LONG QT SYNDROME GENE PANEL DG 3.6.0 (10 GENES)

Releasedate: 05-04-2023

| Gene | TWIST X2 covered | TWIST X2 covered | Associated Phenotype description and OMIM disease ID |
|---------|------------------------|------------------------|---|
| | >10x | >20x | |
| CACNA1C | 100% | 100% | Timothy syndrome, 601005 |
| | | | Long QT syndrome 8, 618447 |
| | | | Neurodevelopmental disorder with hypotonia, language delay, and skeletal defects with or without seizures, 620029 |
| | | | Brugada syndrome 3, 611875 |
| CALM1 | 100% | 100% | Ventricular tachycardia, catecholaminergic polymorphic, 4, 614916 |
| | | | Long QT syndrome 14, 616247 |
| CALM2 | 73% | 73% | Long QT syndrome 15, 616249 |
| CALM3 | 100% | 100% | Long QT syndrome 16, 618782 |
| | | | ?Ventricular tachycardia, catecholaminergic polymorphic 6, 618782 |
| KCNE1 | 100% | 100% | Jervell and Lange-Nielsen syndrome 2, 612347 |
| | | | Long QT syndrome 5, 613695 |
| KCNE2 | 100% | 100% | Long QT syndrome 6, 613693 |
| | | | Atrial fibrillation, familial, 4, 611493 |
| KCNH2 | 100% | 100% | Short QT syndrome 1, 609620 |
| | | | Long QT syndrome 2, 613688 |
| KCNQ1 | 100% | 100% | Short QT syndrome 2, 609621 |
| | | | Atrial fibrillation, familial, 3, 607554 |
| | | | Long QT syndrome 1, 192500 |
| | | | Jervell and Lange-Nielsen syndrome, 220400 |
| SCN5A | 100% | 100% | Ventricular fibrillation, familial, 1, 603829 |
| | | | Heart block, progressive, type IA, 113900 |
| | | | Cardiomyopathy, dilated, 1E, 601154 |
| | | | Heart block, nonprogressive, 113900 |
| | | | Long QT syndrome 3, 603830 |
| | | | Sick sinus syndrome 1, 608567 |

| | | | Brugada syndrome 1, 601144 |
|------|-----|-----|---|
| | | | Atrial fibrillation, familial, 10, 614022 |
| TRDN | 99% | 99% | 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. 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 is the chemistry used for WES analysis.

Covered 10x describes the percentage of a gene's coding sequence that is covered at least 10x.

Covered 20x describes the percentage of a gene's coding sequence that is covered at least 20x.

Genes with coverage denoting NC are non-protein coding genes.

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 3.6.0

Ad 1. "No OMIM Disease ID" signifies a gene without a current OMIM association Ad 2. OMIM phenotype descriptions between {} signify risk factors