

Template for Reporting Results of Biomarker Testing of Specimens From Patients With Non-Small Cell Carcinoma of the Lung

Version: Lungbiomarker 1.3.0.2

Protocol Posting Date: June 2016

Completion of the template is the responsibility of the laboratory performing the biomarker testing and/or providing the interpretation. When both testing and interpretation are performed elsewhere (eg, a reference laboratory), synoptic reporting of the results by the laboratory submitting the tissue for testing is also encouraged to ensure that all information is included in the patient's medical record and thus readily available to the treating clinical team. **This template is not required for accreditation purposes.**

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Summary of Changes

Version 1.3.0.2:

Updated notes to RET Rearrangement

Version 1.3.0.2:

Updated Explanatory Notes

Version 1.3.0.1:

Updated Explanatory Notes

Version 1.3.0.0:

RESULTS

Terminology changes (from Indeterminate to Equivocal).
Added data elements for *ALK* Rearrangements identified.

METHODS

Added Sequencing Type.
Added reporting for Anchored multiplex PCR.
Added more options for reporting MET Region.

Biomarker Reporting Template

Template web posting date: June 2016

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LUNG: Biomarkers

Select a single response unless otherwise indicated.

+ SPECIMEN ADEQUACY

+ Adequacy of Sample for Testing (Note A)

- + Adequate
 - + Estimated tumor cellularity (area used for testing): _____%
- + Suboptimal (explain): _____

Note: If "Adequate" not selected, please refer to original laboratory report for explanation.

+ SPECIMEN TYPE

- + Untreated diagnostic specimen
- + Relapse specimen (after treatment; specify: _____)#

When data is available, specify treatment type. This is most relevant to targeted inhibitors associated with specific genomic changes conferring treatment resistance (especially erlotinib, gefitinib, and other EGFR tyrosine kinase inhibitors).

+ RESULTS

+ EGFR Mutational Analysis (Note B)

- + No mutation detected
- + Mutation(s) identified (select all that apply)
 - + Exon 18 Gly719#
 - + Exon 19 deletion#
 - + Exon 20 insertion##
 - + Exon 20 Thr790Met###
 - + Exon 21 Leu858Arg#
 - + Other (specify)####: _____
- + Cannot be determined (explain): _____

EGFR activation mutation associated with response to EGFR tyrosine kinase inhibitors.

Exon 20 EGFR activating mutations are generally associated with resistance to EGFR tyrosine kinase inhibitors such as erlotinib, afatinib, and gefitinib, although insertions at or before position 768 can be associated with sensitivity.

The T790M mutation is typically secondary to other EGFR activating mutations and is associated with acquired resistance to tyrosine kinase inhibitor therapy. If seen in untreated/pre-treated patients, may be present in the germline and indicate a hereditary cancer syndrome, in which case genetic counseling is suggested.

There is limited data on response to EGFR tyrosine kinase inhibitors for many of the uncommon EGFR activating mutations.

+ EGFR by Mutation-Specific Immunohistochemistry

- + EGFR L858R (clone 43B2)
- + ___ Negative[#]
- + ___ Positive^{##}
- + ___ Equivocal^{###} (explain): _____

+ EGFR Exon 19 Deletion (E746_A750del) (clone 6B6)

- + ___ Negative[#]
- + ___ Positive^{##}
- + ___ Equivocal^{###} (explain): _____

[#] A negative result does not exclude the possibility of EGFR mutations, and testing with molecular methods should be performed if a suitable sample is available.

^{##} Diffuse mutation-specific protein expression in tumor cells is highly correlated with EGFR mutation and as such predicts response to EGFR tyrosine kinase inhibitors.

^{###} Tumors with faint cytoplasmic labeling should be designated as equivocal. This result can rarely occur both with and without mutation.

+ ALK Rearrangement by Molecular Methods (Note C)

- + ___ No rearrangement detected[#]
- + ___ Rearrangement identified^{##}
 - + ___ EML4-ALK (specify variant type, if known): _____
 - + ___ KIF5B-ALK
 - + ___ TFG-ALK
 - + ___ KLC1-ALK
 - + ___ Other ALK rearrangement (specify, if known): _____
- + ___ Cannot be determined (explain): _____

+ Polysomy:

- + ___ Present^{###}
- + ___ Absent

[#] Absence of ALK rearrangement in cancer cells suggests that this tumor is unlikely to respond to treatment with a targeted ALK inhibitor, such as crizotinib.

