BRCA1/2 Analyses with CancerNext®

RESULTS

Pathogenic Mutation(s): None Detected
Variant(s) of Unknown Significance: None Detected
Gross Deletion(s)/Duplication(s): None Detected

SUMMARY

NEGATIVE: No Clinically Significant Variants Detected

INTERPRETATION

- No pathogenic mutations, variants of unknown significance, or gross deletions or duplications were detected.
- Risk Estimate: low likelihood of variants in the genes analyzed contributing to this individual's clinical history.
- Genetic counseling is a recommended option for all individuals undergoing genetic testing.

Genes Analyzed (36 total): APC, ATM, AXIN2, BARD1, BMPR1A, BRCA1, BRCA2, BRI1, C4H1, CDK4, CDKN2A, CHEK2, DICER1, MLH1, MSH2, MSH3, MSH6, MUTYH, NBN, NF1, NTHL1, PALB2, PMS2, PTEN, RAD51C, RAD51D, RECC1, SMAD4, SMARCA4, STK11 and TP53 (sequencing and deletion/duplication); HOXB13, POLD1 and POLE (sequencing only); EPCAM and GREM1 (deletion/duplication only).

Order Summary: The following products were included in the test order for this individual. Please note: tests on hold and those that have been cancelled (including reflex testing steps canceled due to a positive result in a preceding test) are excluded. For additional information, please contact Ambry Genetics.

- BRCA1/2 seq and del/dup (Product Code 9336)
- CancerNext® (Product Code 8824)
AmbryScore: Personalized Breast Cancer Risk Estimate

Supplement to Test Results

Remaining Lifetime Risk:

5.4%

- This individual’s remaining lifetime risk for breast cancer is estimated to be 5.4%, which is at or below the general population risk of 12.6%.

- General population breast cancer screening is appropriate.

Breast Cancer Lifetime Risk

Average for Patient Age & Ethnicity

12.6%

This Patient

5.4%

20% Risk Level*

*Recommendations for modified breast cancer screening exist for women estimated above 20% lifetime risk by models such as Tyer-Cuzick.

Interpretation

- This individual’s remaining lifetime breast cancer risk of 5.4% is at or below the average risk for women of this age and ethnicity.
- Women at average risk should discuss timing and frequency of breast cancer screening with their healthcare provider.
- The below scores were used to estimate the remaining lifetime risk for this individual:
  - Tyer-Cuzick remaining lifetime risk estimate: 4.5%
  - Polygenic risk score (PRS): RR=1.2
- Use of the AmbryScore risk estimate in medical management and planning should be left to the discretion of the healthcare provider and interpreted in the context of patient age, clinical history, and family history.

Technical Details

The AmbryScore tool provides a personalized estimate of remaining lifetime breast cancer risk (up to age 85) based on the following patient-specific factors: age at testing, ethnicity, clinical and family history data, and results of single nucleotide polymorphism (SNP) profiling. A population-standardized PRS is computed as the sum of the patient’s risk alleles across 155 SNPs, weighted by the SNP-specific effects reported in large breast cancer studies, and ethnicity-specific allele frequencies (PMID: 20566762, 26069314, 26077605, 29059563). A patient’s absolute risk of breast cancer is computed according to the Tyer-Cuzick model (v0.8) (PMID: 26029312), which is based on her age, family history and clinical information, and combined with her PRS to produce an estimate of her remaining lifetime risk. The AmbryScore calculation is highly-dependent on the accuracy of clinical-provided clinical data. Other factors not accounted for in the AmbryScore calculation may impact lifetime breast cancer risk including, but not limited to, germline mutations not analyzed by the ordered genetic test. The AmbryScore provided is patient-specific and cannot be used to infer risk to relatives. Additional technical details and supporting references can be found here:

ASSAY INFORMATION

General Information: Cancer is a complex, multifactorial disease diagnosed in approximately 1 out of every 2 men and 1 out of every 3 women over the course of a lifetime. Mutations in cancer predisposition genes appear to be responsible for between 5-10% of cancer diagnoses.

