MAYO CLINIC LABORATORIES

1-800-533-1710

MFRGP

Marfan Syndrome and Related Disorders Multi-Gene Panel, Varies

Patient ID	Patient Name		Birth Date	Gender	Age
SA00108989	TESTINGRNV, MFRGP		1981-09-04	M	36
Order Number	**Client Order Number**	**Ordering Physician**	**Report Notes**		
SA00108989	SA00108989	CLIENT, CLIENT			
Account Information		**Collected**			
C7028846 DLMP Rochester		30 Jul 2018 00:00			

Result Summary

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Negative

Result

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ACTA2	CBS	COL3A1	COL5A1	COL5A2	FBN1	FBN2	FLNA	MFAP5
MYH11	MYLK	NOTCH1	PRKG1	SKI	SLC2A10	SMAD3	SMAD4	TGFB2
TGFB3	TGFBR1	TGFBR2						

The sequencing and deletion/duplication results for all genes on this panel are negative.

Interpretation

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This result decreases the likelihood of, but does not rule out, involvement of the genes evaluated on this panel. Some affected individuals may have a pathogenic variant in one of these genes that is not detectable by the methods utilized. Additionally, the clinical phenotype that is observed in this individual and/or family may be due to a pathogenic variant(s) in a different gene(s).

This result should be interpreted in the context of clinical findings, family history, and other laboratory testing. Consultation with a genetics professional may be of benefit for interpretation of this result.

Next generation sequencing may not detect all types of genetic variants. If results do not match clinical findings, alternative testing methods could be considered.

Performing Site Legend

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

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Method

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Next generation sequencing and/or Sanger sequencing was performed to test for the presence of sequence variants in all coding regions and intron/exon boundaries of the genes tested.

Utilization of an algorithm designed to detect intragenic deletions and duplications, with sensitivity down to a single exon, allows for the detection of most intragenic deletions and duplications. However some samples may not meet the required standards for this analysis. If these standards are not met, the lack of deletion/duplication analysis will be noted in the patient's results.

Disclaimer

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CAUTIONS:

CLINICAL CORRELATIONS

Test results should be interpreted in context of clinical findings, family history, and other laboratory data. Misinterpretation of results may occur if the information provided is inaccurate or incomplete.

If testing was performed because of a clinically significant family history, it is often useful to first test an affected family member. Identification of a pathogenic variant in an affected individual would allow for more informative testing of at risk individuals.

TECHNICAL LIMITATIONS

Next generation sequencing may not detect all types of genetic variants. Additionally, rare variants may be present that could lead to false negative or positive results. If results do not match clinical findings, consider alternative methods for analyzing these genes., If the patient has had an allogeneic blood or marrow transplant or a recent (i.e. less than 6 weeks from time of sample collection) heterologous blood transfusion these results may be inaccurate due to the presence of donor DNA.

RECLASSIFICATION OF VARIANTS POLICY

At this time, it is not standard practice for the laboratory to systematically review likely pathogenic variants or variants of uncertain significance that are detected and reported. The laboratory encourages health care providers to contact the laboratory at any time to learn how the status of a particular variant may have changed over time.

Consultation with a genetics professional should be considered for interpretation of this result. A list of benign and likely benign variants identified for this patient is available from the lab upon request. Please contact the laboratory if additional information is required regarding the transcript and/or human genome assembly used for the analysis of this patient's results.

VARIANT EVALUATION

Evaluation and categorization of variants is performed using the most recent published ACMG recommendations as a guideline. Variants are classified based on known, predicted, or possible pathogenicity and reported with interpretive comments detailing their potential or known significance.

Multiple in silico evaluation tools may be used to assist in the interpretation of these results. The accuracy of predictions made by in silico evaluation tools is highly dependent upon the data available for a given gene, and predictions made by these tools may change over time. Results from in silico evaluation tools should be interpreted with caution and professional clinical judgment.

Unless reported or predicted to cause disease, alterations found deep in the intron or alterations that do not result in an amino acid substitution are not reported. 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.

Reviewed by

MCR

Mary Karow

Received: 31 Jul 2018 11:46 **Reported:** 31 Jul 2018 11:51

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