JAX **CLINIC**A**L** GENOMICS

Neuro-Oncology Testing

The JAX Clinical Genomics Laboratory offers molecular testing methods for primary brain tumor biomarkers to complement standard histopathological assessment. This provides clinicians and their patients with a comprehensive profile of each tumor, supporting diagnostic, prognostic and treatment decision-making.

JAX SOMASEQ™

The JAX SOMASEQ™ is a 517 gene next-generation sequencing-based tumor profiling assay utilizing DNA and RNA from FFPE specimens. Reports identify variants in WHO-classified key diagnostic genes in primary CNS tumors including ATRX, BRAF, EGFR, IDH1/2, NF1, NF2, and the TERT promoter.[1]

JAX OncoMethyl Array™

CNS Tumor Classification from DNA Methylation Profiling
The JAX OncoMethyl Array™ utilizes a machine learning algorithm intended to provide supplemental information for the classification of central nervous system (CNS) tumors based on genomic methylation profiling data.[2] The 2021 WHO Classification of Tumors of the Central Nervous System has identified methylome profiling as "an effective ancillary method for brain and spinal cord tumor classification when used alongside other, standard technologies, including histology."[1]

Coming Soon: MGMT Promoter Methylation

[1]Louis et al., The 2021 WHO Classification of Tumors of the Central Nervous System: a summary. Neuro Oncol. 2021 Aug 2;23(8):1231-1251. doi: 10.1093/neuonc/noab106. PMID: 34185076; PMCID: PMC8328013.

[2]Capper et al., DNA methylation-based classification of central nervous system tumours. Nature. 2018 Mar 22;555(7697):469-474. doi: 10.1038/nature26000. Epub 2018 Mar 14. PMID: 29539639; PMCID: PMC6093218.

CLINICAL GENOMICS JAX

BRINGING THE POWER OF GENOMICS TO TREATMENT DECISIONS