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**		
X100515183	X100515183	UNKNOWN,PROVIDER			
Account Information		**Collected**			
C7028846 DLMP Rochester		01 Dec 2025 05:00			

Neuro-Onc Expanded Panel

Result

MCR

Provided diagnosis: glioma

Microsatellite Instability (MSI) status: Stable (MSS)

NO reportable CLINICALLY RELEVANT SEQUENCE VARIANTS detected within the analyzed regions of the tested genes, including IDH1, IDH2 and H3–3A (previously H3F3A).

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

Interpretation

1 MCR

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

An abnormality involving the genes evaluated in this panel is not excluded since sequence variants and 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

Microscopic examination was 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 (unless otherwise specified) and exon/intron boundaries of the following 89 targeted genes: ACVR1, AKT1, APC, ARID1A, ATRX, BAP1, SCOR, BRAF, CDKN2A, CDKN2B, CIC, CTNNB1, CYSLTR2, DAXX, DDX3X, DGCR8, DICER1, DROSHA, EEO, EGFR, EIF1AX, ERBB2, FGFR1, FGFR2, FGFR3, FUBP1, GNA11, GNAQ, GNAS, H3–3A, H3–3B, H3C2, H3C3, HIST2H3C, HRAS, IDH1, IDH2, KBTBD4, KDM6A, KIT, KLF4, KRAS, LZTR1, MAP2K1, MET, MLH1, MSH2, MSH6, MTOR, NF1, NF2, NOTCH1, NRAS, NTRK1, NTRK2, NTRK3, PBRM1, PDGFRA, PIK3CA, PIK3R1, PLCB4, PMS2, POLD1, POLE, POLR2A, PPM1D, PRKCA, PRKAR1A, PTCH1, PTEN, PTPN11, RB1, SETD2, SF381, SMARCA2, SMARCA4, SMARCAL1, SMARCB1, SMARCE1, SMO, SUFU, SUZ12, TCF12, TERT (Promoter), TP53, TRAF7, TSC1, TSC2, and VHL

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 NONCP). 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.

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 insertion/deletion mutations will be detected in 89 genes. This test may detect single exon deletions

Test Environment TCSFD Template

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
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but does not detect multi-exon deletions, duplications, or genomic copy number variants in any of the genes tested. Deletions-insertions (delins) of 1000 base pairs or less are detectable with at least 50 supporting reads.

This test cannot reliably determine if a variant identified in PMS2 exons 11–15 originated from PMS2 or the highly homologous pseudogene PMS2CL. In the instance that a reportable variant is detected in PMS2 exons 11–15, additional testing will be recommended in the patient report.

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

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 intronic 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 [PMID: 27144058, PMID: 29769535].

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

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

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 formalin-fixed, paraffin-embedded tissues; other fixatives are discouraged. Improper treatment of tissues, such as decalcification, may cause polymerase chain reaction failure.

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.

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

Specimen

MCR

Tissue, Tumor

Tissue ID

MCR

13245

Released By

MCR

Cristiane M. Ida, M.D.

Received: 02 Dec 2025 12:25 **Reported:** 04 Dec 2025 16:32

First Test LTCSF Sample

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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C7028846 DLMP Rochester		01 Dec 2025 05:00			

Test Environment
LTCSEQ Template

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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