditary breast cancer–related disorders (e.g., hereditary breast cancer, hereditary ovarian cancer, hereditary endometrial cancer), targeted mRNA sequence analysis panel (13 genes)
0132U	Hereditary ovarian cancer–related disorders (e.g., hereditary breast cancer, hereditary ovarian cancer, hereditary endometrial cancer), targeted mRNA sequence analysis panel (17 genes)
0134U	Hereditary pan cancer (e.g., hereditary breast and ovarian cancer, hereditary endometrial cancer, hereditary colorectal cancer), targeted mRNA sequence analysis panel (18 genes)
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)
0172U	Oncology (solid tumor as indicated by the label), somatic mutation analysis of BRCA1 (BRCA1, DNA repair associated), BRCA2 (BRCA2, DNA repair associated) and analysis of homologous recombination deficiency pathways, DNA, formalin-fixed paraffin-embedded tissue, algorithm quantifying tumor genomic instability score

ICD-10 DIAGNOSES	
C25.0-C25.9	Malignant neoplasm of pancreas code range
C50.011-C50.929	Malignant neoplasm of nipple and breast, code range
C56.0-C56.9	Malignant neoplasm of ovary; code range
C57.00-C57.02	Malignant neoplasm of fallopian tube code range
C79.60-C79.63	Secondary malignant neoplasm of ovary, code range
D05.01-D05.99	Carcinoma in situ of breast; code range
D07.30-D07.39	Carcinoma in situ of other and unspecified female genital organs; code range
Z13.71-Z13.79	Encounter for screening for genetic and chromosomal anomalies code range
C61	Malignant Neoplasm of Prostate

ICD-10 DIAGNOSES	
C79.81	Secondary malignant neoplasm of breast
C79.89	Secondary malignant neoplasm of other specified sites
Z80.3	Family history of malignant neoplasm of breast
Z80.41	Family history of malignant neoplasm of ovary
Z85.3	Personal history of malignant neoplasm of breast
Z85.41	Personal history of malignant neoplasm of ovary

REVISIONS	
01-01-2012	In the Policy section: Formatting changes to the policy language.
	In the Coding section: Added new codes: 81211, 81212, 81213, 81214, 81215, 81216, 81217
10-04-2012	Updated Description section.
	In the Policy section: ▪ In Item II, removed "Further genetic testing by rearrangement analysis (BART—BRAC Analysis Rearrangement Test) is experimental / investigational (rearrangement analysis includes sequencing the coding regions and intron/extron splice sites as well as tests to detect large dilations and rearrangements that can be missed with sequence analysis only)" and inserted "Testing for genomic rearrangements of the *BRCA1* and *BRCA2* genes (BART—BRAC Analysis Rearrangement Test)may be considered medically necessary in patients who meet criteria for *BRCA* testing, whose testing for point mutations is negative and either (1) there are 3 or more family members (one lineage) affected with breast or ovarian or fallopian tube or primary peritoneal cancer or (2) who have a risk of a *BRCA* mutation of at least 10%." ▪ In the Policy Guidelines, added "#7 Comprehensive mutation analysis currently includes sequencing the coding regions and intron/exon splice sites, as well as tests to detect common large deletions and rearrangements (BART—BRAC Analysis Rearrangement Test) that can be missed with sequence analysis alone. However, current routine laboratory testing for genomic rearrangement is more limited than the criteria noted in the policy statement; automatic testing is specified for those with a risk of *BRCA* mutation of at least 30%. In addition, prior to August 2006, testing for large deletions and rearrangements was not performed, thus some patients with familial breast cancer who had negative *BRCA* testing prior to this time may consider repeat testing for the rearrangements (see Policy statement for criteria). These rates are calculated using the Myriad II risk model (Available online at: www.myriadtests.com)."
	Updated Reference section.
	Updated Reference section.
10-26-2012	In the Policy section: ▪ In the Policy Guidelines section, #7, corrected website, "www.myriadtests.com" to "www.myriadpro.com/brca-risk-calculator".
01-15-2013	In the Coding section: ▪ Added CPT code: 81406 ▪ Removed CPT codes: 83890, 83891, 83892, 83893, 83894, 83896, 83912, 83913 (Effective 12-31-2012)
02-26-2013	Updated Description section.
	In the Policy section:

