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**		
X100515184	X100515184	UNKNOWN,PROVIDER			
Account Information		**Collected**			
C7028846 DLMP Rochester		01 Dec 2025 06:00			

Neuro-Onc Expanded Panel

Result

MCR

Provided diagnosis: meningioma

The following CLINICALLY RELEVANT VARIANT was detected:
Gene: NF2
DNA Change: c.488del (Exon 5)
Amino Acid Change: p.L163Wfs*11 (Leu163Trpfs*11)
Variant Allele Frequency: 74.4%

Microsatellite Instability (MSI) status: Stable (MSS)

NO reportable CLINICALLY RELEVANT SEQUENCE VARIANTS detected within the analyzed regions of the remaining tested genes, including TERT.

NO reportable CLINICALLY RELEVANT FUSIONS/TRANSCRIPT VARIANTS detected involving the tested genes, including YAP1.

Interpretation

1 MCR

This result should be interpreted in correlation with histopathological and clinico-radiological findings and other available genetic test results.

1) NF2 c.488del (p.L163Wfs*11) (Exon 5)

NF2 encodes the tumor suppressor protein Merlin, which inhibits cell growth in the setting of contact between cells [PMID:17971776, PMID:22012890]. Functional loss of NF2 results in aberrant signaling of multiple pathways and contributes to tumorigenesis [PMID:18632626, PMID:25893302].

NF2 mutations contribute to biallelic NF2 inactivation, which is a diagnostic molecular biomarker for meningioma [WHO Classification of Tumours Editorial Board. Central nervous system tumours. Lyon (France): International Agency for Research on Cancer, 5th ed., vol. 6, 2021]. NF2 mutations have been primarily described in low-grade meningioma with fibrous and transitional morphology, atypical/anaplastic meningioma, schwannoma and spinal ependymoma [COSMIC, cBioPortal for Cancer Genomics, PMID:28195122, PMID:28713588]. NF2 mutations have also been recurrently reported in adult-type diffuse gliomas [COSMIC, cBioPortal for Cancer Genomics]. In other central and peripheral nervous system tumors, NF2 mutations are rare or have not been reported [COSMIC, cBioPortal for Cancer Genomics].

Germline (inherited) mutations in NF2 are associated with a hereditary cancer syndrome. This test does not distinguish between germline and somatic (not inherited) genetic variants. If a hereditary cancer syndrome is suspected for this patient, clinical correlation with their personal and family history as well as a referral for genetic counseling is recommended.

There are currently no known clinically approved therapies that specifically target NF2 mutations.

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

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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 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.

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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 TRANSCRIPT

Sequence variant nomenclature is based on the following RefSeq accession number (build GRCh37 (hg19)):NF2 NM_000268.

Specimen

MCR

Tissue, Tumor

Tissue ID

MCR

12345

Released By

MCR

Cristiane M. Ida, M.D.

Received: 02 Dec 2025 12:26 **Reported:** 04 Dec 2025 16:33

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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