MAYO CLINIC LABORATORIES

TEST CHANGE

Notification Date: December 30, 2025
Effective Date: January 29, 2026

Neuro-Oncology Expanded Gene Panel with Rearrangement, Tumor

Test ID: NONCP

Explanation: On the effective date, testing algorithm will be updated and new reflex tests added. RNA methodology will also update.

Current Testing Algorithm
When this test is ordered, slide review will always be performed at an additional charge.

New Testing Algorithm
When this test is ordered, slide review will always be performed at an additional charge. Standalone orderable tests will only be used if the specimen received is insufficient for both portions of testing. Appropriate test code will be added per the direction of testing prioritization. This test includes DNA mutation and RNA fusion analyses. A reflex test is added only when there is insufficient specimen for both test components. Indicate the preferred prioritization of testing on paperwork. If the specimen is insufficient for all portions of testing, the lab will use this prioritization to select the appropriate reflex test ID, reducing communication delays. If additional tests are ordered on same specimen, include them in the prioritization preferences.

Current Reflex Tests
None

New Reflex Tests			
Test ID	Reporting Name	Available Separately	Always Performed
NONCM	Neuro-Onc Panel, Mutations Only	Yes	No
MCRSP	MayoComplete Targeted RNAseq Panel	Yes	No

Current Genetics Information	New Genetics Information
This test uses next-generation sequencing to evaluate for microsatellite instability (MSI) status, somatic mutations, and rearrangements (fusions and abnormal transcript variants) involving 160 genes associated with tumors of the central nervous system. This panel includes a DNA subpanel for the detection of sequence alterations in 89 genes and an RNA subpanel for the detection of rearrangements in 81 genes, including 104 known gene fusions and 29 known abnormal transcript variants. See Targeted DNA Gene Regions Interrogated by Neuro-Oncology Panel and RNA Targeted Gene Fusions and Abnormal Transcript Variants for details regarding the targeted gene regions identified by this test. Of note, this test is performed to evaluate for somatic (ie, tumor-specific) mutations within the genes listed. Although germline (ie, inherited) alterations may be detected, this test cannot distinguish between germline alterations and somatic mutations with absolute certainty. Follow-up germline testing using non-neoplastic (normal) tissue can be performed for confirmation of suspected clinically relevant germline alterations. Germline testing should be performed along with genetic counseling.	This test uses next-generation sequencing to evaluate for microsatellite instability (MSI) status, somatic mutations within 89 genes associated with tumors of the central nervous system, gene fusions within 1445 genes, known abnormal transcript variants in the *MET* and *EGFR* genes, and *BCOR* exon 15 internal tandem duplications. See Targeted DNA Gene Regions Interrogated by Neuro-Oncology Panel and Targeted Fusion Genes for Neuro-Onc Expanded Panel for details regarding the targeted gene regions identified by this test. Of note, this test is performed to evaluate for somatic (ie, tumor-specific) mutations within the genes listed. Although germline (ie, inherited) alterations may be detected, this test cannot distinguish between germline alterations and somatic mutations with absolute certainty. Follow-up germline testing using non-neoplastic (normal) tissue can be performed for confirmation of suspected clinically relevant germline alterations. Germline testing should be performed along with genetic counseling.

Current Method	New Method
Sequence Capture and Targeted Polymerase Chain Reaction (PCR)-Based Next-Generation Sequencing (NGS)	Sequence Capture and Targeted Next-Generation Sequencing (NGS)

Current Method Description	New Method Description
Hybridization and capture-based next-generation sequencing (NGS) are performed to determine microsatellite instability (MSI) status and evaluate the presence of a mutation in targeted regions of 89 genes. Polymerase chain reaction amplification-based NGS is also performed to test for the presence of rearrangements in 81 genes, including 104 known gene fusions and 29 known abnormal gene transcript variants. See Targeted DNA Gene Regions Interrogated by Neuro-Oncology Panel and RNA Targeted Gene Fusions and Abnormal Transcript Variants for details regarding the targeted gene regions identified by this test.(Unpublished Mayo method) A pathology review and macro dissection to enrich for tumor cells is performed prior to slide scraping.	Next-generation sequencing (NGS) is performed to determine microsatellite instability status and evaluate the presence of a somatic mutation in targeted regions of 89 genes. RNA-based NGS is performed to test for the presence of rearrangements involving 1445 genes, selected splice variants in *MET* and *EGFR* genes and *BCOR* exon 15 internal tandem duplications. See Targeted DNA Gene Regions Interrogated by Neuro-Oncology Panel and Targeted Fusion Genes for Neuro-Onc Expanded Panel for details regarding the targeted gene regions identified by this test.(Unpublished Mayo method) A pathology review and macro dissection to enrich for tumor cells is performed prior to slide scraping.

Questions

Contact Melissa Tricker-Klar, Laboratory Resource Coordinator at 800-533-1710.