REVISIONS	
	▪ In Item I, B, added "10. Diagnosed at any age with breast cancer or pancreatic cancer, who are not from families with high risk of *BRCA1* or *BRCA2* mutation, but are affected with one of the following: o Early onset breast cancer o Two breast primary cancers with the first cancer diagnosis occurring prior to age 50 years; o Triple negative breast cancer (neither express estrogen receptor and progesterone receptor, nor overexposure HER2) diagnosed at younger than age 60. o Two or more close blood relatives with pancreatic cancer at any age. ▪ In Item II, removed "and either (1) there are 3 or more family members (one lineage) affected with breast or ovarian or fallopian tube or primary peritoneal cancer or (2) who have a risk of a BRCA mutation of at least 10%." to read "Testing for genomic rearrangements of the *BRCA1* and *BRCA2* genes (BART-BRAC Analysis Rearrangement Test) may be considered medically necessary in patients who meet criteria for BRCA testing, whose testing for point mutations is negative."
	Updated Rationale section.
	In Coding section: ▪ Removed HCPCS codes: S3818, S3819, S3820, S3822, S3823
	Updated Reference section.
07-22-2013	In Coding section: ▪ Maintenance completed on coding section, correcting "V16.4" to read "V16.41".
12-11-2013	In Coding section: ▪ Added ICD-10 Diagnosis *(Effective October 1, 2014)*
08-28-2014	Description section updated.
	In Policy section: ▪ The following medical policy language was removed from the policy and replaced with policy language that mirrors the NCCN criteria (See policy section). This update liberalized the policy and did not restrict any portion of the policy. "I. Genetic testing may be considered medically necessary under any one of the following circumstances: A. Member of family with a known *BRCA1*/*BRCA2* mutation B. Personal history of breast cancer plus one or more of the following: 1. Diagnosed at 45 years of age or younger 2. Diagnosed at 50 years of age or younger with: a. one or more close blood relatives with breast cancer at 50 years of age or younger; and/or b. one or more close blood relatives with epithelial ovarian / fallopian tube / primary peritoneal cancer 3. Two breast primaries when first breast cancer diagnosis occurred prior to age 50 4. Diagnosed at any age with two or more close blood relatives with breast and/or epithelial ovarian / fallopian tube / primary peritoneal cancer at any age 5. Close male blood relative with breast cancer 6. For an individual of ethnicity associated with deleterious mutations (e.g., founder populations of Ashkenazi Jewish, Icelandic, Swedish, Hungarian or other) no additional family history may be required 7. Diagnosed age < 60 years with a triple negative breast cancer [estrogen receptors (ER-), progesterone receptors (PR-), and HER2 (HER2-)] 8. Diagnosed age <50 years with a limited family history (see policy guidelines)

REVISIONS	
	9. Personal history of breast and / or ovarian cancer at any age with ≥ 2 close blood relatives with pancreatic cancer at any age 10. Diagnosed at any age with breast cancer or pancreatic cancer, who are not from families with a high risk of *BRCA1* or *BRCA2* mutation, but are affected with one of the following: ▪ Early onset breast cancer ▪ Two breast primary cancers with the first cancer diagnosis occurring prior to age 50 years; ▪ Triple negative breast cancer (neither express estrogen receptor and progesterone receptor, nor overexposure HER2) diagnosed at younger than age 60. ▪ Two or more close blood relatives with pancreatic cancer at any age. C. Personal history of epithelial ovarian / fallopian tube / primary peritoneal cancer D. Personal history of pancreatic cancer at any age with ≥ 2 close blood relatives with breast and / or pancreatic cancer at any age breast cancer E. Personal history of male breast cancer F. Family history only – 1. Close family member meeting any of the above criteria 2. Third-degree blood relative with breast cancer and /or ovarian / fallopian tube/ primary peritoneal cancer with ≥ 2 close blood relatives with breast cancer (at least one with breast cancer ≤50 years) and / or ovarian cancer. II. Testing for genomic rearrangements of the *BRCA1* and *BRCA2* genes (BART—BRAC Analysis Rearrangement Test) may be considered medically necessary in patients who meet criteria for *BRCA* testing, whose testing for point mutations is negative. III. Genetic testing when policy requirements are not met is experimental / investigational. <u>Policy Guidelines</u> 1. Close family member is defined as a first, second, or third degree relative, which includes: Parent, Full Sibling, Half Sibling, Child, Grandparent, Great-Grandparent, Grandchild, Aunt, Great Aunt, Uncle, Great Uncle, Nephew, Niece, and First Cousin. 2. For purposes of this policy, breast cancer includes both invasive and ductal carcinoma in situ (DCIS). 3. For individuals with family history only, an affected family member should be tested first whenever possible to identify specific site mutations. 4. The maternal and paternal sides should be considered independently. 5. Other malignancies reported in some HBOC families include prostate and melanoma. 6. Individuals with limited family history, such as fewer than 2 first- or second-degree female relatives surviving beyond 45 years in either lineage, may have an underestimated probability of a familial mutation. 7. Comprehensive mutation analysis currently includes sequencing the coding regions and intron/exon splice sites, as well as tests to detect common large deletions and rearrangements (BART—BRAC Analysis Rearrangement Test) that can be missed with sequence analysis alone. However, current routine laboratory testing for genomic rearrangement is more limited than the criteria noted in the policy statement; automatic testing is specified for those with a risk of *BRCA* mutation of at least 30%. In addition, prior to August 2006, testing for large deletions and rearrangements was not performed, thus some patients with familial breast cancer who had negative *BRCA* testing prior to this time may consider repeat testing for the rearrangements (see Policy statement for criteria). These rates are calculated using the Myriad II risk model (Available online at: www.myriadpro.com/brca-risk-calculator).

