SUPPLEMENTAL MATERIAL

Supplemental Tables

Supplemental Table 1. Selected polymorphisms

Gene	rs number	References	Minor allele frequency in European (1000Genomes)	Minor allele frequency in East Asian (1000Genomes)	Minor allele frequency in European (Hapmap)	Minor allele frequency in Japanese (Hapmap)
ADRA2C	rs61767072	[1]	-	-	-	-
ADRB1	rs1801252	[2]	0.216	0.273	-	0
ADRB1	rs1801253	[1, 2]	0.227	0.168	0.308	0.151
ADRB2	rs28365031	[3]	-	-	-	-
ATP1B1	rs10919071	[4, 5]	0.125	0.023	0.129	-
KCNE1	rs1805128	[5-9]	0.009	0.003	0.023	0.011
KCNH2	rs1805123	[5, 7, 9-12]	0.177	0.031	0.239	0.035
KCNH2	rs3778873	[4]	0.170	0.302	0.162	0.284
KCNH2	rs3807375	[4, 9, 12, 13]	0.359	0.762	0.376	0.805
KCNH2	rs3815459	[4, 11, 14]	0.223	0.736	-	0.807
KCNJ2	rs17779747	[4]	0.340	0.077	0.310	0.088
KCNQ1	rs12296050	[4, 13]	0.244	0.374	0.186	0.372
KCNQ1	rs2074238	[5, 6]	0.065	0.033	0.065	0.045
KCNQ1	rs757092	[11, 14]	0.405	0.369	0.346	0.367
NOS1AP	rs10494366	[4, 9, 13, 15-22]	0.361	0.647	0.350	0.686
NOS1AP	rs12029454	[6, 13]	0.177	0.358	0.146	0.367
NOS1AP	rs12143842	[4-6, 13, 18, 23, 24]	0.244	0.318	0.188	0.363
NOS1AP	rs16857031	[6]	0.119	0.205	0.141	0.136
NOS1AP	rs4657139	[9, 15, 16, 19, 25]	0.344	0.696	0.292	0.750
NOS1AP	rs4657178	[4]	0.284	0.517	0.257	0.500
CNOT3	rs36643	[26]	0.380	0.220	0.350	0.181
PLN	rs11970286	[4]	0.460	0.217	0.491	0.155
PLN	rs12210810	[4, 5]	0.049	0.000	0.081	0
SCN5A	rs12053903	[5, 6]	0.372	0.556	0.301	0.522
SCN5A	rs1805124	[7, 9, 27]	0.183	0.103	0.179	0.129

Minor alleles were defined according to alleles frequencies in Europeans.

Supplemental Table 2. Methods and primers used for genotyping

A. FRET

Gene	rs number	Forward primer	Reverse primer	Anchor probe (Red640)	Sensor probe
KCNH2	rs1805123	CCCGGCAGTACGGAGTTA	AAGGTCTGAGGCCTGGGTA	CGCCTGCGGAAGGACAACTTGC	GCCTCACCC**G**TGTCCGT
NOS1AP	rs12029454*	TATTTATTCATTTAAACACGGGGTG	GTATTGGCTCAAAAAGGGAAGT	GACAGTTCTAATCATTCCATCACACGCT	TTGATTTGTTTC**C**TTTGACTGAGA

SNP allelic variants are bolded
* in the discovery cohort

B. HRM with an unlabeled probe

Gene	rs number	Forward primer	Reverse primer	Probe
KCNQ1	rs12296050	GTGCTTAGACTGTGCCCG	GGGAGACCCTGTCTCGAA	CTCCTGGGCTCC**T**AACCTTTCACAG-3'P
SCN5A	rs12053903	GGTCCTCAAACCACACTTTGAATA	CCATCTTCTACATCTTGGGTTCTC	GCTGGGTGGGCA**A**GATACTAAGCAG-3'P

SNP allelic variants are bolded

C. Sequencing

Gene	rs number	Forward primer	Reverse primer
ADRA2C	rs61767072	AGCCGGACGAGAGCAGCGCA	AGGCCTCGCGGCAGATGCCGTACA
ADRB2	rs28365031	AACGGACACTCGAAGTCCAC	GCTGAAGAAGAAGGGGAACC

