

JAX OncoMethyl™ Array Service

Comprehensive methylome profiling provides precise tumor classification of central nervous system tumors

In 2021, the World Health Organization identified methylome profiling as “an effective ancillary method for brain and spinal cord tumor classification when used with other, standard technologies, including histology.”

The JAX Advanced Precision Medicine Laboratory offers an innovative OncoMethyl Array service to classify central nervous system (CNS) tumors based on genomic methylation profiling. Scientists use a well-characterized methylome assay paired with a machine learning algorithm to reveal clinically relevant information about these tumors for more precise classification and personalized patient management.

PROVEN TECHNOLOGY

The JAX OncoMethyl™ Array works with genomic DNA extracted from FFPE tissue that is subjected to bisulfite conversion. The converted DNA is amplified and then analyzed with the Illumina Infinium MethylationEPIC Array. Raw data files are processed through the CNS methylation classifier developed by the molecular neuropathology group at the German Cancer Research Center (DKFZ). (PMID: 29539639)

The JAX® Advantage



EXPERTISE:

The JAX Advanced Precision Medicine Laboratory aims to maintain a CNS tumor center of excellence through the expertly trained team of scientists and analysts, and via collaborations with JAX Cancer Center researchers and local clinicians.



VALIDATED PERFORMANCE:

During clinical validation, 98% of samples with reportable calibration scores were found to confirm, refine, or correct the original pathological diagnosis



SPEED:

Receive results within a clinically actionable time frame to accelerate treatment decisions



POWERFUL PROFILING:

Our approach utilizes arrays to interrogate methylation patterns across the genome. This process has been described as “a powerful approach to CNS classification” by the WHO 2021 CNS Classification Guidelines (PMID: 34185076)



ADVANCED MACHINE LEARNING:

Our algorithm detects distinct methylation patterns found across 184 CNS tumor subclasses (PMID: 29539639)



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SUBMISSION CRITERIA

FFPE SLIDES

- Sample packaging: uncoated, unbaked slides in plastic slide containers
- Slide format: 1 H&E slide and 10 adjacent unstained 5 μ M sections
- Minimum content area: 3 x 3 mm or 5,000 cells (\geq 70% neoplastic content with mild / less necrosis or inflammation)

FFPE BLOCK

- Sample packaging: sealed biohazard bag
- Content area: 3 x 3 mm or 5,000 cells (\geq 70% neoplastic content with mild / less necrosis or inflammation)

DNA

- Sample concentration: \geq 12.5 ng/uL
- Sample quality: $<$ 5 (\blacktriangle CT)
- Amount of material: \geq 250 ng
Amount of material: \geq 200 ng

REQUEST A SHIPPING KIT

Request your kit by email at CGL_CS@jax.org or by phone at (860) 837-2320.

SHIP TO:

The Jackson Laboratory
Attn: Advanced Precision Medicine Laboratory
10 Discovery Drive
Farmington, CT 06032

ABOUT JAX APML

The JAX Advanced Precision Medicine Laboratory is a CLIA-certified, CAP-accredited, and NCI-MATCH-designated laboratory delivering precise genomic testing and critical data analysis services to help improve treatment options for patients.

