Supplementary information for

Genetic association study of QT interval highlights role for calcium signaling pathways in myocardial repolarization

The QT Interval - International GWAS Consortium (QT-IGC)

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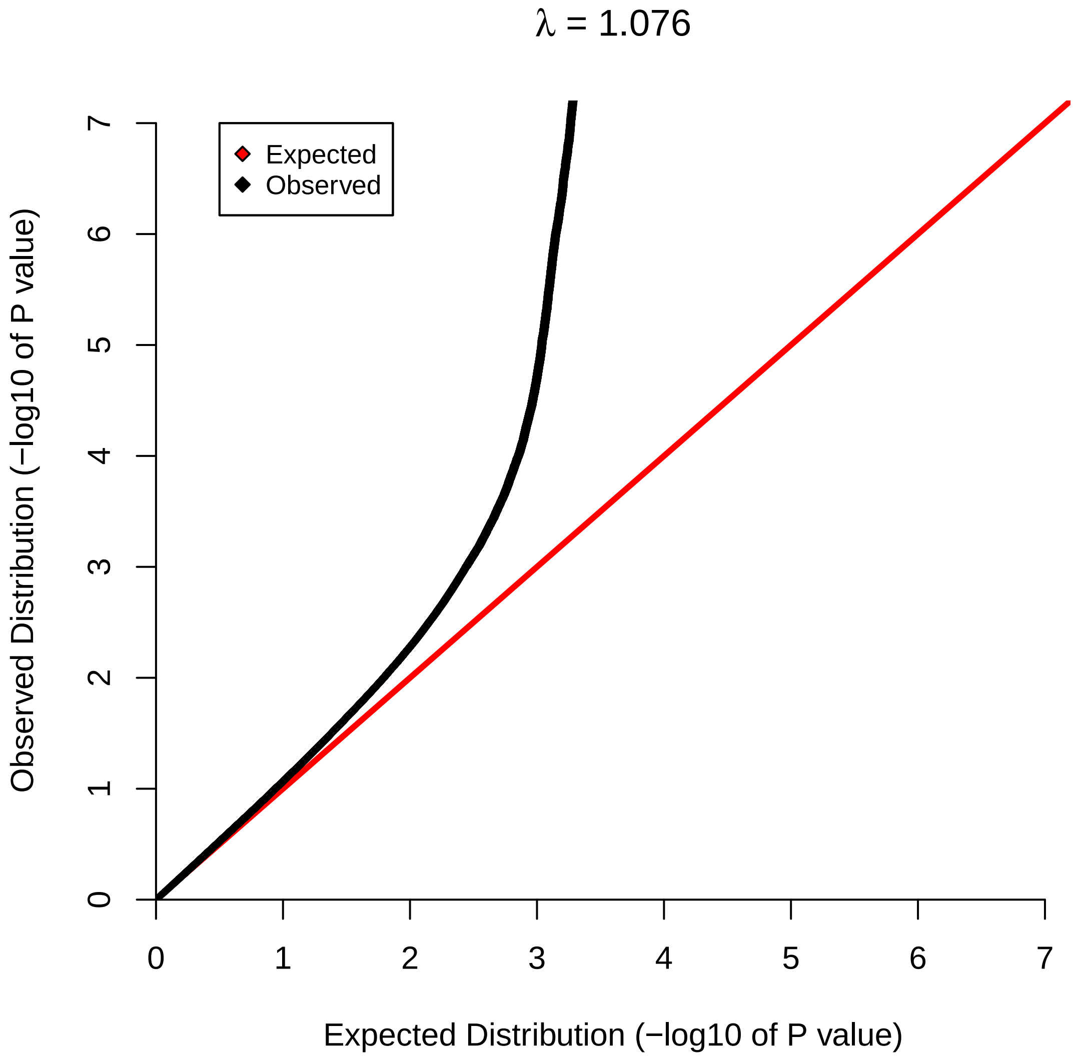
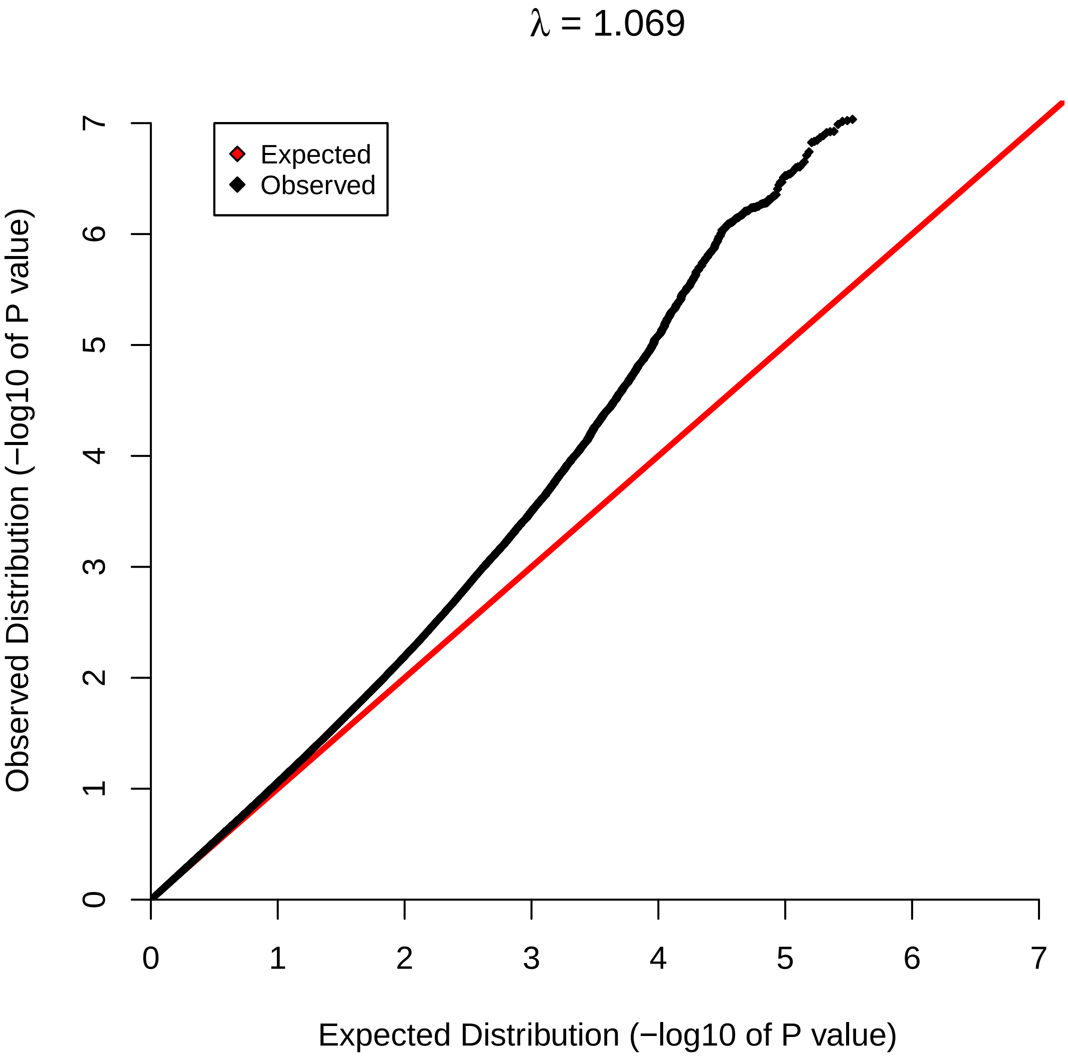
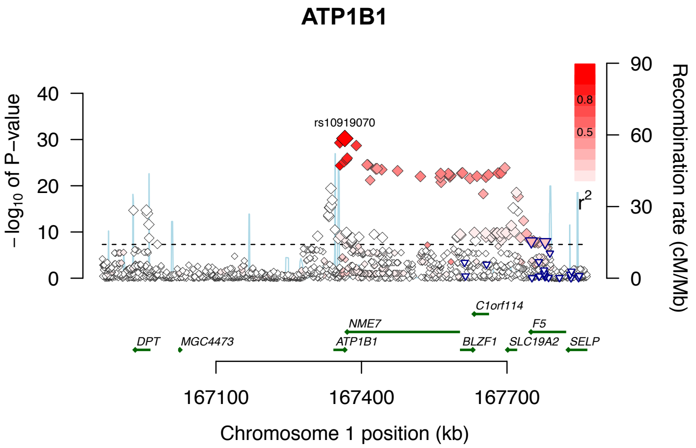


Supplementary Figure 1A. Quantile-quantile plot of GWAS test statistics. Plotted in Supplementary Figure 1A are the observed (y-axis) versus the expected (x-axis) –log(P) for the ~2.5 million SNPs tested for association with QT interval in the meta-analysis of GWAS results for 76,198 individuals of European ancestry, along with the ratio of the observed to expected median test statistic (λGC). In Supplementary Figure 1B, the same results are presented after removing all results within 500kb of the index SNP at each locus.



Supplementary Figure 1B

Supplementary Figure 2: Regional association plots for 35 genome-wide significant loci. Plotted on the following pages are the –log(P) from meta-analysis of association of SNPs with QT interval in the 76,198 individuals of European ancestry with GWAS. For comparability of SNP association no replication results are incorporated, hence some top SNPs in the GWAS-only results presented fail to achieve genome-wide significance (dashed line) because replication results were needed to cross this threshold. At the extreme, minimal association with rs1805128, a missense SNP in KCNE1, is found in the GWAS-only results depicted in the figure due to very low MAF (~1%) and resultant poor imputation using common variants on most genotyping arrays. Only with direct replication genotyping in several of the GWAS samples was this SNP able to reach genome-wide significance. Results are shown for any SNP within 500kb of the index SNP at each locus.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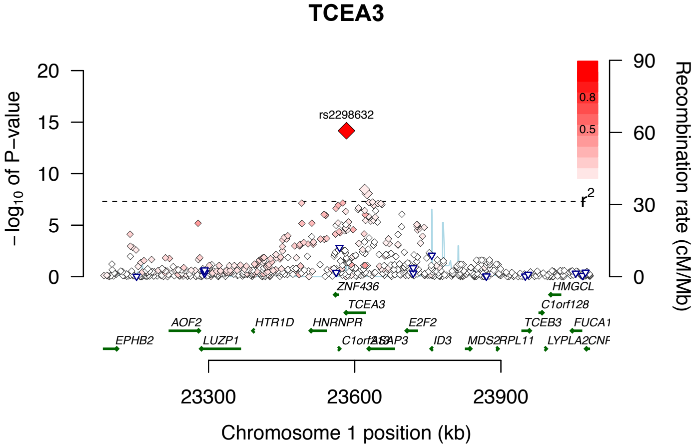
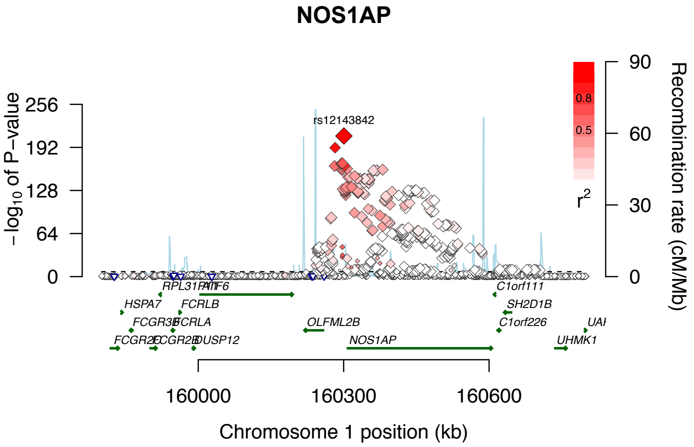

TCEA3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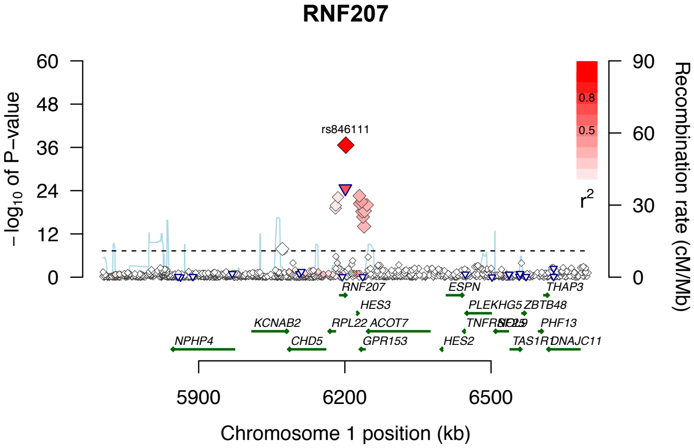
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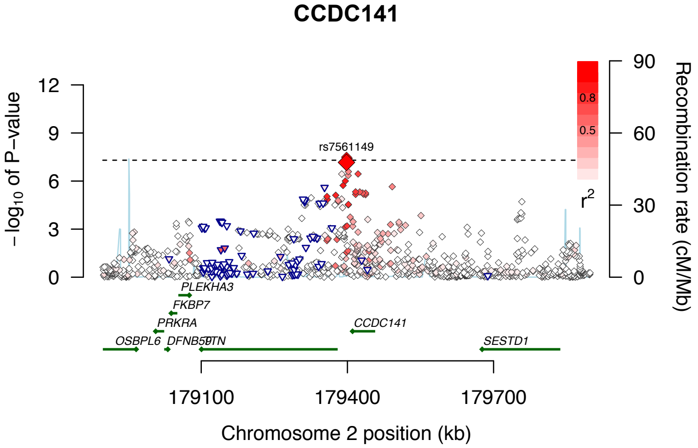
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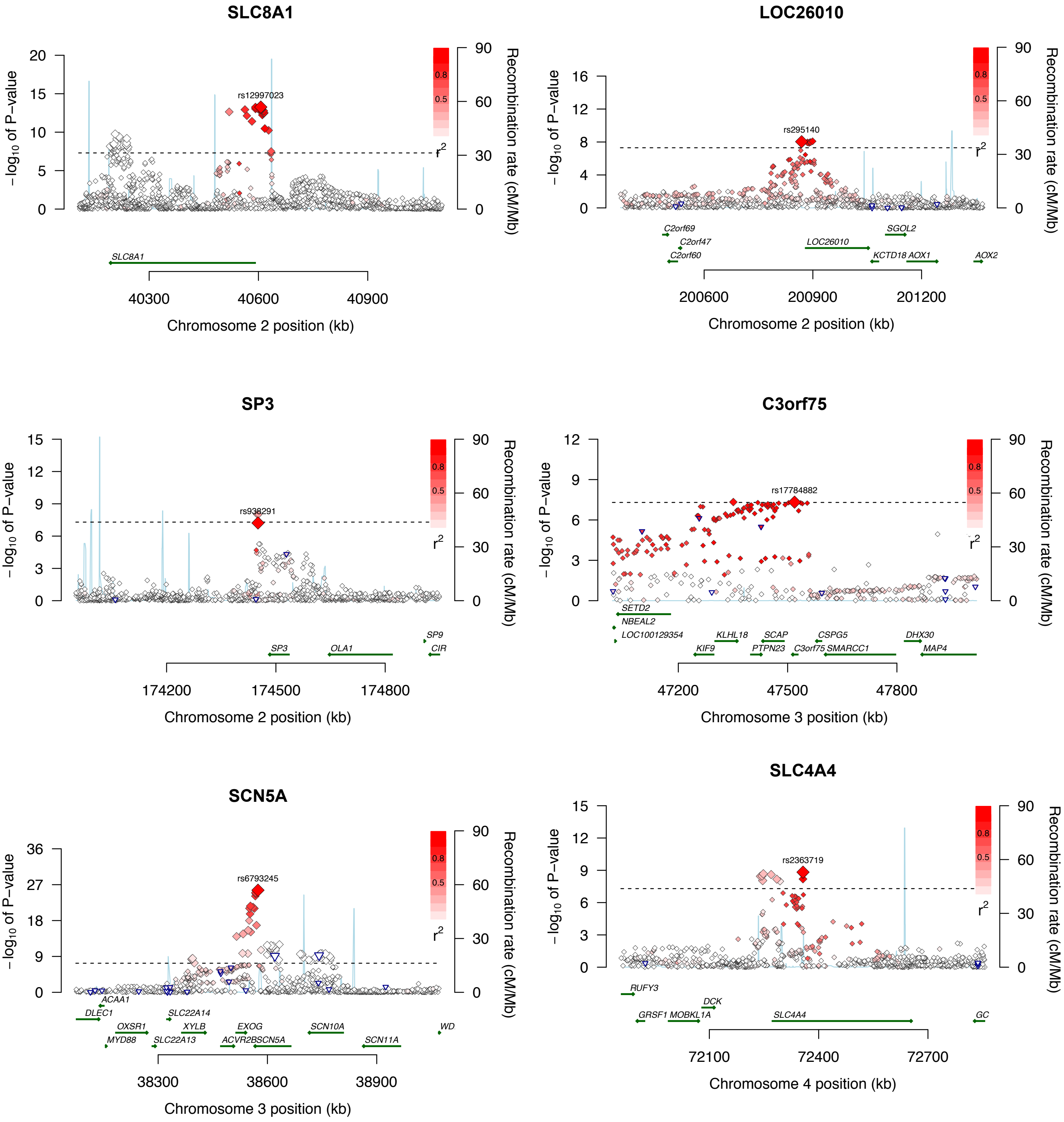
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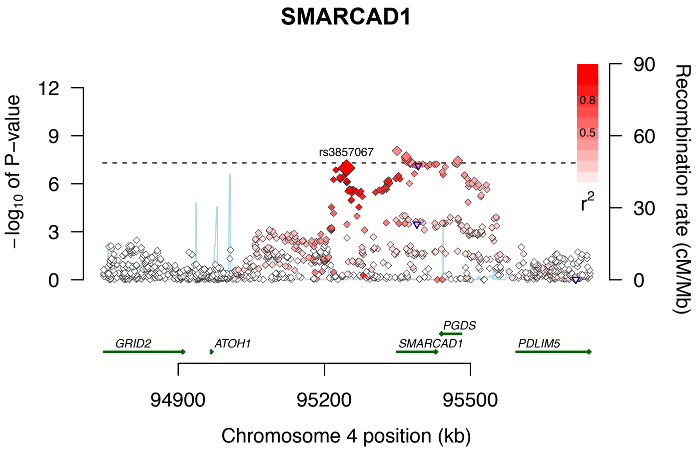
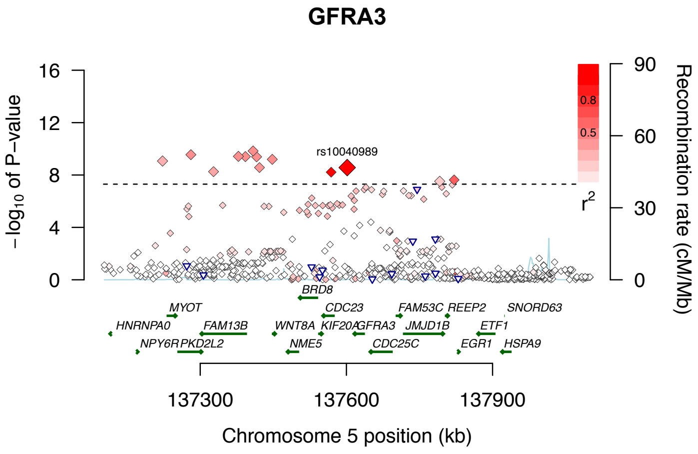
rs12997023
−log10 of P−value
Recombination rate (cM/Mb)
SLC8A1
40300
40600
40900
Chromosome 2 position (kb)
LOC26010
rs295140
C2orf69
C2orf47
C2orf60
LOC26010
SGOL2
KCTD18
AOX1
AOX2
200600
200900
201200
Chromosome 2 position (kb)
SP3
rs938291
SP3
OLA1
SP9
CIR
174200
174500
174800
Chromosome 2 position (kb)
C3orf75
rs17784882
SETD2
NBEAL2
LOC100129354
KIF9
KLHL18
SCAP
PTPN23
C3orf75
CSPG5
SMARCC1
DHX30
MAP4
47200
47500
47800
Chromosome 3 position (kb)
SCN5A
rs6793245
ACAA1
DLEC1
OXSR1
MYD88
SLC22A14
SLC22A13
XYLB
EXOG
ACVR2B
SCN5A
SCN10A
SCN11A
WD
38300
38600
38900
Chromosome 3 position (kb)
SLC4A4
rs2363719
RUFY3
GRSF1
MOBKL1A
DCK
SLC4A4
GC
72100
72400
72700
Chromosome 4 position (kb)
r2
0.8
0.5


