MAYO CLINIC LABORATORIES

1-800-533-1710

MCSMP

MayoComplete Sarcoma Mutation Panel, Next-Generation Sequencing, Tumor

Patient ID	Patient Name		Birth Date	Sex	Age
SA00175007	TESTINGRNV, ABNORMAL		1985-03-25	F	40
Order Number	**Client Order Number**	**Ordering Physician**	**Report Notes**		
SA00175007	SA00175007	CLIENT,CLIENT			
Account Information		**Collected**			
C7028846 DLMP Rochester		28 Mar 2025 00:00			

MayoComplete Sarcoma Mutation Panel

Result

MCR

Provided diagnosis: soft tissue sarcoma

The following CLINICALLY RELEVANT VARIANT was detected:
Gene: GNA11
DNA Change: c.548G>A (Exon 4)
Amino Acid Change: p.R183H (Arg183His)
Variant Allele Frequency: 35.2%

Microsatellite Instability (MSI) status: Stable (MSS)

The following VARIANT OF UNCERTAIN SIGNIFICANCE was detected:
Gene: PDGFRA
DNA Change: c.2816A>G (Exon 21)
Amino Acid Change: p.K939R (Lys939Arg)
Variant Allele Frequency: 12.9%

No other reportable sequence variants were detected within the analyzed regions of the tested genes listed in the method description.

This assay only evaluates mutations and small insertion/deletions. FUSION testing was NOT PERFORMED. If fusion testing is desired, consider Sarcoma Targeted Gene Fusion/Rearrangement Panel, Next-Generation Sequencing, **Tumor (Mayo Test ID:** SARCP) or FISH assays. Refer to mayocliniclabs.com or call 1–800–533–1710 for more information about specimen requirements for this test.

Interpretation

MCR

1) GNA11 c.548G>A (p.R183H) (Exon 4)

GNA11 encodes the Guanine nucleotide-binding protein subunit alpha-11 (G alpha-11), which is one of the Gq subunits [PMID:1902575, PMID:8838318]. Gq proteins activate phospholipase C and act as modulators of transmembrane signaling. Activation of GNA11, mainly through mutations at codons Q209 and R183, leads to activation of the MAPK pathway and oncogenic transformation [PMID:21083380, PMID:23640210].

GNA11 mutations have been reported in 1% of sarcoma samples [COSMIC, cBioPortal for Cancer Genomics].

There are currently no known clinically approved therapies that specifically target GNA11 mutations.

MSI: Stable (MSS)
NO evidence of microsatellite instability was detected suggesting the presence of normal DNA mismatch repair function within the tumor. Current data suggest that advanced stage solid tumors with intact mismatch repair (MSS) are less likely to be responsive to treatment with immunotherapies such as anti-PD-1 therapies [PMID 28596308, PMID 29355075].

Additional Information

MCR

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

REFERENCE TRANSCRIPTS

Sequence variant nomenclature is based on the following RefSeq accession numbers (build GRCh37 (hg19)):GNA11 NM_002067 and PDGFRA NM_006206.

Specimen

MCR

Tissue, Tumor

Tissue ID

MCR

12345

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

Patient ID	Patient Name		Birth Date	Sex	Age
SA00175007	TESTINGRNV, ABNORMAL		1985-03-25	F	40
Order Number	**Client Order Number**	**Ordering Physician**	**Report Notes**		
SA00175007	SA00175007	CLIENT,CLIENT			
Account Information		**Collected**			
C7028846 DLMP Rochester		28 Mar 2025 00:00			

Method

MCR

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 microsatellite instability and a mutation within all coding regions and exon/intron boundaries of the following targeted genes (unless otherwise specified): ALK, APC, BAP1, BCOR (exon 15 only), BRAF, CDKN2A, CTNNB1, DICER1, EED, EGFR, FGFR4, GNA11, GNA14, GNAQ, GNAS, H3–3A (excludes exon 4), H3–3B, KIT, MDM2, MED12 (excludes exon 43), MYOD1, NF1, PDGFRA, PDGFRB, PTPRD, ROS1, SMARCB1, SUZ12 (excludes exons 3, 4, 6, and 9), TERT (promoter), TP53, and TSC2.

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 MCSMP).

Disclaimer

[1] MCR

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.

DNA variants of uncertain significance may be identified.

A negative result does not rule out the presence of a variant 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 at least 20% 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 only. 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 (LOH), or epigenetic modifications such as promoter methylation. DELINS of 1,000 bp or less are detectable with at least 50 or more supporting reads.

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 [PMID: 27144058, PMID: 29769535].

Rare polymorphisms may be present that could lead to false-negative or false-positive results.

The presence or absence of a variant 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 PCR failure.

Released By

MCR

Sounak Gupta, M.B.B.S., Ph.D.

Received: 29 Mar 2025 16:25 **Reported:** 02 May 2025 08:04

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.

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