^{##} ALK rearrangement predicts response to therapy with a targeted ALK inhibitor, such as crizotinib or ceritinib. Some evidence suggests the type of FISH pattern (breakapart versus 5' probe deletion) may have implications for treatment response and outcomes.

^{###} Polysomy involving the ALK locus confirms that fluorescence in situ hybridization (FISH) scoring was carried out in tumor cells but does not predict response to therapy with targeted ALK inhibitors.

+ ALK by Immunohistochemistry

- + ___ Negative[#]
- + ___ Positive^{##}
- + ___ Equivocal^{###} (explain): _____

[#] Absence of ALK protein expression in cancer cells suggests that this tumor is unlikely to harbor ALK rearrangement and to respond to treatment with a targeted inhibitor, such as crizotinib and ceritinib.

^{##} ALK protein expression in cancer cells (based on platform criteria) predicts the presence of ALK rearrangement and response to therapy with a targeted inhibitor, such as crizotinib and ceritinib.

^{###} Tumors with faint cytoplasmic labeling should be designated as equivocal. This result can rarely occur both with and without mutation.

+ ROS1 Rearrangement by Molecular Methods (Note C)

- + ___ No rearrangement detected[#]
- + ___ Rearrangement identified^{##}
- + ___ Cannot be determined (explain): _____

+ Polysomy:

- + Present^{###}
- + Absent

[#] Absence of ROS1 rearrangement in cancer cells suggests that this tumor is unlikely to respond to treatment with a targeted ROS1 inhibitor, such as crizotinib.

^{##} ROS1 rearrangement predicts a high response rate to therapy with a targeted inhibitor, such as crizotinib.

^{###} Polysomy involving the ROS1 locus confirms that fluorescence in situ hybridization (FISH) scoring was carried out in tumor cells but does not predict response to therapy with targeted inhibitors.

+ ROS1 by Immunohistochemistry

- + Negative[#]
- + Positive^{##}
- + Equivocal^{###} (explain): _____

[#] Absence of ROS1 protein expression in cancer cells suggests that this tumor is unlikely to harbor ROS1 rearrangement and to respond to treatment with a targeted inhibitor, such as crizotinib.

^{##} ROS1 protein expression in cancer cells is highly sensitive for a rearrangement involving ROS1 but is not entirely specific. Therefore, confirmatory molecular methods should be used when ROS1 protein expression is detected.

^{###} Tumors with faint cytoplasmic labeling should be designated as equivocal. This result can rarely occur both with and without mutation.

+ RET Rearrangement by Molecular Methods (Note C)

- + No rearrangement detected[#]
- + Rearrangement identified^{##}
- + Cannot be determined (explain): _____

+ Polysomy:

- + Present^{###}
- + Absent

[#] Absence of RET rearrangement in cancer cells suggests that this tumor is unlikely to respond to treatment with a targeted RET inhibitor.

^{##} RET rearrangement is associated with response to targeted RET inhibitor therapies, such as cabozantinib and vandetanib.

^{###} Polysomy involving the RET locus confirms that fluorescence in situ hybridization (FISH) scoring was carried out in tumor cells but does not predict response to therapy with targeted inhibitors.

+ KRAS Mutational Analysis

- + No mutation detected
- + Mutation(s) identified[#] (select all that apply)
 - + Codon 12
 - + Gly12Cys (GGT>TGT)
 - + Gly12Asp (GGT>GAT)
 - + Gly12Val (GGT>GTT)
 - + Gly12Ser (GGT>AGT)
 - + Gly12Ala (GGT>GCT)
 - + Gly12Arg (GGT>CGT)
 - + Specific codon 12 mutation not stated
 - + Other codon 12 mutation (specify): _____
 - + Codon 13
 - + Gly13Asp (GGC>GAC)
 - + Gly13Arg (GGC>CGC)
 - + Gly13Cys (GGC>TGC)
 - + Gly13Ala (GGC>GCC)
 - + Gly13Val (GGC>GTC)
 - + Specific codon 13 mutation not stated

- + ___ Other codon 13 mutation (specify): _____
- + Codon 61
- + ___ Gln61Leu (CAA>CTA)
- + ___ Specific codon 61 mutation not stated
- + ___ Other codon 61 mutation (specify): _____
- + Other
- + ___ Other codon (specify): _____
- + ___ Cannot be determined (explain): _____

No specific tyrosine kinase inhibitors have been approved for lung adenocarcinomas with KRAS mutations. In addition, KRAS mutations are typically mutually exclusive of EGFR, ALK, and other driver molecular alterations.

