What is BRCATrue®

Pathway Genomics’ BRCATrue® is a next-generation sequencing test that searches for mutations in BRCA1 and BRCA2 genes. Having mutations in either the BRCA1 or the BRCA2 gene significantly increases a patient’s risk for breast, ovarian and other types of cancer.

Why BRCATrue®?

- Easy to interpret and clinically actionable
- Rapid 2-3 week turnaround time
- Variant classification
- Full sequencing, deletion and duplication analysis of BRCA1 and BRCA2 genes

For more information about Pathway Genomics’ BRCATrue® or other hereditary cancer tests please visit www.pathway.com today!
**BRCATrue® High Risk Patient Criteria**

The test is best suited for individuals with either a history of early onset breast or ovarian cancer or a strong family history of breast and/or ovarian cancer. Individuals with the following medical or family history factors should consider testing for mutations in BRCA1/2:

- Early onset breast cancer (under 50 years of age)
- Bilateral or multiple breast cancers
- Diagnosed with both breast and ovarian cancer
- Family history of breast and/or ovarian cancer
- Two or more BRCA1 or BRCA2-related cancers in a single family member
  - Breast
  - Ovarian
  - Pancreatic
  - Aggressive Prostate
  - And more
- Male breast cancer within family
- Ashkenazi Jewish ethnic background

**BRCATrue® Test Specifications**

Pathway Genomics uses next-generation sequencing (NGS) technology to search for variants in the coding regions of BRCA1 and BRCA2. All variants are confirmed using Sanger chemistry sequencing technology. Large deletions and duplications within BRCA1 and BRCA2 genes are detected using MLPA technology. Pathway Genomics classifies variants using a 5-tier system. Likely Benign and Benign variants are not reported.

- **Pathogenic** | Mutations with known clinical significance and demonstrated to increase the risk of cancer
- **Likely Pathogenic** | Genetic changes that have some preliminary clinical data suggesting an association with cancer but not sufficient to make a definitive determination of pathogenicity and associated cancer risk
- **Uncertain Pathogenicity (VUS)** | Genetic changes with either conflicting data or no supporting data, thus a determination of pathogenicity cannot be made
- **Likely Benign** | Genetic changes with strong but limited evidence to be classified as benign and are not likely to increase the risk for cancer
- **Benign** | Genetic changes that are previously reported and have sufficient evidence to be classified as benign with no clinical relevance

**Familial Studies Program**

In the process of sequencing the patient’s DNA, we may identify a genetic change with no clear cancer association, or a change in which conflicting data exist. These genetic changes are called variants of uncertain significance (VUS). Pathway Genomics offers a complimentary Familial Studies Program to help understand the significance of these genetic changes, and how the patient and family members may be affected.

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