

	<p align="center">Document name: REP-2-020 Attachment F - Patient Informed Consent for BRCA Testing</p>	<p align="right">Eurofins Document Reference: 1-P-QM-CF -9061962 NTD Labs SOP ID: REP-2-020 Attachment F Revision:1</p>
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REP-2-020 Attachment F - Patient Informed Consent for BRCA Testing

Eurofins Document Reference	1-P-QM-CF -9061962	Type of document	CF - Controlled Form
NTD Labs SOP ID	REP-2-020 Attachment F	Division	1-P Pharma
Effective Date	Aug 1, 2018	Business Line(s) / Unit(s)	(1-DU) Clinical Diagnostics US : (2-59) Clinical Diagnostics Services North-East US : (EUUSME2) Eurofins NTD (US)
Status	Effective	Periodic Review Date	Jul 31, 2020
		Functional Area	QM - Quality Management

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Functional Document Owner	Eurofins D CDS US Quality Management Department; Eurofins D CDS US Reporting Department; Eurofins D CDS US Laboratory Management
Review and Approval	<ul style="list-style-type: none"> • Reviewers: Christina Deer; Jonathan Hayden; Lisa Schmitt • Approver (Laboratory Director Only): Terrence Hallahan
Reason for Revision	

Revision Log

Date	Rev.	Author	Description
Aug 1, 2018	1	Eurofins D CDS US Quality Management Department; Eurofins D CDS US Reporting Department; Eurofins D CDS US Laboratory Management	

Electronic Signatures

<p>Christina Deer;Review;Jul 2, 2018 4:04 PM EDT Jonathan Hayden;Review;Jul 3, 2018 8:48 AM EDT Lisa Schmitt;Review;Jul 11, 2018 10:42 AM EDT Terrence Hallahan;Approval;Jul 18, 2018 9:51 AM EDT</p>

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Patient Informed Consent for Hereditary Breast and Ovarian Cancer Testing

PLEASE NOTE: A signed Physician Acknowledgement of NY Informed Consent for Genetic Testing must be on file at Eurofins NTD, LLC to permit testing and processing.

Test Specific Information (check those that apply)

MM071 BRCA1/BRCA2 Gene Sequencing Panel

In-solution hybridization of all coding exons is performed on the patient's genomic DNA. Direct sequencing of the captured regions is performed using next generation sequencing. The patient's gene sequences are then compared to a standard reference sequence. Potentially causative variants and areas of low coverage are Sanger-sequenced. Sequence variations are classified as pathogenic, likely pathogenic, benign, likely benign, or variants of unknown significance. Variants of unknown significance may require further studies of the patient and/or family members.

Limitations:

- o Mutations in the promoter region, some mutations in the introns and other regulatory element mutations cannot be detected by this analysis.
- o Large deletions/duplications will not be detected by this analysis.
- o Results of molecular analysis should be interpreted in the context of the patient's clinical/biochemical phenotype.
- o Clinical sensitivity is unknown. Analytical sensitivity is approximately 99%.

MM072 BRCA1/BRCA2 Deletion/Duplication Panel

DNA isolated from peripheral blood is hybridized to a CGH array to detect deletions and duplications. The targeted CGH array has overlapping probes which cover the entire genomic region.

Sequence analysis is required before deletion/duplication analysis by targeted CGH array. If sequencing is performed outside of EGL Genetics, please submit a copy of the sequencing report with the test requisition.

Please note that a "backbone" of probes across the entire genome is included on the array for analytical and quality control purposes. Rarely, off-target copy number variants causative of disease may be identified that may or may not be related to the patient's phenotype. Only known pathogenic off-target copy number variants will be reported. Off-target copy number variants of unknown clinical significance will not be reported.

Limitations:

- o Detection is limited to duplications and deletions. The CGH array will not detect point or intronic mutations.
- o Results of molecular analysis must be interpreted in the context of the patient's clinical and/or biochemical phenotype.

MM070 BRCA1/BRCA2 Gene Sequencing and Deletion/Duplication Panel

Both BRCA1/BRCA2 gene sequencing and deletion/duplication panels described above are performed.

General Information, Limitations, and Risks:

- Mutations in the genes *BRCA1* and *BRCA2* cause hereditary breast and ovarian cancer syndrome (HBOC), an autosomal dominant cancer predisposition syndrome. Mutations in these genes are rare and account for only a small percentage of cancers; about 5-10% of all breast cancers and 10-15% of ovarian cancers are due to mutations in the *BRCA1* or *BRCA2* genes. Individuals with mutations in these genes, however, are at a significantly increased risk for developing breast, ovarian, and other cancers than those in the general population. This test is indicated for the following individuals: males or females with a personal or family history of breast and/or ovarian cancer that could be consistent with HBOC.
- This analysis can have the following outcomes:
 - o **Positive:** A pathogenic variant (disease-causing) could be identified in one or more of the genes being tested for and the person is identified as being affected.
 - o **Negative:** No pathogenic variant is identified. This reduces the risk of being affected by the diseases specifically tested for, but does not eliminate it completely.
 - o **Inconclusive:** Due to technical issues the results were inconclusive and the test might need repeating. Results may also be inconclusive due to the identification of a variant of unknown significance.
- DNA-based studies performed are specific to the condition indicated above. The accuracy of genetic testing is limited by the methods employed, the clinical diagnosis, and the nature of the specific condition for which testing is requested. In some cases, the test will detect an abnormality, called a mutation, in the gene. In other cases the test is unable to identify an abnormality although an abnormality may still exist. This event may be due to the current lack of knowledge of the complete gene structure or an inability of the current technology to identify certain types of changes (mutations) in a gene. These analyses may not detect pathogenic

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A signed physician acknowledgement of NY informed consent for genetic testing must be on file at Eurofins NTD, LLC to permit testing and processing.

This Patient Informed Consent form is to be maintained by the physician in the patients' medical file. DO NOT Return to Eurofins, NTD, LLC.

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