MAYO CLINIC

1-800-533-1710

STK11 Full Gene Analysis

STK1Z

PATIENT NAME				ORDER NUMBER
TESTRNV, IMPLEMENTATION				**L002000272**
PATIENT ID X100366928	DATE OF BIRTH 02/19/1968	AGE 53 Y	SEX Female	REQUESTED BY CLIENT TESTING
COLLECTED 9/2/2021, 7:30 AM	RECEIVED 9/3/2021, 2:02 PM	REPORTED 9/9/2021, 6:28 PM		
The collected, received, and reported dates and times on the report are in the time zone of the performing location.				CLIENT ORDER NUMBER X100366928
7028846 MCL RochesterCampus Rochester MN 55901				CLIENT MRN 321

TEST DESCRIPTION

Evaluation of the STK11 gene associated with Peutz-Jeghers syndrome

SPECIMEN

WB Whole Blood

RESULT SUMMARY

Pathogenic Variant Detected

RESULT

Gene (Transcript)	Variant	Zygosity	Classification
STK11 NM_000455.5	p.K84* p.Lys84* c.250A>T Chr19(GRCh37):g.1207162	heterozygous	PATHOGENIC

The following heterozygous PATHOGENIC variant was detected:
STK11 (NM_000455.5), p.K84* (p.Lys84*), c.250A>T, Chr19(GRCh37):g.1207162

INTERPRETATION

STK11 c.250A>T (p.K84*), PATHOGENIC
The heterozygous c.250A>T (p.K84*) nonsense variant in the STK11 gene (MIM:602216) is an established pathogenic variant. Variants in the STK11 gene have been associated with autosomal dominant Peutz-Jeghers syndrome (PJS) (1). Taken together, the evidence supports a classification of pathogenic for this STK11 deletion. This result is supportive of a diagnosis of Peutz-Jeghers syndrome for this individual. Clinical correlation is recommended.

This result should be interpreted in the context of clinical findings, family history, and other laboratory testing.

Consultation with a genetics professional is recommended for interpretation of this result and to determine whether reproductive risk assessment and familial testing may be of benefit to this family. Genetic testing for family members is available by ordering FMTT / Familial Mutation, Targeted Testing for the specific variant(s) detected. Please contact the laboratory at 1-800-533-1710 or the online test catalog at www.mayocliniclabs.com for information about FMTT.

REFERENCES:
1) GeneReviews: Peutz-Jeghers Syndrome (https://www.ncbi.nlm.nih.gov/books/NBK1266/) (PMID: 20301443)

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METHOD

Next generation sequencing (NGS) and/or Sanger sequencing is performed to test for the presence of variants in coding regions and intron/exon boundaries of the genes analyzed, as well as some other regions that have known pathogenic variants. The human genome reference GRCh37/hg19 build was used for sequence read alignment. At least 99% of the bases are covered at a read depth over 30X. Sensitivity is estimated at above 99% for single nucleotide variants, above 94% for indels less than 40 base pairs (bp), above 95% for deletions up to 75 bp and insertions up to 47 bp. NGS, and/or a polymerase chain reaction (PCR)-based quantitative method is performed to test for the presence of deletions and duplications in the genes analyzed. See the Genes Analyzed field for a list of genes tested.

There may be regions of genes that cannot be effectively evaluated for sequencing or deletion and duplication analysis as a result of technical limitations of the assay, including regions of homology, high GC content, and repetitive sequences. Confirmation of select reportable variants was performed by alternate methodologies based on internal laboratory criteria. See www.mayocliniclabs.com STK1Z for details regarding genes with regions not routinely covered.

GENES ANALYZED

STK11

DISCLAIMER

Clinical Correlations
If testing was performed because of a clinically significant family history it is often useful to first test an affected family member. Detection of a reportable variant(s) in an affected family member would allow for more informative testing of at risk individuals.

To discuss the availability of further testing options or for assistance in the interpretation of these results, Mayo Clinic Laboratory genetic counselors can be contacted at 1-800-533-1710.

Technical Limitations
Next generation sequencing may not detect all types of genomic variants. In rare cases, false negative or false positive results may occur. The depth of coverage may be variable for some target regions, but assay performance below the minimum acceptable criteria or for failed regions will be noted. Given these limitations, negative results do not rule out the diagnosis of a genetic disorder. If a specific clinical disorder is suspected, evaluation by alternative methods can be considered.

There may be regions of genes that cannot be effectively evaluated for sequencing or deletion and duplication analysis as a result of technical limitations of the assay, including regions of homology, high GC content, and repetitive sequences. Confirmation of select reportable variants was performed by alternate methodologies based on internal laboratory criteria.

Additionally, low level mosaic variants may not be detected.

This test is not designed to differentiate between somatic and germline variants. If there is a possibility that any detected

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variant is somatic, additional testing may be necessary to clarify the significance of results.

Reclassification of Variants Policy
See www.mayocliniclabs.com STK1Z for information regarding the laboratory's policy for reclassification of variants.

Variant Evaluation
Variant curation is performed using published ACMG-AMP recommendations as a guideline. Other gene-specific guidelines may also be considered. Variants classified as benign or likely benign are not reported.

Results from in silico evaluation tools may change over time and should be interpreted with caution and professional clinical judgment.

TEST CLASSIFICATION
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.

RELEASED BY

Sounak Gupta, M.B.B.S., Ph.D. 8-2183

Code : MCR Laboratory : Mayo Clinic Laboratories - Rochester Main Campus Address : 200 FIRST STREET SW
Lab Director : WILLIAM G MORICE, II MD, PhD CLIA Certificate : 24D0404292 ROCHESTER MN 55905