MAYO CLINIC LABORATORIES

NEW TEST

Notification Date: July 3, 2023
Effective Date: July 11, 2023

FH Mutation Analysis, Next-Generation Sequencing, Tumor

Test ID: TFH

Useful for:
Identifying specific mutations within the *FH* gene to assist in tumor diagnosis/classification, including renal cell carcinoma, uterine/cutaneous leiomyoma, and pheochromocytoma/paraganglioma

Genetics Information:
- This test uses targeted next-generation sequencing to evaluate for somatic mutations within the *FH* gene. See Targeted Genes and Methodology Details for FH Mutation Analysis for details regarding the targeted gene regions evaluated by this test.
- This test is performed to evaluate for somatic mutations within solid tumor samples. This test **does not assess** for germline alterations within the *FH* gene.

Reflex Tests:

Test ID	Reporting Name	Available Separately	Always Performed
SLIRV	Slide Review in MG	No (Bill Only)	Yes

Testing Algorithm:
When this test is ordered, slide review will always be performed at an additional charge.

Methods:
Sequence Capture Next-Generation Sequencing (NGS)

Reference Values:
An interpretive report will be provided.

Specimen Requirements:
This assay requires at least 20% tumor nuclei.
- Preferred amount of tumor area with sufficient percent tumor nuclei: tissue 216 mm(2)

- Minimum amount of tumor area: tissue 36 mm(2)
- These amounts are cumulative over up to 10 unstained slides and must have adequate percent tumor nuclei.
- Tissue fixation: 10% neutral buffered formalin, not decalcified
- For specimen preparation guidance, see Tissue Requirement for Solid Tumor Next-Generation Sequencing. In this document, the sizes are given as 4 mm x 4 mm x 10 slides as preferred: approximate/equivalent to 144 mm(2) and the minimum as 3 mm x 1 mm x 10 slides: approximate/equivalent to 36 mm(2).

Preferred:

Specimen Type:	**Tissue block**
Collection Instructions:	Submit a formalin-fixed, paraffin-embedded tissue block with acceptable amount of tumor tissue.

Acceptable:

Specimen Type:	**Tissue Slide**
Slides:	1 Stained and 10 unstained
Collection Instructions:	Submit 1 slide stained with hematoxylin and eosin and 10 unstained, nonbaked slides with 5-micron thick sections of the tumor tissue.
Note:	The total amount of required tumor nuclei can be obtained by scraping up to 10 slides from the same block.
Additional Information:	Unused unstained slides will not be returned.

Specimen Type:	**Cytology slide (direct smears or ThinPrep)**
Slides:	1 to 3 Slides
Collection Instructions:	Submit 1 to 3 slides stained and coverslipped with a preferred total of 5000 nucleated cells, or a minimum of at least 3000 nucleated cells.
Note:	Glass coverslips are preferred; plastic coverslips are acceptable but will result in longer turnaround times.
Additional Information:	Cytology slides will not be returned.

Specimen Stability Information:

Specimen Type	Temperature	Time	Special Container
Varies	Ambient (preferred)		
	Refrigerated		

Ordering Guidance:

- Multiple oncology (cancer) gene panels are available. For more information see Oncology Somatic NGS Testing Guide.
- For guidance on hereditary cancer test selection see Oncology Hereditary NGS Testing Guide.

Necessary Information:

A pathology report (final or preliminary), at minimum containing the following information, **must accompany specimen for testing to be performed**:

1. Patient name
2. Block number-must be on all blocks, slides, and paperwork (can be handwritten on the paperwork)
3. Tissue collection date
4. Source of the tissue

Cautions:

- This test cannot differentiate between somatic and germline alterations. Additional testing may be necessary to clarify the significance of results if there is a potential hereditary risk.
- DNA variants of uncertain significance may be identified.
- A negative result does not rule out the presence of a variant that may be present below the limits of detection of this assay. In a specimen with 20% or more tumor content, the analytical sensitivity of this assay for sequence reportable alterations is 5% mutant allele frequency with a minimum coverage of 500X.
- Point mutations and small deletion-insertion mutations will be detected in *FH* gene only. This test may detect single exon deletions but does not detect multi-exon deletions, duplications, or genomic copy number variants.
- Variant allele frequency (VAF) is the percentage of sequencing reads supporting a specific variant divided by the total sequencing reads at that position. In somatic testing, VAF should be interpreted in the context of several factors, including, but not limited to, tumor purity/heterogeneity/copy number status (ploidy, gains/losses, loss of heterozygosity) and sequencing artifact/misalignment.(2,3)
- Rare alterations (ie, polymorphisms) may be present that could lead to false-negative or false-positive results.
- Test results should be interpreted in the context of clinical, tumor sampling, histopathological, and other laboratory data. If results obtained do not match other clinical or laboratory findings, contact the laboratory for discussion. Misinterpretation of results may occur if the information provided is inaccurate or incomplete.
- Reliable results are dependent on adequate specimen collection and processing. This test has been validated on cytology slides and formalin-fixed, paraffin-embedded tissues; other types of fixatives are discouraged. Improper treatment of tissues, such as decalcification, may cause polymerase chain reaction failure.

CPT Code:

88381 – Microdissection, manual
81405

Day(s) Performed: Monday through Friday

Report Available: 12-20 days

Questions

Contact Michelle Raths, Laboratory Resource Coordinator at 800-533-1710.