REVISIONS	
	Testing eligible individuals who belong to ethnic populations in which there are well characterized founder mutations should begin with tests specifically for these mutations (multisite testing)."
	Rationale section updated
	In Coding section: ▪ Updated nomenclature for CPT code: 81215 ▪ Updated nomenclature for ICD-9 codes: 174.8, 174.9, 175.9, 183.0, 198.6, 198.81, 233.0, V10.43, V16.41, V16.8 ▪ Added ICD-9 codes: 233.30, 233.39 ▪ Removed ICD-9 code: 233.3 ▪ Removed ICD-10 codes: C50.129, C50.229, C50.529, C50.819
	Removed Revision dates: 08-29-2006 effective 11-01-2-06, 10-31-2006 effective 01-01-2007, 11-23-2009, 10-08-2010, 09-02-2011.
	References updated
04-02-2015	Updated Description section
	In Policy section: ▪ In Item A, added "or With History of Cancer," to read, "Patients with Cancer or With History of Cancer" ▪ In Item B, added "or Without History of Cancer," to read, "Patients Without Cancer or Without History of Cancer" ▪ In Item B, added "[d]For example, fewer than 2 1st- or 2nd-degree female relatives having lived beyond age 45 in either lineage. In families with a large number of unaffected female relates, the likelihood of mutation detection may be very low.", and removed, "Unknown or limited family history / structure is defined as fewer than 2 first- or second degree female relatives having lived beyond age 45 in either lineage" ▪ Removed Item C, "Testing for genomic rearrangements of the *BRCA1* and *BRCA2* genes may be considered medically necessary in patients who meet criteria for *BRCA* testing, whose testing for point mutations is negative." ▪ Removed Item E, "Testing for *CHEK2* abnormality (mutations, deletions, etc.) is considered experimental / investigational in affected and unaffected patients with breast cancer, irrespective of family history." ▪ Added Item D, "Genetic testing in minors for *BRCA1* and *BRCA2* mutations is considered experimental / investigational." ▪ Removed "NOTE: Clinical judgment should be used to determine if the patient has reasonable likelihood of a mutation, considering the unaffected patient's current age and the age of female unaffected relatives who link the patient with the affected relatives.", and "NOTE: Testing of unaffected individuals should only be considered when an appropriate affected family member is unavailable for testing." ▪ In Policy Guidelines, removed, "4. Comprehensive Mutation Analysis. Comprehensive BRCA mutation analysis should be performed in patients with breast cancer, ovarian cancer, cancer of the fallopian tube, or primary peritoneal cancer who are: ● Eligible for testing, and ● From families without a known deleterious BRCA1 or BRCA2 mutation, and ● Not from ethnic groups with known founder mutations." ▪ In Policy Guidelines, added "9. A Recommended Testing Strategy. Patients who meet criteria for genetic testing as outlined in the Policy Statements above should be tested for mutations in BRCA1 and BRCA2. A. In patients with a known familial BRCA mutation, targeted testing for the specific mutation is recommended. B. In patients with unknown familial BRCA mutation: 1) Non-Ashkenazi Jewish descent