D. Taqman

Gene	rs number	Applied Biosystems Taqman Assay
ADRB1	rs1801252	C___8898508_10
ADRB1	rs1801253	C___8898494_10
ATP1B1	rs10919071	C___1264222_10
KCNH2	rs3815459	C___3219498_10

Gene	rs number	Applied Biosystems Taqman Assay
KCNQ1	rs2074238[†]	C__15862454_10
KCNQ1	rs757092	C___2990605_10
NOS1AP	rs4657139	C___1777005_10
NOS1AP	rs4657178	C____133678_10
NOS1AP	rs12029454[‡]	C__31087211_10
SCN5A	rs1805124	C__11987864_10

[†] in the discovery and the replication populations
[‡] in the replication populations

E. Tm shift primers

Gene	rs number	Allele-specific primers		Common primer
KCNE1	rs1805128	GCGGGCAGGGCGGCGTCCTTCTCTTGCCAGGCcT**C**	GCGGGCGTCCTTCTCTTGCCAGGCcT**T**	CTGAGCTACATCCGCTCCAAGAA
KCNH2	rs3778873	GCGGGCAGGGCGGCCACCTAATCCAACCCATcC**G**	GCGGGCCACCTAATCCAACCCATcC**C**	ACTGGTCATCAGACCTCTGCTTCT
KCNH2	rs3807375	GCGGGCAGGGCGGCTAGAGAACTTCTGCGTTTAaA**G**	GCGGGCTAGAGAACTTCTGCGTTTAaA**A**	CTCTATACTGGGAGGGGGCAATG
KCNJ2	rs17779747	GCGGGCAGGGCGGCCAAAGACAGAATTCTGGCcA**C**	GCGGGCCAAAGACAGAATTCTGGCcA**A**	CACTCACAGTTCCAGGATTTCTT
NOS1AP	rs10494366	GCGGGCAGGGCGGCATATTTATGGGAGGTATGCgG**G**	GCGGGCATATTTATGGGAGGTATGCgG**T**	GAGATGTGTCCTAGATAGAGACCAGTA
NOS1AP	rs12143842	GCGGGCAGGGCGGCCCAGGGTCACATCCCAGcT**C**	GCGGGCCCAGGGTCACATCCCAGcT**T**	TGGGAACAGAGTCAGGAGACAGC
NOS1AP	rs16857031	GCGGGCAGGGCGGCCTAACTATGACACTGCTCAtA**G**	GCGGGCCTAACTATGACACTGCTCAtA**C**	GCAAATGTGACAGGGTGTTTACC
CNOT3	rs36643	GCGGGCAGGGCGGCAGAGGAGAATGACTGTaC**C**	GCGGGCAGAGGAGAATGACTGTaC**T**	CGTGCATAGCAGAATTGGTTGG
PLN	rs11970286	GCGGGCAGGGCGGCCCAAAGGCATGAGAACTcG**C**	GCGGGCCCAAAGGCATGAGAACTcG**T**	GGCTCATACACCCTCACCTACCTT
PLN	rs12210810	GCGGGCAGGGCGGCCACTGTCCTGTGTTCACACAaA**G**	GCGGGCCACTGTCCTGTGTTCACACAaA**C**	CTGACATCAGTCTTATTCTGATTACA

The GC-rich tails are underlined

SNP allelic variants are bolded

Mismatched nucleotides are in lowercase

Supplemental Table 3. Sequencing primers used for validating other genotyping methods

