Supplementary table 1. Genes screened in the present study

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| A2ML1, AARS2, ABCB4, ABCC9, ACAD8, ACAD9, ACADS, ACADVL, ACTA1, ACTA2, ACTC1, ACTN2, ACVRL1, AGK, AGL, AGPAT2, AHCY, AIP, AKAP9, ALG10, ALMS1, ALPK3, AMN, ANK2, ANKRD1, ANO5, APOA1, APOPT1, ARSB, ASPH, ATP1B1, ATP2A2, ATPAF2, BAG3, BIN1, BMPR1B, BMPR2, BOLA3,BRAF, BSCL2, C1QBP, CACNA1C, CACNA1D, CACNA2D1, CACNA2D4, CACNB2, CALM1, CALM2, CALM3, CALR, CALR3, CASQ2, CAV1, CAV3, CBL, CCDC78, CDKN1C, CHD7, CHKB, CHRM2, CIDEC, CNGA2, CNGA3, CNGA4, CNGA1, CNOT1, COA5, COA7, COL4A1, COQ2,COQ4, COQ6, COQ7, ADCK3, COQ9, CORIN, COX10, COX14,COX15,COX20, COX6B1, CPT1A, CPT2,CRYAB, CSRP3,CTC1,CTF1,CTNNA3, CUBN, CXADR, D2HGDH, DAG1,DBH, DCAF8,DES, DMD, DNAJC19,DOLK,DPH2, DPP10,DPP6, DSC2, DSC3, DSG2,DSP,DTNA,DYSF,EIF2AK4,ELAC2,ELN,EMD, ENG,EPG5, ETFA, ETFB,ETFDH,EYA4,FASTKD2,FBXL4,FBXO32,FGF12,FHL1,FHL2,FIG4,FKRP,FKTN,FLNA,FLNC,FOXC1,FOXF1,FOXH1,FOXRED1,FXN,G6PC3,GAA,GATA4,GATA5,GATA6,GATAD1,GBE1,GDF2,GFM1,GINS3,GJA1,GJA5,GLA,GLB1,GMPPB,GNAS,GNB5,GNE,GPC3,GPC4,GPD1L,GSN,GTPBP3,GUSB,GYG1,HADHA,HADHB,HAMP,HCCS,HCN4, HEY2,HFE,HFE2,HPS1,HRAS,HSD17B10,IBA57,IDH2,IDUA,IGF2,IGHMBP2,ILK,ISPD, ITGA6,ITGB4,JAG1,JPH2,JUP,KANK2,KCNA5,KCNAB2,KCNB2,KCND3,KCNE1,KCNE2,KCNE3,KCNE4,KCNE1L,KCNH2,KCNJ16,KCNJ2,KCNJ5,KCNJ8,KCNK3,KCNQ1,KCNT1,KRAS,L2HGDH,LAMA2,LAMA4,LAMP2,LARGE,LDB3,LIG3,LIMS2,LIPE,LITAF,LMNA,LMNB2,LPAR6,LZTR1,MAP2K1,MAP2K2,MIB1,MLYCD,MRPL3,MRPL44,MTO1,MURC,MUT,MYBPC3,YH6,MYH7,MYL2,MYL3,MYLK2,MYO6,MYOT,MYOZ1,MYOZ2,MYPN,NDRG4,NDUFA1,NDUFA11,NDUFAF1,NDUFAF2,NDUFAF4,NDUFAF5,NDUFB11,NDUFB3,NDUFB9,NDUFS1,NDUFS2,NDUFS3,NDUFS4,NDUFS6,NDUFV1,NDUFV2,NEBL,NEU1,NEXN,NF1,NKX25,NODAL,NOS1AP,NOTCH1,NOTCH2,NPPA,NRAS,NSD1,NSUN2,NUBPL,PCCA,PCCB,PDLIM3,PDSS1,PDSS2,PERP,PET100,PEX7,PHYH,PKP2,PKP4,PLEC,PLEKHM2,PLN,PMM2,PNN,PNPLA2,POLG,POMGNT1,POMT1,POMT2,PPARG,PPP1R3A,PRDM16,PRKAG2,PRKAR1A, PSEN1,PSEN2,PTPLA,PTPN11,RAB3GAP2,RAF1,RANGRF,RASA1,RASA2, RBCK1,RBM20,RFFL,RIT1,RMND1,RNF207,RRAS,RYR2,SCN10A,SCN1B, SCN2B,SCN3B,SCN4A,SCN4B,SCN5A,SCN9A,SCNN1A,SCNN1B,SCNN1G, SCO1,SCO2,SDHA,SEPN1,SEMA3A,SETD6,SGCA,SGCB,SGCD,SGCG,SGOL1, SHOC2,SLC19A2,SLC22A5,SLC25A20,SLC25A3,SLC25A4,SLC8A1,SLMAP, SMAD4,SMAD9,SMCHD1,SNTA1,SOS1,SPEG,SPRED1,SRL,SUCLG1,SYNE2,TACO1,TAZ,TBX1,TBX20,TBX4,TBX5,TCAP,TFAP2B,TGFB3,TGFBR2, TIMMDC1,TLL1,TMEM126B,TMEM43,TMEM70,TMPO,TNNC1,TNNI3, TNNI3K,TNNT2,TPM1,TRDN,TRIM32,TRIM37,TRIM63,TRPM4,TRPM7,TSFM,TTN,TTR,C10orf2,TXNRD2, VCL,WFS1, ZFPM2, ZIC |

