NGS RESULTS

The NGS data showed that the index patient was **Positive for a heterozygous BRCA1 pathogenic variant**. No pathogenic/likely pathogenic/VUS variant was detected in the BRCA2 gene.

Gene	Exon	Variant details	Type of variant	Zygosity	Allele frequency	*Insilico* predictors
BRCA1	10	chr17:41246153A>C NM_007294.3:c.1395T>G (p.Tyr465Ter)	Nonsense	Heterozygous	gnomAD: Absent	SSIFT: N/A PolyPhen: N/A Mutation Taster: N/A

gnomAD - Genome Aggregation Database. N/A - Not Applicable

Note: The identified variant has been confirmed by Sanger sequencing

- The identified variant is predicted to creates an early stop codon, which may lead to premature truncated non-functional protein
- The variant seems to be a novel variant as it has not been reported previously in patients or in population database (gnomAD)
- However, several truncating variants, such as p.Val863fs and p.Val899fs, downstream of the identified variant, have been reported as pathogenic in the ClinVar database
- Based on American College of Medical Genetics and Genomics (ACMG) guidelines [PMID: 25741868], this variant has been classified as pathogenic (Class 1)