



Test Update 747

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Effective Date 11/18/2020

Update Type [Test Methodology Changed](#)

CPT Code 81120, 81121, 88381-TC

Effective November 18, 2020, MLabs has changed IDH1 and IDH2 Mutation for Glioma (IDHG) testing from sanger to our NGS platform.

Test Usage:

This test is intended to detect IDH1 or IDH2 mutations within glioma or suspected glioma specimens. IDH1 and IDH2 encode the cytoplasmic and mitochondrial isocitrate dehydrogenase enzymes that normally convert isocitrate into alpha-ketoglutarate. Mutations affecting arginine residues in these proteins result in the production of 2-hydroxyglutarate which functions as an oncometabolite. 2-hydroxyglutarate inhibits alpha-ketoglutarate dependent dioxygenases such as TET enzymes, leading to global DNA and histone methylation changes. Mutation status for IDH1 and IDH2 determines the final classification of diffuse astrocytic and oligodendroglial tumors according to the World Health Organization Classification of Tumors of the Central Nervous System. IDH mutations in glioma (most frequently IDH1 R132H) impart a significantly better prognosis than grade-matched IDH wild-type gliomas and these mutations are associated with superior response to chemotherapy. These mutations can be associated with 1p/19q co-deletion and/or MGMT promoter methylation.

Specimen Requirements:

Normal Volume: Formalin-fixed paraffin-embedded tissue; Diff-Quik stained aspirate smear, Papanicolaou stained aspirate smear.

Alternate Specimen: For exhausted formalin-fixed paraffin-embedded blocks, the original Hematoxylin and Eosin stained slide(s) may be extracted at the discretion of the Molecular Diagnostics Laboratory Director. The extraction process will result in destruction of the slide(s). A digital image of the slide(s) must be collected prior to extraction and retained for a minimum of 10 years from the specimen collection date.

Previously extracted DNA from a CLIA certified laboratory may be accepted; however, the extracting laboratory must take responsibility for ensuring that viable, neoplastic cells comprise at least 10% of cellularity within the extracted sample.

Methodology: Next-Generation Sequencing