REVISIONS	
	a) To identify clinically significant mutations, NCCN advises testing a relative who has breast or ovarian cancer, especially with early-onset disease, bilateral disease, multiple primaries, or ovarian cancer, because that individual has the highest likelihood for a positive test result. b) If no living family member with breast or ovarian cancer exists, NCCN suggests testing first- or second-degree family members affected with cancer thought to be related to deleterious *BRCA1*/*BRCA2* mutations (e.g., prostate cancer, pancreatic cancer, melanoma). c) If no familial mutation can be identified, two possible testing strategies are: i. Full sequencing followed by testing for common large genomic rearrangements (deletions/duplications) only if sequencing detects no mutation (negative result). i. More than 90% of BRCA mutations will be detected by full sequencing.(4) ii. Alternatively, simultaneous full sequencing and testing for common large genomic rearrangements (also known as comprehensive BRCA testing; see Comprehensive Mutation Analysis, below) may be performed as is recommended by NCCN. i. Comprehensive testing can detect 92.5% of *BRCA1*/*BRCA2* mutations.(4) d) If comprehensive BRCA testing is negative, testing for uncommon large genomic rearrangements (e.g., BART™) may be done. i. Testing for uncommon large rearrangements should not be done unless both sequencing and testing for common large rearrangements have been performed and are negative. ○ Among patients with negative comprehensive testing, BART™ identified a deleterious mutation (positive result) in less than 1%.(4) C. Ashkenazi Jewish descent ○ In patients of known Ashkenazi Jewish descent, NCCN recommends testing for the 3 known founder mutations (185delAG and 5182insC in *BRCA1*; 6174delT in *BRCA2*) first. ○ If testing is negative for founder mutations, comprehensive genetic testing may be considered (see Comprehensive Mutation Analysis, above)."
	In Coding section: ▪ Removed CPT code 81406.
	Updated Rationale section.
	In Coding section: ▪ Removed CPT code 81406.
	Updated References section.
01-01-2016	Updated Description section.
	In Policy section: ▪ In Policy Guidelines, added paragraph on Genetic Counseling.
	Updated Rationale section.
	In Coding section: ▪ Added CPT code: 81162
	Updated References Section.
	Added Appendix section.
01-04-2017	Updated Description section.
	Updated Rationale section.
	Updated References section.
03-17-2018	Updated Description section.
	In Policy section: ▪ Changed "mutation" to "variant" throughout policy language.

REVISIONS	
	▪ In Item A, added "Personal" to read, "Patients With Cancer or With Personal History of Cancer." ▪ In Item A 2 c, added "pancreatic cancer or prostate cancer" to read, "One or more 1st-, 2nd, or 3rd-degree relative[a] with breast cancer (at any age), pancreatic cancer or prostate cancer[b], or". ▪ In Item A 6, added "Personal history of" and "at any age AND ≥2 or more 1st-, 2nd-, or 3rd-degree relatives[a] with breast, pancreatic, or prostate cancer[b] at any age" to read, "Personal history of pancreatic or prostate cancer[b] at any age AND ≥2 or more 1st-, 2nd-, or 3rd-degree relatives[a] with breast, pancreatic, or prostate cancer[b] at any age." ▪ Removed previous Item C, "Unless the criteria above are met, genetic testing either for those affected by breast, ovarian, fallopian tube, or primary peritoneal cancer or for unaffected individuals, including those with a family history of pancreatic cancer, is considered experimental / investigational." ▪ Added new Item C, "Genetic testing for *BRCA1* and *BRCA2* variants when criteria above are not met is considered experimental / investigational." ▪ Updated Policy Guidelines.
	Updated Rationale section.
	In Coding section: ▪ Removed ICD-9 codes.
	Updated Revisions section.
01-01-2019	In Coding section: ▪ Added CPT codes: 81163, 81164, 81165, 81166, 81167. ▪ Deleted CPT codes: 81211, 81213, 81214. ▪ Revised nomenclature to CPT codes: 81162, 81212, 81215, 81216, 81217. ▪ Added ICD-10 code: Z80.41.
04-12-2019	Policy posted to the bcbsks.com website on 03-13-2019; effective 04-12-2019.
	Updated Description section.
	In Policy section: ▪ Removed previous policy language: "A. Patients With Cancer or With Personal History of Cancer Genetic testing for *BRCA1* and *BRCA2* variants in cancer-affected individuals may be considered medically necessary under any of the following circumstances: 1. Individual from a family with a known *BRCA1/BRCA2* mutation 2. Personal history of breast cancer and ≥1 of the following: a. Diagnosed at age ≤45 years b. Two primary breast cancers when 1st breast cancer diagnosis occurred at age ≤50 years c. Diagnosed at age ≤50 years AND: i. One or more 1st-, 2nd-, or 3rd-degree relative[a] with breast cancer (at any age), pancreatic cancer or prostate cancer[b], or ii. Unknown or limited family history[c] d. Diagnosed at age ≤60 years with a triple negative (estrogen receptor–negative, progesterone receptor–negative, human epidermal growth factor receptor 2–negative) breast cancer e. Diagnosed at any age AND ≥1 1st-, 2nd-, or 3rd-degree relative[a] with breast cancer diagnosed at ≤50 years f. Diagnosed at any age AND ≥2 1st-, 2nd-, or 3rd-degree relative[a] with breast cancer at any age g. Diagnosed at any age AND ≥1 1st-, 2nd-, or 3rd-degree relative[a] with epithelial ovarian, fallopian tube, or primary peritoneal cancer

