

MayoComplete Comprehensive Sarcoma Panel, Next-Generation Sequencing, Tumor

Test ID: MCSRC

Useful for:

- Primarily for identifying mutations that help in the diagnosis of specific soft tissue and bone tumors (sarcoma)
- Secondly for identifying mutations that have therapeutic or prognostic significance
- Assessment of microsatellite instability for immunotherapy decisions

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.

Methods:

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

Reference Values:

An interpretive report will be provided.

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 Requirements:

This assay requires at least 20% tumor nuclei.

- Preferred amount of tumor area with sufficient percent tumor nuclei: tissue 360mm(2)
 - Minimum amount of tumor area: tissue 72mm(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 Requirement for Solid Tumor Next-Generation Sequencing](#).
- 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 slides

Slides: 1 Stained and 15 unstained

Collection Instructions: Submit 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 15 slides from the same block.

Additional Information: Unused unstained slides will not be returned.

Specimen Type: Cytology slides (direct smears or ThinPrep)

Slides: 2 to 4 Slides

Collection Instructions: Submit 2 to 4 slides stained and cover slipped with a preferred total of 10,000 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		

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 there are sometimes 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 but 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 insertion/deletion mutations will be detected in the *ALK*, *APC*, *BAP1*, *BCOR* (exon 15), *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, or genomic copy number variants in any of the genes tested.
- 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.
- Rare alterations (ie, polymorphisms) may be present that could lead to false-negative or false-positive results.
- 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.
- 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 and/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
81445

Day(s) Performed: Monday through Friday

Report Available: 12-20 days

Questions

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