tar**GT**
FIR**S**t

TEST REPORT

4baseCare
Together, *We Beat* Cancer

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Together, We Beat Cancer

PATIENT ID: IN-423-WBTD
CANCER SITE: BREAST
SAMPLE ID: IN-423-WBTD-F
REGISTRATION DATE: 20/02/2023

SCOPE OF THE TEST

SNVs, InDels, CNAs, Gene Fusions status

CLINICAL INDICATION

Adenocarcinoma of Breast

REPORT DETAILS

Name : ANILA

Gender : Female

Age/DOB : 43 Years

Reporting Date : 21/03/2023

Cancer Celltype : Adenocarcinoma, NOS

Sample Source : B-22-8939-1/2

Tumor content : 75%

Consulting Clinician : Dr. Amit Jain

Hospital : Valentis Cancer Hospital, Mussoorie Mawana Road

RESULTS

GENOMIC FINDINGS FROM TUMOR PROFILING

Genomic Alteration	Relevant Therapies (in Same Cancer Type)		Relevant Therapies (in Different Cancer)		
	Therapy	*Clinical Relevance*	*Therapy*	*Clinical Relevance*	*Cancer Type*
EGFR Exon 20 (p.Asp770_Val774dup) Allelic burden: 10%	NA	NA	Mobocertinib	RESPONSIVE	Non-Small Cell Lung Cancer
			Amivantamab-vmjw	RESPONSIVE	Non-Small Cell Lung Cancer

*NA: Not Applicable

STATUS OF VARIANTS IN CANCER RELATED BIOMARKERS

Gene	PIK3CA	ERBB2	BRCA1	BRCA2	ATM	BRIP1	BARD1	CDK12
Status	Not Detected	Not Detected	Not Detected	Not Detected	Not Detected	Not Detected	Not Detected	Not Detected

Gene	CHEK1	CHEK2	FANCL	PPP2R2A	RAD51C	RAD54L
Status	Not Detected	Not Detected	Not Detected	Not Detected	Not Detected	Not Detected

Note:

EGFR mutations and its significance in breast cancer is not well documented in the literature. Kindly correlate clinically.

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VARIANT DETAILS:

Gene	Variant Location	Variant Consequence	Clinical Significance	Variant Type	Reference
EGFR	chr7:g.55249010_55249024dup, ENST00000275493, Exon 20	c.2308_2322dup, p.Asp770_Val774dup , 10%	Pathogenic	Inframe insertion	rs1554350367, VCV000177955.4
CDKN2A	chr9:g.21974715G>A, ENST00000304494, Exon 1	c.112C>T,p.Pro38Ser , 80%	VUS	Nonsynonymous SNV	rs1587339752, VCV000822217.12

*NA: Not Applicable

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4baseCare Oncosolutions Pvt. Ltd

Vaishnavi Signature No. 78/9, Outer Ring Road,

Bellandur Village Varthur Hobli

Bengaluru-560103, Karnataka, India

*Please note that this is not a medical report

VARIANTS WITH CLINICALLY RELEVANT THERAPIES

Gene (Variant) - Drug association

- *EGFR* Exon 20 insertion :
  Mobocertinib - RESPONSIVE
  Non-Small Cell Lung Cancer

- *EGFR* Exon 20 insertion :
  Amivantamab-vmjw - RESPONSIVE
  Non-Small Cell Lung Cancer

Summary

The drug mobocertinib has been approved for the treatment of adult patients with locally advanced or metastatic non-small cell lung cancer (NSCLC) *EGFR* exon 20 insertion mutations with disease progression on or after platinum-based chemotherapy (FDA).
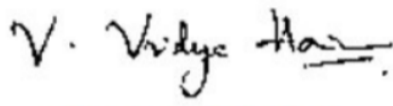The approval was based on the clinical study Study 101 (NCT02716116). The overall response rate among 114 patients was 28% (95% CI: 20%, 37%). The median response duration was 17.5 months (95% CI: 7.4, 20.3).

The drug amivantamab-vmjw has been approved for the treatment of adult patients with locally advanced/ metastatic non-small cell lung cancer (NSCLC) with *EGFR* exon 20 insertion mutations who progressed on/ after platinum-based chemotherapy (FDA).
The approval was based on the clinical study Chysalis trial (NCT02609776). Among the 81 amivantamab-vmjw efficacy evaluable population, the overall response rate was 40% (95%CI, 29 to 51) with three full responses with a median response duration of 11.1 months (95% CI, 6.9 to not reached). The median time without progression was 8.3 months (95% CI, 6.5 to 10.9).

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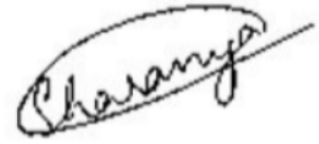*Please note that this is not a medical report*

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TEST DESCRIPTION

TAR**GT** First is a Next Generation Sequencing based test which identifies genetic alterations in a comprehensive panel of well curated 53 tumor genes which can impact response to approved therapy for a particular cancer type. Some of the alterations detected may have bearing on prognosis and/or therapeutic options and may provide relevant information that allows oncologists/clinicians to consider various lines of targeted treatment for the patient.