Methodology: The CancerNext® test is a comprehensive screen of 36 genes associated with hereditary cancer predisposition. Genomic deoxyribonucleic acid (gDNA) is isolated from the patient's specimen using standardized methodology and quantified. Sequence enrichment of the targeted coding exons and adjacent intronic nucleotides is carried out by a bait-capture methodology using long biotinylated oligonucleotide probes followed by polymerase chain reaction (PCR) and Next-Generation sequencing. Additional Sanger sequencing is performed for any regions missing or with insufficient read depth coverage for reliable heterozygous variant detection. Variants in regions complicated by pseudogene interference, variant calls not satisfying depth of coverage and variant allele frequency quality thresholds, and potentially homozygous variants are verified by Sanger sequencing. The BRCA2 Portuguese founder mutation, c.156_157insAlu (also known as 384insAlu), and the MSH2 coding exons 1-7 inversion are detected by next generation sequencing and confirmed by multiplex ligation-dependent probe amplification (MLPA) or PCR and agarose gel electrophoresis. Cross deletion/duplication analysis for the genes sequenced (excluding HOXB13, POLD1, POLE, PMS2) is performed using a custom pipeline based on read-depth from NGS data and/or targeted chromosomal microarray with confirmatory MLPA when applicable. Cross deletion/duplication analysis of PMS2 is performed using MLPA kit P008-B1. If a deletion is detected in exons 13, 14, or 15 of PMS2, double stranded sequencing of the appropriate exon(s) of the pseudogene PMS2CL will be performed to determine if the deletion is located in the PMS2 gene or pseudogene. Sequence analysis is based on the following NCBI reference sequences: APC- NM_000038.5 & NM_001127511.2, ATM- NM_000051.3, AXIN2- NM_004655.3, BARD1- NM_004652.2, BMFRI1A- NM_004329.2, BRCA1- NM_007294.3, BRCA2- NM_000559.3, BRIP1- NM_032043.1, CDH1- NM_004360.3, CDK4- NM_000075.3, CDKN2A- NM_000777.4 and NM_058195.3 (p14ARF), CHEK2- NM_007194.3, DICER1- NM_177432.8, HOXB13- NM_006361.5, MUTYH- NM_00128425.1, MLH1- NM_000249.3, MSH2- NM_000251.1, MSH3- NM_002439.3, MSH6- NM_000179.2, NBN- NM_002485.4, NF1- NM_000267.3, NTHL1- NM_002528.5, PALB2- NM_024675.3, PMS2- NM_000535.5, POLD1-NM_002691.2, POLE-NM_006231.2, PTEN-NM_000314.4, RAD51C-NM_058216.1, RAD51D-NM_000287.3, RECQL- NM_0002907.3, SMAD4- NM_000539.5, SMARCA4- NM_001128849.1, STK11- NM_000455.4, TP53- NM_000546.4.

Analytical Range: The CancerNext® test targets detection of DNA sequence mutations in the sequenced genes (APC, ATM, AXIN2, BARD1, BMFRI1A, BRCA1, BRCA2, BRIP1, CDH1, CDK4, CDKN2A, CHEK2, DICER1, HOXB13, MLH1, MSH2, MSH3, MSH6, MUTYH, NBN, NF1, NTHL1, PALB2, POLD1, POLE, PMS2, PTEN, RAD51C, RAD51D, RECQL, SMAD4, SMARCA4, STK11, and TP53) by either Next-Generation or Sanger sequencing of all coding domains and well into the flanking 5' and 3' ends of all the introns and untranslated regions. For HOXB13, only variants impacting codon 84 are routinely reported. For POLD1 and POLE, only missense variants and in-frame insertions/deletions in the exonuclease domains (codons 311-541 and 299-485, respectively) are routinely reported. For RECQL, only missense variants in the helicase and RQC domains (codons 63-592) and exonic truncating variants are routinely reported. The MSH3 polyalanine repeat region is excluded from analysis. Cross deletion/duplication analysis determines gene copy number for the covered exons and untranslated regions of sequenced genes (excluding HOXB13, POLD1, and POLE) as well as GREM1 and EPCAM. For GREM1, only the status of the 40kb 5’UTR gross duplication is analyzed and reported. For EPCAM, only gross deletions encompassing the 3’ end of the gene are reported. For NTHL1, only full-gene gross deletions and duplications are detected. For APC, all promoter 1B gross deletions as well as single nucleotide substitutions within the promoter 1B YY1 binding motif (NM_001127511 c.-196_186) are analyzed and reported.

Result Reports: Results reported herein may be of constitutional or somatic origin. This methodology cannot differentiate between these possibilities. In result reports, alterations in the following classifications are always reported, and are based on the following definitions and clinical recommendations:

- **Pathogenic Mutation:** alterations with sufficient evidence to classify as pathogenic (capable of causing disease). Targeted testing of at-risk relatives and appropriate changes in medical management for pathogenic mutation carriers recommended. Previously described pathogenic mutations, including intronic mutations at any position, are always reported when detected.
- **Variant, Likely Pathogenic (VLP):** alterations with strong evidence in favor of pathogenicity. Targeted testing of at-risk relatives and appropriate changes in medical management for VLP carriers typically recommended. Previously described likely pathogenic variants, including intronic VLPs at any position, are always reported when detected.
- **Variant, Unknown Significance (VUS):** alterations with limited and/or conflicting evidence regarding pathogenicity. Familial testing via the Family Studies Program recommended. Medical management to be based personal/family clinical histories, not VUS carrier status. Note, intronic VUSs are always reported out to 5 basepairs from the splice junction when detected.

Alterations of unlikely clinical significance (those with strong/very strong evidence to argue against pathogenicity) are not routinely included on results reports. These include findings classified as "likely benign" and "benign" alterations.

Assay Information Continued on Next Page
ASSAY INFORMATION (Supplement to Test Results - Continued)

Resources: The following references are used in variant analysis and classification when applicable for observed genetic alterations.

7. Exome Variant Server, NHLBI Exome Sequencing Project (ESP) [Internet], Seattle WA. Available from: evs.gs.washington.edu/EVS.