Gene	rs number	Forward primer	Reverse primer
ADRB1	rs1801252	CCGGGCTTCTGGGGTGTTCC	GGCGAGGTGATGGCGAGGTAGC
ADRB1	rs1801253	TTCAACCCCATCATCTACTGC	GGCCCTACACCTTGGATTC
ATP1B1	rs10919071	TGCTTTCAAGTATAAGTCTCAGTG	GGAGAAACTGACATCAGTCTTATT
KCNE1	rs1805128	GTTCAGCAGGGTGGCAACAT	GCCAGATGGTTTTCAACGACA
KCNH2	rs1805123	CTGGGGCAAAATCACATTG	AAGGGATGGGAAGGTCTGAG
KCNH2	rs3778873	GAGGAGTTATTGTGGGATCACCTA	GACAAGTTTGAACTTGGGCTG
KCNH2	rs3807375	CTATACTGGGAGGGGGCAAT	AGAGTTTGATGGTGGCCTTG
KCNH2	rs3815459	GGGCTAGGAATGGAAGAAGG	CTCACCCAGCTCTGCTCTCT
KCNJ2	rs17779747	CACTCACAGTTCCAGGATTTCTT	CACAGGCATTCAGTGCAGAT
KCNQ1	rs12296050	GTGCTTAGACTGTGCCCG	GGGAGACCCTGTCTCGAA
KCNQ1	rs2074238	CTCAAGGAGCCTGGTACAGC	GCAATGTCTTGTGAGGAGCA
KCNQ1	rs757092	CACAGGGACACACCCATGTA	GTTCTGCTACCGAGGCTGTC
NOS1AP	rs10494366	GGTGAGGTCAGTCTCTGAAC	CACCCAGAGAGATGTGTCCTA
NOS1AP	rs12029454	TATTTATTCATTTAAACACGGGGTG	GTATTGGCTCAAAAAGGGAAGT
NOS1AP	rs12143842	GGAGACAACACGAGGACGAT	GCTGGGAACAGAGTCAGGAG
NOS1AP	rs16857031	GTGGGGAACATGCCAGTTAT	AAGACGGAAGTGGTGAATGG
NOS1AP	rs4657139	CAGAGGTGGTGCAATTCCTT	TGCAGTCCTTCCCGAGTTAC
NOS1AP	rs4657178	AACAACCCCAAGGGAAAGAT	CCCCACATAACTGCACACTG
CNOT3	rs36643	CCAGACAGGGAAACCGAATA	CCTCGTCTTTCTCCAAGTGC
PLN	rs11970286	GGTGGTGTAATTCAGTCTTGAGTTTG	GGCTCATACACCCTCACCTACCTT
PLN	rs12210810	AAGCAGGGATGGGAATCTTT	CCAGCAATCAACACACTATAGCACC
SCN5A	rs12053903	GGTCCTCAAACCACACTTTGAATA	CCATCTTCTACATCTTGGGTTCTC
SCN5A	rs1805124	GCCCTCAATGCTCTGAGAAG	TAATGAGACCACCCCATTGC

Supplemental Table 4. Polymorphism allele frequencies in Caucasian and Japanese LQTS patients from the discovery cohort

Gene	rs number		Caucasian		Japanese	
ADRA2C	rs61767072		Ins	Del	Ins	Del
		AS	0.92	0.08	0.95	0.05
		S	0.92	0.08	0.95	0.05
		All	0.92	0.08	0.95	0.05
ADRB1	rs1801252		A	G	A	G
		AS	0.89	0.11	0.90	0.10
		S	0.88	0.12	0.85	0.15
		All	0.89	0.11	0.88	0.12
ADRB1	rs1801253		C	G	C	G
		AS	0.73	0.27	0.77	0.23
		S	0.68	0.32	0.79	0.21
		All	0.71	0.29	0.78	0.22
ADRB2	rs28365031		Ins	Del	Ins	Del
		AS	0.76	0.24	0.67	0.33
		S	0.77	0.23	0.62	0.38
		All	0.76	0.24	0.65	0.35
ATP1B1	rs10919071		A	G	A	G
		AS	0.87	0.13	0.90	0.10
		S	0.87	0.13	0.94	0.06
		All	0.87	0.13	0.92	0.08
KCNE1	rs1805128		C	T	C	T
		AS	0.99	0.01	0.98	0.02
		S	0.95	0.05	1.00	0.00
		All	0.97	0.03	0.99	0.01
KCNH2	rs1805123		A	C	A	C
		AS	0.78	0.22	0.96	0.04
		S	0.81	0.19	0.99	0.01
		All	0.80	0.20	0.98	0.02
KCNH2	rs3778873		G	C	G	C
		AS	0.80	0.20	0.73	0.27
		S	0.80	0.20	0.66	0.34
		All	0.80	0.20	0.70	0.30
KCNH2	rs3807375		C	T	C	T
		AS	0.59	0.41	0.17	0.83
		S	0.61	0.39	0.18	0.82
		All	0.60	0.40	0.18	0.82

