Hereditary Cancer

HEREDITARY CANCER PANELS

Eleven different gene panels are available based on clinical indication. If the result is uninformative a reanalysis panel can be ordered within 90 days of the original panel result, free of charge. Refer to panels for gene content and associated order codes.

EPIC- Each gene panel has a unique Order Code.

If EPIC is not an option, please complete and submit a paper requisition to GenomicsLab@upmc.edu
Paper requisition can be found on the INFONET. Search for "hereditary cancer requisition form."

The healthcare provider is also required to complete and submit a consent form. This can be found on the INFONET. Search for "hereditary cancer testing acknowledgment form."

BACKGROUND

Individuals with cancers of the breast, ovary, pancreas, endometrium, and colon are particularly likely to have a heritable cause, especially if there is also a family history of these cancers. Individuals identified to have a heterozygous pathogenic variant have increased lifetime risks of developing cancer.

This information may assist with diagnosis, prognosis, familial screening, and genetic counseling. The identification of a pathogenic variant can inform surgical and chemotherapy decision-making for affected patients, enhanced surveillance and/or surgical prophylaxis for unaffected patients, and predictive testing and risk assessment for at-risk blood relatives.

INDICATIONS FOR TESTING

- Personal history of cancer
- Family history of cancer

RESULTS

1. Positive: A pathogenic or likely pathogenic variant(s) were found which would either explain the patient's symptoms or increases the risk to develop certain types of cancer. The healthcare provider can use the result to guide the patient's medical management. Family members can be tested for the variant to determine their cancer and/or reproductive risk.

2. Negative: No clinically significant variants were found in the gene panel. This does not rule out the possibility of variants in other genes or variants that are not detectable in this assay. Cancer risk may still be increased based on the family history. The healthcare provider will discuss these risks and develop a cancer screening plan based on the patient's personal risk factors. The healthcare provider may also discuss more testing either now or in the future.

3. Variant of Uncertain Significance (VUS): A variant was detected, however, it is uncertain whether this variant is the cause of a patient's symptoms since current information about the variant is limited. The result is not clinically actionable. Cancer screening should be based on personal and family history.

UPMC
LIFE CHANGING MEDICINE

Hereditary Cancer Testing

METHOD
Custom oligonucleotide capture for the complete coding regions and splice sites (±25 bp) in the panel followed by Next-Generation Sequencing (NGS) with 2x250bp reads. Reads are mapped to GRCh37 for variant calling and annotation. The assay detects sequence variants, copy number variants, and Alu insertions. Average sequence coverage is >200x and 100% of targets have at least 25x coverage.

LIMITATIONS
This assay is not intended to detect gross rearrangements, deep intronic variants, regulatory regions, and other unknown abnormalities except for specific regions identified in a gene in a panel. Complexity in some areas of the genome may increase the chance of a variant not being detected. This assay is not designed to detect mosaicism. Other gene limitations are specifically reported when applicable.

SPECIMEN REQUIREMENTS
- Whole blood – EDTA tube required, 3-5 ml
- Previously extracted DNA (concentration >25 ng/ul, volume >20 ul, minimum of 1 ug total DNA, 260/280>1.7)
- Saliva provided in Oragene (OGD-500) collection kits

TURNAROUND TIME
Up to 21 days

CPT CODE
Refer to specific gene panel