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

BRCAssure® *BRCA1* Targeted Analysis

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

PATIENT, ANY

Acct #: 00000000 **Phone:** (000) 000-000
CMBP QA TEST ACCOUNT
CMBP QA DEPT RTP.
RTP
RTP NC 27215-5820

Patient Details		Specimen Details		Physician Details	
DOB:	00/00/0000	**Date collected:**	00/00/0000 00:00 Local	**Ordering:**	
Age(y/m/d):	000/00/00	**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)

RESULTS

NEGATIVE FOR TARGETED VARIANTS

No clinically significant variants or variants of uncertain significance were identified.

GENE	VARIANT
BRCA1	**NEGATIVE** No pathogenic variants were identified.

INTERPRETATION

No pathogenic variants were identified.

ADDITIONAL CLINICAL INFORMATION

NCCN Guidelines

When *BRCA1* and *BRCA2* results are negative, additional testing may be helpful for some patients with breast, ovarian, 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, and pancreatic cancer genes, an Integrated Genetics' Genetic Coordinator is available at 800-345-4363.

Breast cancer diagnosed ≤ age 45	Ovarian cancer at any age
Breast cancer diagnosed age 46-50 with ≥1 close relative with breast, ovarian, pancreatic, or high grade prostate cancer	Breast cancer diagnosed at any age, with ≥1 close relative with breast cancer ≤ age 50, or ovarian, pancreatic, or metastatic prostate cancer
Male breast cancer at any age	Pancreatic cancer at any age
Triple negative breast cancer diagnosed ≤60	Metastatic prostate cancer at any age
Breast, ovarian, or pancreatic cancer at any age; and Ashkenazi Jewish ancestry	A first or second degree relative meeting any of the criteria in this table

Electronically released by: Any Physician, PhD

Testing Performed at Laboratory Corporation of America Holdings, 1912 T.W. Alexander Drive, RTP, NC 27709-0150, 1-800-345-4363, Medical Director: Any Physician, MD.

PATIENT: PATIENT, ANY
DOB: 00/00/0000
Patient ID:
CONTROL ID:
LAB CASE ID: 000000000000000
Specimen ID: 00000000000
Date Collected: 00/00/0000 00:00 Local

RECOMMENDATIONS

Genetic counseling is recommended to discuss the potential clinical and/or reproductive implications of these results, as well as recommendations for testing family members. To access Integrated Genetics Genetic Counselors please visit www.integratedgenetics.com/genetic-counseling or call (855) GC-CALLS (855-422-2557).

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 a different chromosomes; 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 1.2020.
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