Overview

Useful For

Diagnosing specific soft tissue and bone tumors (sarcoma) based on the observed gene fusions (eg, PAX3/FOXO1 gene fusion observed in alveolar rhabdomyosarcoma, EWSR1-FLI1 gene fusion for Ewing’s sarcoma, SS18-SSX1/2 gene fusion for synovial sarcoma)

Genetics Test Information

There are 2 ordering options associated with this test. One of the 2 options below must be selected when this test is ordered.

Comprehensive Sarcoma Targeted Gene Fusion Panel

This ordering option evaluates 138 gene targets for the presence of somatic gene fusions. See Sarcoma Targeted Gene Fusion Panel in Special Instructions for details regarding the targeted gene regions identified by this test.

Custom Sarcoma Targeted Gene Fusion Panel

This ordering option provides a customizable panel in which a subset of the 138 gene targets can be selected to aid in the diagnosis and evaluation of sarcomas. This would allow for selection of a single gene or gene fusion.

If the custom panel option is selected, a unique Gene List ID must be created using the Gene Selection Application. The Gene List ID must be included with the test order. The Gene List ID can be created here: https://orders.mayocliniclabs.com/en/tools/gene_panels/

For a demonstration of this application, Custom Gene Ordering tutorial, click here: https://vimeo.com/299737728/23d56922f1

See Frequently Asked Questions: Custom Gene Ordering Tool in Special Instructions.

Targeted genes: ACTB, AHRR, ALK, ASPSCR1, ATF1, ATIC, BCOR, BRD3, BRD4, CAMTA1, CARS, CCNB3, CDH1, CDX1, CD63, CEP128, CIC, CITED2, CLTC, CNBP, COL1A1, COL1A2, COL3A1, COL6A3, CREB1, CREB3L1, CREB3L2, CSF1, CXorf67, C11orf95, DDIT3, DUX4, DVL2, EML4, EPC1, EP400, ERG, ETV1, ETV4, ETV6, EWSR1, FEV, FGFRI1, FLI1, FN1, FOSB, FOXI1, FOXO4, Fus, GLI1, HAS2, HEY1, HMGA2, IRF2BP2, JAZ1, KIRREL, KLF17, LAMTOR1, LPP, MAML3, MBTD, MEAF6, MED12, MIR143HG, MKL2, MYH9, NAB2, NCOA1, NCOA2, NFATC2, NFIB, NOTCH1, NOTCH2, NR4A3, NTRK1, NTRK3, NUMA1, NUTM1, NUTM2B, OMD, OPHN1, PATZ1, PAX3, PAX7, PBX1, PBX3, PDGFB, PDPN, PHF1, PLAG1, PLPP3, POUS51, PRF1BP1, PRDM10, PRKCA, PRKCB, PRKCD, RAB2A, RAD51B, RANBP2, RNF213, RAGB, SEC31A, SERPINE1, SETBP1, SFMBT1, SMARCA5, SP3, SQSTM1, SRF, SRSF3, SSX1, SSX2, SSX4, SS18, SS18L1, STAT6, SUZ12, S100A10, TAF15, TCF12, TEAD1, TF3, TFG, THRAP3, TPM3, TPM4, TPR, USP6, VCL, VGLL2, WT1, WWTR1, YAP1, YWHAE, ZC3H7B, ZFP36, and ZNF444.

Highlights

This test uses RNA-based next-generation sequencing to evaluate sarcomas for gene fusions that involve at least 1 of 138 genes.

This panel can be modified to interrogate a customized list of gene fusion targets associated with sarcoma. Single gene fusions or single gene targets can be ordered using the Sarcoma Targeted Gene Fusion Panel in Special Instructions.
Reflex Tests

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Testing Algorithm

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

This test includes the option of ordering a predefined comprehensive gene fusion panel or the option to create a custom gene fusion panel. Pricing for the Custom Gene Fusion Panel will be based on the number of genes selected (1-4, 5-50, and 50+). For more information, see Sarcoma Targeted Gene Fusion Rearrangement Panels Test Pricing in Special Instructions.

