

Patient ID SA00179913	Patient Name IMPLEMENTATION, TEST T	Birth Date 2001-05-01	Sex F	Age 24
Order Number SA00179913	Client Order Number SA00179913	Ordering Physician CLIENT,CLIENT	Report Notes	
Account Information C7028846 DLMP Rochester		Collected 17 Apr 2026 00:00		

Neuro-Onc Methylation Array, Tumor

Result

MCR

Provided diagnosis: glioma

NCI/BETHESDA CLASSIFIER v.2.0

Summary: Family MATCHED/Class MATCHED

Family: Glioblastoma

Family Score: 0.991

Family Classification: MATCHED

Class: Methylation_class_GBM_RTK_II

Class Score: 0.996

Class Classification: MATCHED

Nearest-neighbors assisted unsupervised analysis (NN Method)
SUPPORTIVE

MGMT Promoter Methylation

Predicted Status: METHYLATED

Score: 0.755

Confidence Interval: 0.458–0.919

Cutoff: 0.358

Interpretation

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This result should be correlated with histopathological and clinico-radiological findings and other available genetic test results.

NCI/BETHESDA CLASSIFIER v.2.0

The classifier had a MATCHED result for methylation family and methylation class, indicating that the methylation profile of this specimen aligned with high confidence (calibrated score ≥ 0.900) to the reference dataset at the family and class levels.

Methylation class GBM_RTK_II (Glioblastoma, IDH-wildtype, RTK2 subtype) is part of methylation family Glioblastoma and is a supportive diagnostic molecular biomarker for Glioblastoma, IDH-wildtype [WHO Classification of Tumours Editorial Board. Central nervous system tumours. Lyon (France): International Agency for Research on Cancer, 5th ed., vol. 6, 2021]. This class is enriched for CDKN2A/B homozygous deletion, EGFR

amplification, gain of 7/loss of 10 and gene expression profiles resembling the TCGA 'Classical' subgroup [PMID:20129251, PMID:23079654, PMID:38532825].

Nearest-neighbors assisted unsupervised analysis (NN Method)
The NN Method is considered SUPPORTIVE of the classifier methylation class result because the NN Method class was concordant with the classifier methylation class.

The NN method class is defined as the consensus class among at least three of the five closest reference dataset samples ("neighbors"). The NN Method identifies the five "neighbors" to the test sample and provides an objective and quantitative estimation of the test sample methylation class cluster rather than relying on subjective visualization by Uniform Manifold Approximation and Projection (UMAP). The NN Method is complementary to the classifier and interpreted in the context of the classifier methylation class results.

MGMT Promoter Methylation

The MGMT promoter methylation predicted status is METHYLATED, which is a favorable prognostic biomarker and a predictive biomarker for response to alkylating chemotherapy in patients with newly diagnosed glioblastoma, IDH-wildtype [PMID:15758010, PMID:22810491, PMID:22877848, PMID:22578793, PMID:28296618].

Additional studies are needed to assess the clinical significance of MGMT promoter methylation status in other CNS tumor types and organ system tumors.

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

Performing Site Legend

Code	Laboratory	Address	Lab Director	CLIA Certificate
MCR	Mayo Clinic Laboratories - Rochester Main Campus	200 First Street SW, Rochester, MN 55905	Nikola Baumann Ph.D.	24D0404292

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Additional Information

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CLINICAL TRIALS

Possible clinical trials of benefit for this patient can be found at the following sites:

1) ClinicalTrials.gov:

www.clinicaltrials.gov/ct2/search/advanced

2) Mayo Clinic: www.mayo.edu/research/clinical-trials/ 3) National Cancer Institute: www.cancer.gov/clinicaltrials/search

Specimen

Tissue, Tumor

MCR

Tissue ID

12345

MCR

Method

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This assay uses the Illumina Infinium MethylationEPIC v2.0 kit, and data are analyzed using the proprietary NIH-developed NCI/Bethesda central nervous system tumor classifier v2.0, an in-house nearest-neighbors assisted unsupervised analysis (NN Method), and the MGMT promoter methylation mgmtstp27 R package.

Disclaimer

1 MCR

Test results should be interpreted in the context of clinical, tumor sampling, histopathological, and other laboratory data. If results obtained do not match other clinical or laboratory findings, contact the laboratory for discussion.

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 NN Method is complementary to the classifier and the results are not to be used as a stand-alone method.

Performance Characteristics: Validation studies demonstrated that overall concordance of results between samples tested by this assay and those tested at NIH were 88.7% (55/62 samples), with 91.9% (57/62) Family/Class classifier concordance, 98.4% (61/62) NN Method concordance, and 98.4% (61/62) MGMT Promoter Methylation concordance.

This assay has three reportable results:

1) NCI/BETHESDA CLASSIFIER v2.0 generates tumor classification at methylation family and methylation class levels, and is reported as follows:

Family MATCHED/Class MATCHED: methylation family calibrated score ≥ 0.900 and methylation class calibrated score ≥ 0.900

Family MATCHED/Class SUGGESTED: methylation family calibrated score ≥ 0.900 and methylation class calibrated score 0.840–0.899

Family MATCHED/Class NO MATCH: methylation family calibrated score ≥ 0.900 and methylation class calibrated score < 0.840

Family NO MATCH/Class NO MATCH: methylation family calibrated score < 0.900 and methylation class calibrated score of any value

2) NN Method generates an NN Method class that is compared to NCI/BETHESDA CLASSIFIER v2.0 methylation class results, and is reported as follows:

SUPPORTIVE: NN Method class and NCI/BETHESDA CLASSIFIER v2.0 methylation class results are concordant

NON-CONTRIBUTORY: NN Method class and NCI/BETHESDA CLASSIFIER v2.0 methylation class results are discordant or NCI/BETHESDA CLASSIFIER v2.0 methylation class result is NO MATCH, and/or NN Method class did not reach a consensus class among at least three of the five closest reference dataset samples ("neighbors")

3) MGMT promoter methylation testing is reported as follows:

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METHYLATED: score ≥ 0.358

UNMETHYLATED: score < 0.358

Reliable results are dependent on adequate specimen collection and processing. This test has been validated on formalin-fixed, paraffin-embedded tissues; other fixatives are discouraged. Improper treatment of tissues, such as decalcification, may

cause polymerase chain reaction failure. This assay requires at least 60% tumor and 75 ng DNA input.

Released By

Cristiane M. Ida, M.D.

MCR**Received:** 17 Apr 2026 08:04**Reported:** 17 Apr 2026 09:17**Laboratory Notes**

- 1 This test was developed, and its performance characteristics determined by Mayo Clinic in a manner consistent with CLIA requirements. This test has not been cleared or approved by the U.S. Food and Drug Administration.

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