



Gliolab

GLIOBLASTOMA FOUNDATION

WHOLE GENOME DNA METHYLATION PROFILING WITH THE EPIGNOSTIX CLASSIFIER

*TRANSFORMING DIAGNOSIS AND
PERSONALIZED CARE IN GLIOBLASTOMA*



www.gliolab.org

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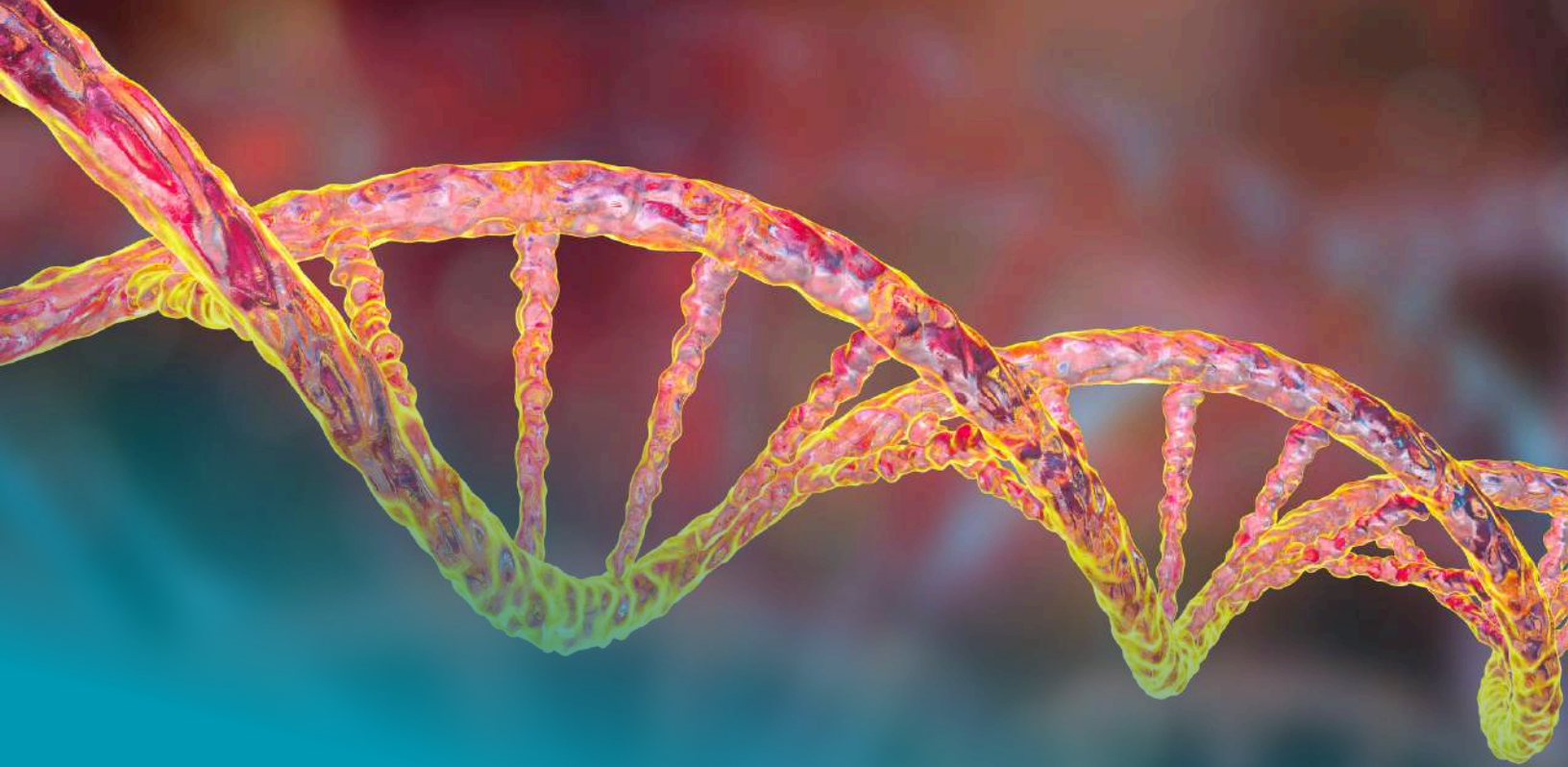


WHAT IS DNA METHYLATION AND WHY IS IT IMPORTANT?