Supplementary Table 2: Demographic data and genetic variants of all 36 patients with SCA

| No | Diagnosis | Symptoms | Rhythm | Sex | Attack age | AED | Underlying | Phenotype* | Family history# | Gene | Alteration† | Outcome | Follow (years) |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 | CPVT | SCA | VF | F | 13 | yes | no | no | No/ refuse | RYR2 c.11836 G>A, p.G3946S | P | ICD appropriate shock | 22 |
| 2 | LQT 2 | SCA | VF | M | 5.4 | no | CHD | prolong QT | No/ negative | KCNH2 c.2335 T>G, p.M645R | P | ICD appropriate shock | 16.5 |
| 3 | ARVC | Syncope | VT | M | 16 | no | no | epislon wave + RV dilate | No/ refuse | RYR2 c.14808+3A>G | LP | ICD appropriate shock | 12 |
| 4 | LVNC | SCA | VT | M | 12.5 | no | LVNC | LVNC | No/ refuse | negative | | ICD then HTX | 3.5 |
| 5 | LQT 7 | Syncope | VT | M | 6.5 | no | no | borderline QT | Yes/positive | KCNJ2 c.575 C>T, p.T192I | P | ICD appropriate shock | 11.5 |
| 6 | Polymorphic VT | Syncope | VT | F | 13 | no | no | no | Yes/negative | negative | VUS | ICD no shock | 9.4 |
| 7 | Idiopathic VF | SCA | VF | M | 17.1 | yes | no | no | No/ positive | CALR3 c.860 C>T, p.T287M | LP | ICD appropriate shock | 6.8 |
| 8 | HCM | SCA | VF | M | 14.2 | no | HCM | mild LV hypertrophy | No/negative | MYH7 c.9090 C>T, p.R453C | P | ICD no shock | 6.4 |
| 9 | LVNC | Syncope | VT | F | 13.5 | no | LVNC | LVNC | No/ positive | DMD p.Ser3666del | P | ICD then HTX | 0.3 |
| 10 | Brugada | SCA | VF | M | 17.8 | yes | no | no | No/ positive | CAV3 c.166 G>A, p.G56S; SCN5A c.3442 C>T, p.A1148T | P | ICD no appropriate shock | 5.6 |

| | | | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 11 | Idiopathic VF | SCA | VF | M | 12.8 | yes | no | no | No/ refuse | CACNA2D2 p.R266Q; MAML3 p.Q788R; MYH7 p.R272G | LP | ICD no shock | 5.6 |
| 12 | LQT 2 | SCA | VT | M | 10 | no | no | prolong QT | Yes/refuse | KCNH2 c.2775dupG, p.P926A fsTer14 | P | alive | 4.3 |
| 13 | Ankyrin syndrome | Syncope | VT | F | 14.3 | no | no | no | No/ positive | ANK2, c.7227G>T, p.L2409F | LP | ICD appropriate shock | 4.7 |
| 14 | HCM | SCA | VF | F | 15.3 | yes | HCM | mild LV hypertrophy | Yes/not done | MYH7 c.9090 C>T, p.R453C | P | ICD no shock | 4.0 |
| 15 | CPVT | SCA | VT | F | 6 | no | no | no | No/ negative | RYR2 c.506G>A p.R169R; SCN10A c.2450G>A p.R817Q | P | alive | 3.2 |
| 16 | CPVT | SCA | VT | F | 4.3 | yes | no | bidirectional VT | No/ negative | RYR2 c.6737 C>T, p.S2246L | P | ICD appropriate shock | 2.6 |
| 17 | CPVT | SCA | VF | M | 13.7 | yes | no | no | Yes/ positive | RYR2 c.1258 C>T, p.R420W | P | ICD appropriate shock | 5.3 |
| 18 | CPVT | SCA | VT | M | 12 | no | no | bidirectional VT at Treadmill | Yes/ positive | RYR2 c.1244C>T,p.T415I | LP | alive | 5.6 |
| 19 | LQT 2 | SCA | VT | F | 18 | no | no | prolong QT | Yes/ not done | KCNH2, p.A561V | P | ICD no shock | 13.8 |
| 20 | Acquired LQT | SCA | VF | M | 11 | yes | cardiac tumor | prolong QT after amiodarone | No/ refuse | negative | negative | alive | 8.6 |
| 21 | LQT 7 | SCA | | M | 12 | no | no | bidirectional VT | No/ refuse | KCNJ2 c.G644A, p.G215D | P | ICD appropriate | 8.4 |

