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 Mahitab Mustafa Hassan Mahgoub
Sex: Female
Date of Birth/Age: 31 years
Disease: Asymptomatic

Clinician

Clinician Name: Dr Amit Verma
Medical Facility: Max Hospital
Pathologist: Not Provided

Specimen

Booking ID: 012109130050
Site: NA
Sample Type: Blood
Date of Collection: 13-09-2021
Date of Booking: 13-09-2021

CLINICAL SYNOPSIS

The index patient Ms. Nagwa Ashri Mohamed Hussien was a case of high grade papillary serous carcinoma of ovary. She was found to harbor a variation in the *BRCA2* gene. Her daughter is being evaluated for the same variation.

RESULTS

Variant is not detected

Gene (Transcript) #	Location	Variant	Zygosity	Clinical condition of family member	Variation reported in family member*
BRCA2 (ENST0000044455.1)	Exon 3	chr13:g.32893302del; c.156del (p.His52GlnfsTer28)	Heterozygous	Asymptomatic	Absent

*The variant analysis in Sanger sequencing is based on the *BRCA2* reference sequence ENST00000544455.1[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 frameshift deletion in exon 3 of the *BRCA2* gene (**chr13:g.32893302del; c.156del**) that results in a premature truncation of the protein 28 amino acids downstream to codon 52 (p.His52GlnfsTer28) was detected in the index patient, Ms. Nagwa Ashri Mohamed Hussien (Sample ID: 7170723; Date of report: 23rd August 2021) by NGS and was further validated by Sanger Sequencing (Figure 1A).

The same variation was not detected in the asymptomatic daughter of the index patient, Ms. Mahitab Mahgoub (Figure 1B).

RECOMMENDATIONS

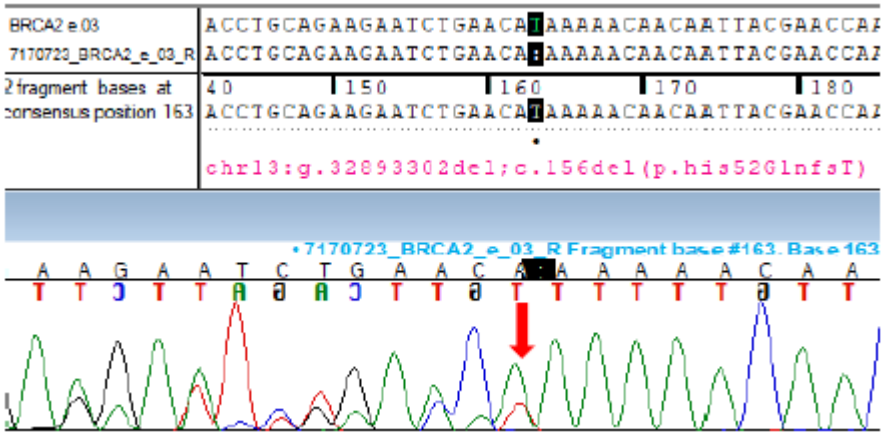
Genetic counselling is advised to discuss the significance of this test. Kindly email us at contact@molq.in for post-test counselling.

REFERENCES

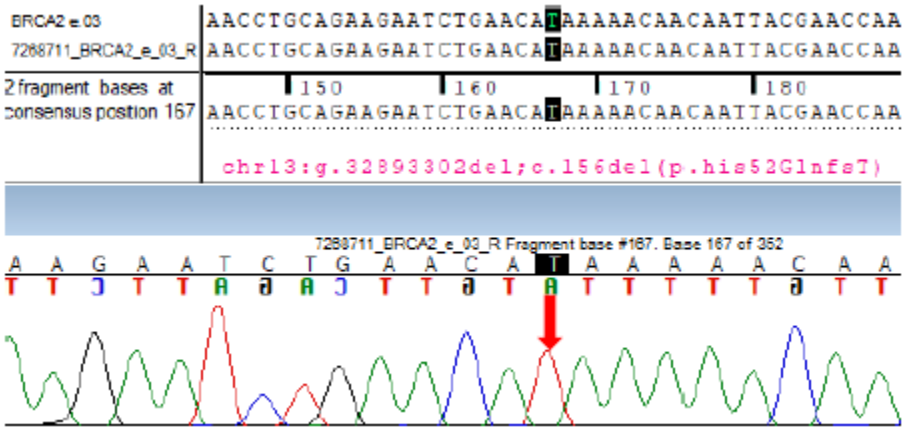
1. ENSEMBL: http://www.ensembl.org.

Figure 1: Sequence chromatogram and alignment to the reference sequence showing the variation in exon 3 of the *BRCA2* gene (chr13:g.32893302del; c.156del; p.His52GlnfsTer28) detected in heterozygous condition in the index patient, Ms. Nagwa Ashri Mohamed Hussien (A) and not detected in the daughter of the index patient, Ms. Mahitab Mahgoub (B).

A. 7170723 – Index patient (Ms. Nagwa Ashri Mohamed Hussien)



B. 7268711 – Daughter of the index patient (Ms. Mahitab Mahgoob)



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APPENDIX 1: TEST METHODOLOGY

Method

Targeted gene Sanger sequencing: Exon 3 of the *BRCA2* gene was PCR-amplified and the products were sequenced using Sanger sequencing. In case of mosaicism in leucocytes, the detection limits of Sanger sequencing for presence of variation is ~12%. The sequence was aligned to available reference sequence ENST00000544455.1[1] to detect variation 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 RC et al. ACMG recommendations for reporting of incidental findings in clinical exome and genome sequencing. Genet Med. 2013, 15(7):565-74.
3. Blais J et al. Risk of Misdiagnosis Due to Allele Dropout and False-Positive PCR Artifacts in Molecular Diagnostics: Analysis of 30,769 Genotypes. J Mol Diagn. 2015, 17(5): 505-14.