



54501229

CONFIDENTIAL

MyRisk™ Hereditary Cancer Test

## MyRisk Genetic Result

MyRisk™

Hereditary Cancer Test

## RECEIVING HEALTHCARE PROVIDER

Test HCP, MD  
 Test Medical Center  
 6609 BLANCO RD STE 200  
 SAN ANTONIO, TX 78216

## SPECIMEN

Specimen Type: Blood  
 Draw Date: Dec 03, 2021  
 Accession Date: Dec 03, 2021  
 Report Date: Dec 03, 2021

## PATIENT

Name: Pt Last Name,  
 Pt First Name  
 Date of Birth: Dec 03, 1981  
 Patient ID: Patient id  
 Gender: Female  
 Accession #: 07007251-BLD  
 Requisition #: 90026818

## GENETIC RESULT: NEGATIVE - NO CLINICALLY SIGNIFICANT MUTATION IDENTIFIED

Note: "CLINICALLY SIGNIFICANT," as defined in this report, is a genetic change that is associated with the potential to alter medical intervention.



## BREAST CANCER RISKSORE®: REMAINING LIFETIME RISK 12.1%

See RiskScore Interpretation Section for more information.



## CLINICAL HISTORY ANALYSIS: NO ADDITIONAL MANAGEMENT GUIDELINES IDENTIFIED BASED ON THE CLINICAL HISTORY PROVIDED

Other clinical factors may influence individualized management. This analysis may be incomplete if details about cancer diagnoses, ages, family relationships or other factors were omitted or ambiguous. If this patient also has a clinically significant mutation, the recommendations based on the clinical history analysis should be considered in light of the possibility that this mutation explains all or some of the cancer history in the family.

## ADDITIONAL FINDINGS: VARIANT(S) OF UNCERTAIN SIGNIFICANCE (VUS) IDENTIFIED

There are currently insufficient data to determine if these variants cause increased risk.

GENE	VARIANT(S) OF UNCERTAIN SIGNIFICANCE	INTERPRETATION
STK11	c.961C>G (p.Pro321Ala)	Uncertain Clinical Significance

**Details About Non-Clinically Significant Variants:** All individuals carry DNA changes (i.e., variants), and most variants do not increase an individual's risk of cancer or other diseases. When identified, variants of uncertain significance (VUS) are reported. Likely benign variants (Favor Polymorphisms) and benign variants (Polymorphisms) are not reported and available data indicate that these variants most likely do not cause increased cancer risk. Present evidence does not suggest that non-clinically significant variant findings be used to modify patient medical management beyond what is indicated by the personal and family history and any other clinically significant findings.

**Variant Classification:** Myriad's myVision™ Variant Classification Program performs ongoing evaluations of variant classifications. In certain cases, healthcare providers may be contacted for more clinical information or to arrange family testing to aid in variant classification. When new evidence about a variant is identified and determined to result in clinical significance and management change, that information will automatically be made available to the healthcare provider through an amended report.



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### ADDITIONAL INFORMATION

**Genes Analyzed:** Sequencing (seq) and large rearrangement analyses were performed for all coding exons in the following genes, unless otherwise indicated:

*APC, ATM, AXIN2, BAP1, BARD1, BMPR1A, BRCA1, BRCA2, BRIP1, CDH1, CDK4, CDKN2A, CHEK2, CTNNA1, FH, FLCN, HOXB13* (seq only), *MEN1, MET, MLH1, MSH2, MSH3* (excluding repetitive portions of exon 1), *MSH6, MUTYH, NTHL1, PALB2, PMS2, PTEN, RAD51C, RAD51D, SDHA, SDHB, SDHC, SDHD, SMAD4, STK11, TP53, TSC1, TSC2, VHL*.

Limited promoter regions may also be analyzed for large rearrangements.

Sequencing (seq) and/or large rearrangement (LR) analyses were performed only for the gene portions indicated in parenthesis for the following genes:

*EGFR* (exons 18-21, seq and LR), *EPCAM* (exons 8-9, LR only), *GREM1* (exon 1 and upstream regulatory regions, LR only), *MITF* (c.952, seq only), *POLE* (exonuclease domain, seq only), *POLD1* (exonuclease domain, seq only), *RET* (exons 5, 8, 10, 11, 13-16 seq and LR), *TERT* (promoter c.DNA -1 to -70, seq only).

\*\* Other genes not analyzed with this test may also be associated with cancer.

**Indication for Testing:** It is our understanding that this individual was identified for testing due to a personal or family history suggestive of a hereditary predisposition for cancer.

