CENTER FOR PRECISION DIAGNOSTICS

Hereditary Melanoma Panel - Expanded (8 genes)

BAP1	*BRCA1*	*BRCA2*	*CDK4*	*CDKN2A*	*PTEN*	*RB1*	*TP53*		

Indication

This Expended Hereditary Melanoma Panel is a comprehensive screen of 8 genes associated with hereditary predisposition to melanoma and other cancers. Most cases of melanoma are isolated and sporadic. However, a small proportion of individuals (approximately 10%) have a family history of the disease typically caused by inherited genetic mutation that increase the risk of developing this type of cancer. Several genes have been associated with hereditary melanoma, including *CDKN2A* and *CDK4*. Individuals with inherited pathogenic variant in *CDKN2A* have 28-67% risk for developing melanoma. This panel also includes genes responsible for rare hereditary cancer syndromes with increased risk for melanoma, such hereditary breast and ovarian cancer syndrome (*BRCA1*, *BRCA2*), Li-Fraumeni syndrome (*TP53*), Cowden syndrome (*PTEN*), BAP1 hereditary cancer predisposition syndrome (*BAP1*), and hereditary retinoblastoma syndrome (*RB1*). Identifying individuals with genetic predisposition to melanoma can allow increased frequency and younger age of initiating screening for cancer, close monitoring of dysplastic nevi for signs of malignant transformation, risk-reducing clinical management options and life style changes, 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
- Multiple primary melanomas in the same person
- Skin findings, such as multiple nevi
- Personal or family history of melanoma and other associated cancer types such as pancreatic, breast, ovarian, uterine, prostate, or kidney cancer (mesothelioma)
- A family history of a mutation in a gene that predisposes to melanoma
- 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 (e.g., triple negative 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, 81321, 81323, 81404, 81405, G0452

References

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Lu KH, Wood ME. Daniels M, Burke C, et al. American Society of Clinical Oncology Expert Statement: collection and use of a cancer family history for oncology providers. J Clin Oncol 2014;32:833-840.

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Aoude LG, Wadt KA, Pritchard AL, Hayward NK. Genetics of familial melanoma: 20 years after CDKN2A. Pigment Cell Melanoma Res. 2015 Mar;28(2):148-60.

Ship Specimens to:

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