Gene	rs number		Caucasian		Japanese	
KCNH2	rs3815459		C	T	C	T
		AS	0.74	0.26	0.21	0.79
		S	0.73	0.27	0.13	0.87
		All	0.73	0.27	0.17	0.83
KCNJ2	rs17779747		G	T	G	T
		AS	0.73	0.27	0.90	0.10
		S	0.67	0.33	0.90	0.10
		All	0.70	0.30	0.90	0.10
KCNQ1	rs12296050		C	T	C	T
		AS	0.78	0.22	0.59	0.41
		S	0.75	0.25	0.56	0.44
		All	0.76	0.24	0.57	0.43
KCNQ1	rs2074238		C	T	C	T
		AS	0.90	0.10	1.00	0.00
		S	0.96	0.04	1.00	0.00
		All	0.93	0.07	1.00	0.00
KCNQ1	rs757092		A	G	A	G
		AS	0.64	0.36	0.59	0.41
		S	0.63	0.37	0.62	0.38
		All	0.63	0.37	0.60	0.40
NOS1AP	rs10494366		T	G	T	G
		AS	0.65	0.35	0.27	0.73
		S	0.65	0.35	0.24	0.76
		All	0.65	0.35	0.26	0.74
NOS1AP	rs12029454		G	A	G	A
		AS	0.84	0.16	0.60	0.40
		S	0.85	0.15	0.59	0.41
		All	0.84	0.16	0.59	0.41
NOS1AP	rs12143842		C	T	C	T
		AS	0.74	0.26	0.61	0.39
		S	0.69	0.31	0.61	0.39
		All	0.71	0.29	0.61	0.39
NOS1AP	rs16857031		C	G	C	G
		AS	0.85	0.15	0.87	0.13
		S	0.87	0.13	0.80	0.20
		All	0.86	0.14	0.84	0.16
NOS1AP	rs4657139		T	A	T	A
		AS	0.67	0.33	0.23	0.77
		S	0.63	0.37	0.22	0.78
		All	0.65	0.35	0.23	0.77

Gene	rs number		Caucasian		Japanese	
NOS1AP	rs4657178		C	T	C	T
		AS	0.70	0.30	0.46	0.54
		S	0.70	0.30	0.44	0.56
		All	0.70	0.30	0.45	0.55
CNOT3	rs36643		T	C	T	C
		AS	0.58	0.42	0.70	0.30
		S	0.58	0.42	0.68	0.32
		All	0.58	0.42	0.69	0.31
PLN	rs11970286		C	T	C	T
		AS	0.54	0.46	0.78	0.22
		S	0.53	0.47	0.77	0.23
		All	0.54	0.46	0.77	0.23
PLN	rs12210810		G	C	G	C
		AS	0.95	0.05	1.00	0.00
		S	0.99	0.01	1.00	0.00
		All	0.97	0.03	1.00	0.00
SCN5A	rs12053903		A	G	A	G
		AS	0.70	0.30	0.45	0.55
		S	0.67	0.33	0.50	0.50
		All	0.69	0.31	0.48	0.52
SCN5A	rs1805124		A	G	A	G
		AS	0.80	0.20	0.91	0.09
		S	0.79	0.21	0.94	0.06
		All	0.79	0.21	0.93	0.07

Asymptomatic patients (AS)

Symptomatic patients (S)

Supplemental Table 5. Polymorphism genotypes in Caucasian and Japanese LQTS patients from the discovery cohort

