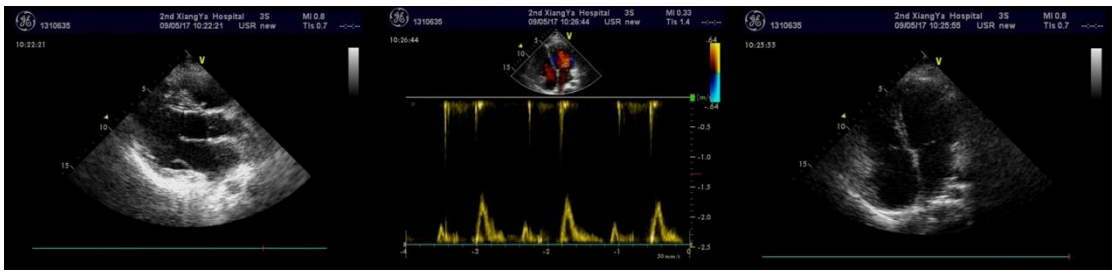

Fig. S1. Color ultrasound results of Patient 1. The patient had enlargement of heart.

Supplementary Table 1. The arrhythmia-related genes list.

ABCC9	*CACNA2D1*	*CMYA5*	*EYA4*	*HCN4*	*KCNJ8*	*MYL3*	*NOS1AP*	*PPP3R1*	*SLMAP*	*TNNI3*
ABRA	*CACNB2*	*COL3A1*	*FBN1*	*HDAC1*	*KCNQ1*	*MYL5*	*NOTCH1*	*PRKAG2*	*SMAD3*	*TNNT1*
ACADVL	*CACNB2B*	*COL5A1*	*FBN2*	*HDAC2*	*KRAS*	*MYL7*	*NPPA*	*PRKCE*	*SMYD1*	*TNNT2*
ACTA1	*CALM1*	*COL5A2*	*FBXL22*	*HEY2*	*LAMA4*	*MYLK*	*NRAP*	*PTPN11*	*SMYD2*	*TPM1*
ACTA2	*CALM2*	*COX15*	*FERMT2*	*HRAS*	*LAMP2*	*MYLK2*	*NRAS*	*RAF1*	*SNTA1*	*TPM2*
ACTC1	*CAML3*	*CRELD1*	*FHL1*	*ILK*	*LBD3*	*MYLK3*	*NRG1*	*RANGRF*	*SOS1*	*TPM3*
ACTN1	*CALR3*	*CRYAB*	*FHL2*	*ITGB1BP2*	*LEFTY2*	*MYO6*	*OBSCN*	*RBM20*	*SYNE1*	*TRDN*
ACTN2	*CAPN1*	*CSRP3*	*FKRP*	*JAG1*	*LIMS1*	*MYOM1*	*OBSL1*	*RYR1*	*SYNE2*	*TRIM54*
ACVR2B	*CAPN2*	*CTNNA3*	*FKTN*	*JPH2*	*LIMS2*	*MYOM2*	*PAK1*	*RYR2*	*SYNM*	*TRIM55*
AKAP13	*CAPN3*	*DES*	*FLNC*	*JUP*	*LMCD1*	*MYOT*	*PALLD*	*SCN1B*	*TAZ*	*TRIM63*
AKAP9	*CAPNS1*	*DICER1*	*FOXH1*	*KBTBD13*	*LMNA*	*MYOZ1*	*PARVB*	*SCN2B*	*TBX20*	*TRPM4*
ALMS1	*CAPZA1*	*DMD*	*GAA*	*KCNA5*	*MAP2K1*	*MYOZ2*	*PDE5A*	*SCN3B*	*TBX5*	*TTN*
ANK2	*CAPZA2*	*DNAJB6*	*GATA4*	*KCND3*	*MAP2K2*	*MYOZ3*	*PDLIM1*	*SCN4B*	*TCAP*	*TTR*
ANKRD1	*CAPZB*	*DNM1L*	*GATD1*	*KCNE1*	*MIB1*	*MYPN*	*PDLIM3*	*SCN5A*	*TGFB2*	*TXNRD2*
ANKRD2	*CASQ2*	*DPP6*	*GDF1*	*KCNE2*	*MIR208*	*MYZAP*	*PDLIM5*	*SCN10A*	*TGFB3*	*UNC45B*
ATP2A2	*CAV3*	*DSC2*	*GJA1*	*KCNE3*	*MYBPC3*	*NEB*	*PDLIM7*	*SDHA*	*TGFBR1*	*VCL*

BAG3	*CBL*	*DSG2*	*GJA5*	*KCNE5*	*MYH11*	*NEBL*	*PKP2*	*SGCD*	*TGFBR2*	*XIRP1*
BCAR1	*CBS*	*DSP*	*GJC1*	*KCNH2*	*MYH6*	*NEURL2*	*PLN*	*SHOC2*	*TMEM43*	*XIRP2*
BMP10	*CFC1*	*DTNA*	*GLA*	*KCNJ2*	*MYH7*	*NEXN*	*POLR2M*	*SLC25A4*	*TMOD1*	*ZIC3*
BRAF	*CFL2*	*ELN*	*GLRX3*	*KCNJ5*	*MYH7B*	*NKX2-5*	*PPP3B*	*SLC2A10*	*TMPO*	
CACNA1C	*CHRM2*	*EMD*	*GPD1L*	*KCNJ5*	*MYL2*	*NODAL*	*PPP3CA*	*SLC8A1*	*TNNC1*	

Supplementary Table 2. Primers and sequences of Sanger sequencing.

