

Patient

Patient Name: John Doe
Date of Birth: 11/11/1855
Accession ID: 231122100047
Sex:

Specimen

Specimen Type: BUCCAL SWAB
Collection Date: DD/MM/20YY
Received Date: DD/MM/20YY

Ordering Physician

Physician: Jane Smith M.D.
Facility:
Report Date: DD/MM/20YY

Test Result

⊕ Positive Result Pathogenic/Likely pathogenic variant(s) detected.

Primary Findings

GENE	VARIANT	POSITION	ZYGOSITY	CLASSIFICATION
BRCA2	c.1189_1190insTTAG p.Gln397LeufsTer25	g.32906804C>CTTAG	Heterozygous	Pathogenic

Primary Findings Summary

BRCA2 p.Gln397LeufsTer25

This patient is heterozygous for variant p.Gln397LeufsTer25 in the *BRCA2* gene. This variant is also defined as c.1189_1190insTTAG. This variant has been reported in families with breast and ovarian cancer (Lalloo et al., 2006. PubMed ID 16644204; Walsh et al., 2011. PubMed ID 22006311; Susswein et al., 2016. PubMed ID 26681312). This variant is reported in 0.00088% of alleles in individuals of European (non-Finnish) descent in gnomAD and is interpreted as pathogenic in ClinVar by an expert panel (https://www.ncbi.nlm.nih.gov/clinvar/variation/51080/?new_evidence=true). Frameshift variants in *BRCA2* are expected to be pathogenic. This variant is interpreted as pathogenic.

Inherited mutations in *BRCA1* and this gene, *BRCA2*, confer increased lifetime risk of developing breast or ovarian cancer. Both *BRCA1* and *BRCA2* are involved in maintenance of genome stability, specifically the homologous recombination pathway for double-strand DNA repair. The largest exon in both genes is exon 11, which harbors the most important and frequent mutations in breast cancer patients. The *BRCA2* gene was found on chromosome 13q12.3 in human. The *BRCA2* protein contains several copies of a 70 aa motif called the BRC motif, and these motifs mediate binding to the RAD51 recombinase which functions in DNA repair. *BRCA2* is considered a tumor suppressor gene, as tumors with *BRCA2* mutations generally exhibit loss of heterozygosity (LOH) of the wild-type allele. [provided by RefSeq, May 2020].

Confirmation by orthogonal technology was performed at Prevention Genetics (3800 S. Business Park Avenue, Marshfield, Wisconsin 54449 USA, CLIA 52D-2065132). Genetic counseling is recommended. For more information, please contact the National Society of Genetic Counselors and locate a practitioner near you at <https://www.nsgc.org/page/find-a-genetic-counselor> or by phone at 312.321.6834.

Test results reviewed and approved by:

John Hanson, Ph.D., HCLD
Section Director

Jan 25, 2026

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Genes Evaluated

BLM, BRCA2, BTK, CFTR, F5, F9, FANCC, G6PC, G6PD, JAK2, MPL, MSH6, MYD88, NRAS, PALB2, PLCG2, PMS2, PTEN, RUNX1, TERT

Test Limitations

This test aims to detect all clinically relevant variants within the coding regions of the genes listed in the method above. Pathogenic and Likely Pathogenic variants in these genes and exons should be confirmed by orthogonal technology. Homopolymer regions, and regions outside of the coding regions cannot be captured by the standard NGS target enrichment protocols. At this time the assay does not detect large deletions and duplications. This analysis also cannot detect pathogenic variants within regions which were not analyzed (e.g. long repeat regions, mitochondrial sequence). This assay is not designed to detect mosaicism; possible cases of mosaicism may be investigated at the discretion of the laboratory director. This test is not designed to detect complex gene rearrangements or genomic aneuploidy events. US Biosciences only reports findings within the genes that are included within the panel. It is important to understand that there may be variants in these genes undetectable using current technology. Additionally, there may be genes associated with hereditary cancer risk whose clinical association has not yet been definitively established. The test may therefore not detect all variants associated with hereditary cancer risk. The interpretation of variants is based on our current understanding of the genes in this panel. These interpretations may change over time as more information about the genes and this individual's clinical phenotype becomes available. Variants that have been classified as benign, likely benign, or uncertain significance are not included in this report.

Regulatory Disclosures

This test for Next-Generation Sequencing of genomic DNA was developed and performance characteristics assessed by **US-Biosciences**, Jessup, PA, CLIA ID: 39D2342948. This laboratory is regulated under the Clinical Laboratory Improvement Amendments of 1988 (CLIA) as qualified to perform High-Complexity clinical testing. This test has not been cleared nor approved by the U.S. Food and Drug Administration (FDA). The FDA has determined that such clearance or approval is not necessary.