+ BRAF Mutational Analysis (Note A)

- + ___ No mutations detected
- + ___ BRAF V600E (c.1799T>A) mutation
- + ___ Other BRAF V600 mutation (specify): _____
- + ___ Cannot be determined (explain): _____

+ ERBB2 Mutational Analysis (Note A)

- + ___ No mutations detected
- + ___ ERBB2 774_775insAYVM insertion mutation
- + ___ ERBB2 776_776G>VC insertion mutation
- + ___ Other ERBB2 exon 20 mutation (specify): _____
- + ___ Other ERBB2 mutation (non-exon 20) (specify): _____
- + ___ Cannot be determined (explain): _____

+ MET Mutational Analysis (Note B)

- + ___ No mutation detected[#]
- + ___ MET D963_splice mutation detected[#]
- + ___ MET D1010N mutation detected[#]
- + ___ MET D1010_splice mutation detected[#]
- + ___ Other MET intron 13 mutation (specify)[#]: _____
- + ___ Other MET intron 14 mutation (specify)[#]: _____
- + ___ Other MET exon 14 mutation (specify)[#]: _____
- + ___ MET exon 14 deletion detected^{##}
- + ___ Cannot be determined (explain): _____

MET mutation detection is typically based on DNA-based sequencing methods and may include coding (exon) or non-coding (intron) variants, most commonly located at or near the intron-exon junctions around exon 14.

RNA-based reverse-transcriptase polymerase chain reaction or RNA sequencing may detect deletion of MET exon 14 without necessarily indicating the mechanism (DNA-based mutation) leading to the deletion.

+ MET Copy Number Analysis

- + ___ No amplification detected
- + ___ Amplification identified (specify copy number and/or ratio to centromere 7): _____ (copies); _____ (ratio)
- + ___ Cannot be determined (explain): _____

+ Other Markers Tested (Note D)

- + Specify marker: _____
- + Specify results: _____

+ METHODS**+ Sequencing Type**

- + ___ Targeted panel sequencing (specify): _____
- + ___ Whole exome sequencing (specify): _____
- + ___ Whole genome sequencing (specify): _____

+ EGFR Exons Assessed (select all that apply)

- + ___ 18
- + ___ 19
- + ___ 20
- + ___ 21
- + ___ Other (specify): _____

+ EGFR Mutational Analysis Testing Method(s) (select all that apply)

- + ___ Direct (Sanger) sequencing
- + ___ Pyrosequencing
- + ___ High-resolution melting analysis
- + ___ Polymerase chain reaction (PCR), allele-specific hybridization
- + ___ Real-time PCR
- + ___ Next-generation (high-throughput) sequencing
- + ___ Mutation-specific immunohistochemistry
 - + ___ 43B2 (L858R) clone
 - + ___ 6B6 (E746_A750del) clone
 - + ___ Other (specify): _____
- + ___ Other (specify): _____

Note: Please specify in Comments section if different testing methods were used for different exons.

+ ALK Rearrangement Testing Method(s) (select all that apply)

- + ___ In situ hybridization (fluorescence [FISH] or chromogenic [CISH])
- + ___ Reverse transcriptase polymerase chain reaction (RT-PCR)
 - + Fusions identified (specify): _____
- + ___ Immunohistochemistry
 - + ___ 5A4 clone
 - + ___ D5F3 clone
 - + ___ Ventana ALK (D5F3) immunohistochemistry (IHC) assay
 - + ___ Other (specify): _____
- + ___ Next-generation (high-throughput) sequencing
- + ___ Anchored multiplex PCR
- + ___ Other (specify): _____

+ ROS1 Rearrangement Testing Method(s) (select all that apply)