SMARCAD1
rs3857067
−log10 of P−value
0
3
6
9
12
90
60
30
0
0.8
0.5
r2
Recombination rate (cM/Mb)
PGDS
GRID2
ATOH1
SMARCAD1
PDLIM5
94900
95200
95500
Chromosome 4 position (kb)


GFRA3
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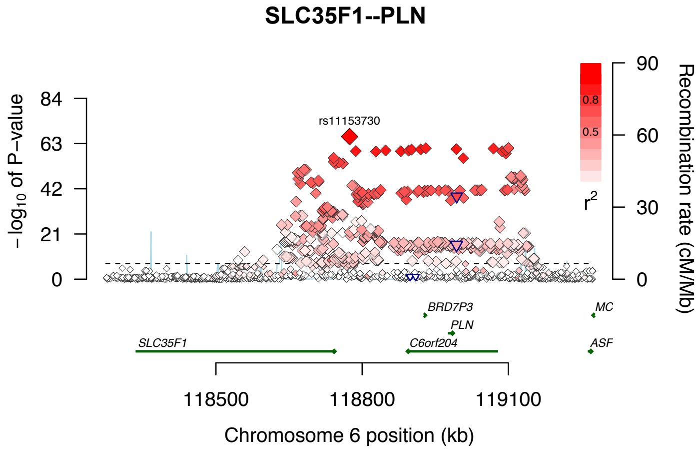
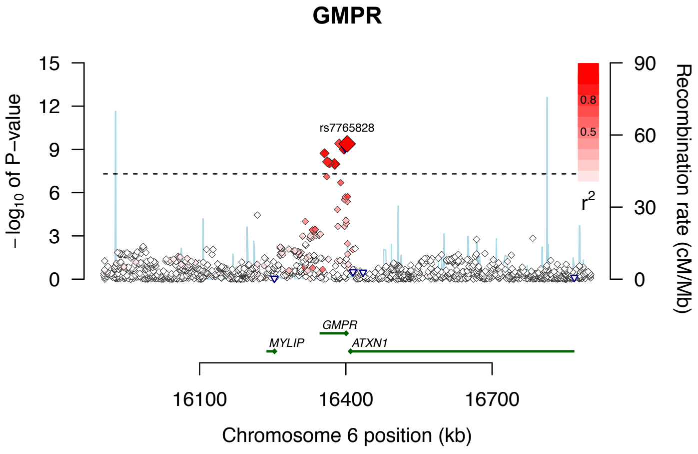
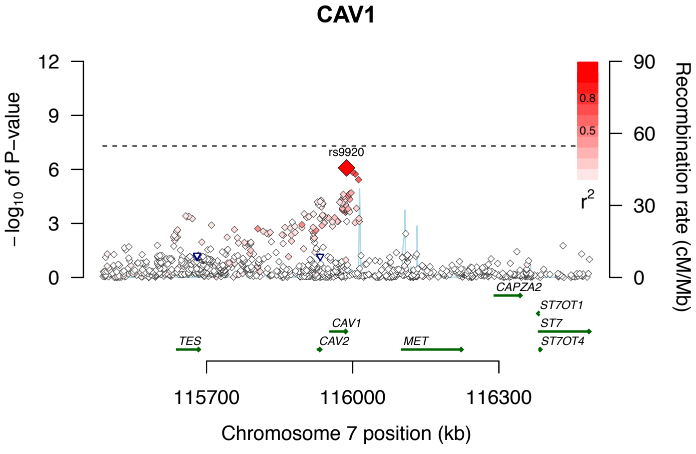
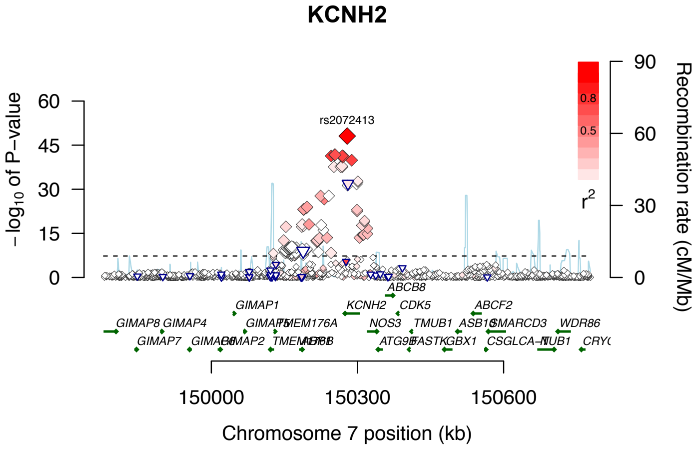
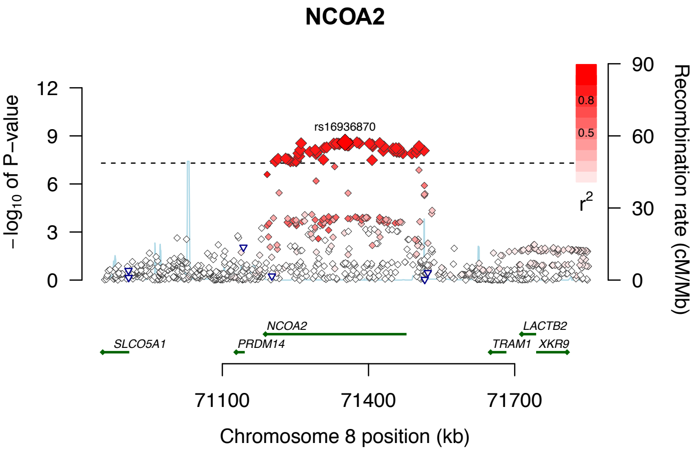
−log10 of P−value
0
4
8
12
16
90
60
30
0
0.8
0.5
r2
Recombination rate (cM/Mb)
BRD8
MYOT
CDC23
FAM53C
REEP2
SNORD63
HNRNPA0
FAM13B
WNT8A
KIF20A
GFRA3
JMJD1B
ETF1
NPY6R
PKD2L2
NME5
CDC25C
EGR1
HSPA9
137300
137600
137900
Chromosome 5 position (kb)


SLC35F1--PLN
rs11153730
−log10 of P−value
0
21
42
63
84
90
60
30
0
0.8
0.5
r2
Recombination rate (cM/Mb)
BRD7P3
MC
PLN
SLC35F1
C6orf204
ASF
118500
118800
119100
Chromosome 6 position (kb)


GMPR
rs7765828
−log10 of P−value
0
3
6
9
12
15
90
60
30
0
0.8
0.5
r2
Recombination rate (cM/Mb)
GMPR
MYLIP
ATXN1
16100
16400
16700
Chromosome 6 position (kb)


CAV1
rs9920
−log10 of P−value
0
3
6
9
12
90
60
30
0
0.8
0.5
r2
Recombination rate (cM/Mb)
CAPZA2
ST7OT1
CAV1
ST7
TES
CAV2
MET
ST7OT4
115700
116000
116300
Chromosome 7 position (kb)


KCNH2
rs2072413
−log10 of P−value
0
15
30
45
60
90
60
30
0
0.8
0.5
r2
Recombination rate (cM/Mb)
ABCB8
GIMAP1
KCNH2
CDK5
ABCF2
GIMAP8
GIMAP4
GIMAP5
TMEM176A
NOS3
TMUB1
ASB10
SMARCD3
WDR86
GIMAP7
GIMAP6
GIMAP2
TMEM176B
AOC3
ATG9B
FASTK
GBX1
CSGLCA−T
NUB1
CRYG
150000
150300
150600
Chromosome 7 position (kb)


NCOA2
rs16936870
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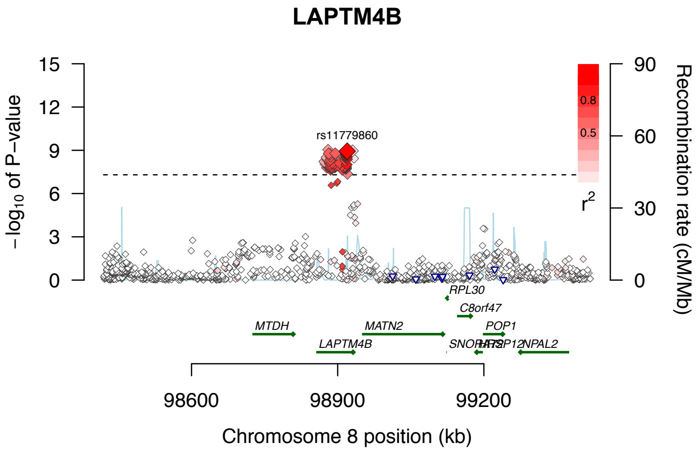
0
3
6
9
12
r2
0.8
0.5
Recombination rate (cM/Mb)
0
30
60
90
SLCO5A1
PRDM14
NCOA2
LACTB2
TRAM1
XKR9
71100
71400
71700
Chromosome 8 position (kb)


LAPTM4B
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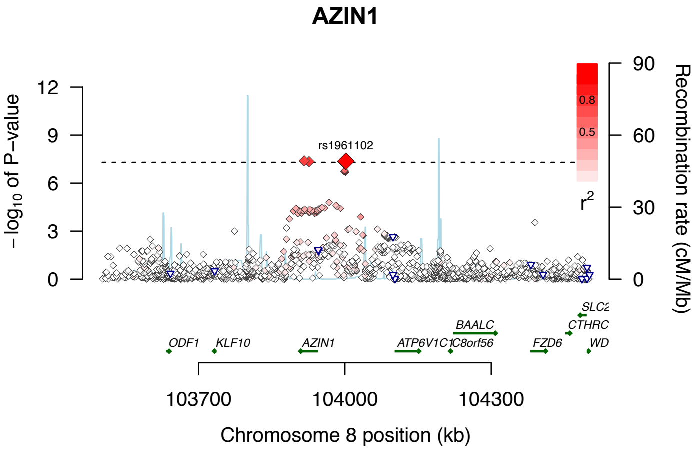
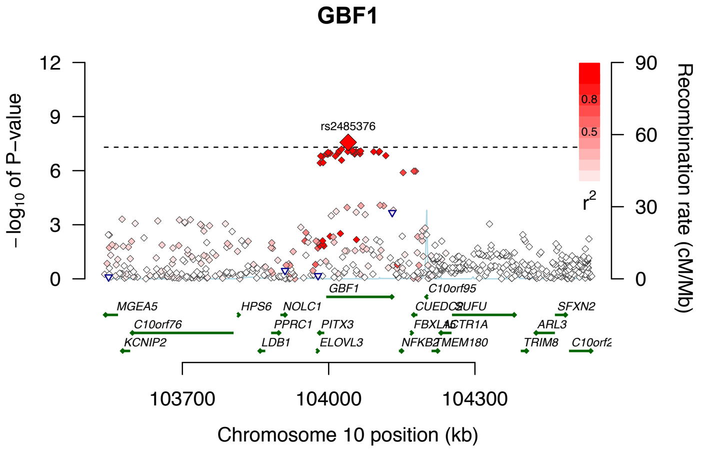
3
6
9
12
15
r2
0.8
0.5
Recombination rate (cM/Mb)
0
30
60
90
RPL30
C8orf47
MTDH
MATN2
POP1
LAPTM4B
SNORD
HRSP12
NPAL2
98600
98900
99200
Chromosome 8 position (kb)


AZIN1
rs1961102
−log10 of P−value
0
3
6
9
12
r2
0.8
0.5
Recombination rate (cM/Mb)
0
30
60
90
SLC2
CTHRC
BAALC
ODF1
KLF10
AZIN1
ATP6V1C1
C8orf56
FZD6
WD
103700
104000
104300
Chromosome 8 position (kb)


GBF1
rs2485376
−log10 of P−value
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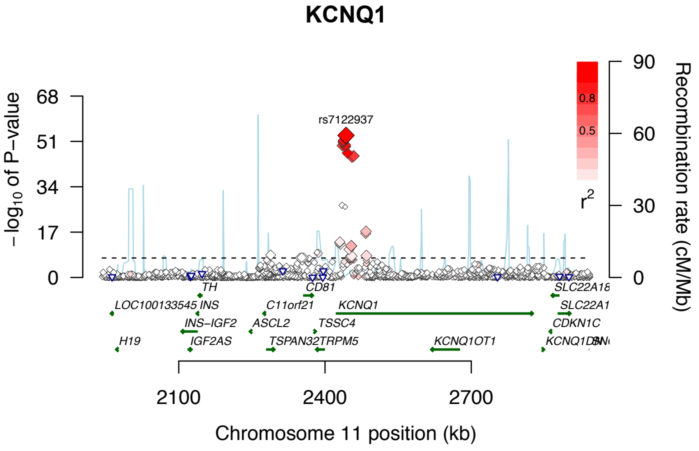
3
6
9
12
r2
0.8
0.5
Recombination rate (cM/Mb)
0
30
60
90
GBF1
C10orf95
MGEA5
HPS6
NOLC1
CUEDC2
SUFU
SFXN2
C10orf76
PPRC1
PITX3
FBXL15
ACTR1A
ARL3
KCNIP2
LDB1
ELOVL3
NFKB2
TMEM180
TRIM8
C10orf2
103700
104000
104300
Chromosome 10 position (kb)


KCNQ1
rs7122937
−log10 of P−value
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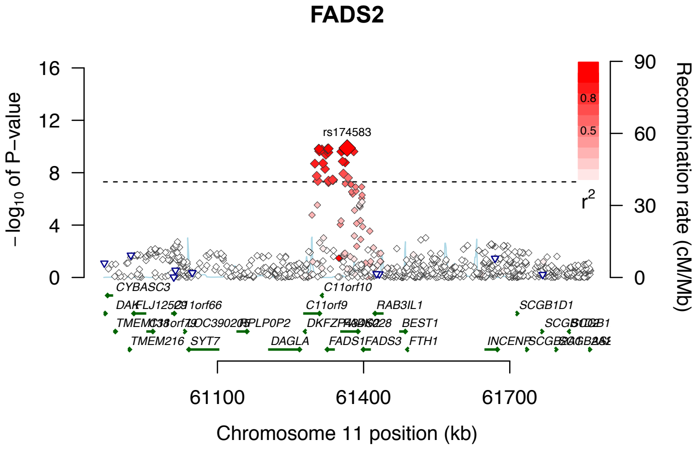
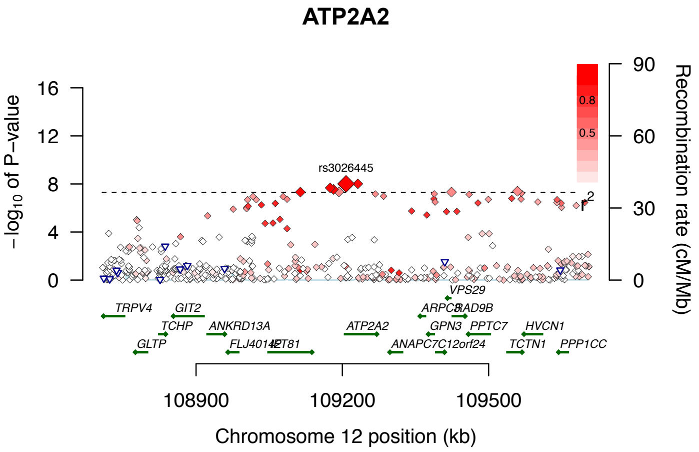
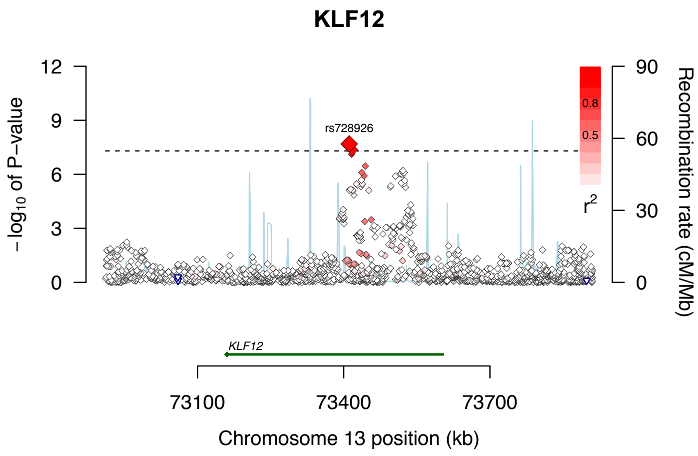
17
34
51
68
r2
0.8
0.5
Recombination rate (cM/Mb)
0
30
60
90
TH
CD81
SLC22A18
LOC100133545
INS
C11orf21
KCNQ1
SLC22A1
INS−IGF2
ASCL2
TSSC4
CDKN1C
H19
IGF2AS
TSPAN32
TRPM5
KCNQ1OT1
KCNQ1DN
2100
2400
2700
Chromosome 11 position (kb)