Disclaimer: This test was developed and its performance characteristics were determined by Ambry Genetics Corporation. It has not been cleared or approved by the US Food and Drug Administration. The FDA does not require this test to go through premarket FDA review. It should not be regarded as investigational or for research. This test should be interpreted in context with other clinical findings. This laboratory is certified under the Clinical Laboratory Improvement Amendments (CLIA) as qualified to perform high complexity clinical laboratory testing. This test analyzes the following types of mutations: nucleotide substitutions, small deletions (up to 25 bp), small insertions (up to 10 bp), small indels and gross deletions/duplications. Unless otherwise noted in the methodology section above, it is not intended to analyze the following types of alterations: gross rearrangements, deep intronic variations, Alu element insertions, and other unknown abnormalities. The pattern of mutation types varies with the gene tested and this test detects a high but variable percentage of known and unknown mutants of the classes stated. A negative result from the analysis cannot rule out the possibility that the tested individual carries a rare unexamined mutation or mutation in the undetectable group. This test is designed and validated to be capable of detecting ~99% of described mutations in the 36 genes represented on the panel (analytical sensitivity). The clinical sensitivity of this test may vary widely according to the specific clinical and family history. Breast, ovarian and colon cancers are complex clinical disorders. Mutations in other genes or the regions not analyzed by this test can also give rise to clinical conditions similar to breast cancer, ovarian or colon cancer. Although molecular tests are highly accurate, rare diagnostic errors may occur. Possible diagnostic errors include sample mix-up, erroneous paternity identification, technical errors, clerical errors, and genotyping errors. Genotyping errors can result from trace contamination of PCR reactions, from maternal cell contamination in fetal samples, from rare genetic variants that interfere with analysis, low-level mosaicism, presence of pseudogenes, technical difficulties in regions with high GC content or homopolymer tracts, presence of pre-malignant or malignant cells in the sample, or from other sources. Rare variants present in the human genome reference sequence (GRCh37 p5/hg19) or rare misalignment due to presence of pseudogenes can lead to misinterpretation of patient sequence data. This report does not represent medical advice. Any questions, suggestions, or concerns regarding interpretation of results should be forwarded to a genetic counselor, medical geneticist, or physician skilled in interpretation of the relevant medical literature.
# Understanding Your Negative Hereditary Cancer Genetic Test Result

**INFORMATION FOR PATIENTS**

<table>
<thead>
<tr>
<th>Result</th>
<th>NEGATIVE</th>
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<tbody>
<tr>
<td></td>
<td>Your testing did not find any disease-causing mutations (changes, like spelling mistakes) in the genes tested.</td>
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<thead>
<tr>
<th>Cancer Risks</th>
<th>VARIES</th>
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<tbody>
<tr>
<td></td>
<td>Even though no mutation was found, you may still have an increased risk of developing cancer based on other possible factors, including the following:</td>
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<tr>
<td></td>
<td>• Your medical and/or family history</td>
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<td></td>
<td>• You could have a mutation in the genes tested that cannot be found with current testing methods</td>
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<tr>
<td></td>
<td>• You could have a mutation in a gene that has not yet been linked to cancer or was not tested</td>
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<td>Your healthcare provider can help you learn more about this.</td>
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<tr>
<th>Risk Management</th>
<th>VARIES</th>
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<tr>
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<td>Risk management decisions are very personal, and depend on many factors. Talk to your healthcare provider about which, if any, options may be right for you.</td>
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<tr>
<th>Family Members</th>
<th>VARIABLE RISKS</th>
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<tbody>
<tr>
<td></td>
<td>Depending on your medical and/or family history, your relatives may still have an increased risk of developing cancer and may be eligible for genetic testing and/or increased cancer screening. They should discuss this with a healthcare provider.</td>
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<th>Next Steps</th>
<th>DISCUSS</th>
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<tr>
<td></td>
<td>Please share this with family members so they can talk with their healthcare providers and learn more. Stay in contact with your healthcare provider for any relevant updates in genetic testing and/or cancer screening. Also, remember to update him/her with any new information about your family history, especially new cancer diagnoses, as this may change how they determine your cancer risks.</td>
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<tr>
<th>Reach Out</th>
<th>RESOURCES</th>
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<tr>
<td></td>
<td>• Ambry's Hereditary Cancer Site for Families <a href="patients.ambrygan.com/cancer">patients.ambrygan.com/cancer</a></td>
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<td></td>
<td>• American Cancer Society <a href="cancer.org">cancer.org</a></td>
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<td></td>
<td>• Genetic Information Nondiscrimination Act (GINA) <a href="ginahelp.org">ginahelp.org</a></td>
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<td>• National Society of Genetic Counselors <a href="nsgc.org">nsgc.org</a></td>
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<td></td>
<td>• Canadian Association of Genetic Counsellors <a href="cagc-acgc.ca">cagc-acgc.ca</a></td>
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</table>

Please discuss this information with your healthcare provider. The cancer genetics field is continuously evolving, so updates related to your genetic test result, medical recommendations, genetic testing options, and/or potential treatments may be available over time. This information is not meant to replace a discussion with a healthcare provider, and should not be considered or interpreted as medical advice.