REVISIONS	
	h. Diagnosed at any age AND ≥2 1st-, 2nd-, or 3rd-degree relative[a] with pancreatic cancer or prostate cancer[b] at any age i. 1st-, 2nd-, or 3rd-degree male relative with breast cancer j. Ethnicity associated with deleterious founder mutations, e.g., Ashkenazi Jewish descent[d] 3. Personal history of epithelial ovarian, fallopian tube, or primary peritoneal cancer 4. Personal history of male breast cancer 5. Personal history of pancreatic cancer or prostate cancer[c] at any age AND ≥1 1st-, 2nd-, or 3rd-degree relative[a] with any of the following: a. Breast cancer ≤50 b. Ovarian, fallopian tube, or primary peritoneal cancer at any age 6. Personal history of pancreatic or prostate cancer[b] at any age AND ≥2 or more 1st-, 2nd-, or 3rd-degree relatives[a] with breast, pancreatic, or prostate cancer[b] at any age 7. For pancreatic cancer, if Ashkenazi Jewish ancestry, only 1 additional affected relative is needed. B. Patients Without Cancer or Without History of Cancer (see Policy Guidelines: Testing Unaffected Individuals) Genetic testing for *BRCA1* and *BRCA2* variants of cancer-unaffected individuals may be considered medically necessary under any of the following circumstances: 1. Individual from a family with a known *BRCA1* or *BRCA2* variant 2. 1st- or 2nd-degree blood relative meeting any criterion listed above for Patients with Cancer 3. 3rd-degree blood relative with breast cancer and/or ovarian, fallopian tube, or primary peritoneal cancer AND ≥2 1st-, 2nd-, or 3rd-degree relatives[a] with breast cancer (≥1 at age ≤50 years) and/or ovarian, fallopian tube, or primary peritoneal cancer [a] For familial assessment, 1st-, 2nd-, and 3rd-degree relatives are blood relatives on the same side of the family (maternal or paternal). • 1st-degree relatives are parents, siblings, and children • 2nd-degree relatives are grandparents, aunts, uncles, nieces, nephews, grandchildren, and half-siblings • 3rd-degree relatives are great-grandparents, great-aunts, great-uncles, great-grandchildren, and first cousins. [b] For familial assessment, prostate cancer is defined as Gleason score ≥7. [c] For example, fewer than 2 1st- or 2nd-degree female relatives having lived beyond age 45 in either lineage. In families with a large number of unaffected female relatives, the likelihood of variant detection may be very low. [d] Testing for Ashkenazi Jewish or other founder mutation(s) should be performed first (see Policy Guidelines: High-Risk Ethnic Groups). C. Genetic testing for *BRCA1* and *BRCA2* variants when criteria above are not met is considered experimental / investigational. D. Genetic testing in minors for *BRCA1* and *BRCA2* variants is considered experimental / investigational." ▪ Added new policy language: "A. Patients With Cancer or With a Personal History of Cancer Genetic testing for *BRCA1* and *BRCA2* variants in cancer-affected individuals may be considered medically necessary under any of the following circumstances: 1. Individual from a family with a known *BRCA1* or *BRCA2* variant 2. Personal history of breast cancer and one or more of the following: a. Diagnosed at age ≤45 years b. Diagnosed 46 to 50 years with:

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	i. One or more 1st-, 2nd-, or 3rd-degree blood relative with breast cancer at any age ii. An unknown or limited family history[c] iii. An additional breast cancer primary at any age iv. One or more 1st-, 2nd-, or 3rd-degree blood relative with high grade (Gleason score ≥7) prostate cancer c. Diagnosed ≤60 years with: i. Triple negative breast cancer d. Diagnosed at any age with: i. One or more 1st-, 2nd-, or 3rd-degree blood relative with v. Breast cancer diagnosed at ≤50 years; or vi. Ovarian, fallopian tube, or primary peritoneal cancer; or vii. Male breast cancer; or viii. Metastatic prostate cancer; or ix. Pancreatic cancer ii. ≥2 additional diagnoses of breast cancer at any age in patient and/or 1st-, 2nd-, or 3rd-degree blood relative e. Ashkenazi Jewish ancestry 3. Personal history of ovarian, fallopian tube, or primary peritoneal cancer 4. Personal history of male breast cancer 5. Personal history of pancreatic cancer 6. Personal history of metastatic prostate cancer 7. Personal history of high-grade prostate cancer (Gleason score ≥7) at any age with: a. One or more 1st-, 2nd-, or 3rd-degree blood relative with ovarian, fallopian tube, or primary peritoneal cancer, pancreatic cancer, or metastatic prostate cancer at any age or breast cancer ≤50 years; or i. Two or more 1st-, 2nd-, or 3rd-degree blood relatives with breast or prostate cancer (any grade) at any age; or b. Ashkenazi Jewish ancestry 8. BRCA1 or BRCA2 pathogenic or likely pathogenic variant detected by tumor profiling on any tumor type in the absence of germline pathogenic or likely pathogenic variant analysis 9. Regardless of family history, some individuals with an BRCA-related cancer may benefit from genetic testing to determine eligibility for targeted treatment 10. An individual who does not meet the other criteria but with one or more 1st- or 2nd-degree blood relatives meeting any of the above criteria. B. Patients Without Cancer or Without History of Cancer (see Policy Guidelines: Testing Unaffected Individuals) 1. Genetic testing for *BRCA1* and *BRCA2* variants of cancer-unaffected individuals may be considered medically necessary under any of the following circumstances: i. Individual from a family with a known *BRCA1* or *BRCA2* variant ii. 1st- or 2nd-degree blood relative meeting any criterion listed above for Patients With Cancer iii. 3rd-degree blood relative with breast cancer and/or ovarian, fallopian tube, or primary peritoneal cancer AND two or more 1st-, 2nd-, or 3rd-degree relatives[a] with breast cancer (≥1 at age ≤50 years) and/or ovarian, fallopian tube, or primary peritoneal cancer [a] For familial assessment, 1st-, 2nd-, and 3rd-degree relatives are blood relatives on the same side of the family (maternal or paternal). • 1st-degree relatives are parents, siblings, and children