FADS2
rs174583
−log10 of P−value
0
4
8
12
16
r2
0.8
0.5
Recombination rate (cM/Mb)
0
30
60
90
CYBASC3
C11orf10
DAK
FLJ12529
C11orf66
C11orf9
RAB3IL1
SCGB1D1
TMEM138
C11orf79
LOC390205
RPLP0P2
DKFZP566K
FADS2
BEST1
SCGB1D2
TMEM216
SYT7
DAGLA
FADS1
FADS3
FTH1
INCENP
61100
61400
61700
Chromosome 11 position (kb)


ATP2A2
rs3026445
−log10 of P−value
16
12
8
4
0
90
60
30
0
0.8
0.5
r2
Recombination rate (cM/Mb)
TRPV4
GIT2
TCHP
ANKRD13A
GLTP
FLJ40142
IFT81
ATP2A2
VPS29
ARPC3
RAD9B
GPN3
PPTC7
HVCN1
ANAPC7
C12orf24
TCTN1
PPP1CC
108900
109200
109500
Chromosome 12 position (kb)


KLF12
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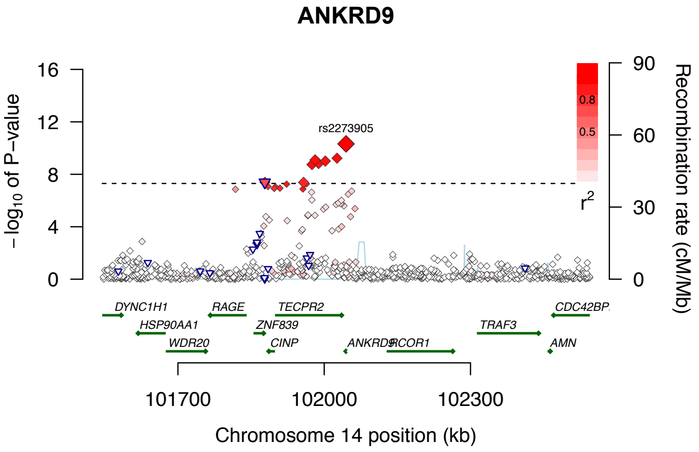
12
9
6
3
0
90
60
30
0
0.8
0.5
r2
Recombination rate (cM/Mb)
KLF12
73100
73400
73700
Chromosome 13 position (kb)


ANKRD9
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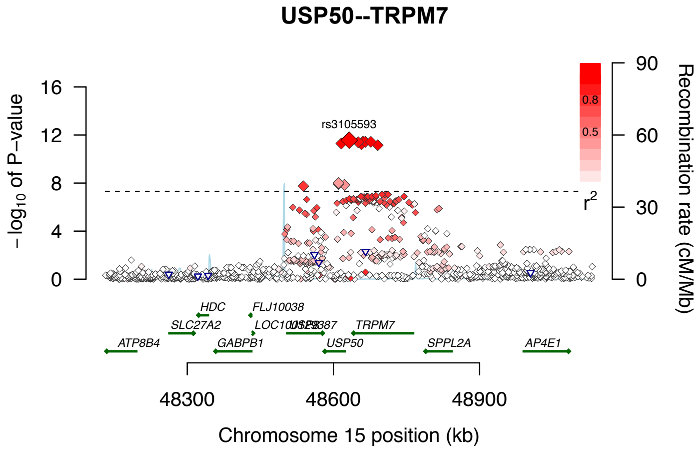
−log10 of P−value
16
12
8
4
0
90
60
30
0
0.8
0.5
r2
Recombination rate (cM/Mb)
DYNC1H1
RAGE
TECPR2
CDC42BP.
HSP90AA1
ZNF839
TRAF3
WDR20
CINP
ANKRD9
RCOR1
AMN
101700
102000
102300
Chromosome 14 position (kb)


USP50--TRPM7
rs3105593
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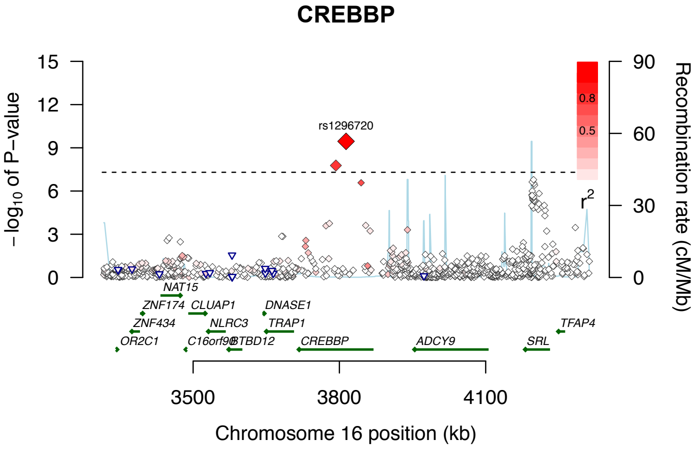
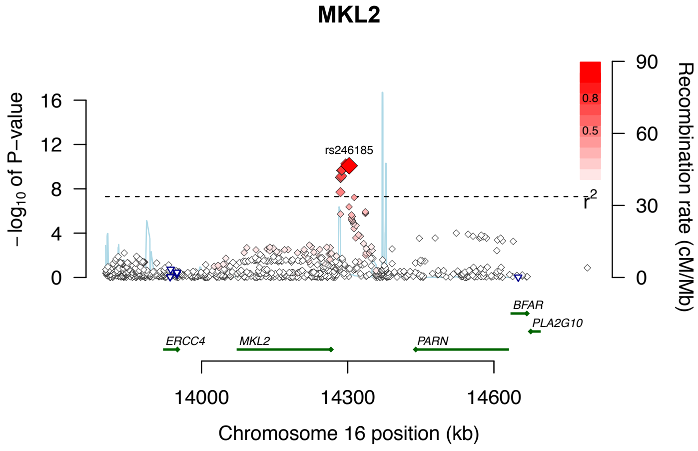
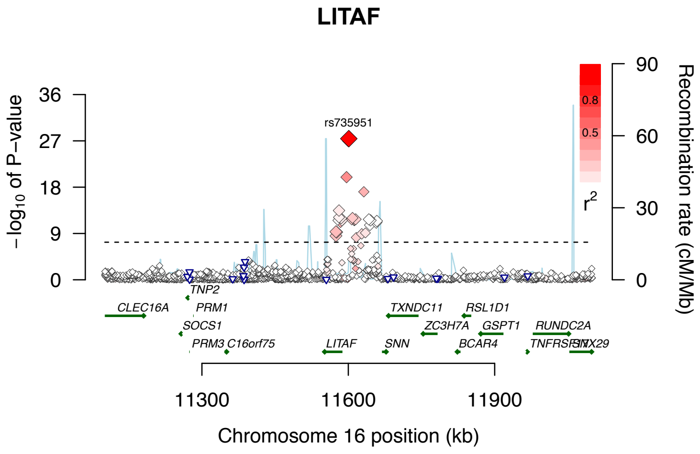
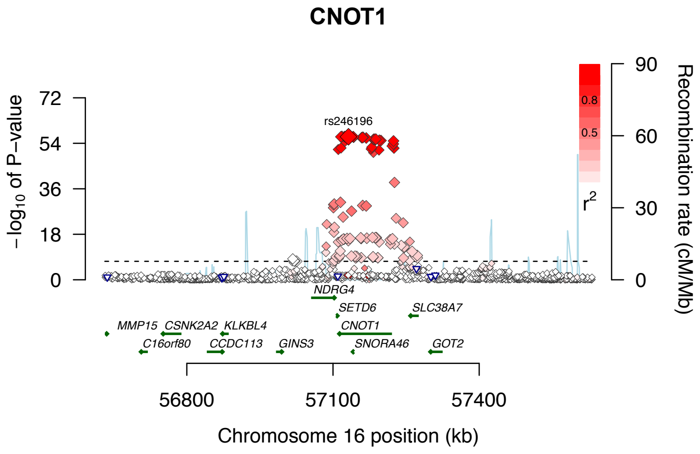
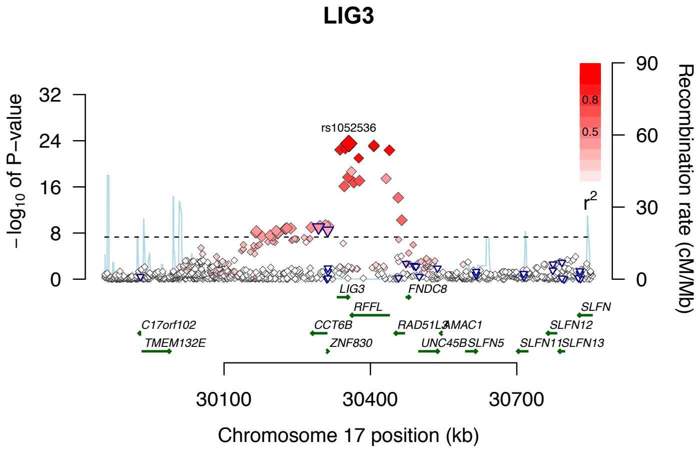
16
12
8
4
0
90
60
30
0
0.8
0.5
r2
Recombination rate (cM/Mb)
HDC
FLJ10038
SLC27A2
LOC100132387
USP8
TRPM7
ATP8B4
GABPB1
USP50
SPPL2A
AP4E1
48300
48600
48900
Chromosome 15 position (kb)

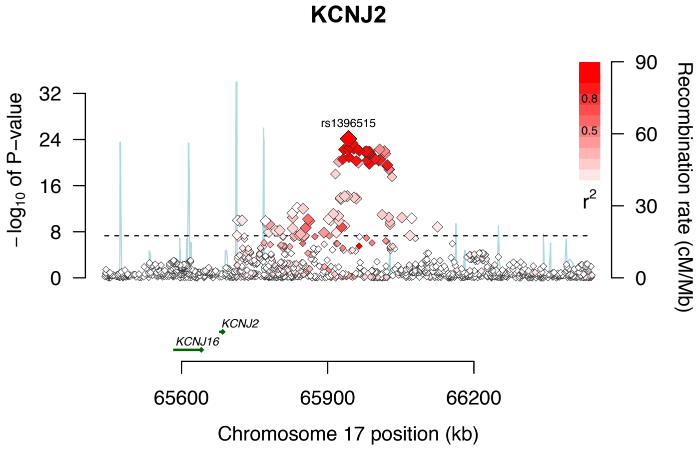

CREBBP
rs1296720
−log10 of P−value
15
12
9
6
3
0
90
60
30
0
0.8
0.5
r2
Recombination rate (cM/Mb)
NAT15
ZNF174
CLUAP1
DNASE1
ZNF434
NLRC3
TRAP1
TFAP4
OR2C1
C16orf90
BTBD12
CREBBP
ADCY9
SRL
3500
3800
4100
Chromosome 16 position (kb)

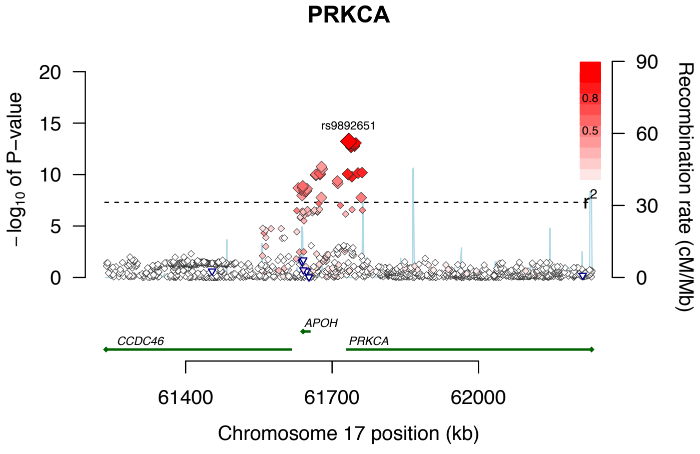

MKL2
rs246185
−log10 of P−value
16
12
8
4
0
90
60
30
0
0.8
0.5
r2
Recombination rate (cM/Mb)
BFAR
PLA2G10
ERCC4
MKL2
PARN
14000
14300
14600
Chromosome 16 position (kb)

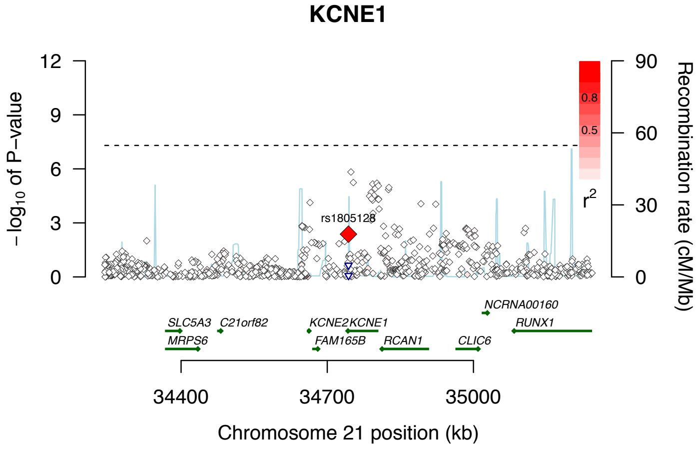

LITAF
−log10 of P−value
36
27
18
9
0
rs735951
0.8
0.5
r2
90
60
30
0
Recombination rate (cM/Mb)
TNP2
CLEC16A
PRM1
SOCS1
PRM3
C16orf75
LITAF
SNN
TXNDC11
ZC3H7A
RSL1D1
GSPT1
BCAR4
RUNDC2A
TNFRSF17
SNX29
11300
11600
11900
Chromosome 16 position (kb)

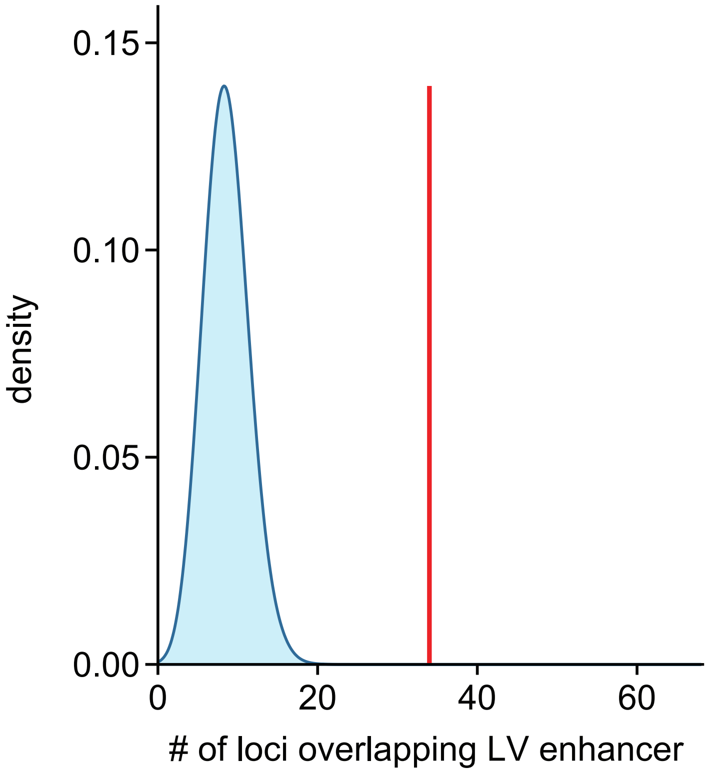

CNOT1
−log10 of P−value
72
54
36
18
0
rs246196
0.8
0.5
r2
90
60
30
0
Recombination rate (cM/Mb)
NDRG4
MMP15
CSNK2A2
KLKBL4
SETD6
SLC38A7
C16orf80
CCDC113
GINS3
CNOT1
SNORA46
GOT2
56800
57100
57400
Chromosome 16 position (kb)


LIG3
−log10 of P−value
32
24
16
8
0
rs1052536
0.8
0.5
r2
90
60
30
0
Recombination rate (cM/Mb)
LIG3
FNDC8
RFFL
SLFN
C17orf102
CCT6B
RAD51L3
AMAC1
SLFN12
TMEM132E
ZNF830
UNC45B
SLFN5
SLFN11
SLFN13
30100
30400
30700
Chromosome 17 position (kb)

