

BRCA1- and BRCA2-Associated Hereditary Breast and Ovarian Cancer Syndrome

Pathogenic variants in the *BRCA1* and *BRCA2* genes are associated with hereditary breast and ovarian cancer (HBOC) syndrome. *BRCA1*- and *BRCA2*-associated HBOC syndrome is often characterized by early age of cancer onset (typically before 50 years of age) and multiple, multifocal, and/or similar cancers in a single individual or in a closely related family member(s). Individuals with a single germline *BRCA1* or *BRCA2* pathogenic variant have an increased risk for breast (female and male), ovarian, fallopian tube, peritoneal, pancreatic, prostate, melanoma, and other cancers. Analysis of the *BRCA1* and *BRCA2* genes is offered through ARUP's *BRCA1* and *BRCA2*-Associated HBOC Syndrome Panel. For a more comprehensive test for hereditary causes of breast and/or ovarian cancer, please see the [Hereditary Breast and Ovarian Cancer Panel](#), which includes analysis of several genes, including *BRCA1* and *BRCA2*.

Disease Overview

Associated Disorder

BRCA1- and *BRCA2*-associated HBOC syndrome

- Caused by a single germline *BRCA1* or *BRCA2* pathogenic variant¹
- Individuals are at increased risk for the following cancers (combined estimated risks for *BRCA1* and *BRCA2* listed below)¹:
 - Breast (female): 38-87%
 - Breast (male): 1.2-8.9%
 - Ovarian (including fallopian tube and peritoneal): 16.5-63%
 - Pancreatic: 1-7%
 - Prostate: 8.6-20%
 - Melanoma: elevated for *BRCA2* only

Etiology

At least 5-10% of all breast cancers and 10-15% of all ovarian cancers are associated with a hereditary cause.^{2,3,4}

Prevalence

One in 400 individuals from the general population or 1 in 40 Ashkenazi Jewish individuals have a *BRCA1* or *BRCA2* pathogenic variant.^{5,6}

Inheritance

- Single pathogenic variants in the *BRCA1* and *BRCA2* genes are inherited in an autosomal dominant manner and are associated with HBOC syndrome.
- *BRCA1* and *BRCA2* pathogenic variants are also associated with autosomal recessive Fanconi anemia.

Test Description

Genes Tested

- *BRCA1* (NM_007294) and *BRCA2* (NM_000059)

Tests to Consider

[BRCA1 and BRCA2-Associated HBOC Syndrome Panel, Sequencing and Deletion/Duplication 3001855](#)

Method: Massively Parallel Sequencing/Multiplex Ligation-dependent Probe Amplification

- Germline analysis of the *BRCA1* and *BRCA2* genes in individuals with a suspected diagnosis of HBOC syndrome
- When a relative has a previously identified pathogenic sequence variant, see Familial Mutation, Targeted Sequencing (2001961)

[Familial Mutation, Targeted Sequencing 2001961](#)

Method: Polymerase Chain Reaction/Sequencing

- Recommended test for a known familial sequence variant previously identified in a family member
- A copy of the family member's test result documenting the familial variant is REQUIRED

[Deletion/Duplication Analysis by MLPA 3003144](#)

Method: Multiplex Ligation-dependent Probe Amplification

- Use to assess for large deletion/duplication previously identified in a family member
- A copy of a relative's lab report is REQUIRED

See [Related Tests](#)



- See [Genes Tested](#) table for more information.



Clinical Sensitivity

BRCA1 and *BRCA2* sequencing and deletion/duplication testing detects 20-60% of hereditary breast and/or ovarian cancers, in general.^{1,2,7}

- >80% of *BRCA1* and *BRCA2* variants are detectable by sequencing.
- ~10% of *BRCA1* and *BRCA2* variants are detectable by large deletion/duplication analysis.

Testing Strategy

Contraindications for Ordering

- Should not be ordered to detect somatic variants associated with malignancy because sensitivity for mosaic variants is low with methodology used for germline assays
- Individuals with hematologic malignancy and/or a previous allogeneic bone marrow transplantation should not undergo molecular genetic testing on a peripheral blood specimen.
 - Testing of cultured fibroblasts is required for accurate interpretation of test results.
- When a relative has a previously identified pathogenic variant, see [Familial Mutation, Targeted Sequencing](#).

Limitations

- A negative result does not exclude a heritable form of cancer.
- Diagnostic errors can occur due to rare sequence variations.
- Interpretation of this test result may be impacted if this individual has had an allogeneic stem cell transplantation.
- The following will not be evaluated:
 - Variants outside the coding regions and intron-exon boundaries of the targeted genes
 - Regulatory region variants and deep intronic variants
 - Breakpoints of large deletions/duplications
- The following may not be detected:
 - Deletions/duplications/insertions of any size by massively parallel sequencing
 - Some variants due to technical limitations in the presence of pseudogenes, repetitive, or homologous regions
 - Low-level somatic variants

Analytical Sensitivity

- Analytical sensitivity for multiplex ligation-dependent probe amplification (MLPA) is 99%.
 - Approximately 99% for single nucleotide variants (SNVs) and >93% for insertions/duplications/deletions from 1-10 base pairs in size
 - Variants >10 base pairs may be detected, but analytical sensitivity may be reduced.

Genes Tested

Gene	MIM Number	Disorder	Inheritance
<i>BRCA1</i>	113705	HBOC syndrome Associated cancer(s)/tumor(s): breast, ovarian, fallopian tube, peritoneal, pancreatic, prostate	AD
		Fanconi anemia, complementation group S	AR
<i>BRCA2</i>	600185	HBOC syndrome Associated cancer(s)/tumor(s): breast, ovarian, fallopian tube, peritoneal, pancreatic, prostate, melanoma	AD
		Fanconi anemia, complementation group D1	AR

AD, autosomal dominant; AR, autosomal recessive





References

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2. Pruthi S, Gostout BS, Lindor NM. [Identification and management of women with BRCA mutations or hereditary predisposition for breast and ovarian cancer](#). Mayo Clin Proc. 2010;85(12):1111-1120. PubMed
3. Couch FJ, Shimelis H, Hu C, et al. [Associations between cancer predisposition testing panel genes and breast cancer](#). JAMA Oncol. 2017;3(9):1190-1196. PubMed
4. Risch HA, McLaughlin JR, Cole DE, et al. [Prevalence and penetrance of germline BRCA1 and BRCA2 mutations in a population series of 649 women with ovarian cancer](#). Am J Hum Genet. 2001;68(3):700-710. PubMed
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Additional Resources

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Walsh T, Casadei S, Lee MK, et al. [Mutations in 12 genes for inherited ovarian, fallopian tube, and peritoneal carcinoma identified by massively parallel sequencing](#). Proc Natl Acad Sci U S A. 2011;108(44):18032-18037. PubMed

Related Information

[Breast Cancer Biomarkers](#)
[Ovarian Cancer](#)

Related Tests

[Hereditary Breast and Ovarian Cancer Panel, Sequencing and Deletion/Duplication 2012026](#)

Method: Massively Parallel Sequencing/Exonic Oligonucleotide-based CGH Microarray

[Hereditary Cancer Panel, Sequencing and Deletion/Duplication 2012032](#)

Method: Massively Parallel Sequencing/Exonic Oligonucleotide-based CGH Microarray

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