Primer	Sequences	Primer	Sequences
RYR2 f	GCACTACACGCAGTCAGAAA	RYR2 r	TCAGGACGCTCTCTGCTAAT
KCNE1 f	GATCCTGTCTAACACCACAGC	KCNE1 r	CATAGGCCTTGTCCTTCTCTTG
KCNQ1 f	TGGGACTCGCTGCCTTA	KCNQ1 r	CCTGGAAGTTTCCGACTTACC
KCNH2 f	AGTGACAGCCATGGACAAC	KCNH2 r	GCCTGGCAGCAGAAGAA
TRPM4 f	GGCAGTCTTCCTGTCTTTCTT	TRPM4 r	AAGTTGACCAGCAGGATGTT

Supplementary Table 3. The ultrasound scan data of Patient 1.

LVEDd	58 mm	LAS	39 mm	RVD	36 mm	RAS	43 mm
IVsd	8 mm	LVPWd	7 mm	AO	23 mm	PA	22 mm
AOV	150 cm/s	PAV	57 cm/s	E/A	Unimodality	EF	37%
FS	18%						

LVEDd, left ventricular end-diastolic dimension; LAD, left atrial diameter; RVD, right ventricular diameter; RAD, right atrial diameter; IVsd, interventricular septal defect; LVPWd, left ventricular posterior wall thickness; AO, aortic diameter; PA, pulmonary artery diameter; AOV, aortic velocity; PAV, pulmonary artery velocity; E/A, E peak/A peak; EF, ejection fraction; FS, fractional shortening.

Supplementary Table 4. The target sequencing results of 6 subjects in this study.

Patient	Gene	Mutation	Mutation Taster	PolyPhen-2	SIFT	1000G	ExAC	gnomAD	OMIM clinical phenotype	ACMG classification
1	*RYR2*	c.12269C>T, p.P4090L	D	D	D	-	-	-	AD, Arrhythmogenic right ventricular dysplasia 2; AD, Ventricular tachycardia, catecholaminergic polymorphic, 1	PS2, PM1, PM2，PP3
	SYNE1	c.18727G>C, p.E6243Q	D	D	D	0.00020	0.00001	0.00006	AR, Arthrogryposis multiplex congenita, myogenic type; AD, Emery-Dreifuss muscular dystrophy 4; AR, Spinocerebellar ataxia	PP3, BS4, BP5
	SYNE1	c.5666A>C, p.Q1889P	D	P	T	-	0.00004	0.00002		BP4 BP5
	COL5A1	c.5335A>G, p.N1779D	D	B	D	-	0.00014	0.00006	AD, Ehlers-Danlos syndrome, classic type, 1	BS4, BP5
	CTNNA3	c.1853A>G, p.H618R	D	D	T	0.00020	0.00002	0.00003	AD, Arrhythmogenic right ventricular dysplasia, familial, 13	PS2, BP5
	CAPN1	c.169C>T, p.R57C	D	D	T	-	0.00005	0.00002	AR, Spastic paraplegia 76	BS4, BP5
	FERMT2	c.1538C>T, p.T513M	D	P	T	0.00200	0.00246	0.00201	-	BP4, BP5
	UNC45B	c.1816G>A, p.E606K	D	D	D	0.00020	0.00001	0.00003	AD, Cataract 43	PP3, BS4, BP5
2	*SLC8A1*	c.959A>G, p.E320G	D	D	D	-	-	-	-	PS2, PM2, PP3, BP5
	XIRP2	c.1985C>T, p.P662L	D	D	D	-	-	-	-	PM2, PP3, BS4, BP5
	TTN	c.82688G>A, p.R27563H	D	B	T	0.00060	0.00020	0.00022	AD, Cardiomyopathy, dilated, 1G; AD, Cardiomyopathy, familial hypertrophic, 9; AR, Muscular dystrophy, limb-girdle; AD, Myopathy, myofibrillar, 9, with early respiratory failure; AR, Salih myopathy; AD, Tibial muscular dystrophy, tardive	BS4, BP4, BP5
	OBSL1	c.3680G>A, p.R1227H	D	D	T	-	0.00005	0.00003	AR, 3-M syndrome 2	BS4, BP5
	TNNC1	c.304C>G,	D	B	D	-	-	-	AD, Cardiomyopathy, dilated, 1Z; AD,	PM2, BS4,