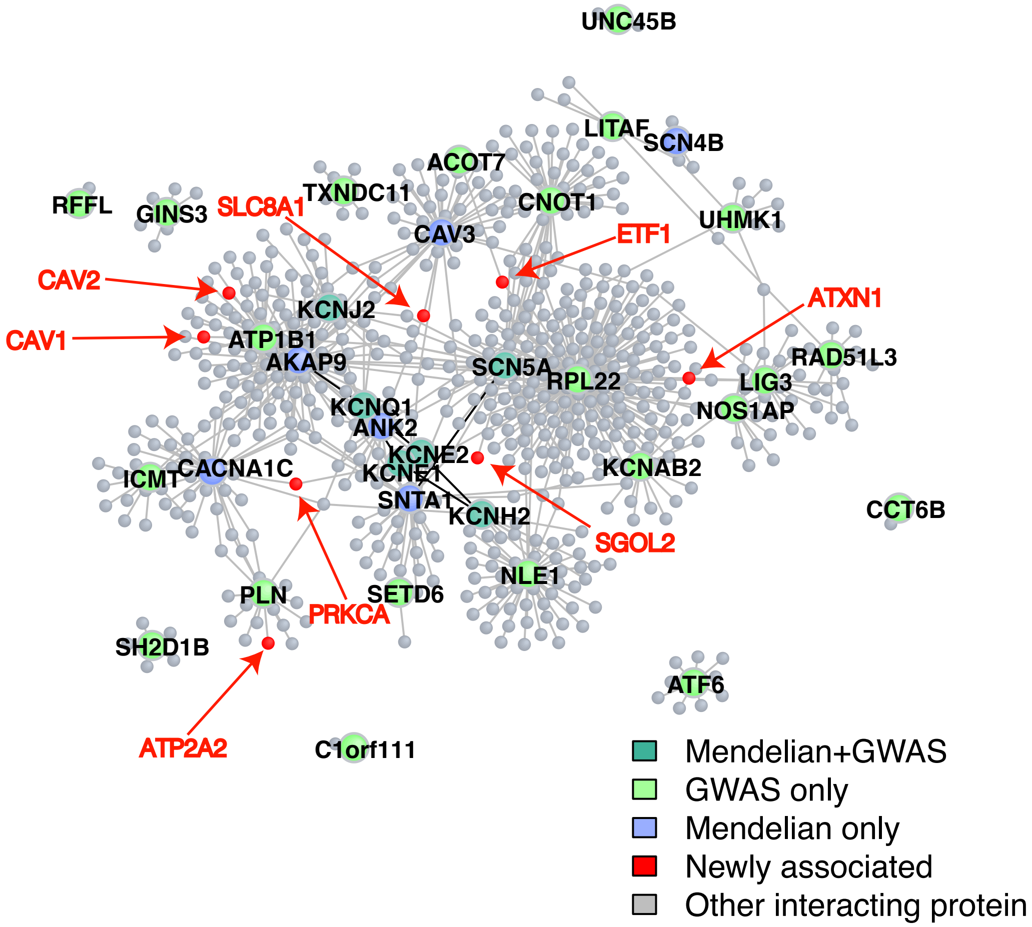

KCNJ2
−log10 of P−value
32
24
16
8
0
rs1396515
0.8
0.5
r2
90
60
30
0
Recombination rate (cM/Mb)
KCNJ2
KCNJ16
65600
65900
66200
Chromosome 17 position (kb)


PRKCA
−log10 of P−value
20
15
10
5
0
rs9892651
0.8
0.5
r2
90
60
30
0
Recombination rate (cM/Mb)
APOH
CCDC46
PRKCA
61400
61700
62000
Chromosome 17 position (kb)

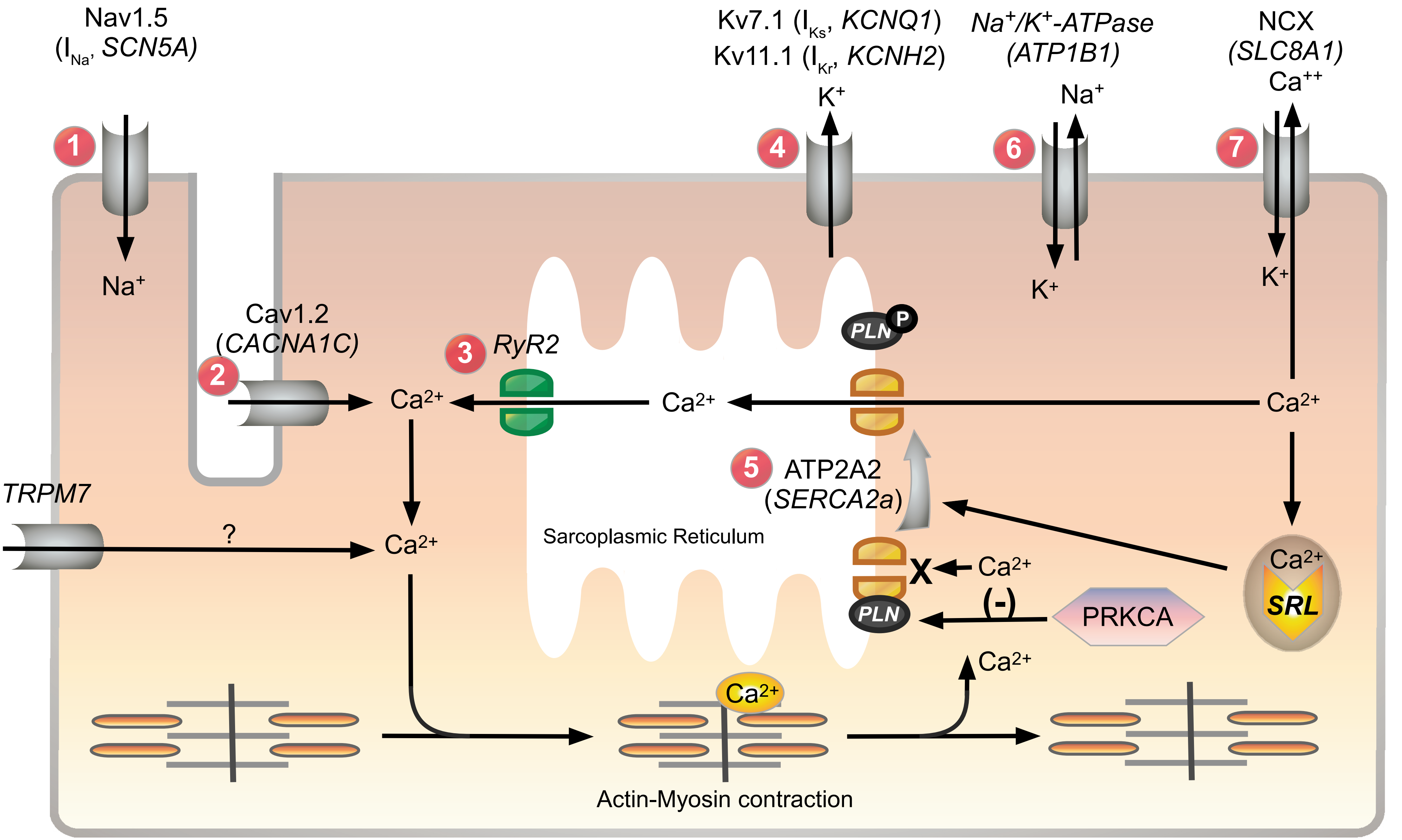

KCNE1
−log10 of P−value
12
9
6
3
0
rs1805128
0.8
0.5
r2
90
60
30
0
Recombination rate (cM/Mb)
NCRNA00160
SLC5A3
C21orf82
KCNE2
KCNE1
RUNX1
MRPS6
FAM165B
RCAN1
CLIC6
34400
34700
35000
Chromosome 21 position (kb)



Supplementary Figure 3. Enrichment of left ventricular enhancers in QT interval-associated loci Enrichment was computed by comparing the number of QT interval loci that include at least one lead or highly correlated (r2>0.8) SNP overlapping an LV enhancer (red line, cf Supplementary Table 13) to 100,000 sets of randomly sampled control loci matched for minor allele frequency, number of SNPs in high LD (r2>0.8) and distance to nearest gene.



Supplementary Figure 4. Protein-protein interaction network. Shown is a network of protein-protein interactions seeded with Mendelian LQTS-susceptibility genes (purple) and genes at 7 previously published QT-associated loci (light green) or both (dark green). We identified 606 proteins interacted directly with the seeds, 8 of which (from 5 loci) were among the 85 newly associated proteins discovered by QT-IGC (Supplementary Table 18), a significant enrichment beyond chance expectation (p=0.029, see Supplementary Methods above).



Supplementary Figure 5. Model of cardiomyocyte ion channel flux underlying myocardial repolarization. Cellular depolarization begins with (1) Na+ influx (INa encoded by SCN5A), which opens (2) voltage-gated L-type Ca2+ channels in the sarcolemma which maintains depolarization and provides the calcium influx that in turn, (3) activates large-scale release of Ca2+ to the cytoplasm through calcium-gated Ca2+ channels (ryanodine receptor, RyR2) in the sarcoplasmic reticulum, with resultant excitation-contraction coupling via calcium-induced calcium release. Repolarization results from (4) efflux of potassium (via Kv7.1 and Kv11.1 channels encoded by KCNQ1 and KCNH2) and (5) reuptake of Ca2+ in the sarcoplasmic reticulum by the sarcoplasmic reticulum Ca2+ ATPase (SERCA2a encoded by ATP2A2) regulated by phospholamban (encoded by PLN), in turn regulated by PRKCA, and stabilized by sarcalumenin (SRL). The Na+ that enters the myocyte in (1) is counterbalanced by an active (6) Na+/K+ ATPase (ATP1B1). The Ca2+ that enters the myocyte in (2) is counterbalanced by (7) the Na+/Ca2+ exchanger (NCX1 encoded by SLC8A1) to ensure net even Ca2+ balance.

	N after exclusions	Age, years, mean ± SD	Sex, Men, %	RR interval, ms, mean ± SD	QT interval, ms, mean ± SD	QTc, Bazett's correction*, ms, mean ± SD	SD of QT residual after covariate adjustment
1a: GWAS cohorts							
AGES	2522	68.6 ± 8.6	40.3%	882.5 ± 164.8	398.6 ± 29.0	426.5 ± 22.5	18.1
Amish studies	1124	49.8 ± 15.8	49.6%	1061.9± 161.6	411.6 ± 62.4	404.4 ± 55.7	18.1
ARIC	8524	54.2 ± 5.7	46.5%	927.7 ± 138.2	399.1 ± 29.4	415.8 ± 17.2	15.0
BLSA	477	68.2 ± 13.9	49.5%	962.0 ± 154.4	415.6 ± 29.8	424.9 ± 22.1	19.0
BRIGHT	1392	502 ± 36.0	56.70%	969.73 ± 89.77	414.5 ± 33.8	421.20 ± 25.08	23.3
Carlantino	383	48.8 ± 16.2	38.2%	891.8 ± 129.4	389.4 ± 27.0	405.1 ± 19.1	19.1
CHS	2457	73 ± 5.5	56.1%	950.9 ± 152.1	414.8 ± 32.8	427.4 ± 20.7	17.3
Croatia - Korcula	363	54.34±13.46	36.6%	938.4±147.0	400.3±28.99	418.42 ± 22.71	18.8
Croatia - Split	365	49.07±14.75	38.9%	934.3± 136.6	399.2± 26.9	415.19 ± 22.15	17.6
DCCT/EDIC	1118	46 ± 7	47.3%	890.0±147	387.6±29.2	413.0±20	17.3
deCODE	8,961	68.9 ± 13.7	45.6%	851.0 ± 201.7	387.7±46.5	421.8 ± 30.7	22.1
eMERGE	5272	55.6 ± 13.7	46.8%	873 ± 131.1	387.5 ± 28.8	415.7 ± 20.0	19.2
ERF	1481	47.9 ± 14.3	40.7%	975.9 ± 157.4	398.0 ± 28.1	404.8 ± 23.5	18.7
FHS	7429	40.0 ± 10.6	45.0%	908.3 ± 165.3	390.6 ± 36.7	412.2 ± 22.0	20.7
FVG Genetic Park	497	50.8 ± 16.3	39.2%	938.1 ± 160.9	401.4 ± 30.1	409.9 ± 27.5	19.2
Health2000	1921	49.9 ± 10.8	47.7%	978.4 ± 161.0	388.5 ± 30.0	394.9 ± 22.3	18.8
HealthABC	1305	73.64 ± 2.78	51.0%	955.15 ± 152.55	412.89 ± 35.39	424.47 ± 27.45	25.5
HNR	346	54.6 ± 5.4	48.6%	905.4 ± 136.4	391.5 ± 28.3	411.4± 23	12.6
KORA-F3	1476	61.8 ± 10.0	49.9%	967.2 ± 162.3	404.3 ± 30.5	411.1±24	19.3
KORA-S4	1736	53.8 ± 8.8	42.0%	940.7 ± 146.4	408.7 ± 26.7	421.4 ± 19.6	19.1
LifeLines	3145	54.9 ± 9.7	39.5%	900.1 ± 146.3	395.7 ± 27.4	419.3 ± 20.7	16.2
MICROS	1013	45.7 ± 16.3	42.1%	900.4 ± 148.5	398.0 ± 28.6	416.8 ± 24.3	15.5
ORCADES	672	53.6 ±15.1	46.6%	1009.2 ± (155.4)	410.2 ± (29.6)	13.0±(0.8)	20.8
PopGen	983	53.5 ± 14.2	54.1%	944.1 ± 154.7	402.9 ± 31.7	416.8 ± 24.3	21.7
PREVEND_GWAS	3608	49.1±12.3	49.2%	897.4±153.0	396.3±27.2	421.1±23.1	17.2
RS-I	4606	68.6 ± 8.5	40.3%	880.4 ± 147.4	398.4 ± 28.8	426.7 ± 22.8	17.9
RS-II	1479	64.9 ± 7.5	44.3%	887.1 ± 137.5	402.8 ± 27.3	429.4 ± 21.8	17.3
SardiNIA - GWAS	4266	43.6 ± 17.6	43.6%	922.1 ± 152.8	370.9 ± 34.3	388.1± 26.4	23.5
SHIP	3221	48.6 ± 15.7	47.5%	854.7 ± 148.1	393.6 ± 28.6	429.0 ± 31.7	22.5
TwinsUK	2838	51.7 ± 12.5	4.5%	922.3 ± 142.8	402.2 ± 28.0	420.8 ± 20.9	16.4
Young Finns Study	1081	31 (4.9)	48.8%	912 (141.5)	351.2 (26.2)	370.2 (23.7)	16.9
1b: Metabochip replication							
PIVUS	833	70.2 ± 0.2	48.1%	983.8 ± 136.5	394.0 ± 30.9	398.6 ± 23.0	21.3
ULSAM	521	76.5 ± 5.1	100.0%	959.9 ± 158.7	411.8 ± 34.8	422.7 ± 28.2	24.8
1c: Targeted SNP replication							
BRHS	3402	68.4 ± 5.4	100.0%	948.8 ± 172.0	408.5 ± 35.6	418.3 ± 24.8	23.7
Bruneck	629	61.0 ± 10.6	52.0%	872.6 ± 139.8	381.8 ± 28.7	410.7 ± 21.6	22.5
Carla	1551	63.3 ± 9.8	53.1%	943.1 ± 148.5	411.2 ± 30.7	425.5 ± 22.4	19.0
Cyprus	804	59.6 ± 10.2	45.6%	909.4 ± 147.9	399.1 ± 28.5	413.0 ± 17.4	20.4
Czech Post-MONICA	289	56.4 ± 10.3	46.7%	928.8 ± 123.5	409.5 ± 25.8	427.1 ± 31.7	22.6
Galicia	797	53.75 ± 18.6	51.4%	932.7 ± 153.0	395.09 ± 33.3	409.8 ± 27.2	18.0
Health2000 - targeted	3128	52.3 ± 15.9	42.9%	973.4 ± 160.6	389.4 ± 30.0	396.8 ± 22.6	18.9
HNR - targeted	4109	59.7 ± 7.8	48.7%	887.1 ± 140.6	390.3 ± 31.6	416.1 ± 18.4	16.0
Intergene	2779	50.6 ± 30.5	45.7%	997.1 ± 158.2	411.6 ± 30.6	414.3 ± 23.9	19.9
KORA-F3 - targeted	908	51.3 ± 12.3	45.8%	955.6 ± 161.2	397.3 ± 28.4	404.7 ± 18.3	18.0
KORA-S4 - targeted	2168	45.1 ± 15.6	49.3%	938.4 ± 155.0	405.7 ± 28.3	419.0 ± 21.3	19.1
MIDSPAN Family Study	2107	45.1 ± 6.2	44.6%	898.3 ± 149.02	391.9 ± 28.9	407.5 ± 21.0	19.9
PREVEND_replication	3865	48 ± 12.8	46.6%	897.7 ± 161.0	396.6 ± 28.62	421.5 ± 23.0	17.2
SAPHIR	1288	50.7 ± 5.95	69.5%	938.4 ± 155.0	405.7 ± 29.2	404.8 ± 27.1	19.4
Whitehall-II	4138	43.7 ± 5.9	75.8%	963.5 ± 161.1	395.3 ± 32.5	402.6 ± 25.0	23.3

Supplementary Table 1: Clinical characteristics of GWAS, replication cohorts. Shown are the distribution of age, sex, RR and QT interval, by cohort for GWAS (1a) and replication (1b, 1c) samples. In addition, we show the Bazett's heart-rate corrected QT interval (QTc), which is used clinically but not in the current analysis. For comparison, we show the standard deviation of QT interval residuals after linear regression to adjust for the effects of age, sex and RR interval. Continuous measures are shown as mean± SD, while categorical traits are shown as percentages.

