

Patient: [REDACTED]
DOB: [REDACTED] Age: 35 Sex: F
Patient Identifiers: [REDACTED]
Visit Number (FIN): [REDACTED]

Client: [REDACTED]
Physician: [REDACTED]

ARUP Test Code: 3003680
Collection Date: 12/02/2022
Received in lab: 12/02/2022
Completion Date: 12/02/2022

Test Information

Test performed at NeoGenomics California, 31 Columbia, Aliso Viejo, CA 92656

Patient Report

Patient's report continues on following page(s).



Patient: [REDACTED]
ARUP Accession: 22-336-101958

Client [REDACTED]
ARUP Laboratories

500 Chipeta Way
 Salt Lake City, UT 84108
 Phone: (800) 242-2787
 Fax: (801) 584-5132



FX 4

Patient Name: [REDACTED]
 Patient DOB / Sex: [REDACTED] / F
 Specimen Type: **Unknown**
 Body Site: **Lung**
 Specimen ID: **22336101958**
 MRN: [REDACTED]
 Other Patient ID / Acct #: [REDACTED]
 Reason for Referral: **diagnosis**

Ordering Physician(s): **NPI Issue**
 Treating Physician(s): **NPI Issue**
 Accession / CaseNo: [REDACTED]
 Collection Date: **12/02/2022 09:37:00 AM**
 Received Date: **12/02/2022 02:26:50 PM EST**
 Report Date: **12/02/2022 02:29:32 PM EST**

Results:

Test	Result
MET Exon 14 Deletion Analysis	Positive
Mutation(s)	Detected

Clinical Significance:

Recurrent somatic splice site alterations at MET exon 14 (METex14) that result in exon skipping and MET activation have been characterized. METex14 mutations are detected most frequently in lung adenocarcinoma (3%), also frequently in other lung neoplasms (2.3%), glioma (0.4%), and tumors of unknown primary origin (0.4%). Tumors with METex14 alterations may respond to MET inhibitor therapy capmatinib or tepotinib.

Methodology:

The MET exon 14 deletion assay is a real-time polymerase chain reaction (RT-PCR) assay performed using RNA extracted from formalin-fixed, paraffin-embedded (FFPE) tissue. In two separate one-step RT-PCR reactions, a wild type (WT) MMX and a deletion MMX are amplified from the same RNA sample. Sample quantity and quality can substantially affect a PCR reaction.

References:

1. Frampton GM, Ali SM, Rosenzweig M, 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;5(8):850-9. PMID: 25971938.
2. Lee J, Ou SH, Lee JM, et al. Gastrointestinal malignancies harbor actionable MET exon 14 deletions. *Oncotarget.* 2015;6(29):28211-22. PMID: 26375439.
3. Drilon A, Cappuzzo F, Ou SI, Camidge DR. Targeting MET in Lung Cancer: Will Expectations Finally Be MET? *J Thorac Oncol.* 2017;12(1):15-26. PMID: 27794501.

Test/Panel	MoDX CPT	AMA CPT
MET Exon 14 Deletion Analysis	81479	81479

Electronic Signature

The Accession Component of this test was performed at NeoGenomics HQ, 9490 NeoGenomics Way, Fort Myers, FL / 33912 / 866-776-5907 / CLIA #10D2235950 / Medical Director(s): Anshil Nowrouzi, MD. The Technical Component Processing and Analysis of this test was completed at NeoGenomics California, 31 Columbia, Aliso Viejo, CA / 92656 / 800-776-5907 / CLIA #05D1021650 / Medical Director(s): Vladislav Chizhevsky, M.D. The Professional Component of this test was completed at NeoGenomics HQ, 9490 NeoGenomics Way, Fort Myers, FL / 33912 / 866-776-5907 / CLIA #10D2235950 / Medical Director(s): Anshil Nowrouzi, MD. The performance characteristics of this test have been determined by NeoGenomics Laboratories. This test has not been approved by the FDA. The FDA has determined such clearance or approval is not necessary. This laboratory is CLIA certified to perform high complexity clinical testing. Images that may be included within this report are representative of the patient but not all testing in its entirety and should not be used to render a result. The CPT codes provided with our test descriptions are based on MoDX and AMA guidelines and are for informational purposes only. Correct CPT coding is the sole responsibility of the billing party. Please direct any questions regarding coding to the payer being billed.



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