



Sample Information

Patient Name: 吳明壽**Gender:** Male**ID No.:** Q101656528**History No.:** 37716226**Age:** 69**Ordering Doctor:** DOC3109L 邱昭華**Ordering REQ.:** D53DPJ6**Signing in Date:** 2020/05/13**Path No.:** S109-99477**MP No.:** F2021**Assay:** Oncomine Focus Assay**Sample Type:** FFPE**Block No.:** S108-29773B**Percentage of tumor cells:** 50%**Note:**

Sample Cancer Type: Non-Small Cell Lung Cancer

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Relevant Non-Small Cell Lung Cancer Findings

Gene	Finding	Gene	Finding
ALK	Not detected	NTRK1	Not detected
BRAF	Not detected	NTRK2	Not detected
EGFR	Not detected	NTRK3	Not detected
ERBB2	Not detected	RET	Not detected
KRAS	Not detected	ROS1	Not detected
MET	MET exon 14 skipping		



Relevant Biomarkers

■ Indicated ■ Contraindicated

Genomic Alteration	Relevant Therapies (In this cancer type)	Relevant Therapies (In other cancer type)	Clinical Trials
MET exon 14 skipping MET proto-oncogene, receptor tyrosine kinase Tier: IA	■ crizotinib	None	19

Public data sources included in relevant therapies: FDA1, NCCN, EMA2, ESMO

Tier Reference: Li et al. Standards and Guidelines for the Interpretation and Reporting of Sequence Variants in Cancer: A Joint Consensus Recommendation of the Association for Molecular Pathology, American Society of Clinical Oncology, and College of American Pathologists. J Mol Diagn. 2017 Jan;19(1):4-23.

Variants (Exclude variant in Taiwan BioBank with >1% allele frequency)

DNA Sequence Variants

Gene	Amino Acid Change	Coding	Variant ID	Locus	Allele Frequency	Transcript	Variant Effect	Coverage
FGFR4	p.(=)	c.483A>G	.	chr5:176517985	10.11%	NM_213647.2	synonymous	1999
MET	p.(D1028Y)	c.3082G>T	.	chr7:116412043	21.00%	NM_001127500.2	missense	2000

Gene Fusions (RNA)

Genes	Variant ID	Locus
MET-MET	MET-MET.M13M15	chr7:116411708 - chr7:116414935

Biomarker Descriptions

MET (MET proto-oncogene, receptor tyrosine kinase)

Background: The MET proto-oncogene encodes a receptor tyrosine kinase for the hepatocyte growth factor (HGF) protein, which is expressed by mesenchymal cells. Ubiquitin-dependent proteolysis regulates the steady state level of the MET protein via recognition of the tyrosine phosphorylation site Y1003 in the MET Cbl-binding domain within the juxtamembrane region^{1,2,3}. Growth factor signaling leads to MET dimerization and subsequent initiation of downstream effectors including those involved in the RAS/RAF/MEK/ERK and PI3K/AKT signaling pathways, which regulate cell migration, proliferation, and survival^{4,5}.

Alterations and prevalence: Recurrent somatic MET alterations include activating mutations, gene amplification, and translocations generating MET gene fusions. Recurrent somatic mutations fall into two classes, mutations in the MET kinase domain, which are uncommon, and splice-site mutations affecting exon 14. Recurrent kinase domain mutations are observed in papillary renal cell carcinoma (PRCC) (1-2%) and include M1250T, H1094Y, and V1070E. Mutation of the Y1003 phosphorylation site is reported in lung cancer but is uncommon (<1%)^{6,7}. In contrast, splice-site mutations flanking exon 14 are observed in 4% of non-small cell lung cancer (NSCLC). These mutations include canonical splice site mutations affecting exon 14 and deletions that extend into the splicing motifs within intron 13^{8,9}. Such mutations disrupt splicing leading to the formation of an alternative transcript that joins exon 13 directly to exon 15 and skips exon 14 entirely. The MET exon 14 skipping transcript lacks the juxtamembrane domain that contains the recognition motif for ubiquitin-dependent proteolysis and thus leads to a marked increase in steady-state level of the MET protein¹⁰. MET exon 14 skipping mutations act as oncogenic drivers in lung cancer mutually exclusive to activating mutations in EGFR and KRAS and other oncogenic fusions such as ALK and ROS1^{8,11,12}. MET is amplified in 2-5% of ovarian cancer, esophageal adenocarcinoma, stomach adenocarcinoma, glioblastoma, and lung adenocarcinoma^{6,7,13}. Recurrent MET fusions, although infrequent, are observed in adult and pediatric glioblastoma, papillary renal cell carcinoma, lung cancer, liver cancer, thyroid cancer, and melanoma^{14,15,16}. MET alterations are believed to be enriched in late-stage cancers where they drive tumor progression and metastasis^{17,18,19}.



