Known Familial Variant for BRCA1

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<th>BRCA1</th>
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**Indication**
This is a targeted mutation analysis for detection of a known familial variant in BRCA1 gene, BReast CAncer gene 1 that codes for protein that helps repair DNA damage. Germline defects in the BRCA1 are the most common cause of predisposition to breast cancer and are diagnostic for the autosomal dominant hereditary breast and ovarian cancer (HBOC) syndrome (OMIM ID: 604370). Inherited mutations in BRCA1 are associated with increased lifetime risk for breast cancer (40-87%), ovarian cancer (16-54%), male breast cancer (1-2%), prostate cancer (up to 20%), and pancreatic cancer (1-3%). Identifying individuals with mutation in BRCA1 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 individuals with deleterious BRCA1 variant include increased frequency and younger age of initiating mammograms and breast MRI, risk-reducing surgery options for breast and ovarian cancer in females, other cancer monitoring and prophylactic treatment options, availability of targeted therapy for cancer treatment (e.g. PARP inhibitors for BRCA1-mutant tumors), and identification of at-risk family members. Updated clinical management guidelines for individuals with BRCA1-associated HBOC syndrome can be found at www.NCCN.org.

**Testing requirements**
This test is designed to detect a known pathogenic mutation in BRCA1 that was previously identified in another member of the family (blood relative). Details about the known familial variant in BRCA1 have to be provided to our laboratory for analysis. This information should include either a copy of previous sequencing report (preferred) or BRCA1 variant information that includes transcript change (e.g., c.68_69delAG), protein change (e.g., p.Glu23Valfs*17) and/or genomic locus corresponding to the known variant (e.g., chr 17: 41276045-41276046). Orders that are missing this information will not be processed.

**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) 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
81215, G0452

References


Ship Specimens to:

Henry Ford Center for Precision Diagnostics
Henry Ford Hospital
Clinic Building, K6, Core Lab E-655
2799 W. Grand Blvd.
Detroit, MI 48202

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