Integrated GENETICS LabCorp Specialty Testing Group | Integrated ONCOLOGY LabCorp Specialty Testing Group

BRCAssure® *BRCA2* Targeted Analysis

Specimen ID: 00000000000
Control ID: **Lab Case ID:** 000000000000000

PATIENT, ANY

Acct #: 00000000
Labcorp Of America
CMBP
1912 TW Alexander Dr
Durham NC 27709

Phone: (000) 000-0000

Patient Details		Specimen Details		Physician Details	
DOB:	00/00/0000	**Date collected:**	00/00/0000 00:00 Local	**Ordering:**	.
Age(y/m/d):	000/00/0000	**Date received:**	00/00/0000 00:00	**Referring:**	
Gender:		**Date entered:**	00/00/0000 00:00	**ID:**	
Patient ID:		**Date reported:**	00/00/0000 00:00 ET	**NPI:**	0000000000

Specimen Type: Whole Blood
Clinical Indication: Testing for familial cancer risk variant(s): *BRCA2* c.2092delC

RESULTS

POSITIVE FOR TARGETED VARIANT(S)
At least one clinically significant variant was detected in the *BRCA2* gene.
No variants of uncertain significance were identified.

GENE	VARIANT
BRCA2	**POSITIVE** Heterozygous for c.2092delC (p.Leu698TyrfsX32) (Pathogenic)

INTERPRETATION

This result increases this individual's risk for cancer.

Variant details

The *BRCA2* c.2092delC (p.Leu698TyrfsX32) targeted variant is associated with HBOC (Hereditary Breast and Ovarian Cancer Syndrome). This frameshift variant is predicted to result in a downstream premature termination codon. The variant is absent in general population databases. It has been reported in ClinVar and in the literature. Based on LabCorp's in-house variant classification protocol and in accord with the American College of Medical Genetics' guidelines, this variant has been classified as pathogenic and is associated with an increased risk for hereditary breast and ovarian cancer.

Gene summary

BRCA1 and *BRCA2* (OMIM 600185) are tumor suppressor genes that play a critical role in normal DNA repair, cell cycle control, and genomic stability. Pathogenic variants in these genes are associated with familial cancers, including breast, ovarian, pancreatic, prostate, and melanoma.

ADDITIONAL CLINICAL INFORMATION

Cancer risks applicable to this individual

A positive *BRCA2* result is associated with the following cancer risks:

Lifetime high risk	Breast >60%; Ovarian 13-29%
Lifetime increased risk	Pancreatic 5-10%; Prostate 19-34%

Electronically released by: Any Physician, PhD

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ADDITIONAL CLINICAL INFORMATION

NCCN Guidelines

When BRCA1 and BRCA2 results are negative, additional testing may be helpful for some patients with breast, ovarian, prostate and pancreatic cancer. Guidelines from the National Comprehensive Cancer Network® (NCCN®) recommend considering germline genetic testing for high-penetrance breast and/or ovarian cancer genes (including, but not limited to, BRCA1/2, CDH1, PALB2, PTEN, and TP53) in patients with any of the criteria in the table below. To discuss comprehensive genetic testing for breast, ovarian, prostate and pancreatic cancer genes, an Integrated Genetics' Genetic Coordinator is available at 800-345-4363.

Breast cancer diagnosed ≤ age 45	Male breast cancer, ovarian cancer, or pancreatic cancer
Breast cancer diagnosed age 46-50 with multiple primary breast cancers or ≥ 1 close relative with breast, ovarian, pancreatic, or prostate cancer	Prostate cancer at any age and Ashkenazi Jewish ancestry, or that is metastatic, high risk or in combination with certain family history criteria
Breast cancer diagnosed at any age and one of the following: • To aid in PARP inhibitor or olaparib treatment • Ashkenazi Jewish ancestry • Triple negative breast cancer • ≥ 1 close relative with breast cancer ≤ age 50, or ovarian, pancreatic, prostate, or male breast cancer at any age • ≥ 3 total diagnoses of breast cancer in patient and/or close blood relatives • ≥ 2 close blood relatives with either breast or prostate cancer at any age	
Patients with a first or second degree relative meeting certain criteria in this table may consider germline genetic testing as well. Complete criteria may be found at NCCN.org.	

RECOMMENDATIONS

NCCN Guidelines provide clinical management recommendations. The most current guidelines may be found at NCCN.org. Modification of surveillance, including initiation of earlier and/or more frequent screening, may be based on guidelines and a patient's personal and/or family history for specific associated cancers.

Genetic counseling is recommended to discuss the potential clinical and/or reproductive implications of these results, as well as recommendations for testing family members. There is a 50% chance (1 in 2) of a first-degree relative having this variant. To access Integrated Genetics' Genetic Counselors please visit www.integratedgenetics.com/genetic-counseling or call (855) GC-CALLS (855-422-2557). To discuss targeted analysis for other family members with a LabCorp Genetic Coordinator please call 800-345-4363.

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METHODS AND LIMITATIONS

Next-generation sequencing: Genomic regions of interest are selected using a custom capture reagent for target enrichment and sequenced via the Illumina(R) next generation sequencing platform. Regions of interest include all exons and intron/exon junctions (+/-20 nucleotides) of the *BRCA1* (NM_007294.3) and *BRCA2* (NM_000059.3) genes. Sequencing reads are aligned with the human genome reference GRCh37/hg19 build. Minimum mean coverage is 40X. Any segment failing minimum read depth coverage is rescued by bi-directional Sanger sequencing to complete sequence analysis. Variants, including SNVs and CNVs, are identified using a custom bioinformatics pipeline.

Reported variants: Pathogenic and likely pathogenic variants and variants of uncertain significance (VUS) are reported. Non-deletion variants are specified using the numbering and nomenclature recommended by the Human Genome Variation Society (HGVS, http://www.hgvs.org/). Benign variants are not reported. Variant classification and confirmation are consistent with ACMG standards and guidelines (Richards, PMID:25741868; Rehm, PMID:23887774). Detailed variant classification information is available upon request. A variant of uncertain significance (VUS) should not be used in clinical decision making; a VUS is classified based on inadequate or conflicting evidence regarding its pathogenicity or clinical relevance.

Limitations: Technologies used do not detect germline mosaicism and do not rule out the presence of large chromosomal aberrations, including rearrangements, gene fusions, or variants in regions or genes not included in this test, or possible inter/ intragenic interactions between variants. Variant classification and/or interpretation may change over time if more information becomes available. False positive or false negative results may occur for reasons that include: genetic variants, pseudogene interference, technical handling, blood transfusions, bone marrow transplantation, mislabeling of samples, or erroneous representation of family relationships. For heterozygous variants in the same gene the assay cannot determine whether they are on the same or different chromosome; to determine phase and clinical significance, rarely, parental testing may be required. Exact breakpoints of exon-level deletions/duplications are not determined. The presence of an inherited cancer syndrome due to a different genetic cause cannot be ruled out. Any interpretation should be clinically correlated with information about the patient's presentation and relevant family history.

REFERENCES

1. NCCN Genetic/Familial High Risk Assessment: Breast, Ovarian, and Pancreatic. Version 1.2022.
2. Petrucelli, et al. *BRCA1*- and *BRCA2*-Associated Hereditary Breast and Ovarian Cancer. GeneReviews, updated 2016. PMID: 20301425.

This test was developed and its performance characteristics determined by LabCorp. It has not been cleared or approved by the Food and Drug Administration.

Electronically released by: Any Physician, PhD