

ARRHYTHMIA AND CARDIAC CONDUCTION DISORDERS

PANEL¹ DG-3.9.0 (28 GENES)

<i>Gene</i>	<i>Twist X2 covered >10x</i>	<i>Twist X2 covered >20x</i>	<i>WGS covered >10x</i>	<i>WGS covered >20x</i>	<i>Associated Phenotype description and OMIM disease ID</i>
CACNA1C	100.0%	100.0%	100.0%	99.0%	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	100.0%	100.0%	100.0%	99.6%	Ventricular tachycardia, catecholaminergic polymorphic, 4, 614916; Long QT syndrome 14, 616247
CALM2	73.5%	73.5%	100.0%	97.3%	Long QT syndrome 15, 616249
CALM3	100.0%	100.0%	100.0%	98.8%	Long QT syndrome 16, 618782; ?Ventricular tachycardia, catecholaminergic polymorphic 6, 618782

CASQ2	100.0%	100.0%	100.0%	98.6%	Ventricular tachycardia, catecholaminergic polymorphic, 2, 611938
DES	100.0%	100.0%	100.0%	98.9%	Scapulooperoneal syndrome, neurogenic, Kaeser type, 181400;Cardiomyopathy, dilated, 11, 604765;Myopathy, myofibrillar, 1, 601419
DPP6	100.0%	99.9%	100.0%	98.2%	Intellectual developmental disorder, autosomal dominant 33, 616311;{Ventricular fibrillation, paroxysmal familial, 2}, 612956
DSC2	100.0%	100.0%	100.0%	98.6%	Arrhythmogenic right ventricular dysplasia 11 with mild palmoplantar keratoderma and woolly hair, 610476;Arrhythmogenic right ventricular dysplasia 11, 610476
DSG2	100.0%	100.0%	100.0%	99.0%	Cardiomyopathy, dilated, 1BB, 612877;Arrhythmogenic right ventricular dysplasia 10, 610193

DSP	100.0%	100.0%	100.0%	98.0%	Arrhythmogenic right ventricular dysplasia 8, 607450;Epidermolysis bullosa, lethal acantholytic, 609638;Keratosis palmoplantaris striata II, 612908;Dilated cardiomyopathy with woolly hair, keratoderma, and tooth agenesis, 615821;Cardiomyopathy, dilated, with woolly hair and keratoderma, 605676
FLNC	100.0%	100.0%	100.0%	99.4%	Cardiomyopathy, familial hypertrophic, 26, 617047;Arrhythmogenic right ventricular dysplasia, familial, 617047;Cardiomyopathy, familial restrictive 5, 617047;Myopathy, distal, 4, 614065;Myopathy, myofibrillar, 5, 609524
GNB2	100.0%	100.0%	100.0%	99.8%	Neurodevelopmental disorder with hypotonia and dysmorphic facies, 619503;?Sick sinus syndrome 4, 619464
HCN4	100.0%	100.0%	100.0%	96.9%	Sick sinus syndrome 2, 163800;{Epilepsy, idiopathic generalized, susceptibility to, 18}, 619521;Brugada syndrome 8, 613123

JUP	100.0%	100.0%	100.0%	99.4%	Naxos disease, 601214;?Arrhythmogenic right ventricular dysplasia 12, 611528
KCNE1	100.0%	100.0%	100.0%	99.7%	Jervell and Lange-Nielsen syndrome 2, 612347;Long QT syndrome 5, 613695
KCNE2	100.0%	100.0%	100.0%	99.8%	Long QT syndrome 6, 613693;Atrial fibrillation, familial, 4, 611493
KCNH2	100.0%	100.0%	100.0%	96.9%	Short QT syndrome 1, 609620;Long QT syndrome 2, 613688
KCNJ2	100.0%	100.0%	100.0%	99.4%	Atrial fibrillation, familial, 9, 613980;Andersen syndrome, 170390;Short QT syndrome 3, 609622
KCNQ1	100.0%	100.0%	100.0%	97.2%	Short QT syndrome 2, 609621;Atrial fibrillation, familial, 3, 607554;Long QT syndrome 1, 192500;{Long QT syndrome 1, acquired, susceptibility to}, 192500;Jervell and Lange-Nielsen syndrome, 220400

LMNA	100.0%	100.0%	100.0%	99.1%	Mandibuloacral dysplasia, 248370;Heart-hand syndrome, Slovenian type, 610140;Cardiomyopathy, dilated, 1A, 115200;Emery-Dreifuss muscular dystrophy 3, autosomal recessive, 616516;Restrictive dermopathy 2, 619793;Charcot-Marie-Tooth disease, type 2B1, 605588;Emery-Dreifuss muscular dystrophy 2, autosomal dominant, 181350;Hutchinson-Gilford progeria, 176670;Lipodystrophy, familial partial, type 2, 151660;Muscular dystrophy, congenital, 613205;Malouf syndrome, 212112
PKP2	99.9%	99.3%	99.9%	98.0%	Arrhythmogenic right ventricular dysplasia 9, 609040
PLN	100.0%	100.0%	100.0%	98.7%	Cardiomyopathy, dilated, 1P, 609909;Cardiomyopathy, hypertrophic, 18, 613874

RYR2	100.0%	100.0%	100.0%	98.3%	Ventricular tachycardia, catecholaminergic polymorphic, 1, 604772;Ventricular arrhythmias due to cardiac ryanodine receptor calcium release deficiency syndrome, 115000
SCN5A	100.0%	100.0%	100.0%	98.6%	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;{Sudden infant death syndrome, susceptibility to}, 272120
TECRL	100.0%	100.0%	100.0%	97.8%	Ventricular tachycardia, catecholaminergic polymorphic, 3, 614021
TMEM43	100.0%	100.0%	100.0%	98.7%	Arrhythmogenic right ventricular dysplasia 5, 604400;Auditory neuropathy, autosomal dominant 3, 619832;Emery-Dreifuss muscular dystrophy 7, AD, 614302

TNNT2	100.0%	100.0%	100.0%	98.9%	Cardiomyopathy, dilated, 1D, 601494;Cardiomyopathy, hypertrophic, 2, 115195;Cardiomyopathy, familial restrictive, 3, 612422;Left ventricular noncompaction 6, 601494
TRDN	99.9%	99.6%	100.0%	96.8%	Cardiac arrhythmia syndrome, with or without skeletal muscle weakness, 615441

Gene symbols used follow HGNC 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 3.9.0

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