Table S1. List of 167 genes in panel gene was used in this study

Including genes associated with arrhythmia and cardiomyopathy:

AARS2, ABCC6, ABCC9, ACADVL, ACTA1, ACTC1, ACTN2, AGK, AGL, AKAP9, ALMS1, ANK2, ANO5, APOA1, BAG3, BRAF, CACNA1C, CACNA1D, CACNA2D1, CACNB2, CALM1, CALM2, CALM3, CALR3, CAPN3, CASQ2, CAV3, CBL, COX15, CPT2, CRYAB, CSRP3, CTF1, DBH, DES, DMD, DNAJC19, DOLK, DSC2, DSG2, DSP, DTNA, DYSF, EMD, ETFA, ETFB, ETFDH, EYA4, FBN2, FHL1, FKPP, FKTN, FLNC, FOXRED1, FXN, GAA, GATAD1, GATA6, GBE1, GDP1L, GFM1, GLA, GLB1, GSN, GUSB, HADHA, HCN4, HFE, HRAS, HTRA1, ISPD, JPH2, JUP, KCNA5, KCNE1, KCNE2, KCNE3, KCNE4, KCNE5, KCND3, KCNH2, KCNJ2, KCNJ5, KCNJ8, KCNQ1, KRAS, LAMA2, LAMA4, LAMP2, LDB3, LMNA, MAP2K1, MAP2K2, MLYCD, MTO1, MYBPC3, MYH6, MYH7, MYL2, MYL3, MYLK, MYOT, MYOZ2, MYPN, NEBL, NEXN, NF1, NKX2-5, NRAS, PCCA, PCCB, PKP2, PLEC, PNPLA2, PRDM16, PRKAG2, PSEN1, PSEN2, PTPN11, RAF1, RBM20, RMND1, RYR2, SALL4, SCN1B, SCN2B, SCN3B, SCN4B, SCN5A, SCN10A, SCNN1B, SCNN1G, SCO2, SDHA, SGCA, SGCB, SGCD, SGCG, SHOC2, SLC4A3, SLC22A5, SLC25A4, SLC25A20, SOS1, SPRED1, TAB2, TAZ, TBX5, TBX20, TCAP, TGFB3, TMEM43, TMEM70, TMPO, TNNC1, TNNI3, TNNI3K, TNNT2, TPM1, TRDN, TRIM32, TRPM4, TSFM, TTN, TTR, VCL, VPS13A.

Table S2. Prediction results using *in silico* tools for splicing variant *SLC4A3:* c.2535+1G>A

MaxEntScan

>widtype
AAGGTGGAG MAXENT: 1.51 MDD: 8.38 MM: 3.88 WMM: 4.57
>mutant
AAGATGGAG MAXENT: -6.67 MDD: 0.20 MM: -4.30 WMM: -3.62

NetGene2 v. 2.4

The sequence: **wildtype** has the following composition:
Donor splice sites, direct strand

pos 5'->3'	phase	strand	confidence	5' exon intron 3'	
159	0	+	1.00	CTTCTTCAAG^GTGAGGCGAA	H
583	0	+	0.60	GCTCTACAAG^GTGGAGGTCC	
599	1	+	0.19	GTCCAGCGAG^GTCTTGGGGG	
662	0	+	0.34	GGAGGGGGAG^GTATGGAGAA	
768	1	+	0.34	GACCCAGGGG^GTGGGTGCCA	
834	2	+	0.46	ACTTGCACAG^GTATGTGATG	

The sequence: **mutant** has the following composition:
Donor splice sites, direct strand

pos 5'->3'	phase	strand	confidence	5' exon intron 3'	
159	0	+	1.00	CTTCTTCAAG^GTGAGGCGAA	H
599	1	+	0.19	GTCCAGCGAG^GTCTTGGGGG	
662	0	+	0.34	GGAGGGGGAG^GTATGGAGAA	
768	1	+	0.34	GACCCAGGGG^GTGGGTGCCA	
834	2	+	0.46	ACTTGCACAG^GTATGTGATG	

