See below for Additional Technical Information topics

**MET Gene Amplification by FISH**

**Indications for Ordering**

Aids in prognostication and therapeutic decisions for neoplasms where amplification has been demonstrated

**Test methodology**

**FISH**

- Fluorescence in situ hybridization (FISH) analysis on formalin-fixed, paraffin-embedded tumor tissue
- DNA probes
  - MET (7q31.2)
  - CEP7 (control probe)
- 40 cells evaluated from regions of tumor identified on histopathologic review of a matching hematoxylin and eosin stained section

**Tests to Consider**

**Primary test**

**MET Gene Amplification by FISH 3001313**

- Screening test for MET gene amplification

**Related test**

**c-MET by Immunohistochemistry 2008652**

- Detects overexpression of c-MET protein

**Disease Overview**

**Prognostic/therapeutic issues**

- In lung cancer, MET gene amplification is associated with acquired resistance to EGFR inhibitors
  - Occurs in 5-20% of patients with EGFR-mutated tumors
  - Amplification is associated with tumor progression and a poor prognosis in other tumors
    - Breast
    - Clear cell ovarian
    - Colorectal
    - Esophageal
    - Gastric
    - Glioma
    - Head and neck
    - Mesenchymal
    - Renal
    - Thyroid
  - Multiple ongoing trials using EGFR inhibitors, with some tumors showing sensitivity to crizotinib

**Genetics**

**Gene – MET**

**Test Interpretation**

**Results**

- Amplified
  - MET/CEP7 ≥ 2.0 OR
  - Average MET copy number per cell is ≥ 6.0
- Nonamplified
  - MET/CEP7 < 2.0

**Limitations**

- Results must be interpreted in the context of morphological and other relevant data
- Results may be compromised if the recommended fixation procedures have not been followed
Lung Cancer Molecular Markers

Indications for Ordering
Mutation testing to aid in selection of tyrosine kinase inhibitor (TKI) and/or immune checkpoint inhibitor therapy

Tests to Consider

Typical Testing Strategy
Minimum initial recommendation – lung cancer panel that includes simultaneous ordering for mutations in ALK, EGFR, and ROS1 genes

Primary Tests
Determine eligibility for TKI therapy (panel tests)

Lung Cancer Panel 2008894
- Screening panel detects
  - EGFR mutations
  - ALK and ROS1 fusion proteins

Lung Cancer Panel with KRAS 2008895
- Screening panel detects
  - EGFR and KRAS mutations
  - ALK and ROS1 fusion proteins

Determine eligibility for TKI therapy (single tests)

ALK (D5F3) with Interpretation by Immunohistochemistry 2007324
- Detects ALK fusion proteins

ALK (D5F3) by Immunohistochemistry with Reflex to ALK Gene Rearrangements by FISH 2011431
- Detects ALK fusion proteins and ALK gene rearrangements in solid tumors

ALK Gene Rearrangements by FISH, Lung 3001302
- Screening test for all ALK fusions
- Use this test if the companion diagnostic test for crizotinib is required
- Does not identify the translocation partner or variant

EGFR Mutation Detection by Pyrosequencing 2002440

KRAS Mutation Detection 0040248
- Predicts response to anti-EGFR and MAPK pathway therapies in a variety of malignancies (eg, colorectal and lung cancer)

c-MET by Immunohistochemistry 2008652
- Detects overexpression of c-MET protein

MET Gene Amplification by FISH 3001313
- Aids in prognostication and therapeutic decisions for neoplasms where amplification has been demonstrated
- Screening test for MET gene amplification

RET Gene Rearrangements by FISH 3001312
- Detects RET gene rearrangements in solid tumors
- Does not identify the translocation partner or variant

ROS1 by FISH 3001308
- Detects ROS1 gene rearrangements in solid tumors
- Does not identify the translocation partner or variant

ROS1 with Interpretation by Immunohistochemistry with Reflex to FISH if Equivocal or Positive 2008414
- Detects ROS1 fusion proteins and ROS1 gene rearrangements

Screening for immune checkpoint inhibitor therapy FDA-approved PD-L1 companion tests

For more information about PD-L1 testing, refer to the ARUP Consult PD-L1 Testing topic and algorithm.
- PD-L1 22C3 IHC with Tumor Proportion Score (TPS) Interpretation, pembrolizumab (KEYTRUDA) 2013284
- Companion diagnostic test to aid in prediction of response to pembrolizumab (KEYTRUDA) as first- or second-line monotherapy for patients with non-small cell lung cancer (NSCLC)
- Can be performed in conjunction with or instead of PD-L1 28-8
- For NSCLC specimens only
  - For gastroesophageal junction (GEJ), urothelial, and cervical specimens, see PD-L1 22C3 IHC with Combined Positive Score (CPS) Interpretation, pembrolizumab (KEYTRUDA) 3000197

PD-L1 28-8 pharmDx by Immunohistochemistry with Interpretation, nivolumab (OPDIVO) 2013684
- FDA-approved complementary codiagnostic test to aid in prediction of response to nivolumab (OPDIVO) for patients with nonsquamous NSCLC, melanoma, urothelial carcinoma, and head and neck squamous cell carcinoma (HNSCC)

Monitor for EGFR T790M resistance

EGFR T790M Mutation Detection in Circulating Tumor DNA by Digital Droplet PCR 2012868
- Monitor blood plasma or cerebrospinal fluid (CSF) for
  - Development of EGFR T790M drug-resistant mutation in patients administered TKI therapy for EGFR-mutant NSCLC
  - Response to therapy and disease progression in patients receiving EGFR T790M-specific TKIs
Related Test

