MAYO CLINIC LABORATORIES

**NEW TEST**

Notification Date: July 3, 2023
Effective Date: July 20, 2023

# Rapid Hereditary Breast Cancer Treatment Decision Panel, Varies

**Test ID:** BRTP

## Useful for:

- Establishing a diagnosis of a hereditary breast cancer syndrome allowing for surgical and management decision making
- Determining therapeutic eligibility with poly adenosine diphosphate-ribose polymerase (PARP) inhibitors based on certain gene alterations (eg, *BRCA1*, *BRCA2*) in selected tumor types
- Evaluating patients with breast cancer who have a personal history suggestive of a hereditary breast or gynecological cancer syndrome
- Identifying genetic variants associated with increased risk for breast cancer, allowing for predictive testing and appropriate screening of at-risk family members

## Genetics Information:

- This test utilizes next-generation sequencing to detect single nucleotide and copy number variants in 11 genes associated with hereditary breast cancer: *ATM, BRCA1, BRCA2, CDH1, CHEK2, PALB2, PTEN* (including promoter)*, RAD51C, RAD51D, STK11,* and *TP53*. See Targeted Genes and Methodology Details for Rapid Hereditary Breast Cancer Treatment Decision Panel and Method Description for additional details.
- Identification of a disease-causing variant may assist with diagnosis, prognosis, clinical management, recurrence risk assessment, familial screening, and genetic counseling for hereditary breast cancer.

## Testing Algorithm:

For more information see Breast, Gynecological, and Prostate Cancer Testing Algorithm

## Methods:

Sequence Capture and Targeted Next-Generation Sequencing (NGS) followed by Polymerase Chain Reaction (PCR) and Sanger Sequencing

## Reference Values:

An interpretive report will be provided.

## Specimen Requirements:

**Patient Preparation:** A previous bone marrow transplant from an allogenic donor will interfere with testing. Call 800-533-1710 for instructions for testing patients who have received a bone marrow transplant.

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|---|---|
| **Specimen Type:** | **Whole blood** |
| **Preferred:** | Lavender top (EDTA) or yellow top (ACD) |
| **Acceptable:** | Any anticoagulant |
| **Specimen Volume:** | 3 mL |
| **Collection Instructions:** | 1. Invert several times to mix blood.<br>2. Send whole blood specimen in original tube. **Do not aliquot.** |
| **Specimen Stability Information:** | Ambient (preferred) 4 days/Refrigerated |

## Shipping Instructions:

Specimen preferred to arrive within 96 hours of collection.

## Specimen Stability Information:

| Specimen Type | Temperature | Time | Special Container |
|---|---|---|---|
| Varies | Varies | | |

## Ordering Guidance:

- This test is for patients diagnosed with cancer for whom results may impact treatment. A rapid turnaround time supports surgical and management decision making. For patients with cancer who do not need rapid results, order BRGYP / Hereditary Breast/Gynecologic Cancer Panel, Varies or COMCP / Common Hereditary Cancer Panel, Varies, depending on the patient's personal and family history.
- This test is **not appropriate for** patients who do not have cancer. If testing is needed based on a previous diagnosis of cancer or family history of cancer, order either BRGYP / Hereditary Breast/Gynecologic Cancer Panel, Varies or COMCP / Hereditary Common Cancer Panel, Varies, depending on the patient's personal and family history.
- Targeted testing for familial variants (also called site-specific or known variants testing) is available for the genes on this panel. For more information see FMTT / Familial Mutation, Targeted Testing, Varies. To obtain more information about this testing option, call 800-533-1710.
- Testing minors for adult-onset predisposition syndromes is discouraged by the American Academy of Pediatrics, the American College of Medical Genetics and Genomics, and the National Society of Genetic Counselors.