DNA methylation involves the *addition of methyl groups to DNA*, influencing gene activity *without altering the DNA sequence*. These patterns are especially important in cancer, *where they can:*

- Classify tumor subtype and lineage
- Diagnose glioblastoma and other brain cancers *with*
- *99.9% accuracy*
- Predict therapy responsiveness
- Reveal diagnostic biomarkers central to subclassification and prognosis of glioblastoma

Whole genome DNA methylation profiling captures over 850,000 sites, generating a tumor-specific epigenetic fingerprint to aid diagnosis, classification, and treatment.



Introducing the Epignostix Classifier

The Epignostix Classifier is a *powerful machine-learning algorithm* developed to:

- Classify CNS tumors based on methylation patterns
- Refine or correct histological diagnoses
- Identify clinically meaningful glioblastoma subtypes
- Report highly accurate MGMT promoter methylation status
- Detect copy number variations (CNVs) in 29 key glioma-related genes



WHY THIS TEST IS ESSENTIAL FOR GLIOBLASTOMA PATIENTS

Refines and Corrects Diagnoses

Methylation profiling often reveals tumors misclassified by histology alone, allowing accurate grading and appropriate treatment selection.

Accurate and Standardized MGMT Methylation Status

MGMT promoter methylation determines chemotherapy responsiveness. Current testing methods (such as MSP, pyrosequencing, etc.) vary in accuracy. Epignostix uses a unified, highly sensitive array-based method, eliminating discrepancies and standardizing MGMT methylation testing across institutions.

29-Gene CNV Analysis

Copy number alterations in key oncogenes and tumor suppressors provide crucial biological insights that may guide treatment.

Supports Clinical Decisions and Trial Matching

Integrating methylation-based classification, with CNV and MGMT status, empowers clinicians to make *more informed therapeutic choices*.



WHAT THE TEST PROVIDES

FEATURE	DETAILS
Tumor Class	WHO-compatible classification + molecular subclass
Classifier Match Score	Confidence of assignment (0 to 1)
MGMT Promoter Methylation Status	Highly reliable methylated/unmethylated result
Copy Number Variation (CNV)	Detailed plot and gene-specific analysis
Molecular Tumor Board Commentary	Optional interpretation and guidance
Turnaround Time	7-10 business days after receipt of specimen

THE 29 GENES ASSESSED FOR CNVS

- | | | |
|-----------|-------------|-------------|
| 1. CDKN2A | 11. BRAF | 21. SMARCA4 |
| 2. CDKN2B | 12. IDH1 | 22. ATRX |
| 3. EGFR | 13. IDH2 | 23. H3F3A |
| 4. PTEN | 14. CDK4 | 24. EZH2 |
| 5. PDGFRA | 15. PIK3CA | 25. FGFR1 |
| 6. MDM2 | 16. PIK3R1 | 26. FGFR2 |
| 7. MDM4 | 17. RB1 | 27. FGFR3 |
| 8. TERT | 18. MYCN | 28. NTRK2 |
| 9. TP53 | 19. MYC | 29. NTRK3 |
| 10. NF1 | 20. SMARCB1 | |

These genes are commonly altered in glioblastoma and other CNS tumors and provide prognostic and therapeutic insight.



Standardizing MGMT Methylation Testing

MGMT promoter methylation is critical for predicting sensitivity to **temozolomide**, yet today's testing landscape is inconsistent:

- **Multiple methods in use:** MSP, qPCR, pyrosequencing, methylation arrays, etc.
- **Variable cutoffs and interpretation criteria**

The Epignostix methylation platform solves this:

- Uses a single, validated methodology (Illumina EPIC array)
- Ensures automated and reproducible analysis of MGMT CpG islands
- Eliminates inter-laboratory variability
- Standardizes MGMT status reporting for clinical use and trials

This test serves as the new standard for MGMT testing in glioblastoma care.



