

HYPERTROPHIC CARDIOMYOPATHY PANEL¹ DG-3.9.0 (24 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>
ACTC1	100.0%	100.0%	100.0%	99.5%	Left ventricular noncompaction 4, 613424;Cardiomyopathy, hypertrophic, 11, 612098;Atrial septal defect 5, 612794;Cardiomyopathy, dilated, 1R, 613424
ACTN2	100.0%	100.0%	99.9%	97.9%	Myopathy, distal, 6, adult onset, 618655;Cardiomyopathy, hypertrophic, 23, with or without LVNC, 612158;Congenital myopathy 8, 618654;Cardiomyopathy, dilated, 1AA, with or without LVNC, 612158
ALPK3	100.0%	100.0%	100.0%	98.3%	Cardiomyopathy, familial hypertrophic 27, 618052
CSRP3	100.0%	100.0%	100.0%	99.7%	?Cardiomyopathy, dilated, 1M, 607482;Cardiomyopathy, hypertrophic, 12, 612124

DES	100.0%	100.0%	100.0%	98.9%	Scapulooperoneal syndrome, neurogenic, Kaeser type, 181400;Cardiomyopathy, dilated, 11, 604765;Myopathy, myofibrillar, 1, 601419
FHL1	100.0%	99.9%	97.9%	69.1%	Myopathy, X-linked, with postural muscle atrophy, 300696;Emery-Dreifuss muscular dystrophy 6, X-linked, 300696;?Uruguay faciocardiomyoskeletal syndrome, 300280;Scapulooperoneal myopathy, X-linked dominant, 300695;Reducing body myopathy, X-linked 1b, with late childhood or adult onset, 300718;Reducing body myopathy, X-linked 1a, severe, infantile or early childhood onset, 300717
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

GLA	90.9%	90.9%	98.3%	73.7%	Fabry disease, cardiac variant, 301500;Fabry disease, 301500
JPH2	100.0%	99.9%	100.0%	99.1%	Cardiomyopathy, dilated, 2E, 619492;Cardiomyopathy, hypertrophic, 17, 613873
LAMP2	100.0%	100.0%	98.0%	72.4%	Danon disease, 300257
MYBPC3	100.0%	100.0%	100.0%	99.7%	Cardiomyopathy, hypertrophic, 4, 115197;Cardiomyopathy, dilated, 1MM, 615396;Left ventricular noncompaction 10, 615396
MYH7	100.0%	100.0%	100.0%	99.0%	Laing distal myopathy, 160500;Cardiomyopathy, hypertrophic, 1, 192600;Left ventricular noncompaction 5, 613426;Cardiomyopathy, dilated, 1S, 613426;Congenital myopathy 7B, myosin storage, autosomal recessive, 255160;Congenital myopathy 7A, myosin storage, autosomal dominant, 608358

MYL2	100.0%	100.0%	100.0%	98.9%	Cardiomyopathy, hypertrophic, 10, 608758;Myopathy, myofibrillar, 12, infantile-onset, with cardiomyopathy, 619424
MYL3	100.0%	100.0%	100.0%	99.3%	Cardiomyopathy, hypertrophic, 8, 608751
PLN	100.0%	100.0%	100.0%	98.7%	Cardiomyopathy, dilated, 1P, 609909;Cardiomyopathy, hypertrophic, 18, 613874
PRKAG2	100.0%	100.0%	100.0%	96.5%	Glycogen storage disease of heart, lethal congenital, 261740;Wolff-Parkinson-White syndrome, 194200;Cardiomyopathy, hypertrophic 6, 600858
PTPN11	100.0%	100.0%	100.0%	98.2%	Noonan syndrome 1, 163950;LEOPARD syndrome 1, 151100;Metachondromatosis, 156250;Leukemia, juvenile myelomonocytic, somatic, 607785
RAF1	100.0%	100.0%	100.0%	98.7%	Cardiomyopathy, dilated, 1NN, 615916;Noonan syndrome 5, 611553;LEOPARD syndrome 2, 611554
RIT1	100.0%	100.0%	100.0%	99.7%	Noonan syndrome 8, 615355

TNNC1	100.0%	100.0%	100.0%	98.2%	Cardiomyopathy, dilated, 1Z, 611879;Cardiomyopathy, hypertrophic, 13, 613243
TNNI3	100.0%	100.0%	100.0%	97.6%	?Cardiomyopathy, dilated, 2A, 611880;Cardiomyopathy, hypertrophic, 7, 613690;Cardiomyopathy, familial restrictive, 1, 115210;Cardiomyopathy, dilated, 1FF, 613286
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
TPM1	100.0%	100.0%	100.0%	98.0%	Left ventricular noncompaction 9, 611878;Cardiomyopathy, hypertrophic, 3, 115196;Cardiomyopathy, dilated, 1Y, 611878
TTR	90.7%	90.7%	100.0%	99.5%	Amyloidosis, hereditary, transthyretin-related, 105210;Carpal tunnel syndrome, familial, 115430;[Dystransthyretinemic hyperthyroxinemia], 145680

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 3.9.0

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