Supplemental Table SI. Complete list of mutated genes, sorted alphabetically, all ACMG class variants, marked from class 3 (VUS) to 5 (pathogenic).

Gene	Full name	Nucleotide change, protein variant	Patients (n)	ACMG class	ClinVar (n)
ABCG5	*ATP-binding cassette, sub-family G, member 5*	ABCG5 p.Arg198Gln	1		Uncertain significance (3)
ACTC1	*actin, alpha, cardiac muscle 1*	ACTC1 c.76G>A p.(Asp26Asn)	1	3	
ACTN2	*actinin, alpha 2*	ACTN2 c.1193G>T p.(Arg398Leu)	1	3	
		ACTN2 c.1549C>T p.(Leu517Phe)	2	3	
		ACTN2 c.1552C>T p.(His518Tyr)	1	3	
		ACTN2 c.1822C>T, p.(Arg608Trp)	1	3	
		ACTN2 c.2147C>T, p.(Thr716Met)	1	3	
		ACTN2 p.Arg93Gln	1		Uncertain significance (3)
		ACTN2 p.His518Tyr	1		Uncertain significance (1)
ANKRD1	*ankyrin repeat domain 1 (cardiac muscle)*	ANKRD1 p.Ala276Val	1		Benign(5); Likely benign(5); Uncertain significance(1)
BAG3	*BCL2-associated athanogene 3*	BAG3 c.1523A>G p.(Tyr508Cys)	1	3	
CACNA1C	*calcium channel, voltage-dependent, L type, alpha 1C subunit*	CACNA1C c.5693+2T>A	1	3	
		CACNA1C c.5893T>C, p.(Ser1965Pro)	1		
		CACNA1C p.Arg518His	1		Likely pathogenic(1); Pathogenic(1); Uncertain significance(1)
CACNA2D1	*calcium channel, voltage-dependent, alpha 2/delta subunit 1*	CACNA2D1 p.Ser709Asn	2		
CAV3	*caveolin 3*	CAV3 c.233C>T, p.(Thr78Met)	1		
		CAV3 c.89A>G p.(Lys30Arg)	1	3	
COL5A2	*collagen, type V, alpha 2*	COL5A2 p.Pro1359Leu	1		
		COL5A2 p.Val95Asp	1		
COX15	*COX15 homolog, cytochrome c oxidase assembly protein (yeast)*	COX15 p.Arg406Gln	1		
CRYAB	*crystallin, alpha B*	CRYAB c.116C>T p.(Pro39Leu)	1	3	
		CRYAB p.Pro51Leu	1		Likely benign(7); Uncertain significance(1)
CSRP3	*cysteine and glycine-rich protein 3 (cardiac LIM protein)*	CSRP3 c.208G>T p.(Gly70Trp)	4	3	
		CSRP3 c.208G>T, p.(Gly70Trp) HOM	1	3	

		CSRP3 c.520A>G, p.(Lys174Glu)	1	3	
		CSRP3 p.Gly70Trp HOM	1		
DES	*desmin*	DES c.728A>G, p.(His243Arg)	1	3	
DMD	*dystrophin*	DMD c.10262+1G>A	1		Benign(1); Uncertain significance(3)
		DMD c.1934A>G, p.(Asp645Gly)	1	3	
		DMD p.Ile99Val	1		Likely benign(1); Uncertain significance(4)
DSC2	*desmocollin 2*	DSC2 c.1223C>T p.(Thr408Ile)	1	3	
		DSC2 c.1661A>G p.(Gln554Arg)	1	3	
DSG2	*desmoglein 2*	DSG2 c.166G>A, p.(Val56Met)	2		Likely benign(5); Pathogenic(1); Uncertain significance(4)
		DSG2 c.216G>T, p.(Lys72Asn)	1	3	
DSP	*desmoplakin*	DSP c.242G>A p.(Cys81Tyr)	1	3	
		DSP c.2684A>G, p.(Tyr895Cys)	1	3	Uncertain significance (5)
		DSP c.3550C>T p.(Arg1184Trp)	1		
		DSP c.3616T>A p.(Leu1206Ile)	1	3	
		DSP c.4961T>C, p.(Leu1654Pro)	1	3	
		DSP c.688G>A, p.(Asp230Asn)	1		
		DSP c.8068C>A p.(Pro2690Thr)	1	3	
		DSP c.8467C>G p.(Pro2823Ala)	1	3	
		DSP p.Thr2665Met	1		Uncertain significance (1)
DTNA	*dystrobrevin, alpha*	DTNA p. p.Thr205Met	1		
		DTNA p.Gln106Glu	1		Uncertain significance (2)
ELN	*elastin*	ELN c.1408C>T p.(Gln470*)	1	4	
EMILIN1	*elastin microfibril interfacer 1*	EMILIN1 p.Leu606ValfsTer43 (delCT)	1		
FHL2	*four and a half LIM domains 2*	FHL2 c.191C>A, p.(Ala64Asp)	1	3	
		FHL2 c.467A>T p.(Lys156Ile)	1	3	
		FHL2 c.501+1G>T	1	3	
		FHL2 p.Leu21Gln	1		Uncertain significance (1)
FKTN	*fukutin*	FKTN c.166-4A>G	1		Benign(1);Uncertain significance(6)

