

ARUP LABORATORIES | aruplab.com

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Tracy I. George, MD, Chief Medical Officer

Patient Report

Patient Age/Gender: 42 years Female

Specimen Collected: 26-Sep-21 15:39

Procedure	Result	Units	Report/Verified: 26-Sep-21 16:02	Reference Interval
CADASIL (NOTCH3) by NGS			Received: 26-Sep-21 15:39	
CADASIL (NOTCH3) Specimen	Whole Blood			
CADASIL (NOTCH3) Interp	Negative ¹¹			

Test Information

i1: CADASIL (NOTCH3) Interp

BACKGROUND INFORMATION: Cerebral Autosomal Dominant Arteriopathy with Subcortical Infarcts and Leukoencephalopathy, CADASIL (NOTCH3), Sequencing

CHARACTERISTICS: CADASIL is a condition characterized predominantly by subcortical ischemic events, including transient ischemic attacks (TIAs) and strokes. Other features of this condition include cognitive defects, dementia, migraines, psychiatric and mood disorders, and epilepsy. Age of onset and clinical presentation are highly variable.

PREVALENCE: 2-4 in 100,000; penetrance may be variable.

INHERITANCE: Autosomal dominant.

CAUSE: Pathogenic variants in the NOTCH3 gene.

CLINICAL SENSITIVITY: 95 percent.

GENE TESTED: NOTCH3 (NM_000435)
Exon 1 is not covered by sequencing.

METHODOLOGY: Capture of all coding exons and exon-intron junctions of the targeted gene, followed by massively parallel sequencing. Sanger sequencing performed as necessary to fill in regions of low coverage and confirm reported variants.

ANALYTICAL SENSITIVITY: The analytical sensitivity of this test is approximately 99 percent for single nucleotide variants (SNVs) and greater than 93 percent for insertions/duplications/deletions from 1-10 base pairs in size. Variants greater than 10 base pairs may be detected by massively parallel sequencing, but the analytical sensitivity may be reduced.

LIMITATIONS: A negative result does not exclude a diagnosis of CADASIL. This test only detects variants within the coding regions and intron-exon boundaries of the specific gene. Regulatory region variants and deep intronic variants will not be identified. Deletions/duplications/insertions of any size may not be detected by massively parallel sequencing. Diagnostic errors can occur due to rare sequence variations. In some cases, variants may not be identified due to technical

*=Abnormal, #=Corrected, C=Critical, f=Result Footnote, H-High, i-Test Information, L-Low, t-Interpretive Text, @=Performing lab

Unless otherwise indicated, testing performed at:

ARUP Laboratories
500 Chipeta Way, Salt Lake City, UT 84108
Laboratory Director: Tracy I. George, MD

ARUP Accession: n/a
Report Request ID: 15050559
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Test Information

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limitations in the presence of pseudogenes, repetitive, or homologous regions. This assay may not detect low-level mosaic or somatic variants associated with disease. Interpretation of this test result may be impacted if this patient has had an allogeneic stem cell transplantation. Noncoding transcripts were not analyzed.

The following regions are not sequenced due to technical limitations of the assay:
NOTCH3 (NM_000435) exon(s) 1

This test was developed and its performance characteristics determined by ARUP Laboratories. It has not been cleared or approved by the US Food and Drug Administration. This test was performed in a CLIA certified laboratory and is intended for clinical purposes.

Counseling and informed consent are recommended for genetic testing. Consent forms are available online.

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