MAYO CLINIC LABORATORIES

1-800-533-1710

MCRSP

MayoComplete Targeted RNA Sequencing Panel, Next-Generation Sequencing, Tumor

Patient ID	Patient Name		Birth Date	Sex	Age
321	IMPLEMENTATION, TEST T		1973-05-01	F	52
Order Number	**Client Order Number**	**Ordering Physician**	**Report Notes**		
X100515180	X100515180	UNKNOWN,PROVIDER			
Account Information		**Collected**			
C7028846 DLMP Rochester		01 Dec 2025 09:00			

MayoComplete Targeted RNAseq Panel

Result

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Provided diagnosis: sarcoma

NO reportable CLINICALLY RELEVANT FUSIONS/TRANSCRIPT VARIANTS were detected involving the tested genes.

Interpretation

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This result is consistent with the absence of reportable fusions/transcript variants involving the targeted regions of the tested genes.

An abnormality involving the genes evaluated in this panel is not excluded since fusions/transcript variants involving non-targeted gene regions, and genomic abnormalities not detectable by this method (e.g. genomic copy number alterations) may be present. If not already performed, consider chromosomal microarray analysis to assess for copy number changes (CMAPT/ Chromosomal Microarray, Tumor, FFPE).

Correlation with histopathological and clinico-radiological findings and other available genetic test results is recommended.

Additional Information

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CLINICAL TRIALS

Possible clinical trials of benefit for this patient can be found at the following sites:
1) ClinicalTrials.gov: www.clinicaltrials.gov/ct2/search/advanced
2) Mayo Clinic: www.mayo.edu/research/clinical-trials/ 3) National Cancer Institute: www.cancer.gov/clinicaltrials/search

Specimen

MCR

Tissue, Tumor

Tissue ID

MCR

12345

Method

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Microscopic examination is performed by a pathologist to identify areas of tumor for enrichment by macrodissection.

Next-generation sequencing is performed to test for the presence of gene rearrangements involving 1,445 genes, transcript variants in the MET and EGFR genes and in-tandem duplications within exon 15 of the BCOR gene.

Variant nomenclature is based on build GRCh37 (hg19). For details about gene transcripts (RefSeq accession numbers), specific targeted regions of each gene, and additional information on this test, see www.mayocliniclabs.com (Test ID MCRSP).

Disclaimer

1 MCR

This assay is not validated for the detection of single nucleotide variations, deletions-insertions, copy number alterations, or gene expression.

Fusions of uncertain significance may be identified.

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 is a minimum coverage of 5 unique variant molecules in a sample with at least 10% tumor content.

This assay can detect in-frame and out-of-frame fusions involving 1,445 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

Performing Site Legend

Code	Laboratory	Address	Lab Director	CLIA Certificate
MCR	Mayo Clinic Laboratories - Rochester Main Campus	200 First Street SW, Rochester, MN 55905	Nikola Baumann Ph.D.	24D0404292

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expressed at very low level, are not detected by this assay.

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 fusion may not be predictive of response to therapy in all patients.

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, contact the laboratory for an updated interpretation. 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 PCR failure.

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

Released By MCR

HUSSAM AL KATEB

Received: 02 Dec 2025 12:23 **Reported:** 04 Dec 2025 14:18

Laboratory Notes

1 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.

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