Gene	rs number		Caucasian			Japanese		
ADRA2C	rs61767072		II	ID+DD	OR [95% CI]	II	ID+DD	OR [95% CI]
		AS	60	11	1.11 [0.60-2.05]	37	4	1.00 [0.37-2.72]
		S	59	12		37	4	
ADRB1	rs1801252		AA	AG+GG	OR [95% CI]	AA	AG+GG	OR [95% CI]
		AS	57	14	1.28 [0.68-2.41]	33	8	1.51 [0.75-3.04]
		S	54	17		30	11	
ADRB1	rs1801253		CC	CG+GG	OR [95% CI]	CC	CG+GG	OR [95% CI]
		AS	39	32	1.33 [0.80-2.21]	25	16	1.00 [0.56-1.78]
		S	34	37		25	16	
ADRB2	rs28365031		II	ID+DD	OR [95% CI]	II	ID+DD	OR [95% CI]
		AS	39	32	0.75 [0.43-1.30]	19	22	1.50 [0.75-2.98]
		S	44	27		15	26	
ATP1B1	rs10919071		AA	AG+GG	OR [95% CI]	AA	AG+GG	OR [95% CI]
		AS	52	19	0.86 [0.46-1.61]	35	6	0.81 [0.40-1.66]
		S	54	17		36	5	
KCNE1	rs1805128		CC	CT+TT	OR [95% CI]	CC	CT+TT	OR [95% CI]
		AS	70	1	7.66 [1.21-48.31]	39	2	-
		S	64	7		41	0	
KCNH2	rs1805123		AA	AC+CC	OR [95% CI]	AA	AC+CC	OR [95% CI]
		AS	43	28	0.78 [0.49-1.27]	38	3	0.32 [0.05-2.15]
		S	47	24		40	1	
KCNH2	rs3778873		GG	GC+CC	OR [95% CI]	GG	GC+CC	OR [95% CI]
		AS	46	25	1.13 [0.69-1.86]	19	22	1.35 [0.74-2.46]
		S	44	27		16	25	
KCNH2	rs3807375		CC	CT+TT	OR [95% CI]	CC	CT+TT	OR [95% CI]
		AS	27	44	0.94 [0.53-1.68]	0	41	-
		S	28	43		2	39	
KCNH2	rs3815459		CC	CT+TT	OR [95% CI]	CC	CT+TT	OR [95% CI]
		AS	40	31	1.12 [0.67-1.88]	1	40	1.00 [0.06-17.17]
		S	38	33		1	40	
KCNJ2	rs17779747		GG	GT+TT	OR [95% CI]	GG	GT+TT	OR [95% CI]
		AS	37	34	1.18 [0.69-2.03]	35	6	1.41 [0.62-3.25]
		S	34	37		33	8	
KCNQ1	rs12296050		CC	CT+TT	OR [95% CI]	CC	CT+TT	OR [95% CI]
		AS	45	26	1.50 [0.85-2.66]	15	26	1.00 [0.55-1.81]
		S	38	33		15	26	
KCNQ1	rs2074238		CC	CT+TT	OR [95% CI]	CC	CT+TT	OR [95% CI]
		AS	57	14	0.38 [0.19-0.73]	41	0	-
		S	65	6		41	0	
KCNQ1	rs757092		AA	AG+GG	OR [95% CI]	AA	AG+GG	OR [95% CI]
		AS	27	44	0.94 [0.51-1.75]	12	29	0.65 [0.33-1.27]
		S	28	43		16	25	

Gene	rs number		Caucasian			Japanese		
NOS1AP	rs10494366		TT	TG+GG	OR [95% CI]	TT	TG+GG	OR [95% CI]
		AS	25	46	0.59 [0.33-1.07]	3	38	1.00 [0.24-4.11]
		S	34	37		3	38	
NOS1AP	rs12029454		GG	GA+AA	OR [95% CI]	GG	GA+AA	OR [95% CI]
		AS	50	21	1.00 [0.59-1.71]	14	27	1.00 [0.51-1.98]
		S	50	21		14	27	
NOS1AP	rs12143842		CC	CT+TT	OR [95% CI]	CC	CT+TT	OR [95% CI]
		AS	37	34	1.00 [0.56-1.77]	15	26	0.90 [0.39-2.11]
		S	37	34		16	25	
NOS1AP	rs16857031		CC	CG+GG	OR [95% CI]	CC	CG+GG	OR [95% CI]
		AS	52	19	0.86 [0.45-1.65]	31	10	1.98 [1.07-3.67]
		S	54	17		25	16	
NOS1AP	rs4657139		TT	TA+AA	OR [95% CI]	TT	TA+AA	OR [95% CI]
		AS	29	42	0.84 [0.45-1.59]	0	41	-
		S	32	39		3	38	
NOS1AP	rs4657178		CC	CT+TT	OR [95% CI]	CC	CT+TT	OR [95% CI]
		AS	35	36	1.00 [0.64-1.57]	9	32	1.16 [0.44-3.07]
		S	35	36		8	33	
CNOT3	rs36643		TT	TC+CC	OR [95% CI]	TT	TC+CC	OR [95% CI]
		AS	22	49	0.94 [0.57-1.54]	20	21	0.91 [0.47-1.74]
		S	23	48		21	20	
PLN	rs11970286		CC	CT+TT	OR [95% CI]	CC	CT+TT	OR [95% CI]
		AS	23	48	1.22 [0.72-2.08]	24	17	0.81 [0.50-1.34]
		S	20	51		26	15	
PLN	rs12210810		GG	GC+CC	OR [95% CI]	GG	GC+CC	OR [95% CI]
		AS	64	7	0.27 [0.05-1.38]	41	0	-
		S	69	2		41	0	
SCN5A	rs12053903		AA	AG+GG	OR [95% CI]	AA	AG+GG	OR [95% CI]
		AS	35	36	1.33 [0.73-2.42]	7	34	0.85 [0.41-1.74]
		S	30	41		8	33	
SCN5A	rs1805124		AA	AG+GG	OR [95% CI]	AA	AG+GG	OR [95% CI]
		AS	43	28	0.84 [0.48-1.44]	36	5	1.00 [0.41-2.45]
		S	46	25		36	5	

