OncoGeneDx: Breast/Gyn Cancer Panel

Panel Gene List: ATM, BARD1, BRCA1, BRCA2, BRIP1, CDH1, CHEK2, EPCAM*, FANCC, FANCM, MLH1, MSH2, MSH6, MUTYH, NBN, NF1, PALB2, PMS2, POLD1, PTEN, RAD51C, RAD51D, RECQL, TP53

*Testing includes sequencing and deletion/duplication analysis for all genes except EPCAM (del/dup only).

Clinical Features:
In the general population, approximately 1 in 8 women (12%) will develop breast cancer in their lifetime, 1 in 75 women (1.4%) will be diagnosed with ovarian cancer in their lifetime, and 1 in 36 women (2.8%) will develop endometrial cancer, also known as uterine cancer.¹ Most cases of breast, ovarian, and endometrial cancer develop sporadically with no family history of the cancer. However, 5-10% of breast and endometrial cancer cases and 15-20% of ovarian cancer cases are due to a hereditary predisposition. The features of a personal and/or family history of cancer that are suggestive of a hereditary cancer predisposition include: young age at diagnosis, multiple primary cancers in a single individual, diagnosis of a cancer type that is not common in general population (such as ovarian cancer, male breast cancer, or pancreatic cancer), and several relatives affected with related cancers spanning multiple generations.

Approximately 20-25% of familial breast cancer risk is thought to be attributed to pathogenic variants in the BRCA1 and BRCA2 genes.²⁻⁴ The additional 21 genes on this panel may also account for a substantial proportion of hereditary breast, ovarian, and endometrial cancer cases. Many of these genes are involved in the Fanconi anemia pathway and/or play a role in DNA damage repair similar to the BRCA1 and BRCA2 genes. Newer genes, such as BARD1, FANCC, and RECQL, have been identified in families with breast and/or ovarian cancer and have been included in the panel to make it as comprehensive as possible. The evidence available to date may be derived from a small number of patients with wide confidence intervals or is based upon an ethnic cohort with one specific variant. Accurate risk assessment may be complicated by the low penetrance of pathogenic variants in these genes and/or ascertainment bias. Since the cancer risks are not yet well defined, no consensus guidelines for medical management are available for these genes.

Inheritance Pattern:
Most genes on this panel are associated with an autosomal dominant cancer risk with the exception of MUTYH, which is associated with an autosomal recessive cancer risk. Some of the genes on this panel are also associated with extremely rare conditions when inherited in an autosomal recessive fashion. The specifics of this inheritance are outlined in the table below.
Test Methods:
Genomic DNA is extracted from the submitted specimen. For skin punch biopsies, fibroblasts are cultured and used for DNA extraction. This DNA is enriched for the complete coding regions and splice site junctions of the genes on this panel using a proprietary targeted capture system developed by GeneDx for next generation sequencing with CNV calling (NGS-CNVS). For PTEN nucleotides c.-700 through c.-1300 in the promoter region are also captured. The enriched targets are simultaneously sequenced with paired-end reads on an Illumina platform. Bi-directional sequence reads are assembled and aligned to reference sequences based on NCBI RefSeq transcripts and human genome build GRCh37/UCSC hg19. After gene specific filtering, data are analyzed to identify sequence variants and most deletions and duplications involving coding exons; however, technical limitations and inherent sequence properties effectively reduce this resolution for some genes. Concurrent MSH2 Exons 1-7 Inversion analysis from NGS data is also performed. For EPCAM, deletion/duplication analysis, but not sequencing, is performed. Alternative sequencing or copy number detection methods are used to analyze regions with inadequate sequence or copy number data by NGS. Reported clinically significant variants are confirmed by an appropriate method. Sequence variants are reported according to the Human Genome Variation Society (HGVS) guidelines. Copy number variants are reported based on the probe coordinates, the coordinates of the exons involved, or precise breakpoints when known. Reportable variants include pathogenic variants, likely pathogenic variants and variants of uncertain significance. Likely benign and benign variants, if present, are not routinely reported but are available upon request.

Test Sensitivity:
The clinical sensitivity of sequencing and deletion/duplication analysis of the 24 genes included in the OncoGeneDx Breast/Gyn Cancer Panel depends in part on the patient’s clinical phenotype and family history. In general, the sensitivity is highest for individuals with features suggestive of a hereditary predisposition to cancer as outlined above. DNA sequencing will detect nucleotide substitutions and small insertions and deletions, while NGS-CNVS analysis, array CGH, or MLPA will detect exon-level deletions and duplications. These methods are expected to be greater than 99% sensitive in detecting pathogenic variants identifiable by sequencing or CNVS technology.

