MET Gene Amplification, FISH

Mesenchymal Epidermal Transition (MET)
Fluorescence *In Situ* Hybridization

Test Description
The mesenchymal-epidermal transition (MET)/ hepatocyte growth factor (HGF) MET, located at 7q21-q31, is a proto-oncogene that encodes the tyrosine kinase receptor for HGF. Different molecular alterations in the *MET* gene have been found to determine the MET/HGF pathway activation: point mutations, amplifications, genetic polymorphisms, enhanced transcription, and autocrine activation, Alterations in the *MET* gene, including overexpression, amplification, and mutations, have been also observed in NSCLC. MET protein overexpression is variable in NSCLC, ranging from 5% to 74.6%

Specimen
Sample Type: FFPE block SB-2842 B/19
Site: Lung
Pathology ID: MOLQ/FISH-02092019
Disease: NSCLC

Methodology
Fluorescence *In Situ* Hybridization (FISH)
Probe: Cytotest LSP MET CytoOrange/LSP CCP7 CytoGreen

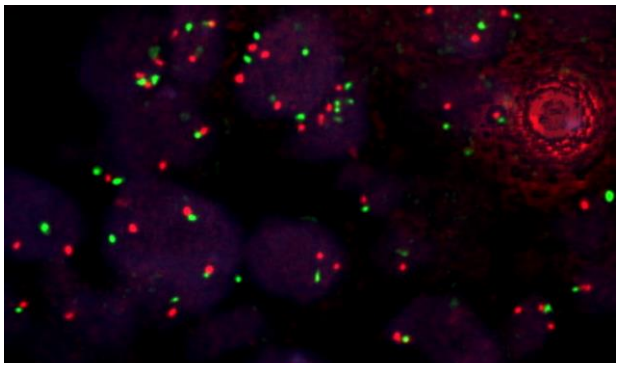
Interpretation
MET gene amplification is
Negative: tumor cells exhibit an average of < 5 copies/cell of the *MET* gene.
Positive: where tumor cells exhibit an average of >5 copies/cell of the *MET* gene, or MET to CEP7 signals ratio is ≥2.

Comments
1. MET/HGF pathway has recently emerged as a potential therapeutic target in several types of human cancers including NSCLC.
2. *MET* gene amplification is seen in 2-4% of previously untreated non-small cell lung carcinomas and 5-20% of patients with EGFR mutated tumors with acquired resistance to EGFR. Increased copy number of *MET* has been associated with poor prognosis in patients with NSCLC.
3. Various studies have shown that *MET* amplified tumors respond favorably to therapy with Crizotinib, an inhibitor of MET and ALK.

References
1. Rosai and Ackerman's Surgical Pathology.
2. Prognostic value of MET copy number gain in non-small-cell lung cancer: an updated meta-analysis Jung Han Kim et al. J Cancer 2018; 9(10).
3. MET amplification assessed using optimized FISH reporting criteria predicts early distant metastasis in patients with non-small cell lung cancer Lianghua Fang et al. Oncotarget. 2018 Feb 27; 9(16).

Result
MET gene amplification: Negative

Clinician
Clinician Name: Dr. Archit Pandit
Medical Facility: Max Hospital, Shalimar Bagh
Pathologist: Not provided

Figure


Microscopic Evaluation

Total number of cells scored	100
Total number of *MET* signals	276
Total number of *CEP7* signals	243
Average of *MET* copies/ cell	2.76
Computed ratio	1.13

Reviewed by
Dr. Jatinder Kaur, Ph.D
Head, Molecular Biology & Genomics

Dr. Gulshan Yadav, MD
Head, Pathology