



Clinical Testing  
Cert. No. 822

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Scientific Director: George Nasioulas PhD

#### SAMPLE INFORMATION

Name :		Date Received :	
Medical ID :		Date of Report :	
Date of Birth :		Req. Physician :	
Material :	PARAFFIN EMBEDDED TISSUE	Barcode :	
Code of sample :		Tumor type	Ovarian Cancer

Somatic mutation analysis of the *BRCA1* and *BRCA2* genes

#### Result

***BRCA1*** - No known pathogenic mutation or rearrangement was identified in the patient's tumor tissue

***BRCA2- Deletion of entire gene***

Large genomic rearrangements, including deletions, duplications or insertions larger than 500 kb, have been identified in the *BRCA1/2* genes, with a frequency between 0 and 28% depending on the population analyzed ([PMID: 26271414, 20232141, 22434521, 22544547, 28212807](#)). The variant detected in this patient is a deletion of the entire *BRCA2* gene. It was identified by NGS and confirmed by MLPA (Multiplex Ligation dependent Probe Amplification, MRC Holland; PMID: 10978226). *BRCA2* gene deletion has been reported to be inactivating. Loss of *BRCA2* has been demonstrated to cause a significant increase in genome-wide error-prone repair of both spontaneous DNA damage and mitomycin C-induced DNA cross-links([PMID: 11532935](#)). To our knowledge, this particular variant has not been described in literature or mutation database ClinVar. However, *BRCA2* deletions have been reported in international literature ([PMID: 29570666, 16199546, 32375709](#)) and in ClinVar mutation database as pathogenic. For these reasons this variant is predicted to be **pathogenic**. Analysis of patient's blood is recommended in order to determine the germline or somatic origin of this alteration.



Electronically Signed by - Eirini Papadopoulou, PhD Molecular Biologist, AMKA:10097202500

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# BRCAsomatic



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## Methodology

Mutations in the *BRCA1* and *BRCA2* genes lead to an increased risk of developing breast or ovarian cancer as part of hereditary breast-ovarian cancer syndrome. Recent studies have established that these genes can also be involved in the development of non-hereditary, sporadic tumors, since a proportion of ovarian, breast cancer and prostate cancer tumors contain somatic (tumor only) *BRCA1* and *BRCA2* pathogenic variants. Patients with tumors that harbor a somatic BRCA mutation may benefit from treatment with PARP inhibitors.

Genomic DNA was extracted from the FFPE tumor tissue. Analysis was carried out using the commercially available Oncomine BRCA assay (Thermo Fisher Scientific). Sequencing was carried out using the Next Generation Sequencing platform Ion GeneStudio™ S5 Prime System (Thermo Fisher Scientific). The presence of large genomic rearrangements is investigated by use of the method MLPA (Multiplex Ligation-dependent Probe Amplification, BRCA1: P002, BRCA2: P045, MRC Holland; AJHG 67:841-50, 2000).

### \*Notes:

<sup>1</sup> Macrodissection was performed on the cancerous tissue

<sup>2</sup> Large genomic rearrangement analysis when performed in FFPE tissue has lower sensitivity compared to whole peripheral blood

<sup>2</sup> Each molecular analysis has an internal error probability of 0,5-1%. This is due to rare molecular events and factors involved in the production and analysis of specimens.



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## References

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