Genetic testing using the methods applied at GeneDx is expected to be highly accurate. Normal findings do not rule out the diagnosis of a genetic disorder since some genetic abnormalities may be undetectable by this test. The methods used cannot reliably detect deletions of 20bp to 250bp in size, or insertions of 10bp to 250 bp in size. Sequencing cannot detect low-level mosaicism. The copy number assessment methods used with this test cannot reliably detect mosaicism and cannot identify balanced chromosome aberrations. Rarely, incidental findings of large chromosomal rearrangements outside the gene of interest may be identified. Regions of certain genes have inherent sequence properties (for example: repeat,
homology, or pseudogene regions, high GC content, rare polymorphisms) that yield suboptimal data, potentially impairing accuracy of the results. False negatives may also occur in the setting of bone marrow transplantation, recent blood transfusion, or suboptimal DNA quality. In individuals with active or chronic hematologic neoplasms or conditions, there is a possibility that testing may detect an acquired somatic variant, resulting in a false positive result. As the ability to detect genetic variants and naming conventions can differ among laboratories, rare false negative results may occur when no positive control is provided for testing of a specific variant identified at another laboratory. The chance of a false positive or false negative result due to laboratory errors incurred during any phase of testing cannot be completely excluded. Interpretations are made with the assumption that any clinical information provided, including family relationships, are accurate. Consultation with a genetics professional is recommended for interpretation of results.