Solid Tumor Mutation Panel by Next Generation Sequencing 2007991
- Aids in therapeutic decisions for solid tumor cancers
- Simultaneously evaluates mutations in multiple genes, including AKT1, ALK, BRAF, EGFR, ERBB2, ERBB4, KRAS, NRAS, and PIKC3CA
- Does not detect translocations

Test Methodology

ALK
- Immunohistochemistry (IHC) using ALK clone D5F3
- Fluorescence in situ hybridization (FISH)

EGFR – polymerase chain reaction (PCR) and pyrosequencing
- Detects mutations at codons 719 (exon 18), 768 and 790 (exon 20), 858 and 861 (exon 21)
- Detects deletions in exon 19

EGFR T790M (serum) – digital droplet PCR

KRAS – PCR and pyrosequencing
- Detects mutations at codons 12, 13 (exon 2), and 61 (exon 3)

c-MET – IHC

MET – FISH

PD-L1 – IHC

RET – FISH
- Detects all RET gene fusions

ROS1 – IHC (using ROS1 clone D4D6) with FISH reflex if equivocal

Test Interpretation

Results
Single gene testing (includes genes in panels) – see table

Limitations
- Results must be interpreted in the context of clinical findings and morphological and other relevant data
- Results may be compromised if the recommended tissue-fixation procedures have not been followed

Disease Overview

Incidence
Lung cancer is the second most common cancer in U.S.

Treatment Issues
- Lung cancer has poor response to traditional chemotherapy agents
  - Dismal 5-year outcome when using these agents
  - Newer targeted agents have better response rates in specific individuals and tumor types
- Tumor response rates to targeted therapy are closely associated with mutation status of the tumor, especially for adenocarcinoma or mixed adenocarcinoma subtypes
- Mutation status
  - Determines TKI therapy eligibility
  - Confers resistance to TKIs (eg, EGFR T790M mutation)
    - Monitoring in serum for EGFR T790M mutation may detect TKI resistance sooner and alter treatment plans
  - PD-L1 expression
    - May predict response to immune checkpoint inhibitor therapy

References
- Francis G, Stein S. Circulating cell-free tumour DNA in the management of cancer. Int J Mol Sci. 2015:16;14122-14142

<table>
<thead>
<tr>
<th>Gene</th>
<th>Testing method</th>
<th>Test result</th>
<th>May predict response to TKI therapy</th>
</tr>
</thead>
<tbody>
<tr>
<td>ALK</td>
<td>IHC</td>
<td>Positive – uniform membranous staining in tumor cells</td>
<td>May predict response to TKI therapy</td>
</tr>
<tr>
<td></td>
<td></td>
<td>Equivocal – very weak cytoplasmic staining visible only on higher power by microscopy</td>
<td></td>
</tr>
<tr>
<td></td>
<td></td>
<td>Negative – no cytoplasmic staining in tumor cells</td>
<td></td>
</tr>
<tr>
<td></td>
<td>FISH</td>
<td>Positive – ALK gene rearrangements detected in ≥15% of nuclei</td>
<td>May predict response to TKI therapy</td>
</tr>
<tr>
<td></td>
<td></td>
<td>• Does not identify translocation partner</td>
<td></td>
</tr>
<tr>
<td>EGFR</td>
<td>PCR/pyrosequencing</td>
<td>Positive – mutation detected</td>
<td>May predict response to TKI therapy</td>
</tr>
<tr>
<td>EGFR T790M (serum)</td>
<td>Digital droplet PCR</td>
<td>Positive – mutation detected</td>
<td>Predicts resistance to TKI therapy</td>
</tr>
<tr>
<td></td>
<td></td>
<td>• Expressed as percentage</td>
<td></td>
</tr>
<tr>
<td>KRAS</td>
<td>PCR/pyrosequencing</td>
<td>Positive – mutation detected</td>
<td>May predict response to TKI therapy</td>
</tr>
<tr>
<td>MET</td>
<td>FISH</td>
<td>Positive – detects gene amplification</td>
<td></td>
</tr>
<tr>
<td></td>
<td></td>
<td>• May predict response to crizotinib TKI therapy</td>
<td></td>
</tr>
<tr>
<td></td>
<td></td>
<td>• Associated with acquired resistance to EGFR inhibitors in 5-20% of patients with EGFR-mutated tumors</td>
<td></td>
</tr>
<tr>
<td>Gene</td>
<td>Testing method</td>
<td>Test result</td>
<td></td>
</tr>
<tr>
<td>------</td>
<td>------------------------</td>
<td>-------------------------------------------------------------------------------</td>
<td></td>
</tr>
<tr>
<td>RET</td>
<td>FISH</td>
<td>Positive – gene rearrangements detected</td>
<td></td>
</tr>
<tr>
<td></td>
<td></td>
<td>• Does not identify translocation partner</td>
<td></td>
</tr>
<tr>
<td>ROS1</td>
<td>IHC FISH reflex</td>
<td>Positive – cytoplasmic staining in tumor cells</td>
<td></td>
</tr>
<tr>
<td></td>
<td></td>
<td>Equivocal – any degree of cytoplasmic staining or focal/weak membranous staining in tumor cells</td>
<td></td>
</tr>
<tr>
<td></td>
<td></td>
<td>• Reflexes to FISH for confirmation</td>
<td></td>
</tr>
</tbody>
</table>