Glioma Solid Tumor Sequencing Panel

This panel detects hotspot mutations and copy number alterations in 15 cancer-related genes (BRAF, CDKN2A, EGFR, H3F3A, HIST1H3B, HRAS, IDH1, IDH2, KRAS, MET, NRAS, PIK3CA, PTEN, TERT, TP53) using DNA extracted from formal fixed paraffin embedded tissues. This test is used for diagnostic, prognostic, and predictive purposes associated with Glioma tumors.

Testing Method and Background

Diagnosis, prognosis and treatment of adult and pediatric glioma tumors relies on identification of molecular genetic alterations that are characteristic to specific tumors subtypes and are now included in the WHO classification of gliomas (PMIDs: 32307792, 26061753, 25314060, 25140036, 30412261). This assay detects hotspot mutations and copy number alterations in multiple cancer-related genes relevant to diagnosis, prognosis and treatment of adult and pediatric glioma tumors. For each gene included on the clinical panel (listed below), the target exons are enriched by hybrid capture method followed by **Next Generation Sequencing (NGS).** This method was optimized for use with low quantity of input DNA (50 ng) obtained from formalin-fixed, paraffin-embedded (FFPE) tissues providing high on-target coverage with coverage uniformity above 95% throughout the entire target region.

Highlights of Glioma Solid Tumor Sequencing Panel

Genes Targeted

SNVs/Indels: *BRAF* (ex 11, 15), *CDKN2A*, *EGFR* (ex 18-21), *H3F3A* (ex 2), *HIST1H3B*, *HRAS* (ex 2-4), *IDH1* (ex 4), *IDH2* (ex 4), *KRAS* (ex 2-4), *MET* (ex 2, 14-20), *NRAS* (ex 2-4), *PIK3CA* (ex 2, 3, 6, 8, 10, 21), *PTEN* (ex 5-9), *TERT* (promoter, ex 1, 8, 9, 13), *TP53*

Amplifications / CNVs: *BRAF, CDKN2A, EGFR, HIST1H3B, HRAS, KRAS, MET, NRAS, PIK3CA, PTEN, TERT, TP53*

- **Accurate Results from Low-Quality Samples**
  Sensitive variant detection with as little as 50 ng of input DNA, and as low as 5% mutant allele frequency, maximizes the results from low input sample types such as formalin fixed, paraffin embedded (FFPE) sections.
- **Wide-ranging Coverage of Variants**
  Assessment of single-nucleotide variants (SNVs) and small insertions/deletions, and whole gene deletions and amplifications

Ordering Information

Get started (non-HFHS): Print a Molecular Solid Tumor requisition form online at www.HenryFord.com/HFCPD

Get started (HFHS): Order through Epic using test "Glioma Solid Tumor Sequencing Panel" (MOL8026)

Specimen requirements:

A surgical pathologist should confirm the presence of adequate tumor in materials submitted for analysis. Section from archival paraffin material or frozen surgical biopsies should be confirmed to contain >50% tumor by a surgical pathologist. If the submitted material for analysis contains < 50% of tumor, areas of predominant tumor will be microdissected, if possible, to enrich for neoplastic cells.

- Formalin-fixed, paraffin-embedded tissue, preferably no older than 2 years
- 5-6 tissue sections at 5-6 micron thickness (include H&E slide and a copy of pathology report)
- Cytology slides (submit cell block with 500+ tumor cells or 5-6 tissue sections at 5-10 micron thickness depending on cellularity)
- Extracted DNA - from a CLIA-certified Laboratory

Cause for Rejection: Clotted, hemolyzed, or frozen specimens, improper anticoagulant, tubes not labeled with dual patient identification, non-dedicated tubes.

TAT: 5-10 business days (after Prior Authorization obtained)

Mail test material to:
Henry Ford Center for Precision Diagnostics
Pathology and Laboratory Medicine
Clinic Building, K6, Core Lab, E-655
2799 W. Grand Blvd., Detroit, MI 48202

CPT Codes: 81445, G0452 (88363 or 88381 may apply)

Contact us: Client Services, Account and Billing Set-up, and connect with a Molecular Pathologist at (313) 916-4DNA (4362)

For more information on Comprehensive Molecular Services, visit our website www.HenryFord.com/HFCPD

Revision: 1; 02-10-2021