



Breast Cancer Risk Assessment & Management Panel (11 genes)

<i>ATM</i>	<i>BRCA1</i>	<i>BRCA2</i>	<i>CDH1</i>	<i>CHEK2</i>	<i>NBN</i>	<i>NF1</i>	<i>PALB2</i>	<i>PTEN</i>	<i>STK11</i>
<i>TP53</i>									

Indication

This Breast Cancer Risk Assessment & Management Panel is a comprehensive screen of 11 genes associated with increased risk for developing breast cancer. Inherited genetic mutations in *BRCA1* and *BRCA2* account for about 20 to 25% of hereditary breast cancers and about 5 to 10% of all breast cancers. This 11-gene panel also includes genes responsible for very rare hereditary cancer syndromes, such as Li-Fraumeni syndrome (*TP53*), Cowden syndrome (*PTEN*), hereditary diffuse gastric cancer (*CDH1*), Peutz-Jeghers syndrome (*STK11*), or neurofibromatosis type I (*NF1*). These syndromes have been associated with increased lifetime risk for multiple cancer types, including breast cancer, and are also characterized by other clinical features specific for each syndrome. Inherited mutations in several other genes associated with breast cancer predisposition (*ATM*, *CHEK2*, *NBN*, *PALB2*) were also included in this analysis. Identifying individuals with genetic predisposition to cancer can allow informed recommendations and personalized medical management that can significantly decrease cancer risks and improve overall survival rates. Some of the current management options for breast cancer include increased frequency and younger age of initiating mammograms and breast MRI, prophylactic mastectomy or other risk-reducing measures, availability of targeted therapy options for individuals with cancer diagnosis (e.g. PARP inhibitors for *BRCA1/BRCA2*), and identification of at-risk family members.

Hereditary cancer syndrome is a genetic predisposition to develop certain types of cancers, often at an early age. Hereditary cancer risk assessment is performed to identify patients and families who may be at risk. Clues that a hereditary cancer syndrome may be present include the following:

- Cancer diagnosed at an unusually young age
- Several different types of cancer in the same person
- Bilateral or multiple primary breast cancers
- Several close blood relatives that have the same type of cancer, especially when on the same side of the family
- Unusual presentation of a specific type of cancer
- The presence of birth defects that are known to be associated with inherited cancer syndromes
- Occurrence of certain types of adult cancer in which the probability of harboring a hereditary cancer syndrome is high:
 - triple negative (ER-/PR-/HER2/neu-) breast cancer
 - ovarian, tubal or peritoneal cancer
 - male breast cancer

Testing method

Next Generation Sequencing (NGS) provides coverage of all coding exons and noncoding DNA in exon-flanking regions (on average 50 bp) enriched using hybrid capture Illumina TruSight Cancer Sequencing Panel. Single base pair (point) mutations, small insertions/deletions (1-25 bp), complex insertions and deletions, or larger deletions and duplication (<100 bp) are detected using a combination of clinically validated computational data analysis methods for sequence variant calling, filtering, and annotation. Gross deletions and duplications at each targeted gene and exon are evaluated through comparative depth of coverage analysis of NGS targeted sequencing data using clinically-validated analysis algorithm. All reportable copy number variants are confirmed by independent methodology using gene-specific Multiplex Ligation-dependent Probe Amplification (MLPA) or genome-wide SNP microarray assay.

Turnaround time

5-10 business days

Sample requirements

3 ml peripheral blood in EDTA (lavender) top tube
Specimen stability: Ambient - 72 hours; Refrigerated - 1 week

CPT codes

81162, 81307, 81321, 81323, 81404, 81405 (x2), 81406, 81408 (x2), G0452

References

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Benafif S, Eeles R. Diagnosis and Management of Hereditary Carcinoids. *Recent Results Cancer Res* 2016;205:149-168.

Antoniou, A, et al. Average risks of breast and ovarian cancer associated with BRCA1 or BRCA2 mutations detected in case Series unselected for family history: a combined analysis of 22 studies. *Am. J. Hum. Genet.* 2003; 72(5):1117-30.

Ship Specimens to:

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