	Platform	Calling algorithm	call rate filter	MAF filter	pHWE filter	Mendelian check
2a: GWAS cohorts						
AGES	Illumina HH 370 CNV	Bead Studio	call rate <95%	MAF < 1%	pHWE < 10-5	
Amish studies	Affymetrix 500k and 6.0	BRLMM	call rate < 95%	MAF < 1%	pHWE < 10-6	
ARIC	Affymetrix 6.0	Birdseed	call rate <95%	MAF < 1%	pHWE < 10-5	
BLSA	Illumina 550 K	Bead Studio	call rate <97%	MAF <1%	pHWE <10-4	
BRIGHT	Affymetrix	CHIAMO	call rate <98%	none	pHWE < 5.7x10-7	
Carlantino	Illumina HH 370 CNV	Bead Studio	call rate <97%	MAF <1%	pHWE < 10-6	
CHS	Illumina HH 370 CNV	Bead Studio	call rate <95%	At least one heterozygote	pHWE < 10-5	> 2 duplicate errors or
Croatia - Korcula	Illumina HH 370 CNV	BeadStudio	call rate <98%	MAF < 1%	pHWE < 10-6	
Croatia-Split	Illumina HH 370 CNV	BeadStudio	call rate <98%	MAF < 1%	pHWE < 10-6	
DCCT/EDIC	Illumina 1M	Bead Studio	call rate <95%	MAF < 1%	pHWE < 10-6	
deCODE	Illumina HH 300, HH 300 Duo, HH610, 1M, 1Mduo	Bead Studio	call rate <95%	MAF < 1%	pHWE < 0.001 in controls	
eMERGE	Illumina 660W-Quadv1_A	BeadStudio	call rate <99%	MAF < 0.1%	pHWE <10-4 (flagged)	excess Mendelian Inco
ERF	Illumina HH 300v2/370CNV	BeadStudio	call rate <95%	MAF < 1%	pHWE < 10^{-5}	
FHS	Affymetrix 500k + 50K Human Gene Focused Panel	BRLMM	call rate <95%	MAF < 1%	pHWE < 10-6	
FVG Genetic Park	Illumina HH 370 CNV	Bead Studio	call rate <97%	MAF <1%	pHWE < 10-6	
Health2000	Illumina 610	Bead Studio	call rate < 95%	MAF < 2%	pHWE < 10-4	
HealthABC	Illumina 1M Duo	BeadStudio	call rate <97%	MAF < 1%	pHWE < 10-6	
HNR	Illumina HH 550v3	BeadStudio	call rate <98%	MAF < 5%	pHWE < 10-5	
KORA-F3	Affymetrix 500k	BRLMM	call rate <93%	MAF < 5%	pHWE < 10-5	
KORA-S4	Affymetrix 6.0	Birdseed	call rate <93%	none	none	
LifeLines	Illumina CytoSNP12 v2	GenomeStudio	call rate <95%	MAF < 1%	pHWE < 10-5	
MICROS	Illumina HH 300v2	BeadStudio	call rate <98%	MAF < 5%	pHWE < 10-5	
ORCADES	Illumina HH 300v2/370CNV	BeadStudio	call rate <95%	MAF < 1%	pHWE < 10^{-5}	
PopGen	Affymetrix 6.0	Birdseed V2	call rate <95%	MAF < 1%	pHWE < 10^{-4}	
PREVEND_GWAS	CytoSNP12-v2	Illumina algorithm	call rate <98%	MAF < 1%	pHWE < 10-5	
RS-I	Illumina HH 550	BeadStudio	call rate <98%	MAF < 1%	pHWE < 10-6	
RS-II	Illumina HH 550	BeadStudio	call rate <98%	MAF < 1%	pHWE < 10-6	
SardiNIA	Affymetrix 500k, Affymetrix 10K	BRLMM	call rate <90%	MAF < 5%	pHWE < 10-6	excess Mendelian Inco
SHIP	Affymetrix 6.0	Birdseed V2	QC call rate < 86% eac	none	none	
TwinsUK	Illumina HH300 HH 300 Duo, HH550, HH610	Illuminus	Call rate <95%	MAF<1%	HWE p<10-4	
Young Finns Study	Illumina 670k custom chip	Illuminus	Call rate < 95%	MAF < 1%	pHWE < 10-6	
2b: Metabochip replication cohorts						
PIVUS	Illumina Metabochip	Illumina GenCall	Call rate <90%		pHWE < 10-5	
ULSAM	Illumina Metabochip	Illumina GenCall	Call rate <90%		pHWE < 10-5	

2c: Replication cohorts

	Platform	call rate filter	HWEp filter
BRHS	Kaspar	<95%	p<0.001
Bruneck	Sequenom	<95%	p<0.001
Carla	Taqman	<95%	p<0.001
Cyprus	Sequenom	<95%	p<0.001
Czech Post-MONICA	Sequenom	<95%	p<0.001
Galicia	Sequenom	<95%	p<0.001
Health2000 - targeted	Sequenom	<95%	p<0.001
HNR - targeted	Sequenom	<95%	p<0.001
Intergene	Kaspar	<95%	p<0.001
KORA-F3 - targeted	Sequenom	<95%	p<0.001
KORA-S4 - targeted	Sequenom	<95%	p<0.001
MIDSPAN Family Study	Taqman	<95%	p<0.001
PREVEND_replication	Kaspar	<95%	p<0.001
SAPHIR	Sequenom	<95%	p<0.001
Whitehall-II	Kaspar	<95%	p<0.001
Young Finns	Taqman	<95%	p<0.001

Supplementary Table 2 (2 pages): Genotyping and imputation methods. Shown are the details of the genotyping platform and quality control filt rs applied at individual cohorts for GWAS (2a) and replication (2b, 2c) samples.

Imputation	Imputation Backbone /	GWAS Statistical Analysis Software used
Mach1 v1.0.15	from build 35	plink
Mach1v1.0.15	from build 35	MMAP
Mach1 v1.0.16	from build 35	Mach2QTL + plink
Mach	from build 35	Merlin offline
IMPUTE	from build 36	SNPTEST v 1.1.5
Mach1	from build 36	GenABEL + ProbABEL
Bimbam	from build 36	R
Mach1 v1.0.15	from build 36	GenABEL + ProbABEL
Mach1 v1.0.15	from build 36	GenABEL + ProbABEL
Mach1 v1.0.15	from build 36	Mach2QTL + plink
IMPUTE v2	from build 36	deCODE software similar to SNPTEST
IMPUTE	from build 36	plink and PLATO
Mach1 v1.0.15	from build 35	Mach2QTL + plink + GenABEL
Mach1 v1.0.15	from build 36	LMEKIN
Mach1	from build 36	GenABEL, ProbABEL
Mach1 v1.0.10	from build 35	plink
Mach1 v1.0.16	from build 36	R
Mach1 v1.0.10	from build 35	Mach2QTL + plink
Mach1 v1.0.10	from build 35	Mach2QTL + plink
Mach1 v1.0.16	from build 36	Mach2QTL + plink
IMPUTE v0.3.2	from build 36	SNPTEST v1.1.4
Mach1 v1.0.10	from build 35	Merlin (--fastassoc)
Mach1 v1.0.15	from build 35	Mach2QTL + GenABEL
Mach1 v1.0.16	from build 36	Mach2QTL + plink
BEAGLE v3.2	Hapmap II CEU r23a	Mach2QTL + plink
Mach1 v1.0.15	from build 35	Mach2QTL
Mach1 v1.0.10	from build 36	Mach2QTL as implemented in GRIMP (PMID: 19700477)
Mach1 v1.0.10	from build 35	Merlin
Impute v0.5.0	from build 36	SNPTEST v1.1.5
IMPUTE v0.3.2	from build 36	SNPTEST v1.1.4
Mach1 v1.0	from build 36	Plink + ProbABEL
IMPUTE v2	from build 36	plink
IMPUTE v2	from build 36	plink

GWAS Cohort	Sample size	Allele frequency exclusion	Imputation quality exclusion	Genomic control lambda after QC
AGES	2522	NA	NA	1.04
Amish Studies	1124	<0.01 or >0.99	NA	1.05
ARIC	8524	NA	NA	1.01
BLSA	477	NA	NA	1.04
BRIGHT	1392	NA	NA	0.99
CARLANTINO	383	NA	NA	0.99
CHS	2457	NA	NA	1.02
Croatia-Korcula	363	NA	NA	0.96
Croatia-Split	365	NA	NA	0.96
DCCT-EDIC	1118	NA	NA	1.03
DECODE	8961	NA	NA	1.09
EMERGE	5272	NA	NA	1.05
ERF	1481	NA	NA	1.03
FHS	7429	NA	NA	1.03
FVG	497	NA	NA	0.98
HEALTH ABC	1305	<0.04 or >0.96	<0.8	1.01
HEALTH2000	1921	NA	NA	1.04
HNR	346	NA	NA	1.00
KORA-F3	1476	NA	NA	0.99
KORA-S4	1736	NA	NA	1.01
LIFELINES	3145	<0.01 or >0.99	<0.3	1.01
MICROS	1013	NA	NA	0.99
ORCADES	672	<0.01 or >0.99	<0.5	0.99
POPGEN	983	NA	NA	1.00
PREVEND	3608	NA	NA	1.05
RS-I	4606	NA	NA	1.02
RS-II	1479	<0.01 or >0.99	NA	1.01
SARDINIA	4266	NA	NA	1.04
SHIP	3221	<0.01 or >0.99	<0.1	1.01
TWINS	2838	NA	NA	1.04
YOUNGFINNS	1081	NA	NA	1.00
TOTAL	**76,061**			

*QC steps for all cohorts: (1) Beta < 100,000, (2) no NA values, (3) allele frequency > 0 and < 1, (4) imputation quality > 1.1

Supplementary Table 3: GWAS quality control. Shown are any filters applied centrally to GWAS results to ensure approximately null distributions based on λGC and quantile-quantile plots.

Supplementary Table 4: Metabochip QT replication + finemapping SNP content. Provided as a separate Excel file at Nature Genetics website.

ST5a: Signal finemapping

TRAIT	RS	CHR	POS	locus	P_GWAS_REPLIC	GRADE
QT	rs12143842	1	160,300,514	NOS1AP	1.95E-123	GOLD
QT	rs11153730	6	118,774,215	PLN	1.10E-38	GOLD
QT	rs37060	16	57,123,805	CNOT1	1.82E-38	GOLD
QT	rs2074239	11	2,441,668	KCNQ1	5.34E-30	GOLD
QT	rs2968863	7	150,254,070	KCNH2	6.51E-24	GOLD
QT	rs846111	1	6,201,957	RNF207/KCNAB2	1.34E-22	GOLD
QT	rs10919070	1	167,365,661	ATP1B1	2.42E-20	GOLD
QT	rs8049607	16	11,599,254	LITAF	3.04E-19	GOLD
QT	rs1396515	17	65,942,588	KCNJ2	2.22E-18	GOLD
QT	rs6793245	3	38,574,041	SCN5A	7.64E-16	GOLD
QT	rs3135967	17	30,337,842	LIG3	1.56E-14	GOLD
QT	rs2298632	1	23,583,062	TCEA3	9.10E-14	BRONZE
QT	rs9303504	17	61,745,828	PRKCA	1.08E-10	GOLD
QT	rs246185	16	14,302,933	MKL2	1.54E-10	SILVER
QT	rs2414059	15	48,660,636	TRPM7	2.43E-10	GOLD
QT	rs295140	2	200,868,944	LOC26010	4.10E-10	BRONZE
QT	rs938291	2	174,450,854	SP3	6.02E-10	SILVER
QT	rs7195486	16	4,195,181	SRL	1.15E-09	GOLD
QT	rs9920	7	115,987,328	CAV1	3.37E-09	GOLD
QT	rs11685090	2	40,217,710	SLC8A1	5.58E-09	GOLD
QT	rs3026445	12	109,207,586	ATP2A2	8.65E-09	GOLD
QT	rs174583	11	61,366,326	FADS1,2,3	1.39E-08	BRONZE
QT	rs4452774	8	98,930,532	LAPTM4B	1.55E-08	SILVER
QT	rs1805128	21	34,743,550	KCNE1	2.28E-08	GOLD
QT	rs1961102	8	104,002,021	AZIN1	2.68E-08	BRONZE
QT	rs7561149	2	179,398,101	TTN	3.96E-08	SILVER

ST5b: Locus finemapping

TRAIT	INDEX_SNP	CHR	START_HG18	END_HG18	LOCUS_GENE	RATIONALE	GRADE
QT	rs12143842	1	160,219,639	160,705,617	NOS1AP	multiple independent signals; strongest effects in genome	GOLD
QT	rs11153730	6	118,534,954	119,189,214	PLN	multiple independent signals; multiple cardiovascular traits	SILVER
QT	rs6793245	3	38,488,369	38,820,319	SCN5A_SCN10A	multiple cardiovascular traits	BRONZE
QT	rs2074239	11	2,419,260	2,846,916	KCNQ1	multiple independent signals; multiple traits	backup

Supplementary Table 5: Metabochip finemapping targets. Shown are the loci selected for finemapping on the Metabochip array. Loci were selected to follow up a specific signal of association (signal finemapping) on the basis of linkage disequilibrium and for a few loci an entire region defined by physical distance on the basis of at least one signal of association and a span defined by a combination of physical and genetic difference. Loci were prioritized on the basis of consensus regarding strength of association and in some cases biologic plausibility as high (GOLD), moderate (SILVER) and lower (BRONZE) priority.

SNP	LOCUS	NEAREST_GENE	Function	CHR	POS	INDEX OTHER SIGNAL	NOVEL?	REPLIC_SNP?	CODED ALLELE	NONCODED ALLELE
rs846111	1	RNF207	NON_SYNONYMOUS_	1	6,201,957	INDEX	KNOWN		C	G
rs2298632	2	TCEA3	INTRONIC	1	23,583,062	INDEX	NOVEL	REPLIC	T	C
rs12143842	3	NOS1AP	INTERGENIC	1	160,300,514	INDEX	KNOWN		T	C
rs10919070	4	ATP1B1	INTRONIC	1	167,365,661	INDEX	KNOWN		C	A
rs12997023	5	SLC8A1	INTERGENIC	2	40,606,486	INDEX	KNOWN		C	T
rs938291	6	SP3	INTERGENIC	2	174,450,854	INDEX	NOVEL	REPLIC	G	C
rs7561149	7	TTN-CCDC141	INTERGENIC	2	179,398,101	INDEX	NOVEL	REPLIC	C	T
rs295140	8	SPATS2L	INTERGENIC	2	200,868,944	INDEX	NOVEL	REPLIC	T	C
rs6793245	9	SCN5A-SCN10A	INTRONIC	3	38,574,041	INDEX	KNOWN		A	G
rs17784882	10	C3ORF75	INTRONIC	3	47,519,007	INDEX	NOVEL		A	C
rs2363719	11	SLC4A4	INTRONIC	4	72,357,080	INDEX	NOVEL		A	G
rs3857067	12	SMARCAD1	INTERGENIC	4	95,245,457	INDEX	NOVEL	REPLIC	A	T
rs10040989	13	GFRA3	INTERGENIC	5	137,601,624	INDEX	NOVEL	REPLIC	A	G
rs7765828	14	GMPR	INTRONIC	6	16,402,701	INDEX	NOVEL	REPLIC	G	C
rs11153730	15	SLC35F1-PLN	INTERGENIC	6	118,774,215	INDEX	KNOWN		T	C
rs9920	16	CAV1	3PRIME_UTR	7	115,987,328	INDEX	NOVEL	REPLIC	C	T
rs2072413	17	KCNH2	INTRONIC	7	150,278,902	INDEX	KNOWN		T	C
rs16936870	18	NCOA2	INTRONIC	8	71,351,896	INDEX	NOVEL		A	T
rs11779860	19	LAPTM4B	INTRONIC	8	98,919,506	INDEX	NOVEL		C	T
rs1961102	20	AZIN1	INTERGENIC	8	104,002,021	INDEX	NOVEL	REPLIC	T	C
rs2485376	21	GBF1	INTRONIC	10	104,039,996	INDEX	NOVEL		A	G
rs7122937	22	KCNQ1	INTRONIC	11	2,443,126	INDEX	KNOWN		T	C
rs174583	23	FADS2	INTRONIC	11	61,366,326	INDEX	NOVEL	REPLIC	T	C
rs3026445	24	ATP2A2	INTRONIC	12	109,207,586	INDEX	NOVEL	REPLIC	C	T
rs728926	25	KLF12	INTRONIC	13	73,411,123	INDEX	NOVEL		T	C
rs2273905	26	ANKRD9	5PRIME_UTR	14	102,044,752	INDEX	NOVEL	REPLIC	T	C
rs3105593	27	USP50-TRPM7	INTERGENIC	15	48,632,310	INDEX	NOVEL		T	C
rs1296720	28	CREBBP	INTRONIC	16	3,813,643	INDEX	NOVEL		C	A
rs735951	29	LITAF	INTERGENIC	16	11,601,037	INDEX	NOVEL		A	G
rs246185	30	MKL2	INTERGENIC	16	14,302,933	INDEX	NOVEL	REPLIC	C	T
rs246196	31	CNOT1	INTRONIC	16	57,131,754	INDEX	KNOWN		C	T
rs1052536	32	LIG3	3PRIME_UTR	17	30,355,688	INDEX	KNOWN		C	T
rs9892651	33	PRKCA	INTRONIC	17	61,734,255	INDEX	KNOWN		C	T
rs1396515	34	KCNJ2	INTERGENIC	17	65,942,588	INDEX	KNOWN		C	G
rs1805128	35	KCNE1	NON_SYNONYMOUS_	21	34,743,550	INDEX	KNOWN		T	C

Supplementary Table 6 (2 pages): 35 genome-wide significant loci associated with QT interval. Shown are the 35 loci with at least one SNP that achieves genome-wide significance on the basis of GWAS and/or replication results. The sentinel (or index) SNP with the lowest p-value from GWAS or GWAS+replication is shown along with annotation of the function of the SNP if falling within a gene, whether the association of the locus is known or novel, whether the top SNP at the locus was selected for replication genotyping, the allele coded 0,1,2 under an additive genetic model, the frequency of the coded allele (weighted average across all studies), the effective sample size (representing the per-SNP sum of per cohort products of samples size and imputation quality [ranging from 0 to 1] for each SNP) and the QT interval effect estimate (beta from linear regression on the scale of milliseconds), the P-value resulting from inverse-variance-weighted fixed-effects meta-analysis and lastly a representation across all GWAS and replication cohorts for whether the effect on QT interval for the coded allele was negative (-), positive (+) or missing (.).