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|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| | | | | | | | | at Treadmill | | | | shock | |
| 22 | Acquired LQT | SCA | VF | M | 13.1 | yes | no | prolong QT after amiodarone | No/ negative | negative | negative | alive | 11.7 |
| 23 | LQT 3 | Syncope | VT | F | 12.3 | no | no | prolong QT | No/ positive | SCN5A c.1993G>T, p.A665S | LP | alive | 4.0 |
| 24 | CPVT | SCA | | F | 14 | yes | no | no | No/ refuse | RyR2 c.13892A>G, p.D4631G | LP | alive | 3.6 |
| 25 | Brugada | SCA | VT | M | 3.8 | yes | no | Brugada EKG | No/ negative | SCN5A c1890+1 G>A | LP | ICD no shock | 2.1 |
| 26 | Idiopathic VF | SCA | VF | F | 18 | yes | no | no | No | ND | | alive | 16.0 |
| 27 | Idiopathic VF | SCA | VF | M | 17 | yes | no | no | No | ND | | ICD appropriate shock | 9.0 |
| 28 | Idiopathic VF | SCA | VT | M | 12.5 | yes | no | no | Yes | ND | | severe sequelae, LOF | 2.3 |
| 29 | Idiopathic VF | SCA | VF | M | 20 | yes | no | no | No | ND | | LOF | 2.6 |
| 30 | LQT | SCA | VF | M | 15.5 | yes | no | prolong QT | No | ND | | death | 0.5 |
| 31 | WPW | SCA | VF | M | 19.7 | yes | WPW | WPW | No | ND | | alive | 10.1 |
| 32 | ARVC | SCA | VF | M | 18.1 | yes | no | RV dilatation | No/refuse | TTN mutation | P | ICD appropriate shock | 2.6 |

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|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 33 | Idiopathic VF | SCA | VF | M | 7.8 | no | no | no | Yes | ND | death | 0 |
| 34 | Idiopathic VF | SCA | VT | F | 18.2 | yes | no | no | No | ND | LOF | 0 |
| 35 | Idiopathic VF | SCA | VF | M | 15.3 | no | no | no | No | ND | LOF | 0.6 |
| 36 | Unknown | SCA | Asystole | M | 6.7 | no | no | no | No | ND | Alive | 5.2 |

* Phenotypes indicated the positive findings of serial electrophysiology and imaging studies for the diagnosis of SCA before genetic test;
# Family history indicates the positive SCA or aborted SCA family history/ genetic test of the family members. Refuse indicates we invited family members for genetic test but they refused to receive test. Not done indicates the family member died before this event so we can't perform the exam.

† means pathogenic mutation according to the American College of Medical Genetics and Genomics guideline

Abbreviation: ARVC: arrhythmogenic right ventricular dysplasia, CPVT: catecholaminergic polymorphic ventricular tachycardia, HCM: hypertrophic cardiomyopathy, ICD: implantable cardioverter defibrillator, HTX: heart transplant, LOF: loss of follow-up, LP: likely pathogenic, LQT: long QT syndrome, LVNC: left ventricular non-compaction, ND: not done, SCA: sudden cardiac arrest, VT: ventricular tachycardia, VF: ventricular fibrillation, WPW: Wolff–Parkinson–White syndrome.

Supplementary Table 3 The clinical characteristics, initial genetic test results and outcome according to the initial genetic test types

| Initial genetic test | Candidate gene | Composite genetic panel | None | p value |
|---|---|---|---|---|
| | 14 | 10 | 12 | |
| Event year (after 2013) | 6 (42.9%) | 9 (90.0%) | 2 (16.7%) | ***0.003*** |
| Family history | 4 (28.6%) | 3 (30.0%) | 2 (16.7%) | 0.714 |
| Onset age | 12.8 ± 3.9 | 11.4 ± 4.9 | 14.7 ± 4.3 | 0.211 |
| Initial symptoms (aborted SCA) | 11 (78.6%) | 8 (80.0%) | 11 (91.7%) | 0.635 |
| Initial positive genetic results | 4 (28.6%) | 9 (90%) | NA | ***0.005*** |
| Final positive genetic results after composite genetic pane | 12 (85.7%) | 9 (90%) | 1 (50%)[#] | |
| Outcome | | | | ***0.011*** |
| Heart transplant | 0 | 0 | 2 (16.7%) | |
| Mortality | 0 | 0 | 2 (16.7%) | |
| ICD appropriate shock* | 9/10 (90%) | 1/5 (20%) | 1/1 (100%) | ***0.018*** |

* excluding those who died or received heart transplant

[#]Only 2 patients received composite genetic panel