MAYO CLINIC LABORATORIES

Test Definition: MCSRC

MayoComplete Comprehensive Sarcoma Panel, Next-Generation Sequencing, Tumor

Overview

Useful For

Primarily for identifying mutations/gene fusions that help in the diagnosis of specific soft tissue and bone tumors (sarcoma)

Secondarily for identifying mutations/gene fusions that have therapeutic or prognostic significance

Genetics Test Information

This test uses targeted next-generation sequencing to evaluate for somatic mutations within the *ALK, APC, BAP1, BCOR, BRAF, CDKN2A, CTNNB1, DICER1, EED, EGFR, FGFR4, GNA11, GNA14, GNAQ, GNAS, H3-3A, H3-3B, KIT, MDM2, MED12, MYOD1, NF1, PDGFRA, PDGFRB, PTPRD, ROS1, SMARCB1, SUZ12, TERT*-promoter, *TP53*, and *TSC2* genes. In addition, this test evaluates 138 gene targets for the presence of somatic gene fusions. It also assesses for microsatellite instability status and *BCOR* internal tandem duplications. See Targeted Genes and Methodology Details for MayoComplete Sarcoma Panels and Targeted Genes Fusions and Methodology Details for MayoComplete Sarcoma Panel for details regarding the targeted gene regions evaluated by this test.

This test is performed to evaluate for somatic mutations within solid tumor samples. It **does not assess** for germline alterations within the genes listed.

Additional 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.

Special Instructions

- Tissue Requirements for Solid Tumor Next-Generation Sequencing
- Targeted Genes and Methodology Details for MayoComplete Sarcoma Panels
- Targeted Gene Fusions and Methodology Details for MayoComplete Sarcoma Panel

Highlights

This test evaluates formalin-fixed, paraffin-embedded tumor or cytology slides to assist in the diagnosis and management of patients with sarcoma.

This test detects *BCOR* internal tandem duplications of exon 15.

Microsatellite instability (MSI) status is determined (microsatellite stable, MSI-High) as part of this test and is often clinically actionable for determining the efficacy of immunotherapy in solid tumors.

Method Name
Sequence Capture and Targeted Next-Generation Sequencing (NGS) and Polymerase Chain Reaction (PCR)-based NGS

NY State Available
Yes

Specimen

Specimen Type
Varies

Ordering Guidance
Multiple oncology (cancer) gene panels are available. For more information see Hematology, Oncology, and Hereditary Test Selection 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

Specimen Required
This assay requires at least 20% tumor nuclei.
-Preferred amount of tumor area with sufficient percent tumor nuclei: tissue 360 mm(2)
-Minimum amount of tumor area: tissue 72 mm(2)
-These amounts are cumulative over up to 15 unstained slides and must have adequate percent tumor nuclei.
-Tissue fixation: 10% neutral buffered formalin, not decalcified
-For specimen preparation guidance, see Tissue Requirements for Sold 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: Submit 3, if available, or 2 of the following specimens.
Acceptable: Submit **at least one** of the following specimens**.**

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

Specimen Type: Tissue slide
Slides: 1 Hematoxylin and eosin-stained and 15 unstained

Collection Instructions:
Submit the followings slides:
1 Slide stained with hematoxylin and eosin
AND
15 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 total of 5000 nucleated cells (preferred) or at least 3000 nucleated cells (minimum).
Note: Glass coverslips are preferred; plastic coverslips are acceptable but will result in longer turnaround times.
Additional Information: Cytology slides will not be returned. An image of the slides will be stored per regulatory requirements.

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
All specimens will be evaluated at Mayo Clinic Laboratories for test suitability.

Specimen Stability Information

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

Clinical & 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. Microsatellite instability status is an increasingly important biomarker for determining effective immunotherapeutic treatment options for patients with solid tumors.

This next-generation sequencing assay interrogates targeted regions for the presence of somatic mutations, chromosomal translocations, interstitial deletions, and inversions that lead to gene fusions that are common in various sarcomas.

Reference Values
An interpretive report will be provided.

Interpretation

The interpretation of molecular biomarker analysis includes an overview of the results and the associated diagnostic, prognostic, and therapeutic implications.