Asymptomatic patients (AS)

Symptomatic patients (S)

Insertion (I)

Deletion (D)

Supplemental Table 6. QTc duration in Caucasian and Japanese LQTS patients from the discovery cohort presented by rs12029454 genotype

			AA		Aa and aa	
Gene	**SNP**		**QTc (ms)**	**n**	**QTc (ms)**	**n**
NOS1AP	rs12029454	Caucasian	474 ± 43	97	485 ± 43	41
		Japanese	463 ± 49	28	483 ± 54	54

Supplemental Table 7. Power to detect previously reported effect on cardiac events or QTc in LQTS patients or healthy populations in our discovery cohort

A. Power to detect previously reported effect on cardiac events in LQTS patients in our discovery cohort

SNP	Previously reported effect		Power[†]
	OR	References	
rs10494366	1.42	Tomas et al., 2010	30%
rs12143842[*]	1.40	Crotti et al., 2009	35 %
rs4657139	1.38	Tomas et al., 2010	27%
	1.80	Crotti et al., 2009	58%

B. Power to detect previously reported effect on QTc in LQTS patients in our discovery cohort

SNP	Previously reported effect		Power[‡]
	Effect size	References	
rs12143842[*]	8 ms	Tomas et al., 2010	39%
rs4657139	7 ms	Tomas et al., 2010	27%

C. Power to detect previously reported effect on QTc in healthy populations in our discovery cohort

SNP	Power[‡]
rs10919071	9-12%
rs1805128	14-17%
rs1805123	9-12%
rs3778873	9%
rs3807375	7-13%
rs3815459	8%
rs17779747	7%
rs12296050	8-9%
rs2074238[§]	14-19%
rs757092	9%
rs10494366	9-14%
rs12029454	15%
rs12143842	13-21%
rs16857031	13%

SNP	Power[‡]
rs4657139	15%
rs4657178	10%
rs36643	7%
rs11970286	8%
rs12210810[§]	7-8%
rs12053903	8%
rs1805124	8%

[*] Effect reported for rs16847548 which is in strong linkage disequilibrium with rs12143842 (r^2>0.8 in Europeans)

[†] Using QUANTO program, we calculated the power to detect previously reported effect, at a significance level of 0.05, under a dominant model, with a prevalence of 35%, according to allele frequencies in our discovery population and for 112 duos constituting our matched case-control study.