REVISIONS	
	• 2nd-degree relatives are grandparents, aunts, uncles, nieces, nephews, grandchildren, and half-siblings • 3rd-degree relatives are great-grandparents, great-aunts, great-uncles, great-grandchildren, and first cousins. 2. Genetic testing for *BRCA1* and *BRCA2* variants in cancer-affected individuals or of cancer-unaffected individuals with a family history of cancer when criteria above are not met is considered experimental / investigational. 3. Genetic testing in minors for *BRCA1* and *BRCA2* variants is considered experimental / investigational.
	Updated Rationale section.
	Updated References section.
	Removed Appendix section.
04-16-2021	Updated Description section
	In Policy section: ITEM A • Added underlined section to and removed the strikethrough text from Item A.2.b.: b. Diagnosed 46 to 50 years with: I. One or more 1st-, 2nd-, or 3rd-degree blood relative with breast cancer, ovarian, pancreatic, or prostate cancer at any age; or II. An unknown or limited family history; or III. An additional breast cancer primary at any age IV. One or more 1st-, 2nd-, or 3rd-degree blood relative with high grade (Gleason score ≥7) prostate cancer • Added underlined text to Item A.2.d.i: x. Metastatic or intraductal/cribriform prostate cancer, or high-risk group or very-high-risk group (see Policy Guidelines) prostate cancer; or • Added "at any age" to Item A.3. and A.5. • Added underlined text to and removed the strikethrough text from Item A.6 and A.7: 6. Personal history of metastatic or intraductal/cribriform histology prostate cancer at any age; or high-risk group or very-high-risk group prostate cancer at any age 7. Personal history of high-grade prostate cancer (Gleason score ≥7) at any age with: a. One or more 1st-, 2nd-, or 3rd-degree blood relative with ovarian, fallopian tube, or primary peritoneal cancer, pancreatic cancer, or metastatic or intraductal/cribriform prostate cancer at any age or breast cancer ≤50 years; or b. Two or more 1st-, 2nd-, or 3rd-degree blood relatives with breast or prostate cancer (any grade) at any age; or c. Ashkenazi Jewish ancestry ▪ Added Item A.8. and Item A.9. ITEM B ▪ Added underlined section to and removed the strikethrough text from Item B.1.b, c, & d: b. An unaffected individual with a 1st- or 2nd-degree blood relative meeting any criterion listed above for Patients With Cancer (except individuals who meet criteria only for systemic therapy decision-making). If the individual with cancer has pancreatic cancer or prostate cancer (metastatic or intraductal/cribriform or high-risk group or very-high-risk group) then only first-degree relatives should be offered testing unless there are other family history indications for testing. c. An unaffected individual who otherwise does not meet the criteria above but has a probability >5% of a *BRCA1/2* pathogenic variant based on prior probability models (*e.g.*, Tyrer-Cuzick, BRCAPro, Pennll)