CODED ALLELE FREQ	N_EFF	BETA	SE	P	DIRECTIONS
0.283	47,041	1.73	0.13	7.4E-40	+++++++++++++++++++++++++.++++...........+..+.
0.496	83,031	0.70	0.09	1.4E-14	+++++-++++++++++++++-+++++++++-.+.---+-.++++.-+.
0.240	75,053	3.50	0.11	1.3E-213	++++++++++++++++++++++++++++++...........+..+.
0.126	75,707	-1.68	0.14	1.1E-31	------------------------------...........-..-.
0.049	70,311	-1.69	0.22	4.7E-14	------------+-+-.------+--.-+--...........-..-.
0.390	101,902	0.53	0.09	5.9E-10	++-+++++++++++++-++++++++-++--++++++-+++++-.++.+
0.420	85,299	-0.52	0.09	7.1E-09	--+++-----------+++-+--+++---+-.-.-.---.+.--..+.
0.423	103,331	0.61	0.08	4.4E-13	+++++-++++++++++++++++++-+++++-+++.-++++++-+.-++
0.317	73,697	-1.12	0.10	4.4E-27	----------+---+---+-----------...........-..-.
0.396	76,184	-0.54	0.10	3.3E-08	--++--+-----+--+-+++--+------+-...........-..+.
0.108	70,821	0.97	0.16	7.8E-10	++++++-++-++-+++-++++-+-++++-++...........+..+.
0.457	101,382	-0.51	0.08	1.2E-09	+-----------+-------+-+-----+-+-.+.-----...--.--
0.133	87,942	-0.85	0.13	5.4E-11	-----+------+----+----+----++--.+.-.---.----.-+.
0.402	93,262	0.55	0.09	3.2E-10	++-++-+++++++++-++-++-++-++-+++-.+++-++-+++-+.++.
0.502	74,932	-1.65	0.10	2.2E-67	-----------------------------...............-.
0.093	102,060	0.79	0.14	2.6E-08	++++--+++++++++--++++++++-++--+++++-+-+++--++-++
0.266	65,331	-1.68	0.11	1.3E-49	--..-------------..-------.----...........-..+.
0.097	74,196	0.99	0.16	1.1E-09	-+--+++++++++-+++++++++++++++++...........+..+.
0.470	73,404	-0.61	0.10	1.7E-10	----------+------++-+-+-+---+--...........-..-.
0.331	82,677	0.57	0.10	3.4E-09	++++-++++++++++++-++-++++++-+++.+.+.-++.++-+.-+.
0.391	70,552	-0.56	0.10	2.7E-08	--++---------+------+-+-.+-----................
0.188	72,978	1.93	0.12	1.2E-54	++++++++++++++-+++++++++++++++++...........+..+.
0.344	100,900	-0.57	0.09	8.2E-11	--+---------+-------+----+--+----+-++---..------
0.356	95,768	0.62	0.09	2.9E-12	++-++-++++++++++++-++-+-++-++++.++.-+++-++-+.+-.
0.362	69,219	0.57	0.10	2.1E-08	++++++++++-++++++++++++--++--+++................
0.355	83,532	0.61	0.09	4.0E-11	++..++++++++-+++-..+++++++.+-++.-+-+-+++-++-..+.
0.446	77,240	0.66	0.10	3.1E-12	++---+++-+++++++++-++-+--+++++++...........+..-.
0.197	59,812	0.83	0.13	3.6E-10	-+++++++++-+++-++-+-++++++-+-+-...........+....
0.455	62,994	-1.15	0.10	2.3E-28	--+--------------------------...........-..-.
0.335	77,411	0.72	0.10	2.6E-13	++++++++++-+++-++-++++-++++++++.+.+++++.+++-.-+.
0.259	76,513	-1.73	0.11	2.0E-57	--------------------------+--...........-..-.
0.530	75,961	0.98	0.10	6.2E-25	++++++-+++++++++--+++++++++++++...........+..+.
0.429	74,683	-0.74	0.10	2.7E-14	--------------++-------+-------...........-..-.
0.521	77,058	-0.98	0.09	2.0E-25	-------------------+----------...........-..-.
0.010	20,061	7.42	0.85	2.0E-18	+++++++

SNP	CHR	POS	CODED ALLELE	NONCODED ALLELE	CODED ALLELE FREQ	N_EFF	BETA FIXED	SE_FIXED	P_FIXED	DIRECTIONS	NEAREST_GENE
rs2298632	1	23,583,062	T	C	0.496	83,031	0.70	0.09	1.38E-14	+++++-++++++++++++++-+++++++++-.+.---+-.++++.-+.	TCEA3
rs1775154	1	203,963,238	A	T	0.43	85,363	0.45	0.09	5.62E-07	++---+++++++++-+-+-++-++++-++++.+...++-.+....++.	NUCKS1
rs11685090	2	40,217,710	G	C	0.375	89,545	0.53	0.09	3.59E-09	+++++++++++++-+++-++---+-+-+++-.+.+--++.+-++..+.	SLC8A1
rs938291	2	174,450,854	G	C	0.39	101,902	0.53	0.09	5.87E-10	++-++++++++++++++-++++++++-++--++++++-+++++-.++.+	SP3
rs7561149	2	179,398,101	C	T	0.42	85,299	-0.52	0.09	7.07E-09	--+++----------+++-+--+++---+-.-.-.---.+.--..+.	CCDC141
rs295140	2	200,868,944	T	C	0.423	103,331	0.61	0.08	4.41E-13	+++++-+++++++++++++++++-+++++-+++.-++++++-+.-++	LOC26010
rs619540	2	220,217,327	C	T	0.145	58,487	0.65	0.15	1.23E-05	++-+++++++++-+-+-++-+++-.+.+-++....---..-.-+..-.	SLC4A3
rs7426919	3	46,721,979	G	A	0.431	76,661	-0.38	0.09	5.62E-05	--..--++----+---+..---+---.----.-.-.+-..-+++..+.	TMIE
rs2593074	4	56,484,374	A	G	0.388	86,226	-0.32	0.09	3.55E-04	----+-+---+---+-----+-+-+----++.+.-.+--.--+..+..	EXOC1
rs3857067	4	95,245,457	A	T	0.457	101,382	-0.51	0.08	1.15E-09	+-----------+-------+-+-----+-+-.+.-----...--.--	SMARCAD1
rs16870629	5	1,068,063	T	C	0.393	70,957	0.45	0.10	7.85E-06	++---+++++++-++++-++-+++.++++++.+.--..+.++-+.++.	NKD2
rs10040989	5	137,601,624	A	G	0.133	87,942	-0.85	0.13	5.41E-11	-----+------+----+----+----++--.+.-.---.----.-+.	GFRA3
rs7765828	6	16,402,701	G	C	0.402	93,262	0.55	0.09	3.21E-10	++-++-++++++++-++-++-++-++-+++-.+++-++-+++-+.++.	GMPR
rs17132774	7	2,892,375	G	T	0.009	48,571	2.37	0.60	8.71E-05	.+.+-.+-.+.+++++.++++..+.+.++-+.-.-..++.-+.-..-.	CARD11
rs404321	7	72,064,058	A	G	0.005	9,781	9.86	2.08	2.00E-06	.+....++.+.+.+...+-+-..+.+..+.-................	NSUN5C
rs7808970	7	99,918,674	G	A	0.383	76,792	0.52	0.10	1.03E-07	++-++++++-++++++-+++++++++++---.+.+-++..+++..-..	C7orf51
rs9920	7	115,987,328	C	T	0.093	102,060	0.79	0.14	2.60E-08	++++--+++++++++--++++++++-++--+++++-+-+++--++-++	CAV1
rs4493911	8	23,229,408	T	C	0.209	91,729	0.28	0.11	9.21E-03	++-+-++--+++-+-++++++++--.-++-++.-----+-+-++-.--.	LOXL2
rs4452774	8	98,930,532	G	C	0.416	83,801	-0.57	0.09	2.30E-10	-------------------+-------+--.+.++-+-.---.....	LAPTM4B
rs1961102	8	104,002,021	T	C	0.331	82,677	0.57	0.10	3.41E-09	++++-++++++++++++-++-++++++-+++.+.+.-++.++-+.-+.	AZIN1
rs10125231	9	22,092,128	A	G	0.022	27,241	1.61	0.53	2.45E-03	.+.+..-+.+++.++..++++..+.+.++.-.-.-+.--.---+.++.	CDKN2BAS
rs16928463	9	114,903,731	T	C	0.013	51,597	1.85	0.48	1.16E-04	.+-++.++.+-++-...+-+++.+.+.+---.+.--.++.---+.+..	C9orf110
rs174583	11	61,366,326	T	C	0.344	100,900	-0.57	0.09	8.21E-11	--+---------+-------+----+--+----+-++---..------	FADS2
rs11233494	11	82,547,804	G	A	0.08	75,687	0.74	0.18	2.75E-05	++++-+++++-+-+-+-++--++-+++++++.+.-.-+....+-.+-.	PCF11
rs3026445	12	109,207,586	C	T	0.356	95,768	0.62	0.09	2.92E-12	++-++-+++++++++++++-++-+-++-++++.++.-+++-++-+.+-.	ATP2A2
rs17217266	13	73,436,467	T	C	0.114	90,391	-0.69	0.14	5.44E-07	-------+--+--+------+-+++-+----.-.-+-+-.-+++.-+.	KLF12
rs2273905	14	102,044,752	T	C	0.355	83,532	0.61	0.09	4.04E-11	++..++++++++-+++-..+++++++.+-++.-+-+-+++-++-..+.	ANKRD9
rs16971598	15	39,269,523	C	T	0.052	42,600	-0.92	0.27	6.78E-04	+---..+---+-----.+---+.-.+--+.-.-.---+-.+..-.--.	EXD1
rs2414059	15	48,660,636	A	T	0.448	86,157	0.59	0.09	7.69E-11	++---+++-++++++++++++-+--+++++++....---.....++.-.	TRPM7
rs12442591	15	83,907,801	A	C	0.077	86,038	0.50	0.17	3.28E-03	++-.++---+++-+++-++++---++++---.+.++-++.-++-.+-.	AKAP13
rs7195486	16	4,195,181	C	G	0.213	76,471	0.55	0.11	9.42E-07	+++-++++++++-+++++-+++.--+.+-+-.-.-++++..+--.+-.	SRL
rs246185	16	14,302,933	C	T	0.335	77,411	0.72	0.10	2.64E-13	++++++++++-+++-++-++++-++++++++.+.+++++.+++-.-+.	MKL2
rs11868136	17	33,704,118	A	G	0.055	68,344	-0.91	0.23	5.96E-05	+-------.---+--+-------+++----+.+.-.-+..+-.+.-+.	MRPL45
rs728478	17	54,821,286	G	A	0.445	86,352	-0.40	0.09	8.27E-06	--+---+-+-------++----+-----++-.+.++---.-.-+..+.	YPEL2
rs9303504	17	61,745,828	G	C	0.428	79,052	-0.71	0.10	8.66E-14	--------------++-------+-------....++-.....-..-.	PRKCA

Supplementary Table 7: Meta-analysis of directly genotyped SNPs + final GWAS. Shown are the association results for 35 SNPs selected for replication at an interim meta-analysis of GWAS results. The directly genotyped SNP results were meta-analyzed with inverse-variance-weighted fixed-effects meta-analysis with the final GWAS results. See Supplementary Table 6 legend for explanation of fields. Note that some SNPs selected for direct genotyping were the most strongly associated SNPs (lowest P-value) at a given locus but others may have been superseded by a SNP based only on available GWAS results. For example, SNP rs9303504 at the locus containing PRKCA showed genome-wide significant association with QT interval with an effective sample size of 79,052 from samples with direct replication genotyping and GWAS (Supplementary Table 7), but another SNP at the locus rs9892651 with an effective sample size of only 74,683 in samples with GWAS only (no direct replication genotyping was performed) had a lower p-value and was therefore reported as the sentinel (index) in Supplementary Table 6.

SNP	LOCUS	NEAREST_GENE	FUNCTION	CHR	POS	INDEX_OTHERSIGNAL	NOVEL?	REPLIC SNP?	Coded/ Noncoded / codfreq	N_EFF	BETA FIXED	SE_FIXED	P_FIXED
rs2273042	1	RNF207	INTRONIC	1	6,071,709	OTHERSIGNAL	KNOWN		A/G/0.11	66,377	0.94	0.16	6.8E-09
rs846111	1	RNF207	NON_SYNONYMOUS	1	6,201,957	INDEX	KNOWN		C/G/0.283	47,041	1.73	0.13	7.4E-40
rs2298632	2	TCEA3	INTRONIC	1	23,583,062	INDEX	NOVEL	REPLIC	T/C/0.496	83,031	0.70	0.09	1.4E-14
rs6669543	3	NOS1AP	INTRONIC	1	160,247,649	OTHERSIGNAL	KNOWN		T/C/0.258	73,090	1.46	0.11	1.6E-39
rs4656345	3	NOS1AP	INTRONIC	1	160,257,861	OTHERSIGNAL	KNOWN		A/G/0.085	12,469	-4.73	0.52	1.0E-19
rs12143842	3	NOS1AP	INTERGENIC	1	160,300,514	INDEX	KNOWN		T/C/0.24	75,053	3.50	0.11	1.3E-213
rs16857031	3	NOS1AP	INTRONIC	1	160,379,534	OTHERSIGNAL	KNOWN		G/C/0.132	71,270	2.37	0.14	6.5E-61
rs17457880	3	NOS1AP	INTRONIC	1	160,434,778	OTHERSIGNAL	KNOWN		A/G/0.055	34,636	-1.90	0.30	2.8E-10
rs4657172	3	NOS1AP	INTRONIC	1	160,446,256	OTHERSIGNAL	KNOWN		C/G/0.125	76,568	-0.81	0.14	1.3E-08
rs3934467	3	NOS1AP	INTRONIC	1	160,449,301	OTHERSIGNAL	KNOWN		T/C/0.222	76,877	2.74	0.11	2.8E-129
rs7545047	3	NOS1AP	INTRONIC	1	160,457,727	OTHERSIGNAL	KNOWN		A/G/0.049	63,238	-1.78	0.24	8.9E-14
rs17460657	3	NOS1AP	INTRONIC	1	160,528,450	OTHERSIGNAL	KNOWN		C/A/0.045	14,788	-4.60	0.56	2.7E-16
rs347272	3	NOS1AP	INTRONIC	1	160,585,122	OTHERSIGNAL	KNOWN		A/G/0.132	72,910	1.80	0.14	1.3E-37
rs164133	3	NOS1AP	INTRONIC	1	160,647,912	OTHERSIGNAL	KNOWN		C/G/0.264	75,936	0.72	0.11	3.0E-11
rs545833	4	ATP1B1	INTRONIC	1	166,956,564	OTHERSIGNAL	KNOWN		T/C/0.266	77,162	0.90	0.11	3.9E-17
rs12061601	4	ATP1B1	UPSTREAM	1	167,337,074	OTHERSIGNAL	KNOWN		C/T/0.117	74,396	-1.41	0.15	3.1E-21
rs10919070	4	ATP1B1	INTRONIC	1	167,365,661	INDEX	KNOWN		C/A/0.126	75,707	-1.68	0.14	1.1E-31
rs12079745	4	ATP1B1	3PRIME_UTR	1	167,367,684	OTHERSIGNAL	KNOWN		A/G/0.059	69,214	-1.34	0.21	1.2E-10
rs1983546	4	ATP1B1	INTRONIC	1	167,712,807	OTHERSIGNAL	KNOWN		G/A/0.348	75,124	-0.81	0.10	9.7E-16
rs6544311	5	SLC8A1	INTRONIC	2	40,206,781	OTHERSIGNAL	KNOWN		A/C/0.376	71,452	0.65	0.10	1.8E-10
rs12997023	5	SLC8A1	INTERGENIC	2	40,606,486	INDEX	KNOWN		C/T/0.049	70,311	-1.69	0.22	4.7E-14
rs938291	6	SP3	INTERGENIC	2	174,450,854	INDEX	NOVEL	REPLIC	G/C/0.39	101,902	0.53	0.09	5.9E-10
rs7561149	7	TTN-CCDC141	INTERGENIC	2	179,398,101	INDEX	NOVEL	REPLIC	C/T/0.42	85,299	-0.52	0.09	7.1E-09
rs295140	8	SPATS2L	INTERGENIC	2	200,868,944	INDEX	NOVEL	REPLIC	T/C/0.423	103,331	0.61	0.08	4.4E-13
rs6793245	9	SCN5A-SCN10A	INTRONIC	3	38,574,041	INDEX	KNOWN		A/G/0.317	73,697	-1.12	0.10	4.4E-27
rs11708996	9	SCN5A-SCN10A	INTRONIC	3	38,608,927	OTHERSIGNAL	KNOWN		C/G/0.148	69,500	-0.92	0.14	2.3E-11
rs11710077	9	SCN5A-SCN10A	INTRONIC	3	38,632,903	OTHERSIGNAL	KNOWN		T/A/0.209	66,926	0.92	0.12	1.4E-13
rs6599234	9	SCN5A-SCN10A	INTERGENIC	3	38,690,304	OTHERSIGNAL	KNOWN		A/T/0.324	71,453	0.70	0.10	2.2E-11
rs6801957	9	SCN5A-SCN10A	INTRONIC	3	38,742,319	OTHERSIGNAL	KNOWN		T/C/0.403	74,534	-0.63	0.10	1.1E-10
rs17784882	10	C3ORF75	INTRONIC	3	47,519,007	INDEX	NOVEL		A/C/0.396	76,184	-0.54	0.10	3.3E-08
rs2363719	11	SLC4A4	INTRONIC	4	72,357,080	INDEX	NOVEL		A/G/0.108	70,821	0.97	0.16	7.8E-10
rs3857067	12	SMARCAD1	INTERGENIC	4	95,245,457	INDEX	NOVEL	REPLIC	A/T/0.457	101,382	-0.51	0.08	1.2E-09
rs10040989	13	GFRA3	INTERGENIC	5	137,601,624	INDEX	NOVEL	REPLIC	A/G/0.133	87,942	-0.85	0.13	5.4E-11
rs7765828	14	GMPR	INTRONIC	6	16,402,701	INDEX	NOVEL	REPLIC	G/C/0.402	93,262	0.55	0.09	3.2E-10
rs457162	15	SLC35F1-PLN	INTRONIC	6	118,642,676	OTHERSIGNAL	KNOWN		T/A/0.059	70,449	-1.85	0.21	2.5E-18
rs12210733	15	SLC35F1-PLN	INTERGENIC	6	118,759,768	OTHERSIGNAL	KNOWN		A/G/0.063	65,356	-2.05	0.21	1.1E-22
rs11153730	15	SLC35F1-PLN	INTERGENIC	6	118,774,215	INDEX	KNOWN		T/C/0.502	74,932	-1.65	0.10	2.2E-67
rs3902035	15	SLC35F1-PLN	INTRONIC	6	119,106,925	OTHERSIGNAL	KNOWN		C/T/0.316	71,216	-0.85	0.11	8.0E-16
rs9489510	15	SLC35F1-PLN	INTERGENIC	6	119,150,591	OTHERSIGNAL	KNOWN		G/A/0.31	68,745	0.61	0.11	1.4E-08
rs9920	16	CAV1	3PRIME_UTR	7	115,987,328	INDEX	NOVEL	REPLIC	C/T/0.093	102,060	0.79	0.14	2.6E-08
rs2072413	17	KCNH2	INTRONIC	7	150,278,902	INDEX	KNOWN		T/C/0.266	65,331	-1.68	0.11	1.3E-49
rs3807375	17	KCNH2	INTRONIC	7	150,298,143	OTHERSIGNAL	KNOWN		T/C/0.36	70,537	1.22	0.10	2.9E-33
rs16936870	18	NCOA2	INTRONIC	8	71,351,896	INDEX	NOVEL		A/T/0.097	74,196	0.99	0.16	1.1E-09
rs11779860	19	LAPTM4B	INTRONIC	8	98,919,506	INDEX	NOVEL		C/T/0.47	73,404	-0.61	0.10	1.7E-10
rs1961102	20	AZIN1	INTERGENIC	8	104,002,021	INDEX	NOVEL	REPLIC	T/C/0.331	82,677	0.57	0.10	3.4E-09
rs2485376	21	GBF1	INTRONIC	10	104,039,996	INDEX	NOVEL		A/G/0.391	70,552	-0.56	0.10	2.7E-08
rs2301696	22	KCNQ1	INTRONIC	11	2,383,560	OTHERSIGNAL	KNOWN		G/C/0.404	22,791	-1.14	0.18	4.3E-10
rs2074238	22	KCNQ1	INTRONIC	11	2,441,379	OTHERSIGNAL	KNOWN		T/C/0.053	17,550	-4.89	0.44	1.9E-28
rs7122937	22	KCNQ1	INTRONIC	11	2,443,126	INDEX	KNOWN		T/C/0.188	72,978	1.93	0.12	1.2E-54
rs174583	23	FADS2	INTRONIC	11	61,366,326	INDEX	NOVEL	REPLIC	T/C/0.344	100,900	-0.57	0.09	8.2E-11
rs3026445	24	ATP2A2	INTRONIC	12	109,207,586	INDEX	NOVEL	REPLIC	C/T/0.356	95,768	0.62	0.09	2.9E-12
rs728926	25	KLF12	INTRONIC	13	73,411,123	INDEX	NOVEL		T/C/0.362	69,219	0.57	0.10	2.1E-08
rs2273905	26	ANKRD9	5PRIME_UTR	14	102,044,752	INDEX	NOVEL	REPLIC	T/C/0.355	83,532	0.61	0.09	4.0E-11
rs3105593	27	USP50-TRPM7	INTERGENIC	15	48,632,310	INDEX	NOVEL		T/C/0.446	77,240	0.66	0.10	3.1E-12
rs1296720	28	CREBBP	INTRONIC	16	3,813,643	INDEX	NOVEL		C/A/0.197	59,812	0.83	0.13	3.6E-10
rs12930096	29	LITAF	INTRONIC	16	11,578,259	OTHERSIGNAL	NOVEL		T/C/0.142	48,027	-1.22	0.17	2.9E-13
rs735951	29	LITAF	INTERGENIC	16	11,601,037	INDEX	NOVEL		A/G/0.455	62,994	-1.15	0.10	2.3E-28
rs12444261	29	LITAF	INTERGENIC	16	11,642,143	OTHERSIGNAL	NOVEL		T/G/0.262	65,791	-0.79	0.11	2.1E-12
rs246185	30	MKL2	INTERGENIC	16	14,302,933	INDEX	NOVEL	REPLIC	C/T/0.335	77,411	0.72	0.10	2.6E-13
rs4784934	31	CNOT1	INTERGENIC	16	57,017,427	OTHERSIGNAL	KNOWN		A/G/0.254	67,425	0.67	0.12	5.5E-09
rs246196	31	CNOT1	INTRONIC	16	57,131,754	INDEX	KNOWN		C/T/0.259	76,513	-1.73	0.11	2.0E-57
rs1052536	32	LIG3	3PRIME_UTR	17	30,355,688	INDEX	KNOWN		C/T/0.53	75,961	0.98	0.10	6.2E-25
rs9892651	33	PRKCA	INTRONIC	17	61,734,255	INDEX	KNOWN		C/T/0.429	74,683	-0.74	0.10	2.7E-14
rs236586	34	KCNJ2	INTERGENIC	17	65,715,141	OTHERSIGNAL	KNOWN		G/A/0.466	70,855	0.64	0.10	6.0E-11
rs10775360	34	KCNJ2	INTERGENIC	17	65,837,463	OTHERSIGNAL	KNOWN		T/C/0.292	73,723	-0.76	0.11	1.1E-12
rs1396515	34	KCNJ2	INTERGENIC	17	65,942,588	INDEX	KNOWN		C/G/0.521	77,058	-0.98	0.09	2.0E-25
rs17763769	34	KCNJ2	INTERGENIC	17	66,072,384	OTHERSIGNAL	KNOWN		A/G/0.146	74,831	0.89	0.14	4.8E-11
rs1805128	35	KCNE1	NON_SYNONYMOUS	21	34,743,550	INDEX	KNOWN		T/C/0.01	20,061	7.42	0.85	2.0E-18