GENES EVALUATED

TAR**GT** First detects mutations (SNVs and Short Indels), Copy Number Variations (CNVs), gene fusions and splice variants in the 53 genes :

SNVs/InDels Covered in TAR**GT** First

ABL1	ALK	AR	ATM	BARD1	BRAF	BRCA1	BRCA2	BRIP1	CDK12
CDK4	CDK6	CDKN2A	CHEK1	CHEK2	EGFR	EPCAM	ERBB2	ERBB3	EZH2
FANCL	FGFR3	GAPDH	IDH1	IDH2	JAK2	KIT	KRAS	MAP2K1	MAP2K2
MDM2	MET	MLH1	MLH3	MSH2	MSH6	NRAS	PALB2	PDGFRA	PDGFRB
PIK3CA	PMS1	PMS2	PPP2R2A	RAD51B	RAD51C	RAD51D	RAD54L	RET	ROS1
STK11	TSC1	TSC2							

CNAs Covered in TAR**GT** First

ABL1	AR	ATM	BARD1	BRCA1	BRCA2	BRIP1	CDK12	CDK4	CDK6
CDKN2A	CHEK1	CHEK2	EGFR	EPCAM	ERBB2	ERBB3	EZH2	FANCL	FGFR3
GAPDH	IDH2	JAK2	KIT	MDM2	NRAS	PALB2	PDGFRA	PDGFRB	PPP2R2A
RAD51B	RAD51C	RAD51D	RAD54L	STK11	TSC1	TSC2			

Gene Fusions Covered in TAR**GT** First

ALK	MET	RET	ROS1

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TEST METHODOLOGY

Sample preparation and Library preparation :

DNA isolated from FFPE, or any other fresh tumor tissue source was used to perform targeted gene capture using a custom capture kit. The libraries were sequenced to mean >250X coverage on Illumina sequencing platform.

Bioinformatics Analysis and Reporting :

The sequences obtained are aligned to human reference genome (GRCh37/hg19) and variant analysis was performed using set of Bioinformatics Pipeline. Only non-synonymous and splice site variants found in the panel consisting of specific set of genes were used for clinical interpretation. Silent variations that do not result in any change in amino acid in the coding region are not reported. Clinically relevant mutations were annotated using published variants in literature and a set of databases – ClinVar, COSMIC and dbSNP. Common variants are filtered based on allele frequency in 1000 Genome Phase 3, ExAC, dbSNP, gnomAD, etc. In the absence of a clinically significant reported known variation(s), pathogenicity will be predicted based on in-silico gene prioritization tools: CADD, SIFT, PolyPhen-2, Condel and Mutation taster and prioritized for clinical correlation. The identified pathogenic variant will be correlated with observed phenotypic features of the patient and interpreted according to American College of Medical Genetics (ACMG) guidelines.

Somatic variants are classified into two tiers based on their level of clinical significance in cancer diagnosis, prognosis, and/or therapeutics as per international guidelines: ACMG, ASCO, AMP, CAP, NCCN and ESMO

LIMITATIONS AND DISCLAIMER

- DNA studies do not constitute a definitive test for the selected condition(s) in all individuals. It should be realized that there are possible sources of error. Errors can result from trace contamination, rare technical errors, rare genetic variants that interfere with analysis, recent scientific developments, and alternative classification systems. This test should be one of the many aspects used by the healthcare provider to help with a diagnosis and treatment plan.
- We are using the canonical transcript for clinical reporting which is usually the longest coding transcript with strong/multiple supporting evidence. However, in rare cases, clinically relevant variants annotated in alternate complete coding transcripts could also be reported.
- The contents of this test should be carefully assessed by the treating physician and further interpreted along with clinical, histopathological findings, contraindications and guidelines before deciding the course of therapy.
- The chromosomal aberrations like copy number variations and rearrangements may not be reliably detected with this assay and have to be confirmed by alternate method.
- The sensitivity of this assay to detect large deletions/duplications of more than 10 bp or copy number variations (CNV) is 70-75%. The CNVs detected have to be confirmed by alternate method.
- Most recent block is recommended for testing as the mutation profile may change in response to treatment and hence differ at different sampling points.
- TARGT FIRST test has been developed, validated and performed by 4baseCare Genomics Pvt. Ltd and has not been cleared or approved by the FDA.
- The identified pathogenic variant will be correlated with observed phenotypic features of the patient and interpreted according to (ASCO) guidelines.
- Certain genes may not be covered completely, and few mutations could be missed. A negative result cannot rule out the possibility that the tested tumor sample carries mutations not previously associated with cancer and hence not included in the panel.

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