High Risk Breast Cancer: Sequencing and Deletion/Duplication Panel

Test Code: MM201
Turnaround time: 4 weeks
CPT Codes: 81211 x1, 81321 x1, 81323 x1, 81404 x1, 81405 x1, 81406 x1

Condition Description

Most cases of breast cancer are sporadic with no family history of the cancer; but, 5-10% of cases are understood to be due to a hereditary predisposition. Nearly 1 in 8 women (12%) will develop breast cancer in their lifetime (SEER). The clinical features suggestive of a hereditary cancer predisposition involve: diagnosis at a young age (< 50), multiple primary cancers in a single individual, diagnosis of a cancer type that is not common in the general population (such as male breast cancer, ovarian cancer, or pancreatic cancer), and several relatives affected with related cancers over multiple generations.

The EGL Genetics High Risk Breast Cancer Panel includes genes involved in hereditary cancer predisposition syndromes, including hereditary breast and ovarian cancer syndrome (BRCA1 and BRCA2), hereditary diffuse gastric cancer syndrome (CDH1), Li-Fraumeni syndrome (TP53 and PTEN), hamartoma tumor syndrome (PTEN), and Peutz-Jeghers syndrome (STK11).

It is estimated that 20-25% of familial breast cancer risk can be ascribed to mutations in the BRCA1 or BRCA2 genes (van der Groep 2011). The contribution of mutations in the CDH1, PTEN, STK11, and TP53 genes to familial breast cancer risk is considerably lower than the contribution of BRCA1 and BRCA2 mutations.

References:

Genes

BRCA1, BRCA2, CDH1, PALB2, PTEN, STK11, TP53

Indications

This test is indicated for:
- Confirmation of a clinical diagnosis of high risk breast cancer.

Methodology

Next Generation Sequencing: In-solution hybridization of all coding exons is performed on the patient’s genomic DNA. Although some deep intronic regions may also be analyzed, this assay is not meant to interrogate most promoter regions, deep intronic regions, or other regulatory elements, and does not detect single or multi-exon deletions or duplications. Direct sequencing of the captured regions is performed using next generation sequencing. The patient's gene sequences are then compared to a standard reference sequence. Potentially causative variants and areas of low coverage are Sanger-sequenced. Sequence variations are classified as pathogenic, likely pathogenic, benign, likely benign, or variants of unknown significance. Variants of unknown significance may require further studies of the patient and/or family members.

Deletion/Duplication Analysis: DNA isolated from peripheral blood is hybridized to a gene-targeted CGH array to detect deletions and duplications. The targeted CGH array has overlapping probes that cover the entire genomic region. Please note that a “backbone” of probes across the entire genome are included on the array for analytical and quality control purposes. Rarely, off-target copy number variants causative of disease may be identified that may or may not be related to the patient's phenotype. Only known pathogenic off-target copy number variants will be reported. Off-target copy number variants of unknown clinical significance will not be reported.

Detection

Next Generation Sequencing: Clinical Sensitivity: Unknown. Mutations in the promoter region, some mutations in the introns and other regulatory element mutations cannot be detected by this analysis. Large deletions/duplications will not be detected by this analysis. Results of molecular analysis should be interpreted in the context of the patient's clinical/biochemical phenotype.

Analytical Sensitivity: ~99%.

Deletion/Duplication Analysis: Detection is limited to duplications and deletions. The CGH array will not detect point or intronic mutations. Results of molecular analysis must be interpreted in the context of the patient's clinical and/or biochemical phenotype.

Specimen Requirements

Submit only 1 of the following specimen types
Type: Whole Blood

Specimen Requirements:

In EDTA (purple top) tube:
Infants (2 years): 3-5 ml
Older Children & Adults: 5-10 ml

Specimen Collection and Shipping: Ship sample at room temperature with overnight delivery.

Type: Isolated DNA

Specimen Requirements:

In microtainer: 60 ug

Isolation using the Qiagen™ Puregene kit for DNA extraction is recommended.

Specimen Collection and Shipping: Refrigerate until time of shipment in 100 ng/ul of TE buffer. Ship sample at room temperature with overnight delivery.

Special Instructions

This test is for germline mutation analysis. DNA isolated from FFPE tumor samples is not suitable for this test.

Related Tests

- BRCA1/BRCA2 Gene Sequencing and Deletion/Duplication Panel
- BRCA1/BRCA2 Gene Sequencing Panel
- BRCA1/BRCA2 Deletion/Duplication Panel
- Hereditary Cancer Syndrome: Sequencing Panel