Biomarker Descriptions (continued)

Potential relevance: The FDA has granted designations for two investigational MET inhibitors— capmatinib²⁰ has been granted FDA orphan drug and breakthrough therapy designations for MET exon 14 skipping positive metastatic NSCLC following platinum-based chemotherapy, and tepotinib²¹ has been granted FDA breakthrough designation (2019) for advanced MET exon 14 skipping NSCLC. MET exon 14 skipping mutations confer sensitivity to approved kinase inhibitors including crizotinib (2011), which is recommended for MET amplifications and exon 14 skipping mutations^{8,11,12,22}. Conversely, amplification of MET has been observed to mediate resistance to EGFR tyrosine kinase inhibitors (TKIs)^{23,24,25,26,27}. In a phase II trial testing the MET inhibitor savolitinib, patients with advanced PRCC exhibited median progression free survival (PFS) of 6.2 and 1.4 months for MET-driven and MET-independent PRCC, respectively²⁸.

Relevant Therapy Summary

● In this cancer type ○ In other cancer type ● In this cancer type and other cancer types ⛔ Contraindicated ⚠ Both for use and contraindicated ✕ No evidence

MET exon 14 skipping

Relevant Therapy	FDA	NCCN	EMA	ESMO	Clinical Trials*
crizotinib	✕	●	✕	●	● (II)
cabozantinib	✕	✕	✕	✕	● (II)
capmatinib	✕	✕	✕	✕	● (II)
capmatinib + nivolumab	✕	✕	✕	✕	● (II)
savolitinib	✕	✕	✕	✕	● (II)
tepotinib	✕	✕	✕	✕	● (II)
bozitinib	✕	✕	✕	✕	● (I/II)
REGN-5093	✕	✕	✕	✕	● (I/II)
glumetinib	✕	✕	✕	✕	● (I)
JNJ-61186372	✕	✕	✕	✕	● (I)
metatinib	✕	✕	✕	✕	● (I)
TPX-0022	✕	✕	✕	✕	● (I)

* Most advanced phase (IV, III, II/III, II, I/II, I) is shown and multiple clinical trials may be available.



Relevant Therapy Details

Current NCCN Information

- ☒ In this cancer type
 ☐ In other cancer type
 ☐ In this cancer type and other cancer types
 ☐ Contraindicated
 ☐ Not recommended
 ☐ Resistance

NCCN information is current as of 2019-11-01. For the most up-to-date information, search www.nccn.org.
For NCCN International Adaptations & Translations, search www.nccn.org/global/international_adaptations.aspx.

MET exon 14 skipping

● crizotinib

Cancer type: Non-Small Cell Lung Cancer

Variant class: MET exon 14 skipping

NCCN Recommendation category: 2A

Population segment (Line of therapy):

- Non-Small Cell Lung Cancer; Emerging targeted agents

Reference: NCCN Guidelines® - NCCN-Non-Small Cell Lung Cancer [Version 2.2020]



Current ESMO Information

☒ In this cancer type ☐ In other cancer type ☐ In this cancer type and other cancer types ☒ Contraindicated ☒ Not recommended ☒ Resistance

ESMO information is current as of 2019-11-01. For the most up-to-date information, search www.esmo.org.

MET exon 14 skipping

☒ crizotinib

Cancer type: Non-Small Cell Lung Cancer

Variant class: MET exon 14 skipping

ESMO Level of Evidence/Grade of Recommendation: III / C

Population segment (Line of therapy):

- Demonstrated potential clinical efficacy that needs to be confirmed (Not specified)

Reference: ESMO Clinical Practice Guidelines - ESMO-Metastatic Non-Small-Cell Lung Cancer [Ann Oncol (2018) 29 (suppl 4): iv192–iv237; <https://www.esmo.org/Guidelines/Lung-and-Chest-Tumours/Metastatic-Non-Small-Cell-Lung-Cancer>]

Signatures

Testing Personnel:

Laboratory Supervisor:

Pathologist:



References

1. Peschard et al. A conserved DpYR motif in the juxtamembrane domain of the Met receptor family forms an atypical c-Cbl/Cbl-b tyrosine kinase binding domain binding site required for suppression of oncogenic activation. *J. Biol. Chem.* 2004 Jul 9;279(28):29565-71. PMID: 15123609
2. Peschard et al. Mutation of the c-Cbl TKB domain binding site on the Met receptor tyrosine kinase converts it into a transforming protein. *Mol. Cell.* 2001 Nov;8(5):995-1004. PMID: 11741535
3. Abella et al. Met/Hepatocyte growth factor receptor ubiquitination suppresses transformation and is required for Hrs phosphorylation. *Mol. Cell. Biol.* 2005 Nov;25(21):9632-45. PMID: 16227611
4. Sierra et al. c-MET as a potential therapeutic target and biomarker in cancer. *Ther Adv Med Oncol.* 2011 Nov;3(1 Suppl):S21-35. PMID: 22128285
5. Mo et al. Targeting MET in cancer therapy. *Chronic Dis Transl Med.* 2017 Sep;3(3):148-153. PMID: 29063069
6. Cerami et al. The cBio cancer genomics portal: an open platform for exploring multidimensional cancer genomics data. *Cancer Discov.* 2012 May;2(5):401-4. PMID: 22588877
7. Brennan et al. The somatic genomic landscape of glioblastoma. *Cell.* 2013 Oct 10;155(2):462-77. PMID: 24120142
8. Frampton et al. Activation of MET via diverse exon 14 splicing alterations occurs in multiple tumor types and confers clinical sensitivity to MET inhibitors. *Cancer Discov.* 2015 Aug;5(8):850-9. PMID: 25971938
9. Schrock et al. Characterization of 298 Patients with Lung Cancer Harboring MET Exon 14 Skipping Alterations. *J Thorac Oncol.* 2016 Sep;11(9):1493-502. PMID: 27343443
10. Pilotto et al. MET exon 14 juxtamembrane splicing mutations: clinical and therapeutical perspectives for cancer therapy. *Ann Transl Med.* 2017 Jan;5(1):2. doi: 10.21037/atm.2016.12.33. PMID: 28164087
11. Reungwetwattana et al. The race to target MET exon 14 skipping alterations in non-small cell lung cancer: The Why, the How, the Who, the Unknown, and the Inevitable. *Lung Cancer.* 2017 Jan;103:27-37. PMID: 28024693
12. Saffroy et al. MET exon 14 mutations as targets in routine molecular analysis of primary sarcomatoid carcinoma of the lung. *Oncotarget.* 2017 Jun 27;8(26):42428-42437. PMID: 28418914
13. Cancer Genome Atlas Research Network. Comprehensive molecular characterization of gastric adenocarcinoma. *Nature.* 2014 Sep 11;513(7517):202-9. doi: 10.1038/nature13480. Epub 2014 Jul 23. PMID: 25079317
14. Yeh et al. Activating MET kinase rearrangements in melanoma and Spitz tumours. *Nat Commun.* 2015 May 27;6:7174. doi: 10.1038/ncomms8174. PMID: 26013381
15. Bao et al. RNA-seq of 272 gliomas revealed a novel, recurrent PTPRZ1-MET fusion transcript in secondary glioblastomas. *Genome Res.* 2014 Nov;24(11):1765-73. PMID: 25135958
16. International Cancer Genome Consortium PedBrain Tumor Project. Recurrent MET fusion genes represent a drug target in pediatric glioblastoma. *Nat. Med.* 2016 Nov;22(11):1314-1320. PMID: 27748748
17. Zeng et al. c-Met gene amplification is associated with advanced stage colorectal cancer and liver metastases. *Cancer Lett.* 2008 Jul 8;265(2):258-69. PMID: 18395971
18. Tsugawa et al. Amplification of the c-met, c-erbB-2 and epidermal growth factor receptor gene in human gastric cancers: correlation to clinical features. *Oncology.* 1998 Sep-Oct;55(5):475-81. PMID: 9732228
19. Di et al. Overexpression and amplification of the met/HGF receptor gene during the progression of colorectal cancer. *Clin. Cancer Res.* 1995 Feb;1(2):147-54. PMID: 9815967
20. <https://www.novartis.com/news/media-releases/novartis-investigational-lung-cancer-therapy-capmatinib-inc280-granted-fda-breakthrough-therapy-designation-patients-met-mutated-advanced-non-small-cell-lung>
21. <https://www.emdgroup.com/en/news/tepotinib-breakthrough-therapy-designation-11-09-2019.html>
22. NCCN Guidelines® - NCCN-Non-Small Cell Lung Cancer [Version 2.2020]
23. Bean et al. MET amplification occurs with or without T790M mutations in EGFR mutant lung tumors with acquired resistance to gefitinib or erlotinib. *Proc. Natl. Acad. Sci. U.S.A.* 2007 Dec 26;104(52):20932-7. PMID: 18093943
24. Chen et al. Clinicopathologic and molecular features of epidermal growth factor receptor T790M mutation and c-MET amplification in tyrosine kinase inhibitor-resistant Chinese non-small cell lung cancer. *Pathol Oncol Res.* 2009 Dec;15(4):651-8. doi: 10.1007/s12253-009-9167-8. Epub 2009 Apr 21. PMID: 19381876



References (continued)

25. Suda et al. Reciprocal and complementary role of MET amplification and EGFR T790M mutation in acquired resistance to kinase inhibitors in lung cancer. Clin. Cancer Res. 2010 Nov 15;16(22):5489-98. PMID: 21062933
26. Zhang et al. Current mechanism of acquired resistance to epidermal growth factor receptor-tyrosine kinase inhibitors and updated therapy strategies in human nonsmall cell lung cancer. J Cancer Res Ther. 2016 Dec;12(Supplement):C131-C137. PMID: 28230005
27. Nguyen et al. Acquired resistance to epidermal growth factor receptor tyrosine kinase inhibitors in non-small-cell lung cancers dependent on the epidermal growth factor receptor pathway. Clin Lung Cancer. 2009 Jul;10(4):281-9. PMID: 19632948
28. Choueiri et al. Biomarker-Based Phase II Trial of Savolitinib in Patients With Advanced Papillary Renal Cell Cancer. J. Clin. Oncol. 2017 Sep 10;35(26):2993-3001. PMID: 28644771