- + ___ In situ hybridization (fluorescence [FISH] or chromogenic [CISH])
- + ___ Reverse transcriptase polymerase chain reaction (RT-PCR)
 - + Fusions identified (specify): _____
- + ___ Immunohistochemistry
 - + ___ D4D6 clone
- + ___ Next-generation (high-throughput) sequencing
- + ___ Anchored multiplex PCR
- + ___ Other (specify): _____

+ RET Rearrangement Testing Method(s) (select all that apply)

- + ___ In situ hybridization (fluorescence [FISH] or chromogenic [CISH])
- + ___ Reverse transcriptase polymerase chain reaction (RT-PCR)
 - + Fusions identified (specify): _____

- + ___ Next-generation (high-throughput) sequencing
- + ___ Anchored multiplex PCR
- + ___ Other (specify): _____

+ KRAS Codons Assessed (select all that apply)

- + ___ 12
- + ___ 13
- + ___ 61
- + ___ Other (specify): _____

+ KRAS Mutational Analysis Testing Method(s) (select all that apply)

- + ___ Direct (Sanger) sequencing
- + ___ Pyrosequencing
- + ___ High-resolution melting analysis
- + ___ Polymerase chain reaction (PCR), allele-specific hybridization
- + ___ Real-time PCR
- + ___ Next-generation (high-throughput) sequencing
- + ___ Other (specify): _____

Note: Please specify in Comments section if different testing methods were used for different codons.

+ BRAF Exons Assessed (select all that apply)

- + ___ 11
- + ___ 15

+ BRAF Mutational Analysis Testing Method(s) (select all that apply)

- + ___ Direct (Sanger) sequencing
- + ___ Pyrosequencing
- + ___ High-resolution melting analysis
- + ___ Polymerase chain reaction (PCR), allele-specific hybridization
- + ___ Real-time PCR
- + ___ Next-generation (high-throughput) sequencing
- + ___ Other (specify): _____

+ ERBB2 Exons Assessed (select all that apply)

- + ___ 8
- + ___ 16
- + ___ 20

+ ERBB2 Mutational Analysis Testing Method(s) (select all that apply)

- + ___ Direct (Sanger) sequencing
- + ___ Pyrosequencing
- + ___ High-resolution melting analysis
- + ___ Polymerase chain reaction (PCR), allele-specific hybridization
- + ___ Real-time PCR
- + ___ Next-generation (high-throughput) sequencing
- + ___ Other (specify): _____

+ MET Region(s) Assessed (select all that apply)

- + ___ Intron 13
- + ___ Intron 14
- + ___ Exon 14
- + ___ Other (specify): _____

+ MET Mutational Analysis Testing Method(s) (select all that apply)

- + ___ Direct (Sanger) sequencing
- + ___ Next-generation (high-throughput) sequencing
- + ___ Reverse transcriptase-PCR (RT-PCR)
- + ___ Other (specify): _____

+ MET Copy Number Testing Method(s) (select all that apply)

- + ___ In situ hybridization (fluorescence [FISH] or chromogenic [CISH])
- + ___ Next-generation (high-throughput) sequencing
- + ___ Array comparative genome hybridization (aCGH)
- + ___ Other (specify): _____

+ Testing Method(s) for Other Markers (Note E)

- + Specify: _____

+ COMMENT(S)

Note: Fixative type, time to fixation (cold ischemia time), and time of fixation should be reported if applicable in this template or in the original pathology report (Note F).

Gene names should follow recommendations of The Human Genome Organisation (HUGO) Nomenclature Committee (www.genenames.org; accessed May 25, 2016).

All reported gene sequence variations should be identified following the recommendations of the Human Genome Variation Society (<http://varnomen.hgvs.org>; accessed May 25, 2016).

Explanatory Notes

Background

Over half of lung adenocarcinomas contain one of a number of identifiable genetic alterations; some of these can be targeted by a specific therapeutic inhibitor that is either approved by the Food and Drug Administration (FDA) or in clinical trials. The National Comprehensive Cancer Network (NCCN) recommends testing for *EGFR* mutations and *ALK* rearrangements in all patients with recurrent or metastatic lung adenocarcinomas in order to guide therapy.¹ The College of American Pathologists (CAP), International Association for the Study of Lung Cancer (IASLC), and Association for Molecular Pathology (AMP) have prepared a joint guideline that provides a detailed description of the patient and specimen requirements and acceptable testing designs and strategies for the detection of these alterations²; the reader is referred to this guideline for details that are beyond the scope of this document.