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.

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

DNA variants and fusions of uncertain significance may be identified.

A negative result does not rule out the presence of a variant or fusion that may be present below the limits of detection of this assay. The analytical sensitivity of this assay for sequence reportable alterations is 5% mutant allele frequency with a minimum coverage of 500X in a sample with 20% or more tumor content.

Point mutations and small deletion-insertion mutations (delins) will be detected in the *ALK, APC, BAP1, BCOR, BRAF, CDKN2A, CTNNB1, DICER1, EED, EGFR, FGFR4, GNA11, GNA14, GNAQ, GNAS, H3-3A, H3-3B, KIT, MDM2, MED12, MYOD1, NF1, PDGFRA, PDGFRB, PTPRD, ROS1, SMARCB1, SUZ12, TERT-promoter, TP53,* and *TSC2* genes. This test may detect single exon deletions but does not detect multi-exon deletions, duplications, larger-scale genomic copy number variants, copy neutral loss of heterozygosity, or epigenetic modifications such as promoter methylation. Delins of 1000 bp or less are detectable with at least 50 or more supporting reads.

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 one gene in the defined gene fusion target list of interest.

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.

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.(1,2)

Rare alterations (ie, polymorphisms) may be present that could lead to false-negative or false-positive results.

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

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.

Supportive Data

Performance Characteristics
The limit of detection for calling a somatic variant (single nucleotide variants [SNV] and deletions-insertions [delins]) is 5% variant allele frequency and having at least 500x deduplicated coverage.

Verification studies demonstrated concordance between this test and the reference method for detection of SNV and delins is 99.7% (699/701) and 96.6% (226/234) of variants, respectively. Concordance for the detection of delins was 98.9% (186/188) in variants 1 to 10 base pair (bp) in size, 95.8% (23/24) in variants 11 to 50 bp in size, and 88.9% (8/9) in variants 51 to 200 bp in size.

Microsatellite instability (MSI) evaluation is accurate at a tumor purity of at least 10% for colorectal tumors and 20% for other tumor types. During verification studies, 98% (200/204) concordance for MSI status was observed between this test and the reference method.

Fusion evaluation was performed in 111 sarcoma formalin-fixed, paraffin-embedded and cytology samples (86 fusion positive and 25 fusion negative). The next-generation sequencing (NGS) assay results were confirmed by reverse-transcription polymerase chain reaction and fluorescent in situ hybridization tests. The overall accuracy of the fusion NGS assay was 95.5% (106/111). No targeted gene fusions were detected in 20 negative control samples (100% specificity).

To ensure accuracy, this test will be performed on cases that are estimated by a pathologist to have at least 20% tumor cells.

Clinical Reference

1. Strom SP. Current practices and guidelines for clinical next-generation sequencing oncology testing. Cancer Biol Med. 2016;13(1):3-11. doi:10.28092/j.issn.2095-3941.2016.0004
2. Spurr L, Li M, Alomran N, et al. Systematic pan-cancer analysis of somatic allele frequency. Sci Rep. 2018;8(1):7735. Published 2018 May 16. doi:10.1038/s41598-018-25462-0
3. US Food and Drug Administration (FDA): Table of Pharmacogenomic Biomarkers in Drug Labeling. FDA; Updated September 23, 2024, Accessed September 4, 2025. Available at www.fda.gov/drugs/science-and-research-drugs/table-pharmacogenomic-biomarkers-drug-labeling
4. Jia Y, Xie Z, Li H. Intergenically spliced chimeric RNAs in cancer. Trends Cancer. 2016;2(9):475-482. doi:10.1016/j.trecan.2016.07.006
5. Jo VY, Fletcher CDM. WHO classification of soft tissue tumours: an update based on the 2013. 4th ed. Pathology. 2014;46(2):95-104. doi:10.1097/PAT.0000000000000050
6. Fletcher CDM. The evolving classification of soft tissue tumours - an update based on the new 2013 WHO classification. Histopathology. 2014;64(1):2-11. doi:10.1111/his.12267
7. Quesada J, Amato R. The molecular biology of soft-tissue sarcomas and current trends in therapy. Sarcoma.