**Associated Cancer Risks and Clinical Management:** The "MyRisk Management Tool" associated with this report provides a summary of cancer risk and professional society medical management guidelines that may be useful in developing a plan for this patient based on any clinically significant test results and/or reported personal/family history. In some cases, a MyRisk Management Tool cannot be provided, such as when the result has a special interpretation or includes a mutation with unusual characteristics.

**Analysis Description:** The Technical Specifications summary ([myriad.com/technical-specifications](http://myriad.com/technical-specifications)) describes the analysis, method, performance, nomenclature, and interpretive criteria of this test. Current testing technologies are unable to definitively determine whether a variant is germline or somatic in origin, which may significantly impact risk estimates and medical management; therefore, these results should be correlated with this patient's personal and family history. The interpretation of this test may also be impacted if the patient has a hematologic malignancy or an allogeneic bone marrow transplant.

### CLASSIFICATION DISCLAIMER

THE CLASSIFICATION AND INTERPRETATION OF ALL VARIANTS IDENTIFIED IN THIS ASSAY REFLECTS THE CURRENT STATE OF MYRIAD'S SCIENTIFIC UNDERSTANDING AT THE TIME THIS REPORT WAS ISSUED. VARIANT CLASSIFICATION AND INTERPRETATION MAY CHANGE FOR A VARIETY OF REASONS, INCLUDING BUT NOT LIMITED TO, IMPROVEMENTS TO CLASSIFICATION TECHNIQUES, AVAILABILITY OF ADDITIONAL SCIENTIFIC INFORMATION, AND OBSERVATION OF A VARIANT IN MORE PATIENTS.



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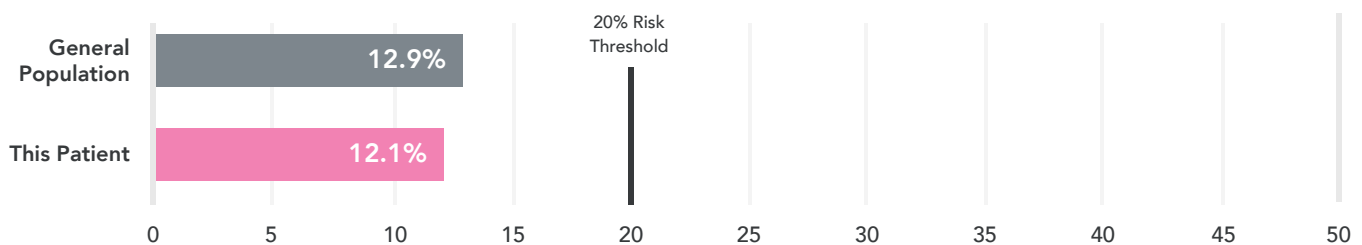
## Breast Cancer RiskScore®

Breast Cancer  
RiskScore®:

12.1%

RESULT: 12.1% Remaining Lifetime Breast Cancer Risk  
0.6% 5-Year Breast Cancer Risk

### Remaining Lifetime Breast Cancer Risk (Age-Adjusted)



### BREAST CANCER RISKSORE® INTERPRETATION

The breast cancer RiskScore provides an estimate of the remaining lifetime risk for breast cancer. A risk estimate at or above 20% is associated with specific modified medical recommendations, including consideration of more aggressive breast cancer screening and additional risk reduction measures. If applicable, details of these recommendations are provided in the accompanying MyRisk Medical Management Tool or other supplemental material. Women with a risk estimate below 20% may still be appropriate for consideration of modified medical management based on other clinical factors or estimates from other breast cancer risk models, such as Tyrer-Cuzick, Claus, and Gail.

### TYRER-CUZICK BREAST CANCER RISK CALCULATION

REMAINING LIFETIME BREAST CANCER RISK: 12.0%

5-YEAR BREAST CANCER RISK: 0.6%

The National Comprehensive Cancer Network (NCCN) provides medical management recommendations for women with an estimated remaining lifetime breast cancer risk greater than 20% based on Tyrer-Cuzick. These recommendations are summarized on the MyRisk Management Tool (MMT). If an MMT is not included with this report, current management recommendations from the NCCN Breast Cancer Screening and Diagnosis panel can be accessed at [www.nccn.org](http://www.nccn.org). Version 7.02 of the Tyrer-Cuzick model was used for this risk estimate. Tyrer-Cuzick model Versions 7.02 and 8.0 are available for download at the EMS-Trials website, <http://www.ems-trials.org/riskevaluator>.