Briefly, approximately 20% of lung adenocarcinomas contain an *EGFR* activating mutation that predicts response to therapy with *EGFR* tyrosine kinase inhibitors such as erlotinib.³⁻⁷ Up to 90% of *EGFR* mutations occur in two hot spots within the kinase domain, as small deletions in the LREA motif of exon 19 or as a leucine to arginine substitution at amino acid 858 (exon 21).^{8,9} Molecular testing (sequencing or PCR-based approaches) is recommended for *EGFR* mutation detection whenever possible.² Immunohistochemistry (IHC) with *EGFR* mutation-specific antibodies has high specificity, but suboptimal sensitivity: 76% for *EGFR* L858R and 60% or less for *EGFR* exon 19 deletions.¹⁰ In addition, these antibodies do not detect less common types of sensitizing *EGFR* mutations. In particular, *EGFR* exon 19 deletion antibody recognizes primarily a 15-base-pair deletion (E746_A750del), which comprises ~50% of exon 19 deletions, but inconsistently detects other types of exon 19 deletions.¹¹ Because of suboptimal sensitivity, IHC for *EGFR* mutations may only have a role in situations in which molecular testing is not available or a sample is insufficient or technically unsuitable for testing, such as due to decalcification. If performed, a note should be included that a negative result does not exclude the possibility of *EGFR* mutations, and testing with molecular methods should be performed if a suitable sample becomes available.

The vast majority of patients with *EGFR*-mutated lung adenocarcinoma treated with *EGFR* tyrosine kinase inhibitors will relapse as a result of resistance to these drugs. The most common resistance mechanism is acquisition of the *EGFR* exon 20 T790M mutation.¹² However, new covalent inhibitors have shown efficacy against relapsed lung adenocarcinomas with *EGFR* T790M mutations in large phase 2 clinical trials^{13,14} but appear less effective in tumors with alternative resistance mechanisms. Therefore, biopsy at the time of relapse may be required to determine the best course of therapy.

Approximately 5% of lung adenocarcinomas have a chromosomal rearrangement involving the *ALK* gene, most commonly in the form of an intrachromosomal inversion leading to the EML4-*ALK* fusion product associated with *ALK* protein overexpression.¹⁵ Patients with this tumor type are responsive to therapy with *ALK* tyrosine kinase inhibitors, such as crizotinib.¹⁶ Fluorescence in situ hybridization (FISH) using break-apart probes is currently considered the “gold standard” for detection of *ALK* rearrangement, which may manifest as separation of the 5' and 3' FISH probes or as deletion of 5' probe. Although both types of alterations are associated with response to *ALK*-targeted therapies, some studies suggest that 5' probe deletion can rarely represent a false positive FISH result.^{17,18} Detection of *ALK* protein overexpression by IHC using the 5A4 or D5F3 clones is highly sensitive and specific for an *ALK* gene rearrangement in lung adenocarcinoma,¹⁹ and the FDA has approved the use of the Ventana *ALK* (D5F3) CDx Assay as a companion diagnostic for crizotinib.²⁰ According to the current guidelines, other carefully-validated, but non-FDA approved, *ALK* immunohistochemistry assays may also be used to screen for *ALK* rearrangement with confirmation by FISH before initiating *ALK*-targeted therapy.²

Patients receiving *ALK*-targeted inhibitors inevitably acquire resistance to these drugs, often in the form of *ALK* kinase domain mutations. The more potent *ALK* inhibitor ceritinib has shown efficacy in these relapsed patients and has been approved for those who developed resistance to, or could not tolerate, crizotinib. The mechanism of resistance does not clearly predict response to this next line therapy; therefore, the role for rebiopsy in patients with *ALK*-rearranged tumors is not clear.²¹