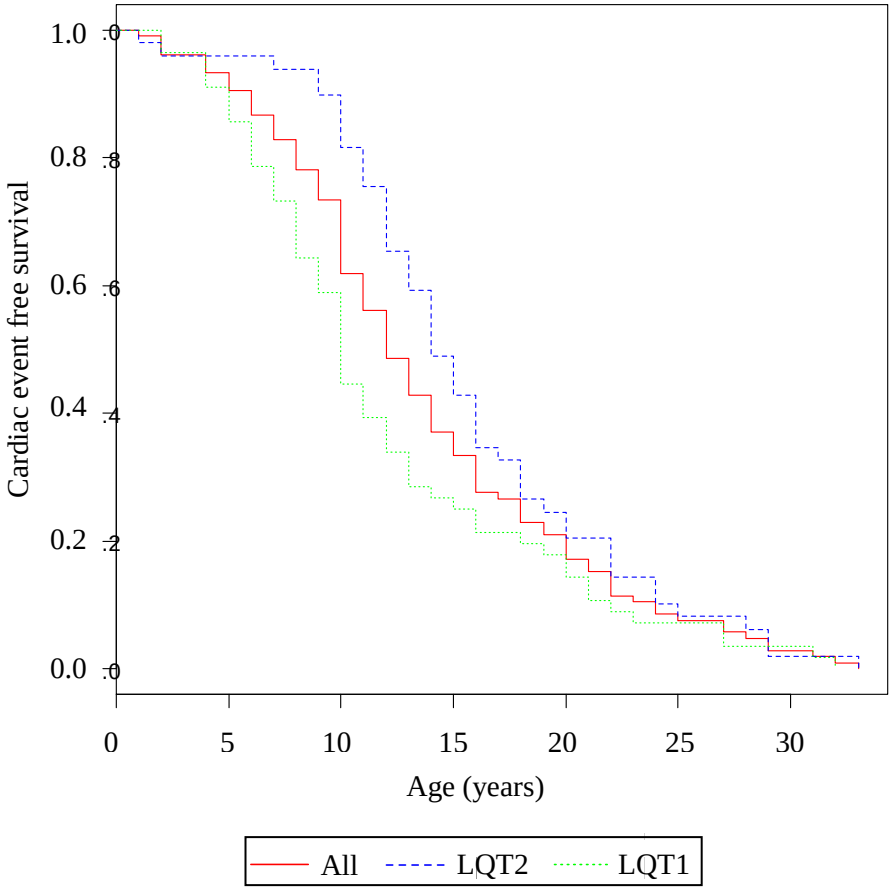
[‡] Using QUANTO program, we calculated the power to detect previously reported effect, at a significance level of 0.05, under a dominant model, with a prevalence of 35%, according to allele frequencies in our discovery population and for 224 individuals constituting our LQTS cohort

[§] Power was calculated according to allele frequencies in Caucasian discovery population and for 142 individuals constituting our Caucasian matched case-control study (SNPs non polymorphic in Japanese)

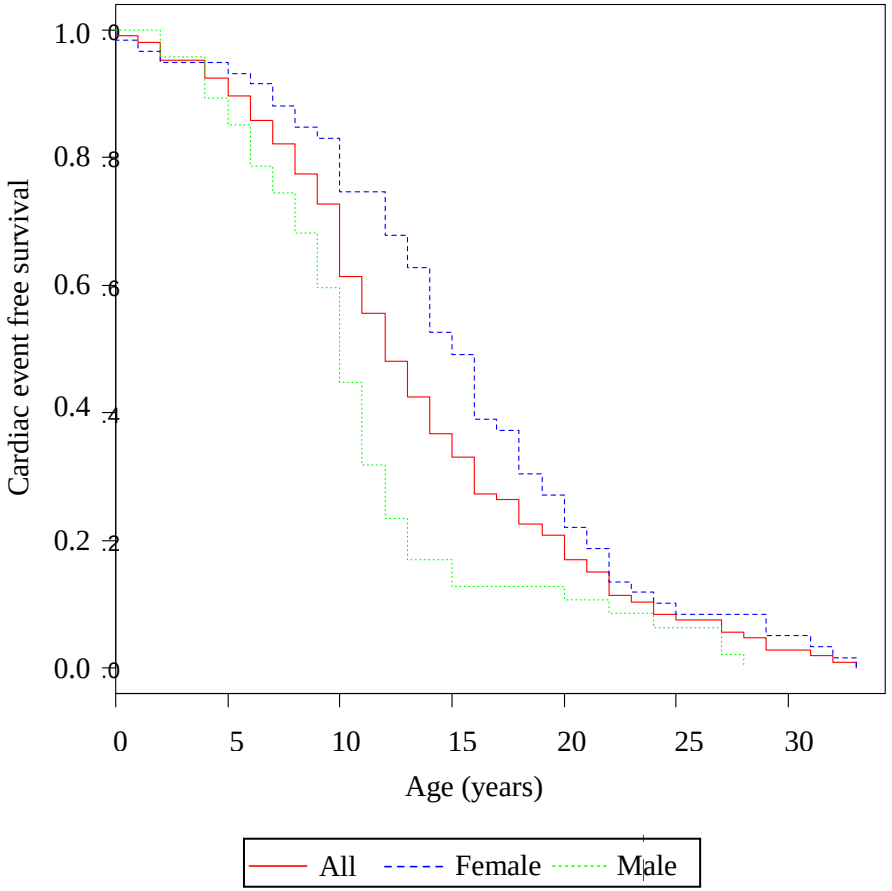
Supplemental Figures

Supplemental Figure 1.