Supplementary Table 8a: 68 independent QT SNPs at 35 QT loci. Shown are the association results for all 68 independent SNPs at 35 loci on the basis of having an $r2<0.05$ in HapMap CEU to any other SNP on the list. See the legend for Supplementary Table 6 for description of fields.

INDEX SNP	LOCUS	NEAREST GENE	MISSENSE SNP	R2	gene	AA change	P vs sentinel
rs846111	1	RNF207	rs846111	same	RNF207	G603A	same
rs6801957	9	SCN5A-SCN10A	rs6795970	0.979	SCN10A	V1073A	6E-10 v 3E-10
rs17784882	10	C3ORF75	rs12487736	0.873	SCAP	V798I	NA
rs17784882	10	C3ORF75	rs2276853	0.873	KIF9	R638W	7E-7 v 5E-8
rs17784882	10	C3ORF75	rs6780013	0.866	PTPN23	A944T	3E-6 v 5E-8
rs17784882	10	C3ORF75	rs4082155	0.844	SETD2	P1962L	7E-6 v 5E-8
rs7765828	14	GMPR	rs1042391	1	GMPR	F256I	1
rs1805128	35	KCNE1	rs1805128	same	KCNE1	D85N	same

Supplementary Table 8b: SNPs correlated with missense SNPs. Missense SNPs are shown for all index and nonindex signals for SNPs with r2>0.8 in HapMap CEU to a given QT-associated SNPs. When a proxy but not the lead SNP was missense, the r2 of proxy to the lead SNP is shown as well as its P-value for association with QT interval in comparison to the P-value for the lead SNP in the GWAS meta-analysis (to allow meaningful comparison of P-values).

QT-IGC	QT-IGC	QT-IGC	QT-IGC	QT-IGC	QT-IGC	QT-IGC	CARE-COGENT	CA-CO	CA-CO	CA-CO	CA-CO	CA-CO	CA-CO	CA-CO	CA-CO	CA-CO	CA-CO
SNP	**LOCUS**	**NEAREST GENE**	**CHR**	**CODED ALLELE**	**CODED ALLELE FREQ**	**BETA**	**SNP**	**CODED ALLELE**	**CODED ALLELE FREQ**	**BETA**	**?flip**	**beta flipped**	**SE**	**N_EFF**	**P GC**	**p < 0.0007**	**direction**
rs2273042	1	RNF207	1	A	0.110	0.94	rs2273042	A	0.130	-0.65	1	-0.65	0.80	9,542	0.43		diff
rs846111	1	RNF207	1	C	0.283	1.73	rs846111	C	0.169	0.65	1	0.65	0.55	8,243	0.25		same
rs2298632	2	TCEA3	1	T	0.496	0.70	rs2298632	C	0.794	-0.68	-1	0.68	0.36	13,102	0.06		same
rs6669543	3	NOS1AP	1	T	0.258	1.46	rs6669543	C	0.379	-0.57	-1	0.57	0.31	10,445	0.07		same
rs4656345	3	NOS1AP	1	A	0.085	-4.73	rs4656345	A	0.395	-4.71	1	-4.71	4.72	497	0.33		same
rs12143842	3	NOS1AP	1	T	0.240	3.50	rs12143842	C	0.802	-3.14	-1	3.14	0.39	12,812	1.8E-15	signif	same
rs16857031	3	NOS1AP	1	G	0.132	2.37	rs16857031	C	0.676	-0.80	-1	0.80	0.29	12,207	0.008		same
rs17457880	3	NOS1AP	1	A	0.055	-1.90	rs17457880	A	0.101	-3.34	1	-3.34	2.15	3,821	0.13		same
rs4657172	3	NOS1AP	1	C	0.125	-0.81	rs4657172	C	0.304	-0.60	1	-0.60	0.29	13,121	0.04		same
rs3934467	3	NOS1AP	1	T	0.222	2.74	rs3934467	C	0.664	-1.69	-1	1.69	0.28	13,170	2.6E-09	signif	same
rs7545047	3	NOS1AP	1	A	0.049	-1.78	rs7545047	A	0.407	-9.14	1	-9.14	3.50	1,584	0.01		same
rs17460657	3	NOS1AP	1	C	0.045	-4.60	rs17460657	A	0.893	-0.35	-1	0.35	2.55	2,912	0.89		diff
rs347272	3	NOS1AP	1	A	0.132	1.80	rs347272	A	0.307	-0.35	1	-0.35	0.29	12,721	0.24		diff
rs164133	3	NOS1AP	1	C	0.264	0.72	rs164133	C	0.340	-0.30	1	-0.30	0.29	12,134	0.31		diff
rs545833	4	ATP1B1	1	T	0.266	0.90	rs545833	C	0.672	-0.42	-1	0.42	0.29	12,650	0.15		same
rs12061601	4	ATP1B1	1	C	0.117	-1.41	rs12061601	C	0.295	-1.89	1	-1.89	0.30	12,608	5.9E-10	signif	same
rs10919070	4	ATP1B1	1	C	0.126	-1.68	rs10919070	A	0.837	2.06	-1	-2.06	1.07	6,825	0.06		same
rs12079745	4	ATP1B1	1	A	0.059	-1.34	rs12079745	A	0.164	-1.28	1	-1.28	0.43	12,524	0.003		same
rs1983546	4	ATP1B1	1	G	0.348	-0.81	rs1983546	A	0.418	0.69	-1	-0.69	0.26	13,103	0.010		same
rs6544311	5	SLC8A1	2	A	0.376	0.65	rs6544311	C	0.505	0.92	-1	-0.92	0.94	1,226	0.33		diff
rs12997023	5	SLC8A1	2	C	0.049	-1.69	rs12997023	C	0.150	-1.68	1	-1.68	0.45	12,873	2.6E-04	signif	same
rs938291	6	SP3	2	G	0.390	0.53	rs938291	C	0.531	-0.36	-1	0.36	0.25	13,039	0.17		same
rs7561149	7	CCDC141	2	C	0.420	-0.52	rs7561149	C	0.249	-0.33	1	-0.33	0.32	12,987	0.31		same
rs295140	8	SPATS2L	2	T	0.423	0.61	rs295140	C	0.638	-0.36	-1	0.36	0.28	13,063	0.20		same
rs6793245	9	SCN5A-SCN	3	A	0.317	-1.12	rs6793245	A	0.570	-0.51	1	-0.51	0.26	13,043	0.05		same
rs11708996	9	SCN5A-SCN	3	C	0.148	-0.92	rs11708996	C	0.443	-2.92	1	-2.92	1.80	2,020	0.11		same
rs11710077	9	SCN5A-SCN	3	T	0.209	0.92	rs11710077	A	0.770	-0.81	-1	0.81	0.42	13,045	0.06		same
rs6599234	9	SCN5A-SCN	3	A	0.324	0.70	rs6599234	A	0.208	0.08	1	0.08	0.36	12,617	0.82		same
rs6801957	9	SCN5A-SCN	3	T	0.403	-0.63	rs6801957	C	0.765	0.95	-1	-0.95	0.35	12,421	0.008		same
rs17784882	10	C3ORF75	3	A	0.396	-0.54	rs17784882	A	0.310	0.17	1	0.17	0.29	12,779	0.58		diff
rs2363719	11	SLC4A4	4	A	0.108	0.97	rs2363719	A	0.150	-0.50	1	-0.50	0.45	13,080	0.27		diff
rs3857067	12	SMARCAD1	4	A	0.457	-0.51	rs3857067	A	0.553	-0.13	1	-0.13	0.30	13,066	0.66		same
rs10040989	13	GFRA3	5	A	0.133	-0.85	rs10040989	A	0.153	0.01	1	0.01	0.44	13,081	0.99		diff
rs7765828	14	GMPR	6	G	0.402	0.55	rs7765828	C	0.233	0.09	-1	-0.09	0.34	12,911	0.79		diff
rs457162	15	SLC35F1-PL	6	T	0.059	-1.85	rs457162	A	0.835	-0.33	-1	0.33	0.46	12,981	0.48		diff
rs12210733	15	SLC35F1-PL	6	A	0.063	-2.05	rs12210733	A	0.125	0.64	1	0.64	1.58	6,732	0.69		diff
rs11153730	15	SLC35F1-PL	6	T	0.502	-1.65	rs11153730	C	0.318	0.57	-1	-0.57	0.29	12,799	0.05		same
rs3902035	15	SLC35F1-PL	6	C	0.316	-0.85	rs3902035	C	0.173	-0.45	1	-0.45	0.70	7,810	0.53		same
rs9489510	15	SLC35F1-PL	6	G	0.310	0.61	rs9489510	A	0.502	-0.03	-1	0.03	0.27	11,722	0.92		same
rs9920	16	CAV1	7	C	0.093	0.79	rs9920	C	0.092	-0.16	1	-0.16	0.90	12,753	0.86		diff
rs2072413	17	KCNH2	7	T	0.266	-1.68	rs2072413	C	0.632	1.34	-1	-1.34	0.38	6,746	5.9E-04	signif	same
rs3807375	17	KCNH2	7	T	0.360	1.22	rs3807375	C	0.368	-0.71	-1	0.71	0.28	13,090	0.01		same
rs16936870	18	NCOA2	8	A	0.097	0.99	rs16936870	A	0.120	0.64	1	0.64	0.61	12,376	0.30		same
rs11779860	19	LAPTM4B	8	C	0.470	-0.61	rs11779860	C	0.408	0.04	1	0.04	0.27	12,098	0.87		diff
rs1961102	20	AZIN1	8	T	0.331	0.57	rs1961102	C	0.815	-0.31	-1	0.31	0.44	11,982	0.49		same
rs2485376	21	GBF1	10	A	0.391	-0.56	rs2485376	A	0.190	-0.04	1	-0.04	0.35	11,695	0.90		same
rs2301696	22	KCNQ1	11	G	0.404	-1.14	rs2301696	C	0.433	-0.94	-1	0.94	0.67	2,188	0.17		diff
rs2074238	22	KCNQ1	11	T	0.053	-4.89	rs2074238	C	0.512	3.11	-1	-3.11	3.48	1,504	0.38		same
rs7122937	22	KCNQ1	11	T	0.188	1.93	rs7122937	C	0.515	-1.35	-1	1.35	0.29	9,959	6.7E-06	signif	same
rs174583	23	FADS2	11	T	0.344	-0.57	rs174583	C	0.718	0.62	-1	-0.62	0.31	10,938	0.05		same
rs3026445	24	ATP2A2	12	C	0.356	0.62	rs3026445	C	0.579	0.47	1	0.47	0.26	13,073	0.08		same
rs728926	25	KLF12	13	T	0.362	0.57	rs728926	C	0.632	-0.35	-1	0.35	0.29	12,013	0.23		same
rs2273905	26	ANKRD9	14	T	0.355	0.61	rs2273905	C	0.781	-1.10	-1	1.10	0.39	12,021	0.005		same
rs3105593	27	TRPM7	15	T	0.446	0.66	rs3105593	C	0.579	-0.98	-1	0.98	0.26	13,088	2.1E-04	signif	same
rs1296720	28	CREBBP	16	C	0.197	0.83	rs1296720	A	0.790	-0.57	-1	0.57	0.85	6,674	0.51		same
rs12930096	29	LITAF	16	T	0.142	-1.22	rs8050461*	A	0.218	0.22	1	0.22	0.41	10,094	0.59		diff
rs735951	29	LITAF	16	A	0.455	-1.15	rs735951	A	0.440	-1.44	1	-1.44	0.31	9,146	5.6E-06	signif	same
rs12444261	29	LITAF	16	T	0.262	-0.79	rs12444261	G	0.790	0.89	-1	-0.89	0.35	12,776	0.01		same
rs246185	30	MKL2	16	C	0.335	0.72	rs246185	C	0.358	0.37	1	0.37	0.31	10,528	0.23		same
rs4784934	31	CNOT1	16	A	0.254	0.67	rs4784934	A	0.316	0.37	1	0.37	0.30	12,117	0.23		same
rs246196	31	CNOT1	16	C	0.259	-1.73	rs246196	C	0.208	-1.40	1	-1.40	0.35	13,143	7.7E-05	signif	same
rs1052536	32	LIG3	17	C	0.530	0.98	rs1052536	C	0.787	0.81	1	0.81	0.36	13,077	0.03		same
rs9892651	33	PRKCA	17	C	0.429	-0.74	rs9892651	C	0.378	-0.72	1	-0.72	0.27	13,023	0.009		same
rs236586	34	KCNJ2	17	G	0.466	0.64	rs236586	A	0.490	-1.00	-1	1.00	0.27	12,161	2.2E-04	signif	same
rs10775360	34	KCNJ2	17	T	0.292	-0.76	rs10775360	C	0.743	0.25	-1	-0.25	0.34	12,265	0.47		same
rs1396515	34	KCNJ2	17	C	0.521	-0.98	rs1396515	C	0.608	-0.45	1	-0.45	0.26	13,078	0.09		same
rs17763769	34	KCNJ2	17	A	0.146	0.89	rs17763769	A	0.151	-0.54	1	-0.54	1.00	7,509	0.60		diff
rs1805128	35	KCNE1	21	T	0.010	7.42	rs1805128	NA	NA	NA	NA	NA	NA	NA	NA		NA
												0.60	correlation EA-AA			same	51
												0.37	r2			diff	16
												9.E-10	P			P	1.1E-05

*SNP rs8050461 is a proxy (r2=1 in 1KG CEU, 0.48 in 1KG YRI) for rs12930096

Supplementary Table 9: Association of QT SNPs in African Americans. Shown are the QT association results in African Americans from the CARe-COGEN GWAS for all 68 independent SNPs (r2<0.05) that achieved genome-wide significance in the QT-IGC samples of European ancestry. One SNP was not found in the CARe-COGENT GWAS results because it was not included in HapMap YRI haplotypes; results for a proxy are shown but the proxy is only modestly correlated (r2=0.48 in 1000Genomes YRI) to the QT-IGC SNP. Statistically significant association in African Americans is claimed for SNPs with 2-sided P<0.0007 (=0.05/68) in the same direction as in QT-IGC. The sign of effect estimates is reversed (beta flip) if the coded allele in CARe-COGENT was the non-coded allele in QT-IGC. Directional consistency is also reported.