REVISIONS	
	d. 3rd-degree blood relative with breast cancer and/or ovarian, fallopian tube, or primary peritoneal cancer AND two or more 1st-, 2nd-, or 3rd-degree relatives[a] with breast cancer (≥1 at age ≤50 years) and/or ovarian, fallopian tube, or primary peritoneal cancer POLICY GUIDELINES ▪ Added underlined section to and removed the strikethrough text from policy guidelines 1, 2, and 3: N. Current U.S. Preventive Services Task Force (USPSTF) guidelines recommend screening women with a personal or any family history of breast, ovarian, tubal, or peritoneal cancer or who have an ancestry associated with *BRCA1/2* gene mutation. Women with positive screening result on the risk assessment tool should receive genetic counseling and, if indicated after counseling, *BRCA* testing (grade genetic testing (B Recommendation). O. Recommended screening tools designed to identify a family history that may be associated with an increased risk for potentially harmful variants mutations in *BRCA1* or *BRCA2* are: o Ontario Family History Assessment Tool (FHAT) o Manchester Scoring System o Referral Screening Tool (RST) o Pedigree Assessment Tool (PAT) o Family History Screen (FHS-7) o International Breast Cancer Intervention Study instrument (Tyrer-Cuziak) o Brief versions of the BRCAPRO P. Prostate Cancer Risk Groups: Risk groups for prostate cancer in this policy include high-risk groups and very-high-risk groups. High-risk group: no very-high-risk features and are T3a (American Joint Committee on Cancer staging T3a = tumor has extended outside of the prostate but has not spread to the seminal vesicles); OR Grade Group 4 or 5; OR prostate specific antigen of 20 ng/ml or greater Very-high-risk group: T3b-T4 (tumor invades seminal vesicle(s); or tumor is fixed or invades adjacent structures other than seminal vesicles such as external sphincter, rectum, bladder, levator muscles, and/or pelvic wall); OR Primary Gleason Pattern 5; OR 2 or 3 high-risk features; OR greater than 4 cores with Grade Group 4 or 5 ▪ Added underlined section to and removed the strikethrough text from policy guidelines 4: In patients with unknown familial *BRCA* variant: 1) Non-Ashkenazi Jewish descent a) To identify clinically significant variants, National Comprehensive Cancer Network (NCCN) advises testing a relative who has breast or ovarian cancer, especially with early-onset disease, bilateral disease, multiple primaries, or ovarian cancer, because that individual has the highest likelihood of obtaining a positive test result. Unless the affected individual is a member of an ethnic group for which particular founder pathogenic or likely pathogenic variants are known, comprehensive genetic testing (*i.e.,* full sequencing of the genes and detection of large gene rearrangements) should be performed b) If no living family member with breast or ovarian cancer exists, NCCN suggests testing first- or second-degree family members affected with cancer thought to be related to deleterious *BRCA1* or *BRCA2* variants (e.g., prostate cancer, pancreatic cancer, melanoma). c) If no familial variant can be identified, two possible testing strategies are:

REVISIONS	
	i. Full sequencing followed by testing for *common* large genomic rearrangements (deletions/duplications) only if sequencing detects no variant (negative result). ii. More than 90% of *BRCA* variants will be detected by full sequencing. ii. Alternatively, simultaneous full sequencing and testing for *common* large genomic rearrangements (also known as comprehensive *BRCA* testing; see Comprehensive Variant Analysis, below) may be performed as is recommended by NCCN. ii. Comprehensive testing can detect 92.5% of *BRCA1* or *BRCA2* variants. d) If comprehensive *BRCA* testing is negative, testing for *uncommon* large genomic rearrangements (e.g., BART) may be done. i. Testing for *uncommon* large rearrangements should not be done unless both sequencing and testing for *common* large rearrangements have been performed and are negative. o Among patients with negative comprehensive testing, BART identified a deleterious variant (positive result) in less than 1%. 2) Ashkenazi Jewish descent a) In patients of known Ashkenazi Jewish descent, NCCN recommends 1 approach is to test for the 3 known founder mutations (185delAG and 5182insC in *BRCA1*; 6174delT in *BRCA2*) first. b) If testing is negative for founder mutations, comprehensive genetic testing may be considered (see Comprehensive Mutation Analysis). c) However, NCCN version 1.2021 states "However, with new panels available, many clinicians are moving away from this stepped approach and are increasingly using comprehensive testing"
	Updated Rationale section
	In Coding section: Added CPT codes 81432, 81433, 0102U, 0103U, 0129U, 0131U, 0132U, 0134U. 0138U, and 0172U Added ICD-10 diagnosis codes C25.0, C25.1, C25.2, C25.3, C25.4, C25.7, C25.8,C57.00, C57.01, C57.02, C61, and Z13.71 Deleted ICD-10 diagnosis code Z80.8
	Updated References section
07-28-2021	In Policy section: ▪ Item B.2 and B.3 were reformatted to become Item C and Item D.
02-14-2022	Updated Title ▪ Added Germline to title
	Updated Description Section
	Updated Policy Section ▪ Added Section A.2: Individuals meeting the criteria below but with previous limited testing (e.g., single gene and/or absent deletion duplication analysis) ▪ Removed Section A.3.d.i."male breast cancer" ▪ Section A.3.d.ii changed "≥ 2 additional" to "≥3 total" ▪ Added Section A.3.e"Diagnosed at any age with male breast cancer" ▪ Removed A.5 "Personal history of male breast cancer" ▪ Section A.6 added word "exocrine" ▪ Section A.10 Changed to read "Personal history of cancer and to aid in systemic therapy decision-making, for PARP-inhibitors for human epidermal receptor 2