ROS1 rearrangement occurs in 1% to 2% of non-small cell lung carcinomas and predicts response to crizotinib therapy.^{15,22,23} *ROS1* fusion partners include *SLC34A2*, *CD74*, *TPM3*, *GOPC* (*FIG*), *SDC4*, *EZR*, *LRIG3*, *KDEL2*, and *CCDC6*. Several methods, including FISH, IHC, anchored multiplex or reverse-transcriptase PCR, and next-generation sequencing, may be considered for *ROS1* rearrangement detection^{21,23}; no "gold standard" method has been defined. Notably, IHC using the available D4D6 antibody appears to be a robust screening tool, but due to suboptimal specificity, positive results should be confirmed by another technique.^{24,25}

Currently, no targeted tyrosine kinase inhibitor therapies are specifically approved for *KRAS* mutations. However, *KRAS* testing is often performed in lung adenocarcinomas because (1) *KRAS* mutations are typically mutually exclusive with *EGFR* and *ALK* alterations, (2) *KRAS* mutations are the most common oncogenic alteration in lung adenocarcinoma (~20% to 30% of tumors), and (3) *KRAS* mutation testing is typically quicker, easier, and less costly than testing for *EGFR* and *ALK*.²⁶ Therefore, *KRAS* mutation analysis may be used in a molecular testing algorithm to eliminate the need for other more costly and time-intensive testing.

BRAF mutations are detected in about 5% of lung adenocarcinomas; V600E mutations comprise approximately half of these and are therefore found in 2% to 3% of tumors.²⁷ The role of *BRAF* as a targetable oncogene was recently established in phase II clinical trials combining the *BRAF* inhibitor dabrafenib with the MEK inhibitor trametinib, where this drug combination was associated with a 63% overall response rate in patients with *BRAF* V600E-mutated non-small cell lung carcinoma.²⁸

The utility of *BRAF* V600E mutation-specific IHC is not well established in lung adenocarcinoma. The variable sensitivity and specificity of this immunohistochemistry assay relative to mutation analysis reported in other tumor types suggests it may not be appropriate as a clinical tool for *BRAF* V600E detection in lung tumors.²⁹

MET has been recognized as a putative biomarker in lung adenocarcinoma for many years, with amplification implicated as a mechanism of resistance to *EGFR* inhibitors.³⁰ In rare cases, de novo *MET* amplification has been associated with profound responses to therapy with crizotinib. Recently, splicing variants and insertion-deletion mutations leading to *MET* exon 14 deletion have been found in about 3% of lung adenocarcinomas; these events lead to *MET* activation and are associated with response to crizotinib and cabozantinib.^{31,32} *MET* amplification can be seen in tumors with *MET* exon 14 deletion. *MET* protein overexpression appears to correlate with *MET* amplification, although *MET* immunohistochemistry is controversial as a biomarker for *MET*-targeted therapies.³³

Oncogenic *RET* gene rearrangements have been reported in 1% to 2% of lung adenocarcinoma and are more common in never-smokers.^{34,35} Due to the relative rarity of *RET*-rearranged tumors, phase 3 clinical trials with targeted agents for *RET* have not been conducted yet, but preliminary data from phase 2 trials of a multi-targeted inhibitor cabozantinib in *RET*-rearranged lung tumors are promising. *RET* rearrangements are detectable by FISH; however, the most commonly described rearrangement, *KIF5B-RET*, is a product of small intrachromosomal inversion leading to only a subtle split in the FISH probe signals. Thus, the rearrangement could be difficult to detect in practice.³⁶ Alternative detection methods such as anchored multiplex PCR or next generation sequencing may be useful. The role of *RET* IHC in predicting *RET* rearrangements has not been well evaluated.

Lung adenocarcinomas contain a number of other less common alterations that may lead to treatment with targeted inhibitors but have not yet been studied in large controlled trials nor emerged as standard of care. *ERBB2* exon 20 insertion mutations are established as oncogenic alterations in lung adenocarcinoma; patients whose tumors harbor these mutations have shown response to HER-tyrosine kinase inhibitors in phase I studies.³⁷ Alterations in *MAP2K1* (*MEK1*) are rare (<1% of lung adenocarcinoma) but are highly correlated with a smoking history and may predict sensitivity to MEK inhibitors.³⁸ Alterations leading to PI3K pathway activation, including *PIK3CA* or *AKT1* activating mutations or *PTEN* loss of function may serve as biomarkers for enrollment in PI3K- or AKT-inhibitor trials.³⁹ Recently identified fusion events involving *NRG1* and *NTRK1* (*TRKA*) appear to be rare but distinctive oncogenic events in a subset of lung adenocarcinomas.^{40,41}