FLNA	*filamin A*	FLNA p.Arg1532Gln	1		
		FLNA p.Leu1540Val	1		
		FLNA p.Lys1538Thr	1		
FLNC	*filamin C*	FLNC c.4564C>A p.(Gln1522Lys)	1	3	
		FLNC c.4660A>C p.(Ile1554Leu)	1	3	
GLA	*galactosidase, alpha*	GLA c.644A>G p.(Asn215Ser)	1	5	
		GLA c.902G>A p.(Arg301Gln)	1	5	
		GLA c.937G>T p.(Asp313Tyr)	1		
GPD1L	*glycerol-3-phosphate dehydrogenase 1-like*	GPD1L c.370A>G, p.(Ile124Val)	1		
		GPD1L c.370A>G, p.(Ile124Val)	1		
HCN4	*hyperpolarization activated cyclic nucleotide-gated potassium channel 4*	HCN4 p.Glu1193Gln	1		Benign(1);Likely benign(2);Uncertain significance(1)
IRX4	*Iroquois Homeobox Protein 4*	IRX4 c.375C>G p.(Tyr125*)	1	3	
JAG1	*jagged 1 (Alagille syndrome)*	JAG1 p.Thr962Ala	1		
JUP	*junction plakoglobin*	JUP p.Ser24Leu	1		Uncertain significance (1)
KCNA5	*potassium voltage-gated channel, shaker-related subfamily, member 5*	KCNA5 c.633G>C, p.(Glu211Asp)	1		
		KCNA5 p.Thr374Ile	1		
KCNH2	*potassium voltage-gated channel, subfamily H, member 2*	KCNH2 c.3107G>A p.(Gly1036Asp)	1	3	
		KCNH2 c.526C>T p.Arg176Trp	1		Likely benign(1);Uncertain significance(5)
KCNJ2	*potassium inwardly-rectifying channel, subfamily J, member 2*	KCNJ5 p.Met210Ile	1		Likely benign (1)
KCNQ1	*potassium voltage-gated channel, KQT-like subfamily, member 1*	KCNQ1 p.Gly269Ser	1		Pathogenic (4) for long QT syndrome
LAMA4	*laminin, alpha 4*	LAMA4 p.Arg730Cys	1		
		LAMA4 p.Ile36Thr	1		
LDB3	*LIM domain binding 3*	LDB3 c.1838C>T, p.(Pro613Leu)	1	3	
		LDB3 p.Ala222Thr	1		
		LDB3 p.Gly508Cys	1		
		LDB3 p.Gly653Arg	1		
LMNA	*lamin A/C*	LMNA c.1930C>T p.(Arg644Cys)	1		
MIB1	*mindbomb homolog 1*	MIB1 c.1111C>T p.(Arg371*)	1	3	

