Germline Cancer Predisposition Panel-focused

Test Description

The MolQ *BRCA* Germline mutation test helps assess your risk of developing cancer by detecting a potentially harmful change (mutation) in *BRCA1* and *BRCA2* genes.

Patient Demographic

Name: Ms Ashley
Sex: Female
Date of Birth/Age: 22 years
Disease: Asymptomatic

Clinician

Clinician Name: Dr Amit Verma
Medical Facility: Dr AV Institute of Personalized Therapy and Cancer Research (IPTCR)
Pathologist: Not Provided

Specimen

Booking ID: 012206180040
Site: NA
Sample Type: Blood
Date of Collection: 18-06-2022
Date of Booking: 18-06-2022

CLINICAL SYNOPSIS

The index patient, Mrs. Anu Kumar was found to harbor a variant, c.9097delA in the *BRCA2* gene. Her daughter is being evaluated for the same variant.

RESULTS

Variant is confirmed to be absent by Sanger sequencing.

Gene (Transcript) #	Location	Variant	Relationship to Index Patient	Clinical condition of family member	Variation reported in family member*
BRCA2 (ENST00000380152.8)	Exon 23	chr13:32954023delA; c.9097del; (p.Thr3033LeufsTer29)	Daughter	Asymptomatic	Absent

*The variant analysis in Sanger sequencing is based on the *BRCA2* reference sequence NM_000059.4[1]. The exon number and nucleotide numbers will differ based on the reference file chosen and the database used.

CLINICAL CORRELATION AND VARIANT INTERPRETATION

Variant description: A variant in exon 23 of the *BRCA2* gene (**chr13:32954023delA; c.9097del; p.Thr3033LeufsTer29**) was detected in the index patient by NGS.

The same pathogenic variant is not detected in the asymptomatic daughter of the index patient, Ms Ashley (Figure 1).

The variant detected in the test and its significance needs to be carefully correlated with the clinical indications of the index patient.

RECOMMENDATION

Genetic counselling is recommended to interpret the significance of the results.

Jatinder Kaur, PhD
Head, Molecular Biology & Genomics

Dr. Gulshan Yadav, MD
Head, Pathology

APPENDIX 1: TEST METHODOLOGY

Method

Targeted gene Sanger sequencing: Exon 11 of the *BRCA2* gene was PCR-amplified, and the product was sequenced using Sanger sequencing. In case of mosaicism in leucocytes, the detection limits of Sanger sequencing for presence of variant are ~20%. The sequence was aligned to available reference sequence ENST00000380152.8[1] to detect variant using variant analysis software programs. Variant classification follows the tenets of American College of Medical Genetics (ACMG) guidelines[2].

DISCLAIMER

About 0.44% of total cases are susceptible to allele dropout/dropin phenomenon, which can lead to misdiagnosis[3].

REFERENCES

1. ENSEMBL: http://www.ensembl.org.
2. Green R. C., et al., American College of Medical Genetics and Genomics. ACMG recommendations for reporting of incidental findings in clinical exome and genome sequencing. Genet Med. 2013 Jul;15(7):565-74
3. Blais, Jonatan et al. Risk of Misdiagnosis Due to Allele Dropout and False-Positive PCR Artifacts in Molecular Diagnostics. The Journal of Molecular Diagnostics, Volume 17, Issue 5, 505 – 514.

Figure 1: Sequence chromatogram and alignment to the reference sequence showing the variation in exon 23 of the *BRCA2* gene (chr13:32954023delA; c.9097del; p.Thr3033LeufsTer29) not detected in the daughter of the index patient, Ms Ashley.