Monoclonal antibodies targeting the programmed death-1 receptor (PD-1) (nivolumab [Opdivo] and pembrolizumab [Keytruda]) and its ligand, PD-L1 (atezolizumab [Tecentriq]), are FDA-approved for use in non-small cell lung carcinoma.⁴²⁻⁴⁷ All three drugs have been approved for use in the second line (after progression on conventional first line therapies) for both lung adenocarcinoma and squamous cell carcinoma, and

pembrolizumab has also been approved for use in first line therapy for these indications. Within the clinical trials, PD-L1 expression levels by immunohistochemistry tended to correlate with improved responses to both PD-1 and PD-L1 inhibitors, however the detection antibodies used and scoring cutoffs for the tumor cells and immune cells were highly variable for each drug. Only pembrolizumab has been approved together with a companion diagnostic immunohistochemistry assay (PD-L1 IHC 22C3 pharmDx test); patient tumors are required to show PD-L1 expression in at least 50% of tumor cells in the first line setting and at least 1% of tumor cells in the second line. In contrast, nivolumab and atezolizumab were approved with "complementary" diagnostics PD-L1 IHC 28-8 PharmDx and VENTANA PD-L1 (SP142) assays, respectively.^{48,49,50} Additional immunotherapeutic and combination therapies are expected to receive FDA approval for use in lung cancer in the future, possibly with distinct paired diagnostics. At this point in time, only pembrolizumab therapy requires knowledge of tumor PD-L1 status. National Comprehensive Cancer Network guidelines currently recommend standard PD-L1 IHC testing in all advanced (stage IIIB and IV) lung squamous cell carcinomas and adenocarcinomas for selection of front line pembrolizumab therapy.⁵¹ At the same time, knowledge of EGFR mutation and ALK rearrangement status is also required, because alterations in these genes predict inferior response to immunotherapies.

A. Suboptimal Specimen Definition

Suboptimal specimens may be defined as those with:

- Improper fixation (see fixation guidelines below).
- Low tumor content, as defined by the molecular diagnostics laboratory. The cutoff for acceptable tumor content depends on the method used by the laboratory. Samples with tumor content below the recommended cutoff may be falsely negative and should be reported as indeterminate if no mutations are detected.

B. Other Mutations

Other mutations include uncommon variants including exon 19 insertions or other missense variants in the kinase domain of *EGFR* (exons 18-21) that are not listed above. Silent mutations that are known, common, single nucleotide polymorphisms in the general population do not need to be included here.

C. Polysomy

Polysomy (multiple copies) at the *ALK*, *RET*, and *ROS1* loci may be seen in lung adenocarcinoma and when present confirms that FISH has been performed in a tumor cell population. Current evidence suggests that it does not, however, predict response/resistance to targeted therapies.

D. Other Markers Tested

"Other Markers Tested" should be used to report results from molecular assays not included here that may be relevant to lung cancer therapy. These assays may include, but are not limited to, detection of mutations in genes such as *BRAF*, *ERBB2*, and *PIK3CA*; rearrangements involving *ROS1* and *RET* genes; and *MET* copy number changes (see "Background" section above).

E. Testing Method for Other Markers

This section should be completed if the "Other Markers Tested" section is filled out and should describe the type of analyses performed for alterations in genes other than *EGFR*, *ALK*, and *KRAS*, as detailed in note D.

F. Fixation

Improper fixation can lead to failure to obtain results with PCR/sequencing-based assays or FISH. Common problems include the following:

- Procedures or fixation involving acid (eg, decalcification, Bouin's) may degrade DNA.
- Fixation with heavy metals (eg, Zenker's, B5, B+, zinc formalin) inhibit the enzymes used in PCR.
- Underfixation or overfixation. Fixation for at least 8 hours and less than 72 hours in buffered formalin is recommended; prolonged fixation, particularly in unbuffered formalin, degrades DNA.

References

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