



MEDGENOME



CNS Tumor Methylation Classifier

India's First
Genome-Wide
Methylation-Based
Precision Diagnostic Test
for CNS Tumors

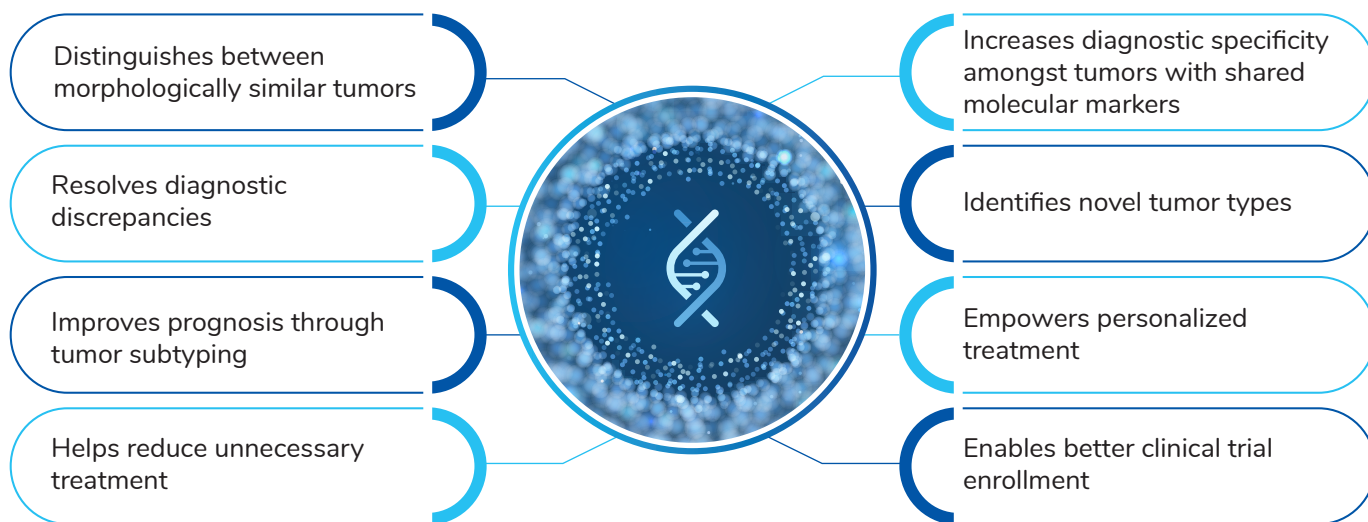
DNA Methylation is an epigenetic modification wherein a methyl group is added to DNA, potentially silencing genes, leading to uncontrolled cell growth and cancer development.

The Challenges in CNS Tumor Diagnosis

Accurate classification of central nervous system (CNS) tumors remains a clinical challenge — even with advancements in histopathology and molecular testing.

According to WHO 2021 guidelines, CNS tumor diagnosis now demands integrated molecular and histological insights.

The methylation-based classifier complements conventional histology



Introducing CNS Tumor Methylation Classifier

A cutting-edge, genome-wide methylation test

How It Works

Platform

Whole Genome Methylation

Technology

Captures methylation patterns across the entire genome

Classification

Categorizes tumors into >90 classes

Diagnostic Strength

>90% sensitivity and specificity

Report Highlights

Confident molecular classification with calibrated scores

WHO Grade assignment

Genome-wide copy number variation (CNV) profiling

Why It Matters — Clinical Value & Impact

Precision Subtyping

e.g. Resolves histologically ambiguous cases and complex differentials (e.g., High grade neuroepithelial tumor (HGNET) vs Atypical teratoid/rhabdoid tumor (AT/RT))

Prognostic Clarity

e.g. WNT-activated medulloblastoma has a significantly better prognosis compared to SHH-activated or Group 3/4 variants

Personalized Management

Enables treatment planning tailored to the tumor's molecular profile — identifies resistance patterns and emerging targets

All CNS tumors can be tested - Adult and pediatric gliomas, gangliogliomas, ependymomas, embryonal tumors, and many more.

All-in-One Precision

Covers every key marker — from genome-wide methylation signatures to critical molecular alterations (WHO guidelines for CNS tumors, 2021).

- Genes like IDH1, IDH2, H3-3A, MGMT, ATRX, TERTp, CDKN2A, CDKN2B, EGFR, GLI2, MET, MYB, MYBL1, MYCN, NF1, NF2, PDGFRA, PTCH1, PTEN, SMARCB1, TP53 ... etc.
- Alterations in all chromosomes including 1p/19q co-deletion, chr7 gain/chr 10 loss, chr 14 alterations.

Test Details

Test Code	Test Name	Sample Type	Turnaround Time
MGM3615	CNS Tumor Methylation Classifier	FFPE block (>30% tumor content) Fresh tissue*	21 Days

*Tumor cellularity for fresh tissue specimens should be pre-evaluated and mentioned in the Test Requisition Form (TRF)