Spliceailookup

SpliceAI scores:

Variant	Gene	Δ type	Δ score	position	REF score	ALT score
chr2-219636875-G-A splice donor variant UCSC, gnomAD	SLC4A3 (ENSG00000114923.17 / ENST00000358055.8 / NM_005070.4) protein coding MANE Select transcript (plus strand) OMIM, GTEx, gnomAD, ClinGen, Ensembl, Decipher, GeneCards	Acceptor Loss	0.00	-255 bp	0.14	0.12
		Donor Loss	0.98	-1 bp	0.98	0.00
		Acceptor Gain	0.07	-63 bp	0.22	0.30
		Donor Gain	0.73	5 bp	0.12	0.85

MANE Select Transcript or All Transcripts

Pangolin scores:

Variant	Gene	Δ type	Δ score	position	REF score	ALT score
chr2-219636875-G-A splice donor variant UCSC, gnomAD	SLC4A3 (ENSG00000114923.17 / ENST00000358055.8 / NM_005070.4) protein coding MANE Select transcript (plus strand) OMIM, GTEx, gnomAD, ClinGen, Ensembl, Decipher, GeneCards	Splice Loss	0.80	-1 bp	0.87	0.07
		Splice Gain	0.37	5 bp	0.13	0.49

EX-SKIP - Results for submitted sequences

Seq	PESS (count)	FAS-ESS hex2 (count)	FAS-ESS hex3 (count)	IIE (count)	IIE (sum)	NI-ESS trusted (count)	NI-ESS all (sum)	PESE (count)	RESCUE -ESE (count)	EIE (count)	EIE (sum)	NI-ESE trusted (count)	NI-ESE all (sum)	ESS (total)	ESE (total)	ESS/ESE (ratio)
SLC4A3	9	102	58	354	6124.2256	157	-218.8672	50	34	312	4030.8882	258	370.1007	680	654	1.04

Allele SLC4A3 has a higher chance of exon skipping than allele .

Fruitfly

Donor site predictions for wildtype:

Start	End	Score	Exon	Intron
152	166	**0.99**	cttcaag	gtgaggcg
655	669	0.44	gggggag	gtatggag
827	841	0.99	tgcacag	gtatgtga
926	940	0.55	gtgtggt	gtgagtat
951	965	0.53	gtgtgat	gtatgtgt

Acceptor site predictions for wildtype:

Start	End	Score	Intron	Exon
251	291	0.87	cccacactcttccttacct	aggggatgggtccctgcattct
307	347	0.84	ttcatccgctgcctattcc	aggggcattgacacccagggc
367	407	0.74	accgctcctacccccacct	agttctgccgagcccaggacct
499	539	0.42	tacatctcgcctttcaccc	aggagatctttgcctttctcat
877	917	0.64	tccttgggtcacctttgt	aggaggtgtgtgtgtgtgtgt

Donor site predictions for mutant:

Start	End	Score	Exon	Intron
152	166	0.99	cttcaag	gtgaggcg
655	669	0.44	gggggag	gtatggag
827	841	0.99	tgcacag	gtatgtga
926	940	0.55	gtgtggt	gtgagtat
951	965	0.53	gtgtgat	gtatgtgt

Acceptor site predictions for mutant:

Start	End	Score	Intron	Exon
251	291	0.87	cccacactcttccttacct	aggggatgggtccctgcattct
307	347	0.84	ttcatccgctgcctattcc	aggggcattgacacccagggc
367	407	0.74	accgctcctacccccacct	agttctgccgagcccaggacct
499	539	0.42	tacatctcgcctttcaccc	aggagatctttgcctttctcat
877	917	0.64	tccttgggtcacctttgt	aggaggtgtgtgtgtgtgtgt