REVISIONS	
	(HER2)-negative metastatic and HER2-negative early stage, high-risk breast cancer (see Policy Guidelines)." ▪ Removed footnote [a]
	Updated Policy Guideline Section ▪ Added Section 3 (C) and 4 (D), ▪ Section 6B Removed B.1-title "Non-Ashkenazi Jewish descent" and B.1.IV.c ▪ Reformatted section to following A.1.a.I.i format
	Updated Rationale Section
	Updated References Section
02-22-2022	Updated Description Section
	Updated Policy Section ▪ Removed section A9 "Personal history of cancer and to aid in systemic therapy decision-making for PARP-inhibitors for human epidermal receptor 2 (HER2)-negative metastatic and HER2-negative early stage, high-risk breast cancer (see Policy Guidelines)"
	Updated Policy Guidelines ▪ Added new section A:"Genetic testing for *BRCA1* and *BRCA2* variants in breast cancer-affected individuals who are considering systemic therapy is addressed separately in BCBSKS medical policy *Germline and Somatic Biomarker Testing (Including Liquid Biopsy) for Targeted Treatment and Immunotherapy in Breast Cancer*" ▪ Removed Section D: "Breast Cancer Risk Groups"
	Updated Rationale Section
	Updated Coding Section ▪ Added ICD 10 codes: D07.30-D07.39 and C79.89
	Updated References Section
01-12-2023	Updated Title ▪ Changed Title to: "Germline Genetic Testing for Hereditary Breast/Ovarian Cancer Syndrome and Other High-Risk Cancers (BRCA1, BRCA2, PALB2)"
	Updated Description Section
	Updated Policy Section ▪ Section A: Added "and *PALB2*" to *BRCA1* and *BRCA2* ▪ Section A1: Changed from "Individuals from a family with a known *BRCA1* or *BRCA2* variant." to "Individuals with any close blood relative with a known *BRCA1* *BRCA2* or *PALB2* pathogenic/likely pathogenic variant (see Policy Guidelines for definitions and for testing strategy)." ▪ Section A3bI, A3dI, A3dII, A7a, A7b: changed "1st-, 2nd-, or 3rd-degree" to "close" ▪ Section A4: Added "epithelial" before ovarian ▪ Section A9: Removed statement "Personal history of cancer and to aid in systemic therapy decision-making for PARP-inhibitors for ovarian cancer prostate cancer, and pancreatic cancer and platinum therapy for prostate cancer and pancreatic cancer." ▪ Section B: Title changed from "Without History of Cancer" to "With Other Personal History of Cancer" ▪ Section B1: Changed from "Genetic testing for *BRCA1,* and *BRCA2,* and variants of cancer-unaffected individuals may be considered medically necessary under any of the following circumstances:" to "Genetic testing for *BRCA1, BRCA2,* and *PALB2* variants of cancer-unaffected individuals and individuals with cancer but not meeting the above criteria (including individuals with cancers unrelated to hereditary breast ovarian cancer syndrome) may be considered medically necessary under any of the following circumstances:"

REVISIONS	
	▪ Section B1a: Removed Statement "Individual from a family with a known *BRCA1 BRCA2* or variant" ▪ Section B1b: Added "An individual with or without cancer not meeting the above criteria but who has a" Removed "An unaffected individual with a" and "(except individuals who meet criteria only for systemic therapy decision-making)." ▪ Section B1c: Added "An individual with any type of cancer" and "or *PALB2*" Removed "An unaffected individual" ▪ Section D: Added "Testing for *PALB2* variants in individuals who do not meet the criteria outlined above is considered experimental / investigational." ▪ Section E: Changed to read "Genetic testing in minors for *BRCA1, BRCA2* and *PALB2* variants for hereditary breast ovarian cancer syndrome is considered experimental / investigational. (see Policy Guidelines)
	Updated Policy Guideline Section ▪ Section A: Added "Testing for *BRCA1, BRCA2,* and/or *PALB2* outside of the above criteria, such as testing all individuals with triple negative breast cancer, may be indicated for guiding cancer therapies." ▪ Section F, F1, and F2, I: Added "*PALB2*" ▪ Section J: Replaced "BRCA" with "*BRCA1, BRCA2,* or *PALB2* variants for identifying hereditary breast ovarian cancer syndrome" ▪ Section K: Added "*PALB2*" and removed "However, the presence of prostate cancer in an individual, or in a family, is not itself considered sufficient justification for BRCA testing."
	Updated Rationale Section
	Updated Coding Section ▪ Updated nomenclature for 81432, 81433, 0102U, 0103U ▪ Added 81307 and 81308
	Updated References Section

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