JAX OncoMethyl Array®

Advanced DNA Methylation Profiling & Copy Number Assessment for CNS Tumors

More Comprehensive Results with Validated Copy Number Calling

The JAX Advanced Precision Medicine Laboratory is excited to launch updates to the JAX OncoMethyl Array® for central nervous system tumors, including updated Heidelberg Epignostix Classifier[1] and clinically-validated copy number assessment.

Why Methylation Profiling?

- Helps resolve diagnostically ambiguous cases
- Distinguishes histologically similar tumor entities
- Identifies rare and newly defined CNS tumor subtypes
- Complements histopathology and targeted molecular testing
- Aligns with current WHO CNS tumor classification

New Features of the JAX OncoMethyl® Array

- **Updated report format** for easier result interpretation (see below)
- **Quality metrics summary** provides transparency for confident result interpretation
- **Latest CNS classifier** version includes updated classes and clinical descriptions
- **Classification evidence levels** provide guidance on the available information about the entities and their alignment with WHO classification
- **Copy number variant** reporting for 57 genes and whole chromosome/arm gains and losses (Table 1)

Test Highlights

- Genome-wide DNA methylation analysis
- Algorithm-based tumor classification
- MGMT promoter methylation status
- Validated copy number variant (CNV) calling with correction for neoplastic content

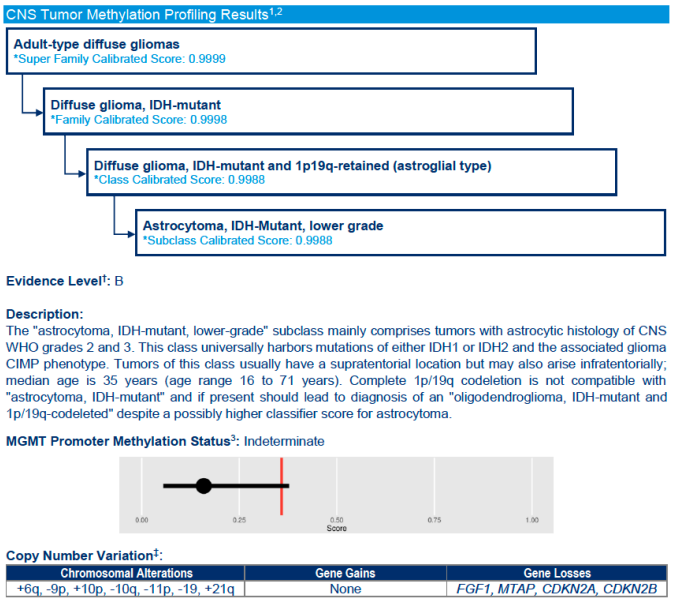
Clinical Utility

Ideal for pediatric and adult CNS tumors when:

- Histology is indeterminate
- Molecular findings are discordant
- Rare or uncommon tumor types are suspected
- Supports diagnostic confidence, prognostic assessment, and treatment planning.

Why The Jackson Laboratory?

- Global leader in genomics and cancer research
- Deep expertise in molecular oncology & bioinformatics
- Trusted precision-medicine partner
- CLIA-certified, CAP-accredited laboratory



CNS Tumor Methylation Profiling Results[1,2]

Adult-type diffuse gliomas
*Super Family Calibrated Score: 0.9999

Diffuse glioma, IDH-mutant
*Family Calibrated Score: 0.9998

Diffuse glioma, IDH-mutant and 1p19q-retained (astroglial type)
*Class Calibrated Score: 0.9988

Astrocytoma, IDH-Mutant, lower grade
*Subclass Calibrated Score: 0.9988

Evidence Level†: B

Description:
The "astrocytoma, IDH-mutant, lower-grade" subclass mainly comprises tumors with astrocytic histology of CNS WHO grades 2 and 3. This class universally harbors mutations of either IDH1 or IDH2 and the associated glioma CIMP phenotype. Tumors of this class usually have a supratentorial location but may also arise infratentorially; median age is 35 years (age range 16 to 71 years). Complete 1p/19q codeletion is not compatible with "astrocytoma, IDH-mutant" and if present should lead to diagnosis of an "oligodendroglioma, IDH-mutant and 1p/19q-codeleted" despite a possibly higher classifier score for astrocytoma.

MGMT Promoter Methylation Status[3]: Indeterminate

Copy Number Variation‡:

Chromosomal Alterations	Gene Gains	Gene Losses
+6q, -9p, +10p, -10q, -11p, -19, +21q	None	*FGF1, MTAP, CDKN2A, CDKN2B*

Table 1: Copy Number Reporting

Genes	Chromosomal Arms*
AKT1, AKT3, ALK, ATRX, AURKB, BRAF, C19MC, CCND1, CCND2, CCNE1, CDK4, CDK6, CDKN2A, CDKN2B, CHEK2, CRKL, EGFR, FGF1, FGF2, FGFR1, FGFR2, FGFR3, FGFR4, FOXM1, FRS2, GATAD1, GLI1, GLI2, GNAS, HMGA2, HOXA5, IGF1R, KRAS, MAPK1, MCL1, MDM2, MDM4, MET, MTAP, MYC, MYCN, NF1, NF2, OTX2, PDGFRA, PLAGL1, PLAGL2, PPM1D, PTEN, RAD21, RB1, SMARCB1, SMARCE1, TERT, TP53, TSPAN31, VEGFA	1p/q, 2p/q, 3p/q, 4p/q, 5p/q, 6p/q, 7p/q, 8p/q, 9p/q, 10p/q 11p/q, 12p/q, 13q, 14q, 15q, 16p/q, 17p/q, 18p/q, 19p/q, 20p/q, 21q, 22q

*Chromosomal arm gains and losses reported for all autosomes, excluding acrocentric arms 13p, 14p, 15p, 21p, 22p.

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[1]Sill M, et al. Advancing CNS tumor diagnostics with expanded DNA methylation-based classification. Cancer Cell. 2026 Feb 9;44(2):340-354.e2. doi: 10.1016/j.ccell.2025.11.002. PMID: 41349541.