		MIB1 c.1971del p.(Asn658Thrfs*7)	1	3	
		MIB1 c.908+2T>A	1	3	
MYBPC3	*myosin binding protein C, cardiac*	MYBPC3 c.1000G>A p.(Glu334Lys)	1	3	
		MYBPC3 c.1028delC p.(Thr343MetfsTer7)	2	5	
		MYBPC3 c.1078A>T p.(Lys360Ter)	1	5	
		MYBPC3 c.1468G>A p.(Gly490Arg)	3	3	
		MYBPC3 c.1484G>A, p.(Arg495Gln)	1	4	Pathogenic/Likely pathogenic (12)
		MYBPC3 c.1558G>T p.(Glu520*)	2	5	
		MYBPC3 c.1577_1580dup, p.(Cys528Thrfs*4)	1	5	
		MYBPC3 c.1736A>C p.(Lys579Thr)	1	3	
		MYBPC3 c.1790G>A p.(Arg597Gln)	1	3	
		MYBPC3 c.1855G>A p.(Glu619Lys)	1		
		MYBPC3 c.185dup p.(Arg63Thrfs*50)	1	5	
		MYBPC3 c.1897+1G>A	1	5	Pathogenic (4)
		MYBPC3 c.2215G>T p.(Glu739*)	1	5	
		MYBPC3 c.2309-3C>G	1		
		MYBPC3 c.2381C>T, p.(Pro794Leu)	1	3	
		MYBPC3 c.2382delG p.(Pro795LeufsTer27)	1	5	
		MYBPC3 c.2429G>A p.(Arg810His)	1	3	
		MYBPC3 c.2540_2547delinsT p.(Tyr847Leufs*30)	1	5	
		MYBPC3 c.2639_2642dup, p.(Ser882Argfs*3)	2	5	
		MYBPC3 c.2686G>A, p.(Val896Met)	2		
		MYBPC3 c.2687T>G, p.(Val896Gly)	1	3	
		MYBPC3 c.2815C>T p.(Arg939Trp)	1	3	
		MYBPC3 c.3097C>T p.(Arg1033Trp)	1	3	
		MYBPC3 c.3130C>T p.(Gln1044*)	1	5	
		MYBPC3 c.3166dup p.(Ala1056Glyfs*9)	1	5	
		MYBPC3 c.3190+5G>A	1	5	Pathogenic/Likely pathogenic (9)

		MYBPC3 c.3343G>A, p.(Val1115Ile)	1	3	
		MYBPC3 c.3392T>C, p.(Ile1131Thr)	1		
		MYBPC3 c.3413G>C, p.(Arg1138Pro)	1	3	
		MYBPC3 c.3490+1G>T	3	5	Pathogenic (2)
		MYBPC3 c.3580dup p.(Ala1194Glyfs*14)	1	5	
		MYBPC3 c.3697C>T, p.(Gln1233*)	10	5	
		MYBPC3 c.373_374del, p.(Ala125*)	1	5	
		MYBPC3 c.3767_3769del p.(Thr1256del)	1	4	
		MYBPC3 c.3811C>T p.(Arg1271*)	1	4	
		MYBPC3 c.442G>A p.(Gly148Arg)	1	3	
		MYBPC3 c.565G>A p.(Val189Ile)	1		
		MYBPC3 c.62T>G p.(Val21Gly)	1	3	
		MYBPC3 c.696del, p.(Phe233Serfs*67)	1	5	
		MYBPC3 c.724T>C, p.(Ser242Pro)	1	3	
		MYBPC3 c.772+1G>A	7	5	Pathogenic/Likely pathogenic (4)
		MYBPC3 c.842G>A p.(Arg281Gln)	1		
		MYBPC3 c.977G>A, p.(Arg326Gln)	9		
MYH6	*myosin, heavy chain 6, cardiac muscle, alpha*	MYH6 c.3010G>T, p.(Ala1004Ser)	1		
		MYH6 c.3346C>A p.(Arg1116Ser)	1	3	
		MYH6 c.3469G>A, p.(Gly1157Arg)	1	3	
		MYH6 c.3607dup p.(Ala1203Glyfs*30)	1	3	
		MYH6 c.3902C>T p.(Ser1301Leu)	1	3	
		MYH6 p.Gln1534His	1		Uncertain significance (1)
MYH7	*myosin, heavy chain 7, cardiac muscle, beta*	MYH7 c.1063G>A, p.(Ala355Thr)	1	4	
		MYH7 c.1207C>T, p.(Arg403Trp)	1	5	
		MYH7 c.1436A>G. p.(Asn479Ser)	1	4	
		MYH7 c.161G>A p.(Arg54Gln)	1	3	
		MYH7 c.1816G>A p.(Val606Met)	1	5	Pathogenic/Likely pathogenic (11)
		MYH7 c.1868A>G p.(Asn623Ser)	1	3	
		MYH7 c.1979C>A, p.(Thr660Asn)	1	3	