Special Instructions

- [Tissue Requirements for Solid Tumor Next-Generation Sequencing](https://orders.mayocliniclabs.com/en/tools/gene_panels/)
- Sarcoma Targeted Gene Fusion Rearrangement Panels Test Pricing
- Sarcoma Targeted Gene Fusion Panel

Method Name

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

NY State Available

Yes

Specimen

Specimen Type

Varies

Necessary Information

Either Sarcoma Targeted Gene Fusion Panel or Custom Gene Fusion Panel must be selected. If Custom Gene Fusion Panel is selected, a Gene List ID must accompany the order (generated through the Custom Gene Ordering Tool: https://orders.mayocliniclabs.com/en/tools/gene_panels/).

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 10% 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 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:** Formalin-fixed, paraffin-embedded (FFPE) tissue

**Container/Tube:** Tissue block

**Collection Instructions:** Submit a formalin-fixed, paraffin-embedded tissue block.

**Acceptable:**

**Specimen Type:** FFPE Tissue

**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.

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

**Slide:** 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 Minimum Volume
See Specimen Required

Reject Due To

| Other                                      | Decalcified specimens; bone marrow in EDTA |

Specimen Stability Information

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Clinical and Interpretive

Clinical Information
Molecular analysis of biomarkers is increasingly being utilized in oncology practices to support and guide diagnosis, prognosis, and therapeutic management of patients. Chromosomal translocations, interstitial deletions, and inversions that lead to gene fusions are common in various sarcomas such as Ewing sarcoma and rhabdomyosarcoma. This next-generation sequencing assay is used to detect specific gene fusions to assist in the diagnosis of sarcomas. See Sarcoma Targeted Gene Fusion Panel in Special Instructions for a table of known fusions associated with specific sarcoma histologies.

Reference Values
An interpretive report will be provided.

Interpretation
An interpretive report will be provided.

Cautions
This assay is not validated for the detection of point variations, indels, copy number alterations, or gene expression.

This assay may detect gene fusions that are present at the RNA level, but not the DNA level, that result from cis-splicing of adjacent genes or trans-splicing.(1)

This panel can detect in-frame and out-of-frame fusions. There may be lower sensitivity in detecting out-of-frame fusions such as exon-intron, intron-intron or big insertions. This assay will only detect fusions involving at least 1 gene in the defined genes of interest list.

This assay will only detect fusions involving gene transcripts that have been defined in UCSC Genome Browser (March 2012 version) available from Illumina's iGenomes Project.(2)

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 PCR failure.
A negative result does not rule out the presence of a gene fusion that may be present but below the limits of detection of this assay (tumor cells comprise <10% of the cell population; targeted fusion read coverage with <10 unique fusion molecules in a sample).

The limit of detection of this assay for specific gene fusions is dependent on a number of variables including decreased sensitivity with decreased tumor percentage and decreased sensitivity with decreased level of expression of the gene fusion.

RNA is particularly labile and degrades quickly. Rapid preservation of the tumor sample after collection reduces the likelihood of degradation but there are sometimes biological factors such as tumor necrosis which interfere with obtaining a high quality RNA specimen despite rapid preservation.

The presence or absence of a fusion may not be predictive of response to therapy or prognosis in all patients.

Fusions of uncertain significance may be identified.

**Supportive Data**

In a verification study, this next-generation sequencing (NGS) assay was performed in 111 sarcoma formalin-fixed, paraffin-embedded (FFPE) and cytology samples (86 fusion positive and 25 fusion negative). The NGS assay results were confirmed by RT-PCR and FISH tests. The overall accuracy of the NGS assay was 95.5% (106/111). No targeted gene fusions were detected in 20 negative control samples (100% specificity).

**Clinical Reference**


Performance

Method Description
Next-generation sequencing is performed to test for the presence of rearrangements involving targeted regions of 138 fusion genes. See Sarcoma Targeted Gene Fusion Panel 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
14 days

Maximum Laboratory Time
21 days

Specimen Retention Time
Unused portions of blocks will be returned to 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
81455 (If Applicable)
81445 (If Applicable)
81405 (If Applicable)
81406 (If Applicable)
81407 (If Applicable)
81408 (If Applicable)
LOINC® Information

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