## Cautions:

### Clinical Correlations:

- Test results should be interpreted in the context of clinical findings, family history, and other laboratory data. Misinterpretation of results may occur if the information provided is inaccurate or incomplete.
- If testing was performed because of a clinically significant family history, it is often useful to first test an affected family member. Detection of a reportable variant in an affected family member would allow for more informative testing of at-risk individuals.

- To discuss the availability of additional testing options or for assistance in the interpretation of these results, contact Mayo Clinic Laboratories genetic counselors at 800-533-1710.

**Technical Limitations:**

- Next-generation sequencing may not detect all types of genomic variants. In rare cases, false-negative or false-positive results may occur. The depth of coverage may be variable for some target regions; assay performance below the minimum acceptable criteria or for failed regions will be noted. Given these limitations, negative results do not rule out the diagnosis of a genetic disorder. If a specific clinical disorder is suspected, evaluation by alternative methods can be considered.
- There may be regions of genes that cannot be effectively evaluated by sequencing or deletion and duplication analysis due to technical limitations of the assay, including regions of homology, high guanine-cytosine (GC) content, and repetitive sequences. Confirmation of select reportable variants will be performed by alternate methodologies based on internal laboratory criteria.
- This test is validated to detect 95% of deletions up to 75 base pairs (bp) and insertions up to 47 bp. Deletions-insertions (delins) of 40 or more bp, including mobile element insertions, may be less reliably detected than smaller delins.

**Deletion/Duplication Analysis:**

- This analysis targets single and multi-exon deletions/duplications; however, in some instances single exon resolution cannot be achieved due to isolated reduction in sequence coverage or inherent genomic complexity. Balanced structural rearrangements (such as translocations and inversions) may not be detected.
- This test is not designed to detect low levels of mosaicism or differentiate between somatic and germline variants. If there is a possibility that any detected variant is somatic, additional testing may be necessary to clarify the significance of results.
- Genes may be added or removed based on updated clinical relevance. Refer to the Targeted Genes and Methodology Details for the Rapid Hereditary Breast Cancer Treatment Decision Panel for the most up to date list of genes included in this test. For detailed information regarding gene specific performance and technical limitations, see Method Description or contact a laboratory genetic counselor.
- If the patient has had an allogeneic hematopoietic stem cell transplant or a recent non-leukoreduced blood transfusion, results may be inaccurate due to the presence of donor DNA. Call Mayo Clinic Laboratories for instructions for testing patients who have received a bone marrow transplant.

**Reclassification of Variants:**

- Currently, it is not standard practice for the laboratory to systematically review previously classified variants on a regular basis. The laboratory encourages health care providers to contact the laboratory at any time to learn how the classification of a particular variant may have changed over time. Due to broadening genetic knowledge, it is possible that the laboratory may discover new information of relevance to the patient. Should that occur, the laboratory may issue an amended report.

**Variant Evaluation:**

- Evaluation and categorization of variants are performed using published American College of Medical Genetics and Genomics and the Association for Molecular Pathology recommendations as a guideline. Other gene-specific guidelines may also be considered. Variants are classified based on known, predicted, or possible pathogenicity and reported with interpretive comments detailing their potential or known significance. Variants classified as benign or likely benign are not reported.
- Multiple in silico evaluation tools may be used to assist in the interpretation of these results. The accuracy of predictions made by in silico evaluation tools is highly dependent upon the data available for a given gene, and periodic updates to these tools may cause predictions to change over time. Results from in silico evaluation tools should be interpreted with caution and professional clinical judgement.
- Rarely, incidental or secondary findings may implicate another predisposition or presence of active disease. Incidental findings may include, but are not limited to, results related to the sex chromosomes. These findings will be carefully reviewed to determine whether they will be reported.

## CPT Code:

81405

81406
81307
81408
81162
81321
81351
81479
81479 (if appropriate for government payers)

**Day(s) Performed:** Varies

**Report Available:** 10-14 days

## Questions

Contact Michelle Raths, Laboratory Resource Coordinator at 800-533-1710.