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### BREAST CANCER RISKSORE<sup>®</sup> ANALYSIS DESCRIPTION

The breast cancer RiskScore provides 5-year and remaining lifetime breast cancer risks, based on an analysis of genetic markers combined with patient clinical and family history data. The Technical Specifications summary (<http://myriad.com/technical-specifications>) describes the RiskScore eligibility criteria, analysis, method, performance and interpretive criteria of this test. Data from 149 biomarkers are analyzed during next generation sequencing (NGS). The allele status of these markers has been weighted to generate a polygenic odds ratio of 1.0 for this patient, which is combined with clinical and family history information to generate the final RiskScore. This odds ratio is adjusted for overlap between the risk captured by the biomarkers and the clinical factors and has not been validated for use with other risk models. The Clinical and Cancer Family History Information section of this report displays the data used for this analysis and explains important limitations on the accuracy of RiskScore (including significant over- or under-estimates of breast cancer risk) that can be caused by errors and/or omissions in the reported clinical and family history data.

Please contact Myriad Medical Services at 1-800-469-7423 X 3850 to discuss any questions regarding this result.

This Authorized Signature  
pertains to this laboratory report:

Benjamin B. Roa, PhD  
Diplomate ABMG  
Laboratory Director

These test results should only be used in conjunction with the patient's clinical history and any previous analysis of appropriate family members. The patient's clinical history and test results should not be disclosed to a third party, unless related to treatment or payment for treatment, without the patient's express written authorization. It is strongly recommended that these results be communicated to the patient in a setting that includes appropriate genetic consultation. This test was developed and its performance characteristics determined by Myriad Genetic Laboratories. It has not been cleared or approved by the U.S. Food and Drug Administration (FDA). The FDA has determined that clearance or approval for laboratory-developed tests is not required.





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## Clinical &amp; Cancer Family History Information

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## PERSONAL / FAMILY CANCER HISTORY SUMMARY

FAMILY MEMBER	CANCER / CLINICAL DIAGNOSIS	AGE AT DIAGNOSIS
Patient	None	

## PATIENT CLINICAL HISTORY SUMMARY

Woman's age	40	Hormone Replacement Therapy (HRT)	No
Ancestry	White/Non-Hispanic	- HRT: Treatment Type	N/A
Height	5 ft 7 in	- HRT: Current user	N/A
Weight	175 lbs	- Number of years ago started	N/A
Age of menarche	13	- Additional years of intended use	N/A
Patient's menopausal status	Pre-menopausal	- HRT: Past user	N/A
- Age of onset	N/A	- Number of years ago ended	N/A
Age of first live birth	27	Breast biopsy	No Benign Disease

## NUMBER OF PATIENT'S FEMALE RELATIVES

Daughters	1	Sisters	2	Maternal Aunts	2	Paternal Aunts	2
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## Clinical & Cancer Family History Information

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The clinical information displayed here was provided by a qualified healthcare provider on the Test Request Form and other documents, and was not verified by Myriad. Family members listed as "other" are not included in a Tyrer-Cuzick breast cancer risk estimate or other personal/family history assessments. For more information see the Specifications for Personal/Family History Analysis at <http://myriad.com/technical-specifications>.

The accuracy and completeness of the information provided in the Clinical and Cancer Family History Information section of the report (e.g. height and weight, age of menarche) may significantly affect the accuracy of breast cancer risk estimates provided based on either Tyrer-Cuzick or RiskScore.

RiskScore is not valid, and may significantly over- or under-estimate breast cancer risk for women who do not meet the eligibility criteria in effect when the testing was performed. The current criteria are: 1) age is 18 to 84 years, 2) no personal history of breast cancer, LCIS, hyperplasia (with or without atypia), or a breast biopsy with unknown results, 3) there is no mutation detected in a breast cancer risk gene (other than a monoallelic *CHEK2* mutation in a White/Non-Hispanic or Ashkenazi Jewish individual), 4) the woman's relatives have not been found to have a mutation in a high-penetrance breast cancer risk gene and 5) the sample was submitted with a current Test Request Form and the ordering healthcare provider has not determined that RiskScore is inappropriate for the patient. If this is an amended report for a patient tested in the past, please refer to the MyRisk Technical Specifications at <http://myriad.com/technical-specifications> for the eligibility criteria in effect at the time of the original testing.



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**GENETIC RESULT: NEGATIVE - NO CLINICALLY SIGNIFICANT MUTATION IDENTIFIED**

Note: "CLINICALLY SIGNIFICANT," as defined in this report, is a genetic change that is associated with the potential to alter medical intervention.

**BREAST CANCER RISKSORE®: REMAINING LIFETIME RISK 12.1%**

See RiskScore Interpretation Section for more information.

