

Long QT Syndrome Panel

Disorder also known as: Ventricular fibrillation with prolonged QT interval; Romano-Ward syndrome (RWS); Jervell and Lange-Nielsen syndrome (JLNS)

Panel Gene List: *AKAP9, ANK2, CACNA1C, CALM1, CALM2, CALM3, CAV3, KCNE1, KCNE2, KCNH2 (HERG), KCNJ2, KCNJ5, KCNQ1, SCN4B, SCN5A, SNTA1, TRDN*

Additional genes from our cardiology test menu may be added to this panel by selecting test code 727C.

Clinical Features:

Long QT syndrome (LQTS) is due to abnormal cardiac ion channel function and characterized by prolongation of the QT interval on ECG. Approximately seventy-five percent of cases of LQTS are due to known genetic causes. LQTS is associated with increased risk for syncope, ventricular arrhythmia, and sudden cardiac death in young adults with normal heart structure. Sudden death is the first and final symptom in 10-15% of individuals with this diagnosis. LQTS has an estimated prevalence 1 in 2000 individuals¹, occurs in all ethnicities, and results in approximately 4000 deaths annually in the US.²

The diagnosis of LQTS is based on clinical history, ECG findings, genetic testing, and family history. Typically, the disorder manifests in patients younger than 40 years of age and may present as early as infancy. Patients often have a history of syncope or palpitations in the absence of any other causes, such as medications, structural heart abnormalities, myocardial ischemia, or electrolyte imbalances. In some patients, syncope may be mistakenly diagnosed as seizures. LQTS may be present even in the absence of any clinical symptoms and, in some patients, sudden cardiac death occurs without any preceding symptoms and without an identifiable cause at autopsy. Inherited LQTS may underlie up to 10-15% of sudden infant death syndrome (SIDS) cases.³

Inheritance Pattern/Genetics: Autosomal Dominant or Autosomal Recessive

Test Methods:

Using genomic DNA extracted from the submitted specimen, the coding regions and splice junctions of the 17 genes (Only exons 1-44 for *CACNA1C*, only the *KCNQ1*-binding domains including Ser1570 residue for *AKAP9*) are enriched using a proprietary targeted capture system developed by GeneDx for next-generation sequencing with CNV calling (NGS-CNV). The enriched targets are simultaneously sequenced with paired-end reads on an Illumina platform. Bi-directional sequence reads are assembled and aligned to reference sequences based on NCBI RefSeq transcripts and human genome build GRCh37/UCSC hg19. After gene specific filtering, data are analyzed to identify sequence variants and most deletions and duplications involving coding exons; however, technical limitations and inherent sequence properties effectively reduce this resolution for some genes. Alternative sequencing or copy number detection methods are used to analyze or confirm regions with inadequate sequence or copy number data by NGS. Reportable variants include pathogenic variants, likely pathogenic variants and variants of uncertain significance. Likely benign and benign variants, if present, are not routinely reported but are available upon request.

Test Sensitivity:

The technical sensitivity of sequencing is estimated to be >99% at detecting single nucleotide events. It will not reliably detect deletions greater than 20 base pairs, insertions or rearrangements greater than 10 base pairs, or low-level mosaicism. The copy number assessment methods used with this test cannot reliably detect copy number variants of less than 500 base pairs or mosaicism and cannot identify balanced chromosome aberrations. Assessment of exon-level copy number events is dependent on the inherent sequence properties of the targeted regions, including shared homology and exon size.

| Gene | Protein | Inheritance | Disease Associations |
|---------------------|---|-------------|---|
| <i>AKAP9</i> | A-KINASE ANCHOR PROTEIN 9 | AD | LQTS |
| <i>ANK2</i> | ANKYRIN 2 | AD | Arrhythmia, LQTS |
| <i>CACNA1C</i> | CALCIUM CHANNEL, VOLTAGE-DEPENDENT, L TYPE, ALPHA-1C SUBUNIT | AD | BrS, Timothy syndrome, LQTS |
| <i>CALM1</i> | CALMODULIN 1 | AD | LQTS, CPVT |
| <i>CALM2</i> | CALMODULIN 2 | AD | LQTS, CPVT |
| <i>CALM3</i> | CALMODULIN 3 | AD | LQTS, CPVT |
| <i>CAV3</i> | CAVEOLIN 3 | AD, AR | HCM, LQTS, LGMD, Rippling muscle disease, Tateyama-type distal myopathy, SIDS |
| <i>KCNE1</i> | POTASSIUM CHANNEL, VOLTAGE-GATED, ISK-RELATED SUBFAMILY, MEMBER 1 | AD, AR | LQTS, JLNS |
| <i>KCNE2</i> | POTASSIUM CHANNEL, VOLTAGE-GATED, ISK-RELATED SUBFAMILY, MEMBER 2 | AD | LQTS |
| <i>KCNH2 (HERG)</i> | POTASSIUM CHANNEL, VOLTAGE-GATED, SUBFAMILY H, MEMBER 2 | AD | LQTS, SQTS |
| <i>KCNJ2</i> | POTASSIUM CHANNEL, INWARDLY RECTIFYING, SUBFAMILY J, MEMBER 2 | AD | Andersen-Tawil syndrome, SQTS, AF |
| <i>KCNJ5</i> | POTASSIUM CHANNEL, INWARDLY RECTIFYING, SUBFAMILY J, MEMBER 5 | AD | LQTS, Hyperaldosteronism |
| <i>KCNQ1</i> | POTASSIUM CHANNEL, VOLTAGE-GATED, KQT-LIKE SUBFAMILY, MEMBER 1 | AD, AR | JLNS, LQTS, SQTS |
| <i>SCN4B</i> | SODIUM CHANNEL, VOLTAGE-GATED, TYPE IV, BETA SUBUNIT | AD | LQTS, AF |
| <i>SCN5A</i> | SODIUM CHANNEL, VOLTAGE-GATED, TYPE V, ALPHA SUBUNIT | AD, AR | BrS, DCM, ARVC, HB, LQTS, SSS, SIDS |
| <i>SNTA1</i> | ALPHA SYNTROPHIN | AD | LQTS |
| <i>TRDN</i> | TRIADIN | AR | CPVT, LQTS |

Abbreviations: AD – Autosomal dominant; AF – Atrial fibrillation; AR – Autosomal recessive; ARVC- Arrhythmogenic right ventricular cardiomyopathy; BrS – Brugada syndrome; CPVT – Catecholaminergic polymorphic ventricular tachycardia; DCM – Dilated cardiomyopathy; HB – Heart block; JLNS – Jervell and Lange-Nielsen syndrome; LGMD – Limb girdle muscular dystrophy; LQTS – Long QT syndrome; SIDS – Sudden infant death syndrome; SQTS – Short QT syndrome; SSS – Sick sinus syndrome

References:

- Lehnart et al. (2007) *Circulation* 116 (20):2325-45 (PMID: 17998470)
- Vincent, et al. (1998) *Annual Review Of Medicine* 49 :263-74 (PMID: 9509262)
- Arnestad et al. (2007) *Circulation* 115 (3):361-7 (PMID: 17210839)
- Ackerman MJ et al. HRS/EHRA expert consensus statement on the state of genetic testing for the channelopathies and cardiomyopathies: this document was developed as a partnership between the Heart Rhythm Society (HRS) and the European Heart Rhythm Association (EHRA). *Europace : European Pacing, Arrhythmias, And Cardiac Electrophysiology : Journal Of The Working Groups On Cardiac Pacing, Arrhythmias, And Cardiac Cellular Electrophysiology Of The European Society Of Cardiology*. 2011 13(8):1077-109.21810866