A

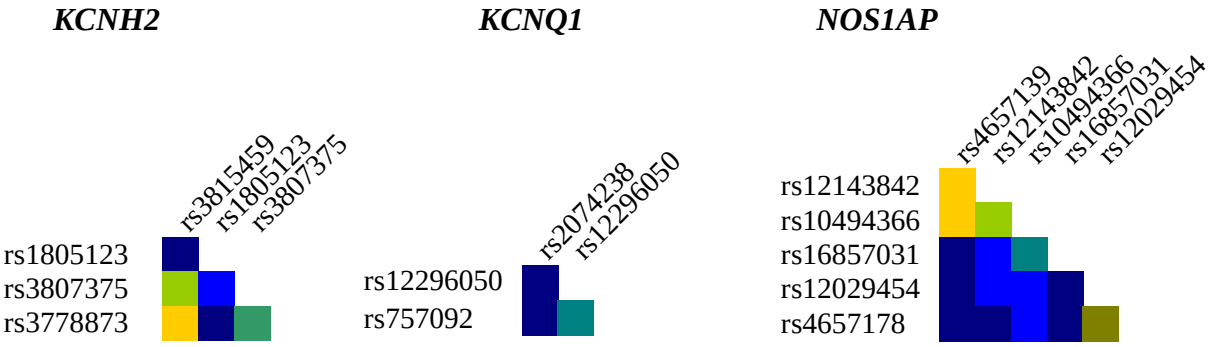


B

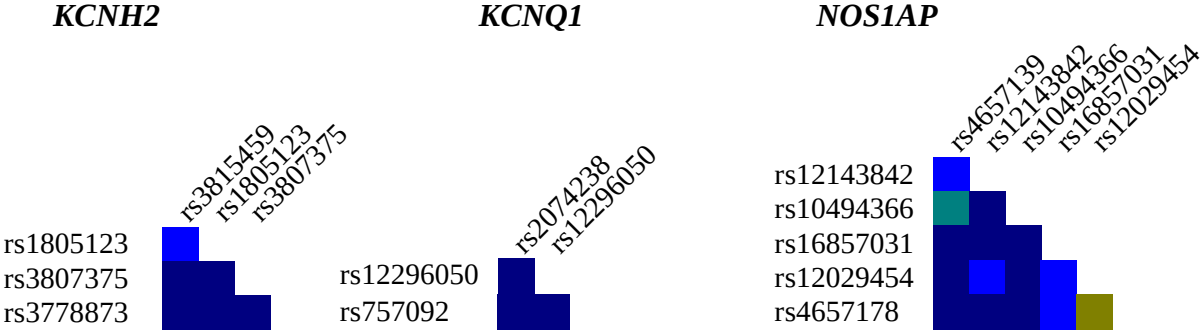


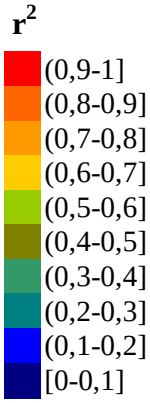
Supplemental Figure 2.

A.



B.





Supplemental Figures Legends

Supplemental Figure 1. Kaplan-Meier curves of survival free from cardiac events among the symptomatic group from the discovery cohort.

The age-related probability of not experiencing a first cardiac event, with birth used as time of origin, was plotted using the Kaplan-Meier method in the symptomatic population by genetic locus (A) or sex (B).

Supplemental Figure 2. Pairwise LD between polymorphisms in LQTS patients from the discovery cohort

A. Pairwise LD calculated from asymptomatic Caucasian patients

   SNPs in *ADRB1*, *PLN* or *SCN5A* have $r^2<0.1$

B. Pairwise LD calculated from asymptomatic Japanese patients

   SNPs in *ADRB1*, *PLN* or *SCN5A* have $r^2<0.1$

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