

Specimen Collected: 10-Mar-21 14:12

Long QT NGS, Deldup Procedure	Result	Received: 10-Mar-21 14:12 Units	Report/Verified: 10-Mar-21 14:15 Reference Interval
Long QT Specimen	Whole Blood		
Long QT Interp	Negative ^{f1 i1}		

Result Footnote

f1: Long QT Interp
INDICATION FOR TESTING
Prolonged QT interval.

RESULT

No pathogenic variants were detected in any of the genes tested.

INTERPRETATION

No pathogenic variants were identified by massively parallel sequencing of the coding regions and exon-intron boundaries of the genes tested. No large exonic deletions and duplications were identified in the genes tested. This result decreases the likelihood of, but does not exclude, a heritable form of long QT syndrome (LQTS). Please refer to the background information included in this report for a list of the genes analyzed and limitations of this test.

RECOMMENDATIONS

Medical screening and management of this individual should rely on clinical findings and family history. Genetic consultation is recommended.

COMMENTS

Likely benign and benign variants are not included in this report.

Test Information

i1: Long QT Interp
BACKGROUND INFORMATION: Long QT Panel, Sequencing and
Deletion/Duplication

CHARACTERISTICS: Long QT syndrome (LQTS) is characterized by prolongation of the QTc interval and T-wave abnormalities on electrocardiogram that are associated with tachyarrhythmias, often torsade de pointes. Cardiac events including syncope, ventricular fibrillation or sudden cardiac death may occur from infancy to middle age, but are most common in preteens and young adults. Forms of LQTS associated with additional non-cardiac features include Andersen-Tawil syndrome (muscle weakness and distinctive facial features), Timothy syndrome (cutaneous syndactyly, neurodevelopmental and facial features), and Jervell and Lange-Nielsen syndrome (congenital sensorineural hearing loss).

EPIDEMIOLOGY: Prevalence of congenital LQTS is approximately 1 in 2,500.

CAUSE: Pathogenic germline variants in genes associated with LQTS.

INHERITANCE: Typically autosomal dominant with incomplete penetrance. Autosomal recessive inheritance for Jervell and Lange-Nielsen syndrome.

*=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: 14708253

Printed: 10-Mar-21 14:17

Page 1 of 3

Test Information

i1: Long QT Interp
PENETRANCE: Variable, influenced by gene involved.

CLINICAL SENSITIVITY: 60-75 percent.

GENES TESTED: CACNA1C, CALM1**, CALM2**, CAV3, KCNE1, KCNE2, KCNH2, KCNJ2, KCNQ1, SCN5A

** - Deletion/duplication detection is not available for this gene.

METHODOLOGY: Capture of all coding exons and exon-intron junctions of the targeted genes followed by massively parallel sequencing. Sanger sequencing was performed as necessary to fill in regions of low coverage and confirm reported variants. A custom tiled comparative genomic hybridization array (aCGH) was used to detect large deletions or duplications in the indicated subset of genes. Human genome build 19 (Hg 19) was used for data analysis.

ANALYTICAL SENSITIVITY/SPECIFICITY: 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, but the analytical sensitivity may be reduced.

LIMITATIONS: A negative result does not exclude a heritable form of LQTS. This test only detects variants within the coding regions and intron-exon boundaries of the targeted genes. Regulatory region variants and deep intronic variants will not be identified and breakpoints of large deletions/duplications will not be determined. Single exon deletions/duplications or deletions/duplications less than 1kb may not be detected. Deletions/duplications/insertions of any size may not be detected by massive parallel sequencing. Diagnostic errors can occur due to rare sequence variations. In some cases, variants may not be identified due to technical 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. Non-coding transcripts were not analyzed.

Single exon deletions/duplications will not be called for the following exons: KCNH2 (NM_000238) 13; KCNQ1 (NM_000218) 16; KCNQ1 (NM_181798) 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.

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Test Information

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

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Page 3 of 3