

Neuro-Oncology Genome-Wide Methylation Array Analysis, Tumor

Test ID: MTNON

Useful for:

Assisting in tumor profiling by identifying methylation family and class that may support a diagnosis or help determine prognosis for patients with central nervous system tumors.

This test is **not intended** for use in hematologic malignancies.

Genetics Information:

This test uses a methylation array to evaluate genome-wide methylation of central nervous system (CNS) tumors. Results are analyzed using the NCI/Bethesda CNS tumor classifier v2.0 developed by the National Institutes of Health, an in-house nearest-neighbors assisted unsupervised analysis (NN Method), and the MGMT promoter methylation mgmtstp27 R package.

Methods:

Methylation Array

Reference Values:

An interpretive report will be provided.

Necessary Information:

Pathology report (final or preliminary), at minimum containing the following information **must accompany specimen for testing to be performed:**

1. Patient name
2. Block number-must be on all blocks, slides, and paperwork (can be handwritten on the paperwork)
3. Tissue collection date
4. Source of the tissue
5. Pathologic diagnosis (final or preliminary)

Specimen Requirements:

This assay requires at least 60% tumor nuclei.

- Preferred amount of tumor area with sufficient percent tumor nuclei: tissue 360 mm(2)
 - Minimum amount of tumor area: tissue 144 mm(2)
 - These amounts are cumulative over up to 20 unstained slides and must have adequate percent tumor nuclei.
 - Tissue fixation: 10% neutral buffered formalin, not decalcified
 - For specimen preparation guidance, see [Tissue Requirements for Solid Tumor Next-Generation Sequencing](#).
- In this document, the sizes are given as 6 mm x 6 mm x 10 slides as preferred: approximate/equivalent to 360 mm(2) and the minimum as 4 mm x 4 mm x 10 slides: approximate/equivalent to 144 mm(2).
- If ordered in conjunction with other tests, please refer to specimen requirements for the specific tests.

Preferred:

Specimen Type: Tissue block

Collection Instructions: Submit a formalin-fixed, paraffin-embedded tissue block with an acceptable amount of tumor tissue

Acceptable:

Specimen Type: Tissue slide

Slides: 1 Hematoxylin and eosin-stained and 20 unstained

Collection Instructions:

Submit the following slides:

1 Slide stained with hematoxylin and eosin

AND

20 Unstained, nonbaked slides with 5-micron thick sections of the tumor tissue

Note: The total amount of required tumor nuclei can be obtained by scraping up to 20 slides from the same block.

Additional Information: Unused unstained slides will not be returned.

Specimen Minimum Volume:

See Specimen Required

Specimen Stability Information:

Specimen Type	Temperature
Varies	Ambient (preferred)
	Refrigerated

Cautions:

Abnormal methylation patterns sufficiently distinct from the reference dataset patterns can impact the ability of the classifier to provide high confidence results.

Discordant methylation profiling results may be obtained using different classifiers and different classifier versions.

The nearest-neighbors assisted unsupervised analysis (NN) method is complementary to the classifier and the results are not to be used as a stand-alone method.

Discordant *MGMT* methylation results may occur due to different testing methodologies and/or evaluation of different CpG sites.

CPT Code:

81524

Day(s) Performed: Varies

Report Available: 10 to 16 days

Questions

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