FREQUENTLY ASKED QUESTIONS (FOR PATIENTS)

Q1. Why should I get this test?

Whole Genome DNA Methylation ensures that your *diagnosis is accurate*, and provides *important molecular information* that can *help guide and personalize your treatment*.

Q2. Does the test hurt?

No, it uses tumor tissue that was already collected from you during surgery or biopsy.

Q3. What is MGMT and why does it matter?

MGMT is a gene that helps repair DNA. If it is *methyalted*, chemotherapy may work better.

Q4. Will my insurance cover this test?

Yes, the test is typically covered by Medicare, private insurance, or provided free by **Gliolab** if you do not have insurance.

Q5. How long does it take to get results?

Results are usually available in 7–10 days after the lab receives the sample.



Frequently Asked Questions (For Providers)

Q1. How is the classifier validated?

The Epignostix classifier is trained on **20,000+** CNS tumor samples and *validated with matched histopathology and outcome data.*

Q2. Is the test performed in a CLIA-certified laboratory?

Yes, all testing is performed in the **Gliolab** CLIA-certified laboratory.

Q3. Can I use the results for diagnosis and treatment decisions?

Yes, this test has high diagnostic utility and also provides MGMT and CNV information with clinical relevance to aid in diagnosis and treatment decisions.

Q4. How are CNVs reported?

Detected CNVs in 29 glioma-relevant genes are displayed in an easily readable plot with gene annotations.

Q5. What tissue types are accepted?

Formalin-fixed paraffin-embedded (FFPE) blocks or unstained slides (minimum of 5 x 5µm sections).



HOW THE TEST IS PERFORMED

Step 1: Tumor sample sent to Gliolab (FFPE block or slides)

Step 2: DNA is extracted from the tissue

Step 3: DNA methylation is measured using the Illumina EPIC array

Step 4: Epignostix Classifier analyzes the data

Step 5: Comprehensive report is generated and reviewed by our tumor board

All Gliolab samples are processed in our secure, HIPAA-compliant, CLIA-certified laboratory.



Interpreting the Report

Includes:

- Tumor match confidence score
- Classifier-based diagnosis
- MGMT promoter status
- CNV plot with key gene highlights
- Optional: molecular tumor board comments

The *Whole Genome DNA Methylation* report is an important part of our Personalized Treatment Roadmap.



