

## **Test Description**

*EGFR* mutation test is an *in vitro* diagnostic test for the qualitative detection of mutations in exons 18, 20, 21; deletions in exon 19 and insertions in exon 20 of *EGFR* oncogene.

**Patient Demographic** 

Name: Abdul Rahman Afghan

Sex: Male

Date of Birth/Age: 58 Years

Disease: Metastatic NSCLC - Adenocarcinoma

PATIENT Abdul Rahman Afghan REPORT DATE 09 June 2019

BOOKING ID 011906080128

#### Clinician

Clinician Name: Dr Sandeep Batra Medical Facility: Max Hospital Pathologist: Not Provided

# **Specimen**

Site: Left lung mark biopsy

Sample Type: FFPE block SC-1756/19 Date of Collection: 08-06-2019 Date of Booking: 08-06-2019

# **EGFR** Mutation Analysis

# Result

# No mutation detected

#### GENOMIC FINDINGS

No mutation detected

### INTERPRETATION

No mutation in exon 18, 19, 20 and 21 of *EGFR* gene is detected.

For valid batch test results specific controls are being run with every batch.

## **METHODOLOGY**

The Biocartis Idylla<sup>M</sup> EGFR Mutation Test is an *in vitro* diagnostic test intended for the qualitative detection of 51 alterations in exon 18 (G719A/C/S), exon 21 (L858R, L861Q), exon 20 (T790M, S768I) mutations, exon 19 deletions and exon 20 insertions in the *EGFR* oncogene. The Test uses formalin-fixed, paraffin-embedded (FFPE) tissue sections from human non-small cell lung cancer (NSCLC) tissue. A conserved fragment in the transmembrane region of the *EGFR* gene is amplified simultaneously. This PCR reaction, EGFR total, serves as a sample processing control (SPC) that checks for adequate execution of the complete process from sample to result, and is present in each of the five multiplexes. In addition, the EGFR control reaction is a measure for the amount of amplifiable DNA in the sample and is used in the analysis of the mutation status of the sample. This test is carried out on Idylla platform using the EGFR/1.0 Cartridge based kit which is CE IVD approved.

The Idylla™ EGFR Mutation Test is able to detect allelic frequencies at:  $\leq 5\%$  for mutations in exons 19, 20 and 21 of the *EGFR* oncogene; and  $\leq 10\%$  for mutations in exon 18 of the *EGFR* oncogene

### REFERENCES

- 1. Montpreville et al. Path Res & Prac (2017) 213:793-98
- 2. Lambros et al. J clin Path (2017) 0:1-6

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Date