Laboratory Analysis and Result

PHYSICIAN	SPECIMEN		PATIENT INFORMATION	
	Specimen:	**Blood**	Name:	
	Collection Date:	**29/Jan/2013**	Date of Birth:	
	Accession Date:	**30/Jan/2013**	Accession #:	**G0000235-BLD**
	Report Date:	**11/Feb/2013**	Requisition #:	**03090034**

BRCA1 Gene: No Deleterious Mutation Detected
BRCA2 Gene: No Deleterious Mutation Detected

It is our understanding that this patient was identified for testing due to a personal or family history suggestive of hereditary breast and ovarian cancer.

No deleterious mutation was found in the BRCA1 or BRCA2 genes in this individual. There are other, uncommon genetic abnormalities in BRCA1 and BRCA2 that this test will not detect. This result, however, rules out the majority of abnormalities believed to be responsible for hereditary susceptibility to breast and ovarian cancer (Ford D et al., Am J Human Genetics 62:676-689, 1998). If this individual has never had breast or ovarian cancer, it is recommended that testing an affected relative be considered to help clarify the clinical significance of this individual's negative test result. If this patient has a relative with a known mutation in BRCA1 or BRCA2, it is important to confirm that this family mutation is detected with the testing as performed for this patient.

Analysis Description: Analysis consists of sequencing of all translated exons and immediately adjacent intronic regions of the BRCA1/BRCA2 genes, as well as large rearrangement analysis (MLPA) of all BRCA1 (OMIM 113705/GenBank entry U14680) and BRCA2 (OMIM 600185/GenBank entry U43746) exons. In cases where Myriad GmbH identifies benign variants for which there is strong evidence that they are not associated with disease, these variants will not be reported. See attached technical specifications for details. The classification and interpretation of all variants identified in this assay reflects the current state of scientific understanding at the time this report was issued. In some instances, the classification and interpretation of such variants may change as new scientific information becomes available. In the future, should Myriad significantly modify the interpretation of one or more variants, an amended report will be issued.

To discuss any questions regarding this result, please contact helpmed-international@myriad.com.

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