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 variants that have therapeutic or prognostic significance

Assessing microsatellite instability for immunotherapy decisions

Reflex Tests

Test Id	Reporting Name	Available Separately	Always Performed
MCSMP	MayoComplete Sarcoma Mutation Panel	Yes	No
MCRSP	MayoComplete Targeted RNAseq Panel	Yes	No

Genetics Test Information

This test uses targeted next-generation sequencing to assess microsatellite instability status and 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 1445 genes for the presence of somatic gene fusions, known abnormal transcript variants in the *MET* and *EGFR* genes, and *BCOR* internal tandem duplications. See Targeted Genes and Methodology Details for MayoComplete Sarcoma Panels and Targeted Fusion Genes for MayoComplete Sarcoma Panel for details regarding the targeted gene regions evaluated by this test.

This test is performed to evaluate for somatic mutations and gene fusions within solid tumor samples. It **does not assess** for germline alterations.

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.

This test includes DNA mutation and RNA fusion analyses. A reflex test is added only when there is insufficient specimen for both test components. Indicate the preferred order of testing on the paperwork. If the specimen is insufficient to perform all portions of testing, the lab will use this prioritization to select the appropriate reflex test ID, reducing

communication delays. If additional tests are ordered on same specimen, include them in the prioritization preferences.

Special Instructions

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

Highlights

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

This test detects *BCOR* internal tandem duplications of exon 15, and splice variants for *EGFR* and *MET* genes.

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)

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
5. Diagnosis, potential diagnosis, or differential diagnosis

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: Hematoxylin and eosin-stained and unstained slides will not be returned.

Specimen Type: Cytology slide (Diff-Quik or Pap stained direct smears or ThinPrep)
Slides: 2 to 6 Slides
Collection Instructions: Submit 2 to 6 slides, stained and coverslipped, with a total of 10,000 nucleated cells (preferred) or 2 slides with at least 2000 nucleated cells per slide (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, and gene fusions that can result from chromosomal translocations, interstitial deletions, and inversions, 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.

Variants and fusions 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. 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.

The sensitivity of this assay for gene fusions depends on several variables including decreased sensitivity with decreased tumor percentage, and decreased sensitivity with decreased level of expression of a variant. A negative result does not rule out the presence of a gene fusion, splice variant, or *BCOR* exon 15 internal tandem duplication that may be present but below the limits of detection of this assay. The analytical sensitivity of this assay for rearrangements is a minimum coverage of 5 unique variant molecules in a sample with at least 10% 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 assay can detect in-frame and out-of-frame fusions involving 1445 genes. Sensitivity for detecting out-of-frame fusions such as exon-intron, intron-intron or big insertions, may be lower due to bioinformatics detection limitations. This assay will only detect fusions involving at least 1 gene in the defined gene fusion target list of interest. This assay may not detect fusions involving deep intron or intergenic regions and will not detect chromosomal rearrangements that do not create a fusion transcript (i.e. enhancer repositioning). Variants not expressed, or expressed at very low level, are not detected by this assay.

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 variants, or alterations derived from the production of a gene fusion, 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

DNA validation studies demonstrated concordance between this test and the reference method for detection of single nucleotide variants (SNV) and deletions-insertions (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.

RNA Validation studies demonstrated that concordance between this test, and the reference method, for detection of gene fusions, *BCOR* in-tandem duplications, and splice variants within *MET* and *EGFR* is 96.6% (256/265). No gene fusions were detected in 14 normal tissues, and no gene fusions were detected in the negative control sample (100%

specificity). The sensitivity of this assay for detecting *CIC*::*DUX4* fusions is lower (approximately 70%-80%), based on preclinical testing; tumors that are fusion negative but suspected to be *CIC*-rearranged may require orthogonal methods including immunohistochemistry, fluorescence in situ hybridization, real-time polymerase chain reaction, gene expression profiling, and/or methylation profiling.

To ensure this assay detects variants based on established sensitivity, this test will be performed on cases that are estimated by a pathologist to have at least 20% tumor cells.

Clinical Reference

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Performance

Method Description

Next-generation sequencing (NGS) is performed to determine microsatellite instability 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 NGS is performed to test for the presence of rearrangements involving 1445 genes, selected splice variants in *MET* and *EGFR* genes, and internal tandem duplications within exon 15 of the *BCOR* gene.

See Targeted Genes and Methodology Details for MayoComplete Sarcoma Panels and Targeted Fusion Genes for MayoComplete Sarcoma Panel for details regarding the targeted gene regions evaluated by this test genes.(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: Hematoxylin and eosin-stained and unstained slides will not be returned. Unused slides are stored for at least 5 years; Extracted DNA/RNA: 3 months

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
81456

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