		MYH7 c.2039C>T p.(Ser680Phe)	1	3	
		MYH7 c.2051T>C p.(Met684Thr)	1	3	
		MYH7 c.2081G>A, p.(Arg694His)	1	3	
		MYH7 c.2167C>G p.(Arg723Gly)	1	5	
		MYH7 c.2207T>C p.(Ile736Thr)	1	5	Pathogenic (9)
		MYH7 c.2221G>A, p.(Gly741Arg)	1	4	Pathogenic (8)
		MYH7 c.2221G>T p.(Gly741Trp)	1	4	Pathogenic (8)
		MYH7 c.2333A>T p.(Asp778Val)	1	4	
		MYH7 c.2347C>T, p.(Arg783Cys)	1	3	
		MYH7 c.2389G>A p.(Ala797Thr)	1	5	Pathogenic/Likely pathogenic (12)
		MYH7 c.2546T>C p.(Met849Thr)	1	4	
		MYH7 c.2609G>A p.(Arg870His)	1	3	
		MYH7 c.2770G>A p.(Glu924Lys)	1	5	
		MYH7 c.2882T>G, p.(Leu961Arg)	2	3	
		MYH7 c.3286G>T, p.(Asp1096Tyr)	1	3	
		MYH7 c.4283T>C p.(Leu1428Ser)	1	3	
		MYH7 c.428G>A p.(Arg143Gln)	2	4	
		MYH7 c.4472C>G, p.(Ser1491Cys)	1		
		MYH7 c.4487A>C p.(Glu1496Ala)	1	3	
		MYH7 c.497T>G p.(Leu166Glu)	1	3	
		MYH7 c.5527A>G p.(Ser1843Gly)	1	3	
		MYH7 c.5561C>T, p.(Thr1854Met)	1	3	
MYL2	*myosin, light chain 2, regulatory, cardiac, slow*	MYL2 c.401A>C p.(Glu134Ala)	1	3	Likely pathogenic(3);Uncertain significance(5)
		MYL2 c.431C>A, p.(Pro144His)	1	3	
		MYL2 c.496G>A p.(Asp166Asn)	1	3	
MYL3	*myosin, light chain 3, alkali; ventricular, skeletal, slow*	MYL3 c.170C>G, p.(Ala57Gly)	1	4	
		MYL3 c.460C>T, p.(Arg154Cys)	1	4	
MYOM1	*myomesin 1*	MYOM1 c.1175-2A>T	1	3	
		MYOM1 c.1230del p.(Lys410Asnfs*13)	1	3	
		MYOM1 c.1482T>G p.(Ser494Arg)	1	3	

		MYOM1 c.4222G>A, p.(Asp1408Asn)	1		
		MYOM1 c.920G>C p.(Arg307Pro)	1	3	
MYOZ2	*myozenin 2*	MYOZ2 c.343C>T, p.(Arg115*)	1	3	
MYPN	*myopalladin*	MYPN c.1012C>T p.(Arg338Cys)	1	3	
		MYPN c.3205C>A p.(Arg1069Ser)	1	3	
NEBL	*nebulette*	NEBL c.267C>G p.(Tyr89Ter)	1	3	
		NEBL c.614A>G p.(Asn205Ser)	1	3	
NEXN	*nexilin (F actin binding protein)*	NEXN c.1190G>A, p.(Arg397Gln)	1	3	
NKX2-5	*NK2 transcription factor related, locus 5*	NKX2-5 p.Ala119Ser het confirmed	1		Benign(1);Likely benign(2);Pathogenic(1) for hypothyroidism
		NKX2-5 c.355G>T p.(Ala119Ser)	1		
PKP2	*plakophilin 2*	PKP2 c.1170+4_1170+7dup	1	3	
		PKP2 c.2552C>T, p.(Thr851Met)	1	3	
		PKP2 p.Val587Ile	1		Benign(3);Likely benign(5);Uncertain significance(2)
PRDM16	*PR domain containing 16*	PRDM16 c.1484C>T p.(Pro495Leu)	1	3	
		PRDM16 p.Asp418Asn	1		
		PRDM16 p.Phe729Leu	1		Likely benign (1)
PRKAG2	*protein kinase, AMP-activated, gamma 2 non-catalytic subunit*	PRKAG2 c.997T>G p.(Ser333Ala)	1	3	
		PRKAG2 p.Asn512Ile	1		Uncertain significance (1)
		PRKAG2 p.Leu341Ser	1		
PTPN11	*protein tyrosine phosphatase, non-receptor type 11*	PTPN11 c.1492C>T, (p.Arg498Trp)	1	5	Pathogenic (5)
		PTPN11 c.1643C>G p.(Ser548Cys)	1	3	
RAF1	*v-raf-1 murine leukemia viral oncogene homolog 1*	RAF1 c.781C>T, p.(Pro621Ser)	3	5	
		RAF1 c.935T>C p.(Val312Ala)	1		
RBM20	*RNA binding motif protein 20*	RBM20 p.Ala818Ser	1		Likely benign(2);Uncertain significance(1)
RYR2	*ryanodine receptor 2 (cardiac)*	RYR2 c.10640C>T p.(Thr3547Met)	1	3	
		RYR2 c.5654G>A p.(Gly1885Glu)	1		
		RYR2 p.Arg3904Trp	1		Uncertain significance (1)

