

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 Sali Mustafa
Sex: Female
Date of Birth/Age: 35 years
Disease: Asymptomatic

Clinician

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

Specimen

Booking ID: 012204130078
Site: NA
Sample Type: Blood
Date of Collection: 13-04-2022
Date of Booking: 13-04-2022

CLINICAL SYNOPSIS

The index patient Ms. Ngwa Ashri Mohamed Hussien’s Morphology and immunoprofile favors high grade papillary serous carcinoma of ovary. Tumor cells are immunoreactive for ER, WT-1 and CK7 [as per the histopathological report dated 14-04-2021 provided along with Test Requisition Form]. The tumor was identifiable in the FFPE block [H-1974/21 A]. Ms. Ngwa Ashri Mohamed Hussien was found to harbor a variation in the BRCA2 gene. Her daughter is being evaluated for the same variation.

RESULTS

Variant is detected

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

*The variant analysis in Sanger sequencing is based on the BRCA2 reference sequence ENST00000544455.1¹. 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 detected in heterozygous condition in the asymptomatic daughter of the index patient, Ms. Sali Mustafa (Figure 1B).

RECOMMENDATIONS

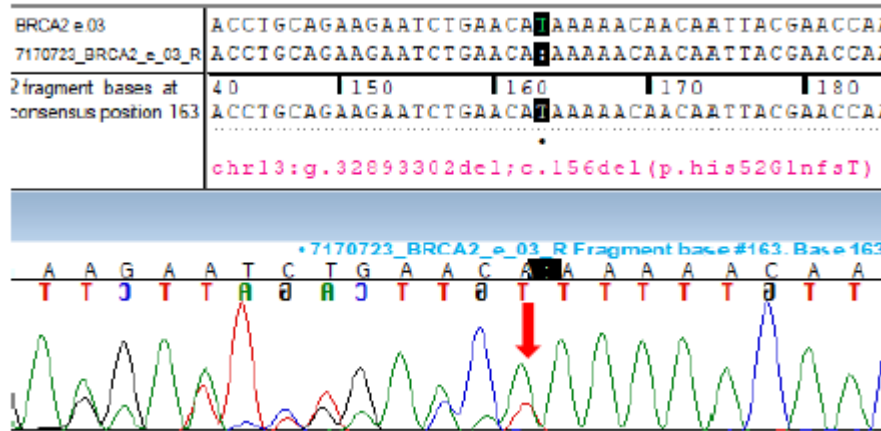
Genetic counselling is recommended to interpret the significance of the results. Kindly email us at contact@molq.in for post-test counselling.

REFERENCES

- 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. Sali Mustafa (B).

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



B. 7538478 - Daughter of the index patient (Ms. Sali Mustafa)



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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 ~20%. The sequence was aligned to available reference sequence ENST00000544455.1¹ to detect variation using variant analysis software programs. Variant classification follows the tenets of American College of Medical Genetics (ACMG) guidelines².

DISCLAIMER

About 0.44% of total cases are susceptible to allele dropout/dropin phenomenon, which can lead to misdiagnosis³.

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.