K.N.D Fernando

AGE: 45 years | **Gender:** Female | **Coupon/UID:** NA **/** AOM0266

Diagnosis: Breast Neoplasms

MEDGENOME

MGM2732 : ESR1 gene testing by NGS -Liquid Biopsy (Hot Spot Mutations)

Report Details		Specimen Information		Ordering Clinician	
Sample ID / Order ID:	9404883 / 1452627	**Specimen Site:**	NA	**Clinician:**	Dr. Mahendra Perera
Collection Date:	16th September 2025	**Specimen Received:**	Blood in streck tube	**Affiliation:**	Aegle Omics Private Limited
Date Received:	19th September 2025	**Specimen Tested:**	Blood in streck tube	**Serviced By:**	18718
Report Date & Time:	27th Sep 2025 12:38 PM	**Tumor Content (%):**	NA	**Report Status:**	Final

Clinical Summary: Invasive mucinous carcinoma of the right breast, pT1 N0 Mx, Stage: I, ER/PR: Positive, Her2Neu: Negative

TEST RESULT SUMMARY

Next Generation Sequencing (NGS) Test Result

Result - NEGATIVE

NO CLINICALLY RELEVANT VARIANT/S DETECTED

AMP Classification ^	CDS variant details	Interpretation	Treatment Recommendations	$Treatment Response
No clinically significant variants detected				

^Refer to Glossary section for the classification criteria details.

$Drug Approvals are based on US-FDA Guidelines. Kindly refer to local guidelines if required.

ADDITIONAL BIOMARKERS DETECTED

This section provides information about variants that do not have any therapeutic value. However, these variants may or may not have a likely oncogenic effect.

No other biomarkers that warrants to be reported was detected

AMP-ASCO-CAP CLASSIFICATION CRITERIA

Genetic test results are reported based on the somatic variant classification recommendations of College of American Pathologists (CAP) /American society for Clinical Oncology (ASCO)/Association of Molecular Pathologists (AMP) [PMID: 27993330] as described in the table below:

Tier	Criteria
Tier I	Variants of strong clinical significance.
Tier II	Variants of potential clinical significance.
Tier III	Variants of unknown clinical significance
Tier IV	Benign or likely benign variants

DISCLAIMER

- This is a screening test and can be used as a treatment monitoring tool, which could help in assessment of treatment response and early recurrence.
- Decisions regarding treatment action plan should not be solely based on these test results. These findings are highly recommended to be correlated with the patient's clinical, pathological, radiological and family history for decisions on diagnosis, prognosis, or therapeutics.
- The therapy information provided in this report is based on FDA approved drugs data, NCCN guidelines, peer reviewed published literature, standard clinical databases, and strength of biomarker results till date. These therapies may or may not be suitable/beneficial to a particular patient. This clinical report summarizes potentially effective medications, potentially ineffective medications, and medications that may pose a higher risk of adverse reactions by mapping the patient's genetic alterations to the biomedical reference information. The report may also provide prognostic and diagnostic biomarkers detected or shown for the given disease context.The treatment recommendations for the variants classified in Tier II are not provided.
- The clinical trials information provided in this report is compiled from www.clinicaltrials.gov as per currently available data, however completeness of information provided herein cannot be guaranteed. This information should only be used as a guide and specific eligibility criteria should be reviewed thoroughly for the concerned patient. MedGenome Labs does not guarantee or promise an enrolment in any clinical trials.
- The identification of a genomic biomarker does not necessarily imply pharmacological effectiveness or ineffectiveness. The medications identified by the treating physician may or may not be suitable for use on a particular patient. Thus, the clinical report does not guarantee that any particular agent will be effective in the treatment of any particular condition. Also, the absence of a treatment option does not determine the effectiveness or predict an ineffective or safety-relevant effect of a medication selected by the treating physician.
- The classification and clinically relevant information for the reported variants is based on peer-reviewed publications, public clinical databases, medical guidelines (NCCN, ASCO, AMP) or other publicly available information and it has been ensured that the information provided is up to date at the time of report generated, however continuous updates may happen in public domains. Also, the classification of variants can change based on the updated literature evidence. Re-analysis of the results can be requested at additional cost.
- This test is performed on the patient's cfDNA sample without a paired blood sample; therefore, it may include variations which may be of germline origin. However, this test is designed and validated for the detection and reporting of somatic genomic variants only and does not discriminate between germline and somatic variants. If clinically warranted, appropriate germline testing and genetic counselling for the patient should be considered for further evaluation.
- Detection of large insertions, deletions, copy number variations, gene rearrangements and deep intronic variations are beyond the scope of this test.
- In-house validation data has shown limit of detection as 0.25% VAF for SNVs and Indels. However, a possibility of false positives cannot be ruled out at lower frequency. Therefore, it is recommended to correlate these findings with tissue testing results wherever available.