2012;2012:849456. doi:10.1155/2012/849456
8. Podnar J, Deiderick H, Huerta G, Hunicke-Smith S. Next-generation sequencing RNA-seq library construction. Curr Protoc Mol Biol. 2014;106:4.21.1-19. doi:10.1002/0471142727.mb0421s106
9. Mertens F, Tayebwa J. Evolving techniques for gene fusion detection in soft tissue tumours. Histopathology. 2014;64(1):151-162. doi:10.1111/his.12272
10. Al-Zaid T, Wang WL, Somaiah N, Lazar AJ. Molecular profiling of sarcomas: new vistas for precision medicine. Virchows Arch. 2017;471(2):243-255
11. Gao Q, Liang WW, Foltz SM, et al. Driver fusions and their implications in the development and treatment of human cancers. Cell Rep. 2018;23(1):227-238e3. doi:10.1016/j.celrep.2018.03.050
12. Lam SW, Cleton-Jansen AM, Cleven AHG, et al. Molecular analysis of gene fusions in bone and soft tissue tumors by anchored multiplex PCR-based targeted next-generation sequencing. J Mol Diagn. 2018;20(5):653-663. doi:10.1016/j.jmoldx.2018.05.007
13. Roy A, Kumar V, Zorman B, et al. Recurrent internal tandem duplications of BCOR in clear cell sarcoma of the kidney. Nat Commun. 2015;6:8891. doi:10.1038/ncomms9891
14. Marino-Enriquez A, Lauria A, Przybyl J, et al. BCOR internal tandem duplication in high-grade uterine sarcomas. Am J Surg Pathol. 2018;42(3):335-341. doi:10.1097/PAS.0000000000000993
15. Marcus L, Lemery SJ, Keegan P, Pazdur R. FDA Approval Summary: Pembrolizumab for the treatment of microsatellite instability-high solid tumors. Clin Cancer Res. 2019;25(13):3753-3758. doi:10.1158/1078-0432.CCR-18-4070

Performance

Method Description

Next-generation sequencing is performed to determine microsatellite instability (MSI) status and evaluate the presence of a mutation in targeted regions of the *ALK, APC, BAP1, BCOR, BRAF, CDKN2A, CTNNB1, DICER1, EED, EGFR, FGFR4, GNA11, GNA14, GNAQ, GNAS, H3-3A, H3-3B, KIT, MDM2, MED12, MYOD1, NF1, PDGFRA, PDGFRB, PTPRD, ROS1, SMARCB1, SUZ12, TERT-promoter, TP53,* and *TSC2* genes. RNA-based next-generation sequencing is performed to test for the presence of rearrangements involving targeted regions of 138 fusion. See Targeted Genes and Methodology Details for MayoComplete Sarcoma Panels and Targeted Genes Fusions and Methodology Details for MayoComplete Sarcoma Panel for details regarding the targeted gene regions evaluated by this test.(Unpublished Mayo method)

PDF Report

No

Day(s) Performed

Monday through Friday

Report Available

12 to 20 days

Specimen Retention Time

Tissue blocks: Unused portions of blocks will be returned; Tissue slides: Unused slides are stored for at least 5 years; Extracted DNA/RNA: 3 months

Test Definition: MCSRC

MayoComplete Comprehensive Sarcoma Panel, Next-Generation Sequencing, Tumor

Performing Laboratory Location

Mayo Clinic Laboratories - Rochester Main Campus

Fees & 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 account representative. 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. It has not been cleared or approved by the US Food and Drug Administration.

CPT Code Information

81457

LOINC® Information

Test ID	Test Order Name	Order LOINC® Value
MCSRC	MayoComplete Sarcoma Panel	95124-4

Result ID	Test Result Name	Result LOINC® Value
617849	Result	82939-0
617850	Interpretation	69047-9
617851	Additional Information	48767-8
617852	Specimen	31208-2
617853	Tissue ID	80398-1
617854	Method	85069-3
617855	Disclaimer	62364-5
617856	Released By	18771-6