PERSONALIZED TREATMENT ROADMAP

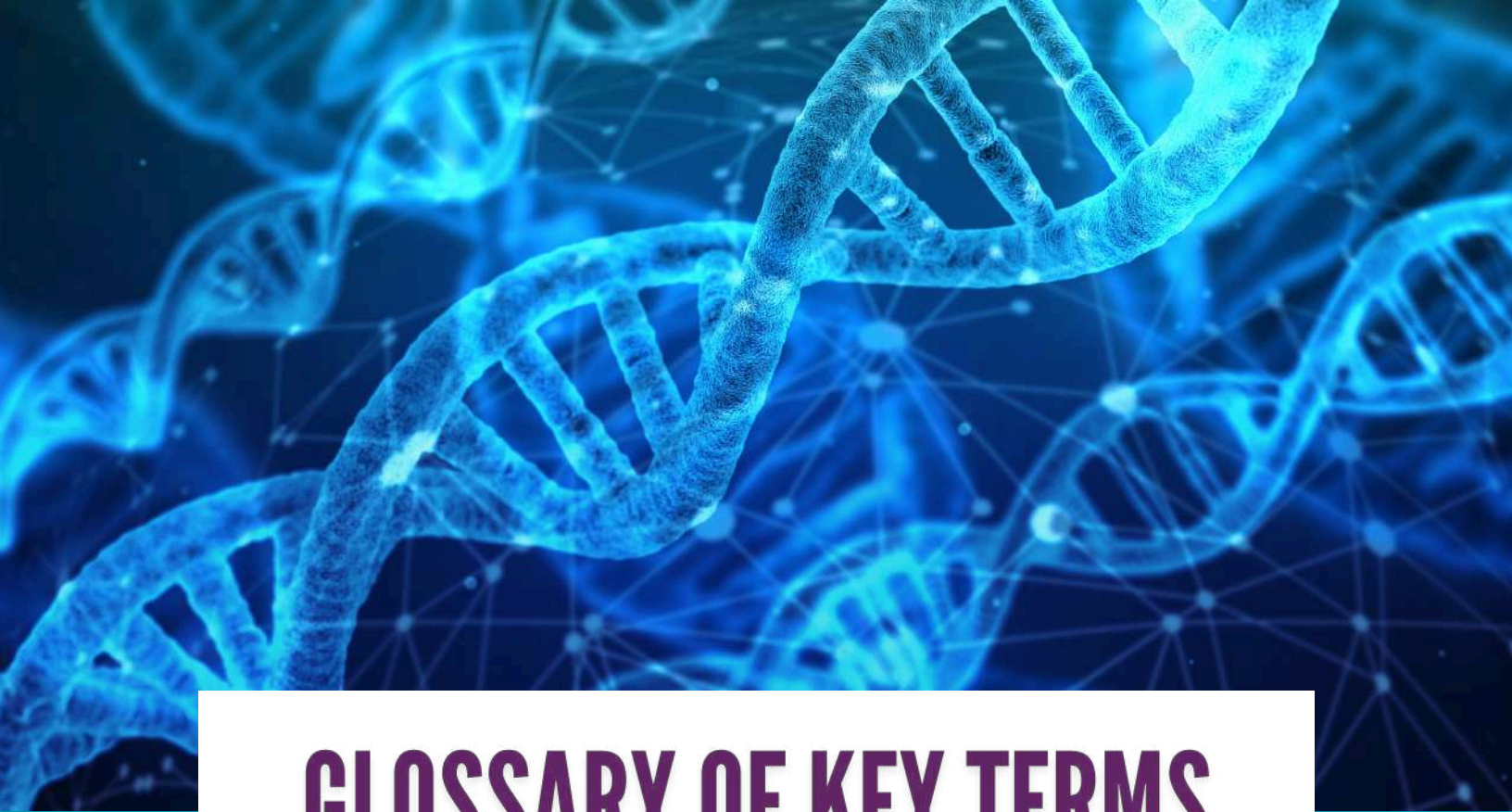
At Gliolab, we help you and your doctor discover the treatment paths designed uniquely for you — based on your tumor profile.

Our **Whole Genome DNA Methylation** test does more than provide data; it's an important part of our personalized treatment roadmap tailored to each patient's tumor biology.

Rather than relying on one-size-fits-all protocols, care teams can use our detailed genomic insights to pinpoint therapies most likely to be effective, explore relevant clinical trials, and avoid treatments unlikely to be effective.

With Gliolab, patients and their physicians gain clarity, direction, and a powerful tool for navigating one of the most complex and aggressive brain cancers.

Personalized Glioblastoma Care Starts at Gliolab.



GLOSSARY OF KEY TERMS

DNA Methylation – A chemical tag on DNA that controls gene activity

MGMT – A DNA repair gene relevant in glioblastoma therapy response

CNV – Copy number variation, meaning extra or missing copies of a gene

Classifier – A machine-learning tool that assigns tumor types/subtypes

RTK Subtype – Receptor Tyrosine Kinase subclass of glioblastoma



Contact and Support

For help with new or existing test orders, please contact our support team at the phone or email below, and we'll provide assistance. Our hours of operation are Monday through Friday 8AM to 6PM Eastern Time. For providers who would like to order a test in the United States (US) please visit our website at www.gliolab.org for ordering instructions and more.

Phone: (919) 309-1489

Email: support@gliolab.org



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