- **A false negative result due to the presence of mutations at low mutant allele fraction below the limit of detection (LOD) of this assay cannot be ruled out.**

TEST DESCRIPTION

The Medgenome's *ESR1* gene test is a high-throughput next generation sequencing based assay performed on liquid biopsy samples. This assay detects SNVs and InDels in the Ligand binding domain (LBD) spanning exons 7, 8, 9 and 10 of *ESR1* gene.It covers all the reported hotspot mutations listed in Appendix 1.

TEST METHODOLOGY

The scope of this test is to assess mutations in the *ESR1* gene by performing NGS on circulating free DNA (cfDNA) from blood plasma (liquid biopsy). cfDNA comprises circulating tumor DNA (ctDNA) present in blood plasma that is shed from tumor tissue and is the source of tumor genetic material. Unlike traditional biopsy, liquid biopsy is non-invasive as it requires only a peripheral blood draw in Streck tube from the cancer patient. Liquid Biopsy NGS testing is very powerful clinically as it provides- (a) real-time treatment monitoring to evaluate the drug response in cancer patients, (b) early detection of acquired resistance mutations to targeted therapy, (c) detection of recurrence at early stages before significant accumulation of tumor cell mass, (d) identification of tumor heterogeneity arising due to multiple clones and hence the disease progression.

Sample Type: Peripheral blood in Streck tube

Extraction and Library Preparation: cfDNA isolated from blood plasma is used to perform UMI-based gene sequencing for *ESR1* exons (7, 8, 9,10).

Sequencing: The QC passed libraries are sequenced to a minimum depth >10000X (pre-UMI) on validated Illumina sequencing platform and compressed to >1000X (post-UMI) for variant analysis.

Data Analysis: The sequences obtained are aligned to human reference genome (GRCh38/hg38) using BWA program [PMID:19451168, PMID: 23155063]. Somatic mutations are identified using UMI corrected Sention pipeline [PMID: 31481971]. Only non-synonymous and splice site variants are used for clinical interpretation. The mutations are annotated using our in-house annotation pipeline (VariMAT).

Reporting: Reportable alterations are prioritized, classified, and reported based on AMP-ASCO-CAP guidelines [PMID: 27993330].

Analytical performance: A minimum of 30ng cfDNA isolated from plasma is considered as an acceptable criterion for proceeding with this testing. Analytical validation of this test in our laboratory has shown sensitivity, and specificity of 100% at Limit of Detection at 0.25% VAF.

Limit of Detection (LOD): The Limit of detection of the assay for somatic mutations is 0.25% for SNVs and short INDELs [PMID: 29379323].

The transcript used for clinical reporting generally represents the canonical transcript (according to Ensembl release 99 human gene model), which is usually the longest coding transcript with strong/multiple supporting evidence. However, clinically relevant variants annotated in alternate complete coding transcripts could also be reported. Variants annotated on incomplete, and nonsense mediated decay transcripts are not reported.

§This test is developed, and its performance characteristics is determined by MedGenome Labs Ltd.

APPENDIX 1

All mutations occurring in Exon 7, 8, 9, & 10 will be covered in this assay. The reported hotspot mutations are listed below

Exon No	Mutations Covered
Exon 7	*E380Q, V392I*
Exon 8	*V418E, S432L*
Exon 9	*S463P, F461D, L466Q, V478L, H476N*
Exon 10	*N532K, V534E, L536H, L536P, L536R, Y537S, Y537N, Y537C, Y537D, D538G, E542G, A576D*

CLINICAL TRIALS

The following trials are potentially best suited for your patient's indication, considering all reported treatment recommendations. See https://clinicaltrials.gov (clinical trials from NCT) or https://trialsearch.who.int (clinical trials from other registries) for more information.

Clinical trials in total : 0 **Trial countries :** IN-India, US-United States

S.No	Title	Phase and ID	Intervention	Disease	Age & Sex
No Clinical Trials.					

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END OF REPORT