

## Patient Information



Name  
JANE TAN

DOB  
01/03/1973

### PATIENT

#### JANE TAN

Age: 45      Sex: Female  
DOB: 01/03/1973  
MRN:  
Citizen ID: NNNN  
Ethnicity: Chinese

### PHYSICIAN

#### YYY YYYY

Order ID: NNNNN  
Account ID: NN  
Copied to:

### SAMPLE

#### LUCENCE ID: BS-18-NNNNN

Date of Report: DD/MM/YYYY  
Date Collected: DD/MM/YYYY  
Date Received: DD/MM/YYYY  
Type: Blood in Streck tubes (22 mL)

## Test Summary

### TEST(S) PERFORMED

#### LiquidHALLMARK®

#### GENES EVALUATED\*

AKT1, ALK, APC, AR, BRAF, CDKN2A, CTNNB1, EGFR, ERBB2 (HER2), ESR1, GNAS, KIT, KRAS, MED12, MET, NRAS, PIK3CA, PTEN, SMAD4, TP53, VHL

#### MICROSATELLITE LOCI

BAT25, BAT26, NR21, NR24, NR27, MONO27

#### VIRAL TARGETS

EBV BamHI-W, EBV EBNA1

*\*Targeted regions selected to maximize detection of known hotspot mutations.*

### ABOUT THE TEST

The LiquidHALLMARK® assay is a next-generation sequencing (NGS) based test that identifies targeted somatic genomic alterations and cancer-associated viral DNA in cell-free DNA (cfDNA).

### RESULTS SUMMARY

#### 2 Clinically Relevant Genomic Alterations Identified

- EGFR L858R
- MET amplification (2.5-fold)

#### 3 Other Genomic Alteration Identified

- MET R992I
- SMAD4 R441C
- TP53 R65\*

#### Other Actionable Target Genes with No Alterations in Patient Sample

- KRAS
- NRAS
- BRAF
- ERBB2
- PIK3CA

#### Other Findings

No detected microsatellite instability at tested markers. No other mutations detected in tested genes.

### CLINICAL DIAGNOSIS

EGFR MUTANT METASTATIC  
LUNG ADENOCARCINOMA

### TREATMENT HISTORY

FIRST LINE: AFATINIB  
SECOND LINE: OSIMERTINIB  
THIRD LINE: CHEMOTHERAPY  
FOURTH LINE: OSIMERTINIB AND CRIZOTINIB

## Clinical Interpretation and Recommendations

### CLINICALLY RELEVANT ALTERATIONS IDENTIFIED

| Gene        | Transcript     | Exon | Alteration                            | Variant Type          | Significance     | % cfDNA/fold-amplification |
|-------------|----------------|------|---------------------------------------|-----------------------|------------------|----------------------------|
| <i>EGFR</i> | NM_005228.3    | 21   | c.2573T>G<br>p.L858R<br>(p.Leu858Arg) | Missense substitution | Gain-of-function | 4.10%                      |
| <i>MET</i>  | NM_001127500.2 | -    | Amplification                         | -                     | Gain-of-function | 2.5-fold                   |

### OTHER GENOMIC ALTERATIONS IDENTIFIED

| Gene         | Transcript     | Exon | Alteration                            | Variant Type          | Significance                              | % cfDNA |
|--------------|----------------|------|---------------------------------------|-----------------------|---|---------|
| <i>MET</i>   | NM_001127500.2 | 14   | c.2975G>T<br>p.R992I<br>(p.Arg992Ile) | Missense substitution | Predicted Splicing variant, Exon skipping | 0.35%   |
| <i>SMAD4</i> | NM_005359.5    | 11   | c.1321C>T<br>p.R441C<br>(p.Arg441Cys) | Missense substitution | Likely loss-of-function                   | 0.83%   |
| <i>TP53</i>  | NM_000546.5    | 4    | c.193A>T<br>p.R65*<br>(p.Arg65Ter)    | Stop gain             | Loss-of-function                          | 10.8%   |

The percentage, or allele frequency, of altered cell-free DNA (% cfDNA) is related to the unique tumour biology of the patient. Several factors may affect the percentages of detected genomic alterations in cfDNA including tumor growth, turnover, size, heterogeneity, vascularization, disease progression or treatment.

### INTERPRETATION OF CLINICALLY RELEVANT ALTERATIONS

| Variant   | Interpretation  |
|---|---|
| <i>EGFR</i><br>NM_005228.3<br>c.2573T>G<br>p.L858R<br>(p.Leu858Arg) | EGFR L858R mutation is one of the most common EGFR mutations in NSCLC (26-40%), and the most common sensitizing mutation to EGFR tyrosine kinase inhibitors. EGFR L858R occurs either as a somatic variant, predominantly in non-small cell lung cancer and lung adenocarcinoma. Gefitinib, erlotinib and afatinib are FDA-approved EGFR TKIs for first-line treatment of metastatic NSCLC with EGFR exon 19 deletions or exon 21 (L858R) substitution mutations.   |
| <i>MET</i><br>amplification   | <p><i>MET</i> amplification, <i>MET</i> mutations, or aberrant c-MET signaling are associated with unfavorable prognosis in NSCLC. <i>MET</i> amplification as a primary driver of tumorigenesis is relatively rare, occurring in only 2% of lung adenocarcinomas, but it can occur in up to 15-20% of <i>EGFR</i>-mutant NSCLCs with acquired resistance to EGFR inhibitors, including osimertinib. <i>MET</i> amplification is independent of the occurrence of EGFR T790M, and has also been identified in EGFR inhibitor-naïve samples. Both <i>MET</i> amplification and exon 14 splice mutations have been associated with clinical responses to MET inhibitors.</p> <p>Crizotinib and cabozantinib are two multi-tyrosine kinase inhibitors (MET/ROS1/ALK inhibitors) that have been approved for metastatic NSCLCs with ALK/ROS, and RET rearrangements, respectively. Multiple combinations of MET inhibition and EGFR inhibition have been reported to result in clinical response in case reports or small clinical studies.</p> |