		p.R102G							Cardiomyopathy, hypertrophic, 13	BP5
	CMYA5	c.10000G>A, p.Q3334K	D	B	D	-	-	-	-	PS2, PM2, BP5
	MYH6	c.2717G>A, p.R906H	D	D	D	0.00020	0.00000	0.00001	AD, Atrial septal defect 3; AD, Cardiomyopathy, dilated, 1EE; AD, Cardiomyopathy, hypertrophic, 14	PP3, BS4, BP5
	FBN1	c.79G>A, p.A27T	D	B	D	0.00120	0.00044	0.00041	AD, Acromicric dysplasia; AD, Ectopia lentis, familial; AD, Geleophysic dysplasia 2; AD, Marfan lipodystrophy syndrome; AD, Marfan syndrome; AD, MASS syndrome; AD, Stiff skin syndrome; AD, Weill-Marchesani syndrome 2	BS4, BP5
	KCNE1	c.169T>C, p.F57L	D	D	T	-	-	-	AD, Long QT syndrome 5; AR, Jervell and Lange-Nielsen syndrome 2	PM1, PM2, PP1, PP3
3	*OBSCN*	c.3140C>T, p.A1047V	D	D	T	0.00180	0.00025	0.00013	-	PM6, BP5
	FHL2	c.62T>G, p.L21R	D	D	T	-	0.00001	0.00002	-	PM6, BP5
	FBN2	c.8674G>T, p.D2892Y	D	B	D	0.00060	0.00040	0.00043	AD, Contractural arachnodactyly, congenital; AD, Macular degeneration, early-onset	PM6, BP5
	FBN2	c.3626A>G, p.N1209S	D	B	T	0.00020	0.00003	0.00006		BP4, PM6, BP5
	RBM20	c.1922G>A, p.R641Q	D	D	D	0.00100	0.00012	0.00022	AD, Cardiomyopathy, dilated, 1DD	PM6, PP3, BP5
	KCNQ1	c.853A>C, p.K285Q	D	D	D	-	-	-	AD, Atrial fibrillation, familial, 3; AD, Long QT syndrome 1; AD, Short QT syndrome 2; AR, Jervell and Lange-Nielsen syndrome	PM1, PM2, PP3
	RYR1	c.13089C>A, p.F4363L	D	B	T	-	0.00010	0.00003	AD, Malignant hyperthermia susceptibility 1; AD/AR, Central core disease; AD, King-Denborough syndrome; AR, Minicore myopathy with external ophthalmoplegia; AD/AR, Neuromuscular disease, congenital, with uniform type 1 fiber	PM6, BP4, BP5
4	*OBSL1*	c.4610-1G>C	D	-	-	-	-	-	AR, 3-M syndrome 2	PM2, PP3, BS4, BP5

	KCNH2	c.793T>C, p.C265R	D	P	D	-	-	-	AD, Long QT syndrome 2; AD, Short QT syndrome 1	PS2, PM2, PP2
	TMOD1	c.1028G>T, p.R343M	D	D	D	-	-	-	-	PM2, PP3, BS4, BP5
	MYH7B	c.649A>G, p.I217V	D	B	D	-	-	-	-	PS2, PM2, BP5
5	*NEB*	c.24862A>G, p.I8288V	D	D	D	0.00080	0.00024	0.00026	AR, Nemaline myopathy 2	PM6, PP3, BS4, BP5
	TTN	c.62723G>A, p.R20908Q	D	D	T	0.00020	0.00008	0.00003	AD, Cardiomyopathy, dilated, 1G; AD, Cardiomyopathy, familial hypertrophic, 9; AR, Muscular dystrophy, limb-girdle; AD, Myopathy, myofibrillar, 9, with early respiratory failure; AR, Salih myopathy; AD, Tibial muscular dystrophy, tardive	PM6, BP5
	TTN	c.60928C>T, p.R20310C	D	D	D	0.00020	0.00008	0.00003		PM6, PP3, BP5
	GATA4	c.1075G>A, p.E359K	D	D	T	-	0.00005	0.00004	AD, Testicular anomalies with or without congenital heart disease; AD, Atrial septal defect 2; AD, Atrioventricular septal defect 4; AD, Tetralogy of Fallot; AD, Ventricular septal defect 1	PS1, PM6, BP5
	SYNE2	c.10556A>G, p.E3519G	D	D	T	-	0.00003	0.00013	AD, Emery-Dreifuss muscular dystrophy 5	PM6, BP5
	TRPM4	c.2985_3012del, p.E996Gfs*118	D	-	-	-	0.00021	0.00016	AD, Erythrokeratodermia veriabilis et progressiva 6; AD, Progressive familial heart block, type IB	PVS1, PM4, PP1, PP3

Red words, mutations identified in this study; D, disease causing; T, tolerated; P, polymorphism; B, benign; AR, autosomal recessive; AD, autosomal dominant.