JAX MGMT Promoter Methylation

Patient

Name: John Doe
Patient ID: ABC123
Source Patient ID: 0123456
Date of Birth: 01/01/1960
Sex: Male
Submitted Diagnosis: Infiltrating glioma

Specimen

Specimen ID: S9876543
Source Specimen ID: X26-01234
Primary Tumor Site: Brain
Specimen Site: Left frontal lobe
Neoplastic Content: 75%
Collection Date: 03/25/2026
Received Date: 04/01/2026

Physician

Name: Dr. Gene
Affiliation: Genomics Institute

MGMT Promoter Methylation Results

MGMT Promoter Methylated

Test Methods & Limitations

As necessary (for FFPE blocks or unstained slides), specimens are sectioned and stained using Fisher Chemical Eosin Y and Richard-Allan Scientific™ Hematoxylin Stain (Modified Mayer). Slides are digitally scanned on the Leica Aperio CS2 Scanner for remote pathologist review of neoplastic content, tissue type, tumor area, and specimen quality (Remote Testing Site: LBH07).

Areas of high tumor cellularity (≥30% neoplastic content, NPC) are macro-dissected for DNA extraction using the QIAamp DNA FFPE Tissue Kit (Qiagen) or AllPrep DNA/RNA FFPE Kit (Qiagen), followed by bisulfite conversion (Zymo Research). The bisulfite-treated DNA is amplified via qPCR on a QuantStudio™ 7 instrument using primers targeting the MGMT promoter (-4 to +93), followed by high-resolution melt (HRM) analysis[1]. The area under the curve (AUC) is calculated for the HRM derivative plots for both methylated and unmethylated peaks, and the ratio of methylated-to-unmethylated is calculated. Specimens with ratios above a 15% methylated control run in parallel are interpreted as “MGMT Promoter Methylated”. Specimens are interpreted as “MGMT Promoter Unmethylated” if the methylated/unmethylated ratio falls within the validated unmethylated range. Specimens with ratios between unmethylated and the 15% methylated control are interpreted as “Indeterminate”.

Review of digital data, results, and/or clinical report was performed at the following remote testing sites: MKH11.

References

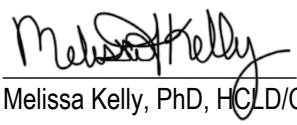
[1]Switzeny OJ, Christmann M, Renovanz M, Giese A, Sommer C, Kaina B. MGMT promoter methylation determined by HRM in comparison to MSP and pyrosequencing for predicting high-grade glioma response. Clin Epigenetics. 2016 May 5;8:49. doi: 10.1186/s13148-016-0204-7. PMID: 27158275; PMCID: PMC4858829.

Disclaimer

Decisions on patient care must be based on the independent medical judgment of the treating physician, taking into consideration all relevant information about the patient's condition, including patient medical and family history, physical examinations, information from other diagnostic tests, and patient preferences. A treating physician's decisions should not be based on a single test, such as this test, or the information contained in this report alone. Results of this test must always be interpreted in the context of all relevant clinical and pathological data and should not be used alone for diagnosis or patient care decisions. Genetic counseling is recommended to discuss the implications of these test results.

This test was developed and its performance characteristics determined by The Jackson Laboratory. It has not been cleared or approved by the U.S. Food and Drug Administration (FDA). This test may be used for clinical purposes and should not be regarded as purely investigational or for research only. This laboratory is certified under the Clinical Laboratory Improvement Amendments of 1988 (CLIA 88) as qualified to perform high complexity clinical testing. The Jackson Laboratory makes no promises or guarantees that a healthcare provider, insurer or other third-party payor, whether private or governmental, will reimburse a patient for the cost of this test.

Electronically Signed By:



Melissa Kelly, PhD, HCLD/CC(ABB), Clinical Laboratory Director

04/10/2026
Date