<table>
<thead>
<tr>
<th>Gene</th>
<th>Protein</th>
<th>Inheritance</th>
<th>Disease Associations</th>
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</thead>
<tbody>
<tr>
<td>ATM</td>
<td>SERINE-PROTEIN KINASE ATM</td>
<td>AD</td>
<td>Breast, colon &amp; pancreatic cancers</td>
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<tr>
<td>BARD1</td>
<td>BRCA1-ASSOCIATED RING DOMAIN PROTEIN 1</td>
<td>AD</td>
<td>Ataxia telangiectasia</td>
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<tr>
<td>BRCA1</td>
<td>BREAST CANCER TYPE 1 SUSCEPTIBILITY PROTEIN</td>
<td>AD</td>
<td>Hereditary Breast and Ovarian Cancer (HBOC) syndrome: breast, ovarian, pancreatic, prostate &amp; endometrial serous cancer</td>
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<tr>
<td>BRCA2</td>
<td>BREAST CANCER TYPE 2 SUSCEPTIBILITY PROTEIN</td>
<td>AD</td>
<td>Hereditary Breast and Ovarian Cancer (HBOC) syndrome: breast, ovarian, pancreatic, prostate, melanoma &amp; endometrial serous cancer</td>
</tr>
<tr>
<td>BRIP1</td>
<td>FANCONI ANEMIA GROUP J PROTEIN</td>
<td>AD</td>
<td>Breast &amp; ovarian cancer</td>
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<tr>
<td>CDH1</td>
<td>CADHERIN 1</td>
<td>AD</td>
<td>Hereditary Diffuse Gastric Cancer (HDGC) syndrome: gastric (diffuse), breast &amp; colon (signet ring) cancer</td>
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<tr>
<td>CHEK2</td>
<td>SERINE/THREONINE-PROTEIN KINASE CHK2</td>
<td>AD</td>
<td>Breast, colon, prostate, gastric &amp; thyroid cancer</td>
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<tr>
<td>EPCAM</td>
<td>EPITHELIAL CELL ADHESION MOLECULE</td>
<td>AD</td>
<td>Lynch syndrome (LS): colorectal, endometrial, ovarian, gastric,</td>
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<tr>
<td>Gene</td>
<td>Protein Name</td>
<td>Inheritance</td>
<td>Common Carcinomas</td>
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<tr>
<td><strong>FANCC</strong>48,49</td>
<td>FANCONI ANEMIA GROUP C PROTEIN</td>
<td>AD</td>
<td>Breast cancer</td>
</tr>
<tr>
<td></td>
<td></td>
<td>AR</td>
<td>Fanconi anemia</td>
</tr>
<tr>
<td><strong>FANCM</strong>60–52</td>
<td>FANCONI ANEMIA GROUP M PROTEIN</td>
<td>AD</td>
<td>Breast &amp; ovarian cancer</td>
</tr>
<tr>
<td><strong>MLH1</strong>42,44–47,53,54</td>
<td>DNA MISMATCH REPAIR PROTEIN MLH1</td>
<td>AD</td>
<td>Lynch syndrome (LS): colorectal, endometrial, ovarian, gastric, pancreatic, biliary tract, urinary tract, small bowel, prostate &amp; brain cancer, sebaceous neoplasms</td>
</tr>
<tr>
<td><strong>MUTYH</strong>66–68</td>
<td>ADENINE DNA GLYCOSYLASE</td>
<td>AR</td>
<td>MUTYH-associated polyposis (MAP): colorectal, small bowel &amp;</td>
</tr>
<tr>
<td>Gene</td>
<td>Description</td>
<td>Inheritance</td>
<td>Associated Cancer Types</td>
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<tr>
<td><strong>NBN</strong>&lt;sup&gt;69–75&lt;/sup&gt;</td>
<td>NIBRIN</td>
<td>AD</td>
<td>Breast &amp; prostate cancer, non-Hodgkin lymphoma</td>
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<tr>
<td><strong>NF1</strong>&lt;sup&gt;76–78&lt;/sup&gt;</td>
<td>NEUROFIBROMIN</td>
<td>AD</td>
<td>Neurofibromatosis type 1 (NF1) syndrome: breast cancer, GIST, optic nerve gliomas, pheochromocytoma, MPNST, neurofibromas, brain tumors</td>
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<tr>
<td><strong>PALB2</strong>&lt;sup&gt;5,79–84&lt;/sup&gt;</td>
<td>PARTNER AND LOCALIZER OF BRCA2</td>
<td>AD</td>
<td>Breast, pancreatic &amp; ovarian cancer</td>
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<tr>
<td><strong>PMS2</strong>&lt;sup&gt;42,44–47,85,86&lt;/sup&gt;</td>
<td>MISMATCH REPAIR ENONUCLEASE PMS2</td>
<td>AD</td>
<td>Lynch syndrome (LS): colorectal, endometrial, ovarian, gastric, pancreatic, biliary tract, urinary tract, small bowel, prostate &amp; brain cancer, sebaceous neoplasms</td>
</tr>
<tr>
<td><strong>POLD1</strong>&lt;sup&gt;87,88&lt;/sup&gt;</td>
<td>DNA POLYMERASE DELTA CATALYTIC SUBUNIT</td>
<td>AD</td>
<td>Colon &amp; endometrial cancer, colon polyps</td>
</tr>
<tr>
<td><strong>PTEN</strong>&lt;sup&gt;66,89–92&lt;/sup&gt;</td>
<td>PHOSPHATIDYLINOSITOL 3,4,5-TRISPHOSPHATE 3-PHOSPHATASE AND DUAL-SPECIFICITY PROTEIN PHOSPHATASE PTEN</td>
<td>AD</td>
<td><em>PTEN</em> hamartoma tumor syndrome (PHTS): breast, thyroid, endometrial, colon, melanoma &amp; renal cancer, gastrointestinal polyps, Lhermitte-Duclos disease</td>
</tr>
<tr>
<td><strong>RAD51C</strong>&lt;sup&gt;93–96&lt;/sup&gt;</td>
<td>DNA REPAIR PROTEIN RAD51 HOMOLOG 3</td>
<td>AD</td>
<td>Breast &amp; ovarian cancer</td>
</tr>
<tr>
<td><strong>RAD51D</strong>&lt;sup&gt;93,94,97,98&lt;/sup&gt;</td>
<td>DNA REPAIR PROTEIN RAD51 HOMOLOG 4</td>
<td>AD</td>
<td>Breast &amp; ovarian cancer</td>
</tr>
<tr>
<td><strong>RECQL</strong>&lt;sup&gt;99–102&lt;/sup&gt;</td>
<td>RECQ PROTEIN-LIKE</td>
<td>AD</td>
<td>Breast cancer</td>
</tr>
</tbody>
</table>
| **TP53**<sup>82,103–107</sup> | CELLULAR TUMOR ANTIGEN P53 | AD | Li-Fraumeni syndrome (LFS): breast cancer, sarcoma, brain cancer, hematologic malignancies, endometrial serous cancer, gastrointestinal polyps, Nijmegen breakage syndrome, Nijmegen breakage syndrome, Neurofibromatosis type 1 (NF1) syndrome, breast cancer, GIST, optic nerve gliomas, pheochromocytoma, MPNST, neurofibromas, brain tumors, Breast, pancreatic & ovarian cancer, Constitutional mismatch repair deficiency syndrome, Colon & endometrial cancer, colon polyps, breast cancer, thyroid, endometrial, colon, melanoma & renal cancer, gastrointestinal polyps, Lhermitte-Duclos disease, Breast & ovarian cancer, Breast & ovarian cancer, Breast cancer, Li-Fraumeni syndrome (LFS): breast cancer, sarcoma, brain cancer, hematologic malignancies,
Because of evolving and expanding phenotypes, this list of cancer/tumor types is not exhaustive. Gene-specific risk for some of the cancers and other features listed are not well-defined.

** High overall risk of cancer: 75% lifetime risk for males to develop cancer, nearly 100% risk for females.

**Abbreviations:**
- AD – Autosomal Dominant
- AR – Autosomal Recessive
- CGH – Comparative genomic hybridization
- MLPA – Multiplex ligation-dependent probe amplification
- MPNST - Malignant peripheral nerve sheath tumors
- GIST - Gastrointestinal stromal tumor

**References:**

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73. Buslov, K. G. et al. NBS1 657del5 mutation may contribute only to a limited fraction of breast cancer cases in Russia. Int. J. Cancer 114, 585–589 (2005).