Overview

Useful For
Identifying solid tumors that may respond to targeted therapies by assessing multiple gene targets simultaneously

Identifying specific variants within genes known to be associated with response or resistance to specific cancer therapies

Identifying variants that may help determine prognosis for patients with solid tumors

Assisting in establishing a diagnosis (e.g., KIT and PDGFRA alterations for gastrointestinal stromal tumors)

Aiding in the determination of clinical trial eligibility for patients with genetic variants not amenable to current FDA-approved targeted therapies

This test is not intended for use for hematological malignancies or assessment of germline variants

Genetics Test Information
This test uses targeted next-generation sequencing to evaluate for somatic variants within 50 genes associated with cancer. See Targeted Gene Regions Interrogated by Solid Tumor Targeted Cancer Gene Panel by Next-Generation Sequencing in Special Instructions for details regarding the targeted gene regions identified by this test.

Additional Tests

<table>
<thead>
<tr>
<th>Test ID</th>
<th>Reporting Name</th>
<th>Available Separately</th>
<th>Always Performed</th>
</tr>
</thead>
<tbody>
<tr>
<td>SLIRV</td>
<td>Slide Review in MG</td>
<td>No, (Bill Only)</td>
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</tr>
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</table>

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

Special Instructions
- Targeted Gene Regions Interrogated by Solid Tumor Targeted Cancer Gene Panel by Next Generation Sequencing
- Tissue Requirements for Solid Tumor Next-Generation Sequencing

Method Name
Polymerase Chain Reaction (PCR)-Based Next Generation Sequencing

NY State Available
Yes

Specimen

Specimen Type
Varies

Necessary Information
Pathology report (final or preliminary), at minimum containing the following information, must accompany specimen in order 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

**Specimen Required**

This assay requires at least 20% tumor nuclei.

- Preferred amount of tumor area with sufficient percent tumor nuclei: tissue 144 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 Special Instructions. In this document, the sizes are given as 4mm x 4mm x 10 slides as preferred: approximate/equivalent to 144 mm(2) and the minimum as 3mm x 1mm x 10 slides: approximate/equivalent to 36mm(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.

**Specimen Type:** Cytology slide (direct smears or ThinPrep)

**Slides:** 1 to 3 slides

**Collection Instructions:** Submit 1 to 3 slides stained and cover slipped 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.

**Forms**
If not ordering electronically, complete, print, and send an [Oncology Test Request](#) (T729) with the specimen.

**Specimen Minimum Volume**
See Specimen Required

**Reject Due To**

<table>
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<tr>
<th>Other</th>
<th>Specimens that have been decalcified (all methods)</th>
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<tr>
<td></td>
<td>Specimens that have not been formalin-fixed, paraffin-embedded</td>
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**Specimen Stability Information**

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<th>Specimen Type</th>
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<th>Time</th>
<th>Special Container</th>
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**Clinical and Interpretive**

**Clinical Information**
Targeted cancer therapies are defined as antibody or small molecule drugs that block the growth and spread of cancer by interfering with specific cell molecules involved in tumor growth and progression. Multiple targeted therapies have been approved by the FDA for treatment of specific cancers. Molecular genetic profiling is often needed to identify targets amenable to targeted therapies and to minimize treatment costs and therapy-associated risks.

Next-generation sequencing has recently emerged as an accurate, cost-effective method to identify variants across numerous genes known to be associated with response or resistance to specific targeted therapies. This test is a single assay that uses formalin-fixed paraffin-embedded tissue to assess for common variants in 50 genes known to be associated with cancer.

See [Targeted Gene Regions Interrogated by Solid Tumor Targeted Cancer Gene Panel](#) by Next-Generation Sequencing in Special Instructions for details regarding the targeted gene regions identified by this test.

**Reference Values**
An interpretive report will be provided.

**Interpretation**
An interpretive report will be provided.
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 (wild-type) result does not rule out the presence of a variant that may be present but below the limits of detection of this assay (approximately 5%-10%).

This test does not detect large single or multi-exon deletions or duplications or genomic copy number variants.

Rare polymorphisms may be present that could lead to false-negative or false-positive results. Test results should be interpreted in the context of clinical findings, tumor sampling and other laboratory data. If results obtained do not match other clinical or laboratory findings, please contact the laboratory for updated interpretation. Misinterpretation of results may occur if the information provided is inaccurate or incomplete.

Clinical Reference


Performance
Method Description
Next-generation sequencing is performed to test for the presence of a mutation in targeted regions of the following 50 genes: ABL1, AKT1, ALK, APC, ATM, BRAF, CDH1, CDKN2A, CSF1R, CTNNB1, EGFR, ERBB2, ERBB4, EZH2, FBXW7, FGFR1, FGFR2, FGFR3, FLT3, GNA11, GNAQ, GNAS, HNF1A, HRAS, IDH1, IDH2, JAK2, JAK3, KDR, KIT, KRAS, MET, MLH1, MPL, NOTCH1, NPM1, NRAS, PDGFRA, PIK3CA, PTEN, PTPN11, RB1, RET, SMAD4, SMARCB1, SMO, SRC, STK11, TP53, and VHL. See Targeted Gene Regions Interrogated by Solid Tumor-Targeted Cancer Gene Panel by Next Generation Sequencing in Special Instructions for details regarding the targeted gene regions identified by this test. (Unpublished Mayo method)

PDF Report
No

Day(s) and Time(s) Test Performed
Monday through Friday; Varies

Analytic Time
12 days

Maximum Laboratory Time
20 days

Specimen Retention Time
Unused portions of blocks will be returned to the client. Unused slides are stored indefinitely.
Performing Laboratory Location
Rochester

Fees and Codes

Fees
- Authorized users can sign in to Test Prices for detailed fee information.
- Clients without access to Test Prices can contact Customer Service 24 hours a day, seven days a week.
- Prospective clients should contact their Regional Manager. For assistance, contact Customer Service.

Test Classification
This test was developed and its performance characteristics determined by Mayo Clinic in a manner consistent with CLIA requirements. This test has not been cleared or approved by the U.S. Food and Drug Administration.

CPT Code Information
81445-Targeted genomic sequence analysis panel, solid organ neoplasm

Slide Review
88381-Microdissection, manual

LOINC® Information

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