		RYR2 p.Pro3209Leu	1		
SCN10A	*Sodium Channel, Voltage Gated, Type 10 Alpha Subunit*	SCN10A c.3803G>A, p.(Arg1268Gln)	1	3	
SCN2B	*sodium channel, voltage-gated, type II, beta*	SCN2B c.332C>T, p.(Ser111Leu)	1	3	
		SCN2B c.53G>A p.Ser18Asn	1	3	
SCN5A	*sodium channel, voltage-gated, type V, alpha subunit*	SCN5A c.1199G>A p.(Gly400Glu)	1		
		SCN5A c.1673A>G, p.(His558Arg)	3		
		SCN5A c.4895G>A p.(Arg1632His)	1	4	
		SCN5A c.5216G>A p.(Arg1739Gln)	1	3	
		SCN5A c.615T>A p.(Tyr205Ter)	1	3	
		SCN5A p.Arg569Trp	1		
		SCN5A p.Glu1876Val	1		
		SCN5A p.His558Arg	1		
		SCN5A p.Pro1044Leu	1		
SNTA1	*syntrophin, alpha 1*	SNTA1 p.Ala257Gly	1		Likely benign(4);Uncertain significance(1); Pathogenic (1) for long QT syndrome
SOS2	*SOS Ras/Rho guanine nucleotide exchange factor 2*	SOS1 c.233T>G, p.(Phe78Cys)	1	3	
TBX3	*T-box 3*	TBX3 p.Asp114Asn	1		
TGFB3	*transforming growth factor, beta 3*	TGFB3 c.293C>T, p.(Ser98Leu)	1		
		TGFB3 c.487C>T p.(Arg163Trp)	2	3	
		TGFB3 p.Arg163Trp	1		Uncertain significance (3)
TMEM43	*transmembrane protein 43*	TMEM43 p.Arg240Cys	1		Uncertain significance (4)
		TMPO p.Ile530SerfsTer8	1	3	
TNNC1	*troponin C type 1 (slow)*	TNNC1 c.435C>A p.(Asp145Glu)	2	3	
TNNI3	*troponin I type 3 (cardiac)*	TNNI3 c.497C>T, p.(Ser166Phe)	1	4	Likely pathogenic(2); Pathogenic(1); Uncertain significance(1)
TNNT2	*troponin T type 2 (cardiac)*	TNNT2 c.304C>T p.(Arg102Trp)	1	5	
		TNNT2 c.311G>A p.(Arg104His)	1	5	
		TNNT2 c.275G>A, p.(Gly92Glu)	1	4	
		TNNT2 c.304C>T p.(Arg102Trp)	2	4	

		TNNT2 c.824G>A p.(Arg275Gln)	1	3	
		TNNT2 c.862C>T, p.(Arg285Cys)	1	3	
TPM1	*tropomyosin 1 (alpha)*	TPM1 c.523G>A, p.(Asp175Asn)	1	4	Pathogenic (9)
TRIM63	*tripartite motif-containing 63*	TRIM63 c.481_482delAG p.(Ser161Cysfs*8) HOM	1	3	
		TRIM63 c.831+2T>G	1	3	
		TRIM63 p.Gln247Ter	1	3	Likely pathogenic(1);Uncertain significance(1)
TXNRD2	*thioredoxin reductase 2*	TXNRD2 c.528 + 2T>C	1	3	
VCL	*vinculin*	VCL p.Arg759Gln	1	3	Uncertain significance (1)

*ACMG - American College of Medical Genetics and Genomics, VUS - variant of uncertain significance