**CLINICAL HISTORY ANALYSIS: NO ADDITIONAL MANAGEMENT GUIDELINES IDENTIFIED BASED ON THE CLINICAL HISTORY PROVIDED**

Other clinical factors may influence individualized management. This analysis may be incomplete if details about cancer diagnoses, ages, family relationships or other factors were omitted or ambiguous. If this patient also has a clinically significant mutation, the recommendations based on the clinical history analysis should be considered in light of the possibility that this mutation explains all or some of the cancer history in the family.

No clinically significant mutations were identified in this patient. However, based on personal/family history, the patient's cancer risks may still be increased over the general population. See information below.

Please see the Genetic Test Result for more details on any variant(s) detected in this patient, including variant classification information.

**ADDITIONAL FINDINGS: VARIANT(S) OF UNCERTAIN SIGNIFICANCE (VUS) IDENTIFIED****TYRER-CUZICK BREAST CANCER RISK CALCULATION****REMAINING LIFETIME BREAST CANCER RISK: 12.0%****5-YEAR BREAST CANCER RISK: 0.6%**

The Tyrer-Cuzick breast cancer risk estimate is only calculated for women who meet the following criteria: 1) age is younger than 85 years, 2) no known mutation or inconclusive result has been found in the woman or any of her relatives, and 3) the sample was submitted with a current Test Request Form that includes all of the fields required to collect the information used in the calculation, and the provider has not indicated on the Test Request Form that the Tyrer-Cuzick calculation is not appropriate for the patient. Version 7.02 of the Tyrer-Cuzick model was used for this risk estimate. Tyrer-Cuzick model Versions 7.02 and 8.0 are available for download at the EMS-Trials website, <http://www.ems-trials.org/riskevaluator>.

**Notes for Personalized Management:**

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### INFORMATION ON HOW CANCER RISKS AND MANAGEMENT ARE DETERMINED

The MyRisk Management Tool provides cancer risk levels based on analysis of genetic test results (see MyRisk Genetic Result) and a summary of medical society management recommendations based on both the genetic test results and a limited analysis of the patient's clinical history related to the risk for breast, colorectal, prostate, melanoma and pancreatic cancers. Here are some important points to understand as you interpret this test report and decide on the best plan for management:

- Comprehensive patient management. The management recommendations presented in this report are a summary of management options recommended by the National Comprehensive Cancer Network (NCCN) and other established medical societies and are general in nature. The patient's actual management should be modified based on personal medical history, surgeries and other treatments. A comprehensive risk assessment and management plan may take into account this report and other aspects of the patient's personal/family medical history (e.g., all known clinical diagnoses), as well as lifestyle, environmental and other factors.
- Risk estimates based on provider-supplied information. Some of the risk estimates and management recommendation summaries provided in this report are based on our interpretation of information supplied by the ordering health care provider on the test request form (see Specifications for Personal/Family History analysis at [myriad.com/technical-specifications](http://myriad.com/technical-specifications)). The patient's actual risks and appropriate management may be significantly different if details provided for cancer diagnoses, ages, family relationships or other factors were incorrect, omitted, ambiguous or have since changed. Please review the clinical history listed on the Clinical & Family History Information page of this report to make sure that the information used was provided and interpreted correctly.
- Variability in Tyrer-Cuzick risk estimates. Tyrer-Cuzick estimates of breast cancer risk can vary significantly based on the way in which the model is used, and the estimate provided here may be higher or lower than what would be calculated by other users. For complete details of how Myriad calculates Tyrer-Cuzick risk estimates, including how Myriad handles information provided in a format not compatible with the model, please see the Specifications for Personal/Family History analysis at [myriad.com/technical-specifications](http://myriad.com/technical-specifications). These Specifications also include information for recalculating the Tyrer-Cuzick breast cancer risk estimate if desired.
- What is meant by "High Risk" and "Elevated Risk"? In the Genetic Test Result Summary, a gene-associated cancer risk is described as "High Risk" for a cancer type if all of the following conditions are met: the absolute risk of cancer is approximately 5% or higher, the increase in risk over the general population is approximately 2 to 3-fold or higher, and there is significant data from multiple studies supporting the cancer risk estimate. A gene is described as "Elevated Risk" for a cancer type if there is sufficient data to support an increase in cancer risk over the general population risk, but not all criteria for "High Risk" are met.

### INFORMATION FOR FAMILY MEMBERS

Family members should talk to their healthcare providers about hereditary cancer testing to help define their own risk and assist in the interpretation of this patient's genetic test result.

**Please contact Myriad Medical Services at 1-800-469-7423 X 3850 to discuss any questions regarding this result.**

### END OF MANAGEMENT TOOL