# WES LONG QT SYNDROME [1] DG 3.7

| Gene | Twist X2 covered >10x | Twist X2 covered >20x | WGS covered >10x | WGS covered >20x | Associated Phenotype description and OMIM disease ID |
|---|---|---|---|---|---|
| CACNA1C | 100.0% | 100.0% | 100.0% | 99.4% | Timothy syndrome, 601005<br>Long QT syndrome 8, 618447<br>Neurodevelopmental disorder with hypotonia, language delay, and skeletal defects with or without seizures, 620029<br>Brugada syndrome 3, 611875 |
| CALM1 | 100.0% | 100.0% | 100.0% | 99.6% | Ventricular tachycardia, catecholaminergic polymorphic, 4, 614916<br>Long QT syndrome 14, 616247 |
| CALM2 | 73.5% | 73.5% | 100.0% | 98.8% | Long QT syndrome 15, 616249 |
| CALM3 | 100.0% | 100.0% | 100.0% | 99.4% | Long QT syndrome 16, 618782<br>?Ventricular tachycardia, catecholaminergic polymorphic 6, 618782 |
| KCNE1 | 100.0% | 100.0% | 100.0% | 100.0% | Jervell and Lange-Nielsen syndrome 2, 612347<br>Long QT syndrome 5, 613695 |
| KCNE2 | 100.0% | 100.0% | 100.0% | 99.9% | Long QT syndrome 6, 613693<br>Atrial fibrillation, familial, 4, 611493 |
| KCNH2 | 100.0% | 100.0% | 100.0% | 98.8% | Short QT syndrome 1, 609620<br>Long QT syndrome 2, 613688 |

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|---|---|---|---|---|---|
| KCNQ1 | 100.0% | 100.0% | 100.0% | 99.6% | Short QT syndrome 2, 609621<br>Atrial fibrillation, familial, 3, 607554<br>Long QT syndrome 1, 192500<br>Jervell and Lange-Nielsen syndrome, 220400 |
| SCN5A | 100.0% | 100.0% | 100.0% | 99.4% | Ventricular fibrillation, familial, 1, 603829<br>Heart block, progressive, type IA, 113900<br>Cardiomyopathy, dilated, 1E, 601154<br>Heart block, nonprogressive, 113900<br>Long QT syndrome 3, 603830<br>Sick sinus syndrome 1, 608567<br>Brugada syndrome 1, 601144<br>Atrial fibrillation, familial, 10, 614022 |
| TRDN | 99.9% | 99.6% | 100.0% | 98.4% | Cardiac arrhythmia syndrome, with or without skeletal muscle weakness, 615441 |

*Gene symbols used follow HGCN guidelines: Gray KA, Yates B, Seal RL, Wright MW, Bruford EA. Nucleic Acids Res. 2015 Jan 43(Database issue):D1079-85.*
*TWIST X2 Covered 10x describes the percentage of a gene's coding sequence that is covered at least 10x when analyzed by WES using TWIST X2 chemistry.*
*TWIST X2 Covered 20x describes the percentage of a gene's coding sequence that is covered at least 20x when analyzed by WES using TWIST X2 chemistry.*
*srWGS GRCh38 Covered 10x describes the percentage of a gene's coding sequence that is covered at least 10x when analyzed by WGS mapped against GRCh38.*
*srWGS GRCh38 Covered 20x describes the percentage of a gene's coding sequence that is covered at least 20x when analyzed by WGS mapped against GRCh38.*
*non-protein coding genes are covered, but as coverage statistics are based on protein coding regions, statistics could not be generated.*
*OMIM release used for OMIM disease identifiers and descriptions : March 17th, 2023.*
*This list is accurate for panel version DG 3.7.0.*