Supplementary Table 10: Association of QT SNPs with heart rate and QRS duration. Shown are the effects on heart rate and on QRS duration of the 68 independent (r2<0.05) SNPs that show genome-wide significant association with QT interval. The sign of effect estimates is reversed (beta_flipped) if the coded allele in the heart rate GWAs or QRS duration was the non-coded allele in QT-IGC. Statistical significance is claimed for SNPs with 2-sided P<0.0007 (=0.05/68), regardless of directionality. Directional consistency of effects is reported.

QT-IGC	QT-IGC	QT-IGC	QT-IGC	QT-IGC	QT-IGC	HRGEN	HRGEN	HRGEN	HRGEN	HRGEN	HRGEN	HRGEN	HRGEN	HRGEN	HRGEN	compai	QRS	QRS	QRS	QRS	QRS	QRS	QRS	QRS	QRS	QRS	compariso
SNP	LOCUS	NEAREST GENE	CODED ALLELE	CODED ALLELE FREQ	BETA	SNP	CODED ALLELE	codfreq	beta (bpm)	?flip	beta flipped	SE (bpm)	P GC	N_EFF	P < 0.0007	directi on	SNP	CODED ALLELE	CAF	beta	?flip	beta flipped	SE	P	N_EFF	p<0.0 007	direction
rs2273042	1	RNF207	A	0.110	0.94	rs2273042	a	0.112	0.013	1	0.013	0.085	0.88	84,513		same	rs2273042	A	0.13	-0.01	1	-0.01	0.11	0.92	38,057		opp
rs846111	1	RNF207	C	0.283	1.73	rs846111	c	0.286	-0.009	1	-0.009	0.078	0.91	79,422		opp	rs846111	C	0.29	-0.04	1	-0.04	0.09	0.67	25,193		opp
rs2298632	2	TCEA3	T	0.496	0.70	rs2298632	t	0.492	0.049	1	0.049	0.053	0.38	85,032		same	rs2298632	C	0.49	0.25	-1	-0.25	0.07	5.3E-04	35,155	signif	opp
rs6669543	3	NOS1AP	T	0.258	1.46	rs6669543	t	0.278	-0.016	1	-0.016	0.058	0.79	92,700		opp	rs6669543	C	0.73	0.14	-1	-0.14	0.08	0.07	37,864		opp
rs4656345	3	NOS1AP	A	0.085	-4.73	rs4656345	a	0.097	1.459	1	1.459	0.830	0.09	11,207		opp	rs4656345	A	0.10	0.43	1	0.43	0.36	0.23	9,654		opp
rs12143842	3	NOS1AP	T	0.240	3.50	rs12143842	t	0.257	0.030	1	0.030	0.059	0.63	92,664		same	rs12143842	C	0.74	0.29	-1	-0.29	0.08	1.9E-04	38,973	signif	opp
rs16857031	3	NOS1AP	G	0.132	2.37	rs16857031	g	0.125	0.023	1	0.023	0.081	0.79	87,444		same	rs16857031	C	0.86	0.30	-1	-0.30	0.10	0.002	39,130		opp
rs17457880	3	NOS1AP	A	0.055	-1.90	rs17457880	a	0.069	0.136	1	0.136	0.173	0.46	66,219		opp	rs17457880	A	0.05	-0.08	1	-0.08	0.21	0.70	20,607		same
rs4657172	3	NOS1AP	C	0.125	-0.81	rs4657172	c	0.135	-0.028	1	-0.028	0.074	0.72	93,154		same	rs4657172	C	0.14	-0.06	1	-0.06	0.10	0.58	40,030		same
rs3934467	3	NOS1AP	T	0.222	2.74	rs3934467	t	0.251	-0.006	1	-0.006	0.058	0.92	93,134		opp	rs3934467	C	0.77	0.13	-1	-0.13	0.08	0.10	40,230		opp
rs7545047	3	NOS1AP	A	0.049	-1.78	rs7545047	a	0.052	-0.095	1	-0.095	0.130	0.49	81,355		same	rs7545047	A	0.08	0.04	1	0.04	0.17	0.83	34,431		opp
rs17460657	3	NOS1AP	C	0.045	-4.60	rs17460657	c	0.045	0.205	1	0.205	1.184	0.87	11,207		opp	rs17460657	A	0.95	-0.27	-1	0.27	0.38	0.48	11,695		opp
rs347272	3	NOS1AP	A	0.132	1.80	rs347272	a	0.146	-0.044	1	-0.044	0.073	0.57	93,089		opp	rs347272	A	0.15	0.00	1	0.00	0.10	0.99	38,819		same
rs164133	3	NOS1AP	C	0.264	0.72	rs164133	c	0.266	0.084	1	0.084	0.057	0.16	93,143		same	rs164133	C	0.28	-0.09	1	-0.09	0.07	0.21	40,166		opp
rs545833	4	ATP1B1	T	0.266	0.90	rs545833	t	0.290	-0.004	1	-0.004	0.057	0.95	88,647		opp	rs545833	C	0.73	0.08	-1	-0.08	0.08	0.26	40,179		opp
rs12061601	4	ATP1B1	C	0.117	-1.41	rs12061601	c	0.120	-0.092	1	-0.092	0.082	0.29	84,880		same	rs12061601	C	0.14	0.08	1	0.08	0.10	0.42	39,428		opp
rs10919070	4	ATP1B1	C	0.126	-1.68	rs10919070	c	0.126	-0.156	1	-0.156	0.079	0.06	86,031		same	rs10919070	A	0.87	0.21	-1	-0.21	0.10	0.04	39,818		same
rs12079745	4	ATP1B1	A	0.059	-1.34	rs12079745	a	0.080	-0.108	1	-0.108	0.104	0.33	84,463		same	rs12079745	A	0.09	-0.10	1	-0.10	0.14	0.50	36,583		same
rs1983546	4	ATP1B1	G	0.348	-0.81	rs1983546	g	0.366	0.004	1	0.004	0.054	0.94	82,939		opp	rs1983546	A	0.64	0.11	-1	-0.11	0.07	0.13	40,231		same
rs6544311	5	SLC8A1	A	0.376	0.65	rs6544311	a	0.399	-0.035	1	-0.035	0.054	0.54	82,179		opp	rs6544311	A	0.38	0.05	1	0.05	0.07	0.47	38,651		same
rs12997023	5	SLC8A1	C	0.049	-1.69	rs12997023	c	0.051	-0.082	1	-0.082	0.117	0.51	93,156		same	rs12997023	C	0.07	-0.30	1	-0.30	0.16	0.07	39,443		same
rs938291	6	SP3	G	0.390	0.53	rs938291	g	0.418	-0.034	1	-0.034	0.053	0.54	86,983		opp	rs938291	C	0.60	-0.06	-1	0.06	0.07	0.41	38,509		same
rs7561149	7	CCDC141	C	0.420	-0.52	rs7561149	c	0.418	-0.111	1	-0.111	0.052	0.04	89,347		same	rs7561149	C	0.41	-0.12	1	-0.12	0.07	0.08	39,688		same
rs295140	8	SPATS2L	T	0.423	0.61	rs295140	t	0.445	-0.052	1	-0.052	0.050	0.32	93,139		opp	rs295140	C	0.58	-0.14	-1	0.14	0.07	0.04	39,961		same
rs6793245	9	SCN5A-SCN1	A	0.317	-1.12	rs6793245	a	0.343	-0.069	1	-0.069	0.056	0.24	84,350		same	rs6793245	A	0.32	0.66	1	0.66	0.07	5.2E-20	39,070	signif	opp
rs11708996	9	SCN5A-SCN1	C	0.148	-0.92	rs11708996	c	0.155	-0.154	1	-0.154	0.074	0.05	84,790		same	rs11708996	C	0.16	0.79	1	0.79	0.10	1.3E-16	38,632	signif	opp
rs11710077	9	SCN5A-SCN1	T	0.209	0.92	rs11710077	t	0.252	0.083	1	0.083	0.068	0.25	87,055		same	rs11710077	A	0.79	0.84	-1	-0.84	0.09	5.7E-22	35,941	signif	opp
rs6599234	9	SCN5A-SCN1	A	0.324	0.70	rs6599234	a	0.337	0.184	1	0.184	0.054	0.001	89,333		same	rs6599234	A	0.33	-0.66	1	-0.66	0.07	3.1E-20	39,808	signif	opp
rs6801957	9	SCN5A-SCN1	T	0.403	-0.63	rs6801957	t	0.419	-0.187	1	-0.187	0.052	6.5E-04	87,454	signif	same	rs6801957	C	0.59	-0.77	-1	0.77	0.07	1.1E-28	39,009	signif	opp
rs17784882	10	C3ORF75	A	0.396	-0.54	rs17784882	a	0.401	-0.056	1	-0.056	0.051	0.30	93,126		same	rs17784882	A	0.40	-0.09	1	-0.09	0.07	0.19	39,374		same
rs2363719	11	SLC4A4	A	0.108	0.97	rs2363719	a	0.118	-0.002	1	-0.002	0.087	0.98	83,264		opp	rs2363719	A	0.13	0.19	1	0.19	0.11	0.08	36,483		same
rs3857067	12	SMARCAD1	A	0.457	-0.51	rs3857067	a	0.446	-0.047	1	-0.047	0.050	0.38	92,460		same	rs3857067	A	0.46	0.03	1	0.03	0.07	0.66	39,927		opp
rs10040989	13	GFRA3	A	0.133	-0.85	rs10040989	a	0.151	-0.214	1	-0.214	0.074	0.006	86,577		same	rs10040989	A	0.15	0.06	1	0.06	0.10	0.51	40,258		opp
rs7765828	14	GMPR	G	0.402	0.55	rs7765828	g	0.431	0.026	1	0.026	0.053	0.65	90,125		same	rs7765828	C	0.59	-0.20	-1	0.20	0.07	0.006	36,766		same
rs457162	15	SLC35F1-PLI	T	0.059	-1.85	rs457162	t	0.065	0.411	1	0.411	0.107	2.6E-04	89,365	signif	opp	rs457162	A	0.94	0.55	-1	-0.55	0.14	1.5E-04	40,059	signif	same
rs12210733	15	SLC35F1-PLI	A	0.063	-2.05	rs12210733	a	0.062	0.339	1	0.339	0.119	0.007	77,307		opp	rs12210733	A	0.09	-0.66	1	-0.66	0.14	4.7E-06	36,273	signif	same
rs11153730	15	SLC35F1-PLI	T	0.502	-1.65	rs11153730	t	0.515	0.393	1	0.393	0.051	1.3E-13	91,235	signif	opp	rs11153730	C	0.49	0.59	-1	-0.59	0.07	1.3E-18	39,200	signif	same
rs3902035	15	SLC35F1-PLI	C	0.316	-0.85	rs3902035	c	0.307	0.197	1	0.197	0.056	8.3E-04	86,302		opp	rs3902035	C	0.32	-0.27	1	-0.27	0.07	1.8E-04	38,861	signif	same
rs9489510	15	SLC35F1-PLI	G	0.310	0.61	rs9489510	g	0.315	-0.078	1	-0.078	0.057	0.19	87,429		opp	rs9489510	A	0.68	-0.16	-1	0.16	0.08	0.04	35,924		same
rs9920	16	CAV1	C	0.093	0.79	rs9920	c	0.091	-0.111	1	-0.111	0.092	0.25	85,874		opp	rs9920	C	0.12	0.51	1	0.51	0.12	1.8E-05	37,692	signif	same
rs2072413	17	KCNH2	T	0.266	-1.68	rs2072413	t	0.266	0.099	1	0.099	0.071	0.18	58,822		opp	rs2072413	C	0.72	-0.03	-1	0.03	0.08	0.73	35,778		opp
rs3807375	17	KCNH2	T	0.360	1.22	rs3807375	t	0.388	-0.091	1	-0.091	0.055	0.12	87,428		opp	rs3807375	C	0.63	0.06	-1	-0.06	0.07	0.45	37,023		opp
rs16936870	18	NCOA2	A	0.097	0.99	rs16936870	a	0.129	-0.076	1	-0.076	0.079	0.36	93,118		opp	rs16936870	A	0.12	0.28	1	0.28	0.11	0.01	38,863		same
rs11779860	19	LAPTM4B	C	0.470	-0.61	rs11779860	c	0.464	0.021	1	0.021	0.051	0.70	92,680		opp	rs11779860	C	0.46	-0.10	1	-0.10	0.07	0.14	38,465		same
rs1961102	20	AZIN1	T	0.331	0.57	rs1961102	t	0.325	0.081	1	0.081	0.056	0.17	87,456		same	rs1961102	C	0.65	-0.05	-1	0.05	0.08	0.48	35,781		same
rs2485376	21	GBF1	A	0.391	-0.56	rs2485376	a	0.380	0.042	1	0.042	0.055	0.47	81,911		opp	rs2485376	A	0.37	-0.01	1	-0.01	0.07	0.83	39,118		same
rs2301696	22	KCNQ1	G	0.404	-1.14	rs2301696	g	0.413	0.121	1	0.121	0.137	0.40	36,372		opp	rs2301696	C	0.60	0.13	-1	-0.13	0.15	0.37	11,282		same
rs2074238	22	KCNQ1	T	0.053	-4.89	rs2074238	t	0.070	0.013	1	0.013	0.207	0.95	44,886		opp	rs2074238	C	0.94	-0.18	-1	0.18	0.34	0.60	13,464		opp
rs7122937	22	KCNQ1	T	0.188	1.93	rs7122937	t	0.223	-0.110	1	-0.110	0.065	0.11	85,389		opp	rs7122937	C	0.80	0.06	-1	-0.06	0.09	0.49	38,235		opp
rs174583	23	FEN1-FADS2	T	0.344	-0.57	rs174583	t	0.363	0.299	1	0.299	0.056	4.4E-07	80,086	signif	opp	rs174583	C	0.65	0.29	-1	-0.29	0.07	4.6E-05	39,074	signif	same
rs3026445	24	ATP2A2	C	0.356	0.62	rs3026445	c	0.364	-0.223	1	-0.223	0.053	5.9E-05	90,435	signif	opp	rs3026445	C	0.35	0.19	1	0.19	0.07	0.008	40,041		same
rs728926	25	KLF12	T	0.362	0.57	rs728926	t	0.371	0.072	1	0.072	0.054	0.21	90,839		same	rs728926	C	0.62	0.40	-1	-0.40	0.07	4.7E-08	36,508	signif	opp
rs2273905	26	ANKRD9	T	0.355	0.61	rs2273905	t	0.378	-0.043	1	-0.043	0.065	0.52	58,835		opp	rs2273905	C	0.64	0.00	-1	0.00	0.07	0.97	36,243		same
rs3105593	27	USP50-TRPM	T	0.446	0.66	rs3105593	t	0.451	-0.059	1	-0.059	0.050	0.27	93,126		opp	rs3105593	C	0.54	-0.15	-1	0.15	0.07	0.02	40,317		same
rs1296720	28	CREBBP	C	0.197	0.83	rs1296720	c	0.193	0.003	1	0.003	0.071	0.97	82,282		same	rs1296720	A	0.79	-0.26	-1	0.26	0.10	0.007	30,660		same
rs12930096	29	LITAF	T	0.142	-1.22	rs12930096	t	0.132	-0.060	1	-0.060	0.103	0.58	70,799		same	rs12930096	C	0.86	-0.11	-1	0.11	0.12	0.37	27,871		opp
rs735951	29	LITAF	A	0.455	-1.15	rs735951	a	0.441	0.018	1	0.018	0.055	0.76	84,981		opp	rs735951	A	0.45	0.05	1	0.05	0.07	0.55	32,998		opp
rs12444261	29	LITAF	T	0.262	-0.79	rs12444261	t	0.242	-0.048	1	-0.048	0.067	0.50	76,961		same	rs12444261	G	0.73	-0.06	-1	0.06	0.08	0.43	35,812		opp
rs246185	30	MKL2	C	0.335	0.72	rs246185	c	0.326	-0.031	1	-0.031	0.060	0.62	87,052		opp	rs246185	C	0.33	0.14	1	0.14	0.08	0.08	32,205		same
rs4784934	31	CNOT1	A	0.254	0.67	rs4784934	a	0.265	-0.033	1	-0.033	0.060	0.60	87,055		opp	rs4784934	A	0.27	0.04	1	0.04	0.08	0.65	36,849		same
rs246196	31	CNOT1	C	0.259	-1.73	rs246196	c	0.266	-0.043	1	-0.043	0.057	0.47	93,150		same	rs246196	C	0.26	-0.06	1	-0.06	0.08	0.41	40,292		same
rs1052536	32	LIG3	C	0.530	0.98	rs1052536	c	0.516	-0.027	1	-0.027	0.051	0.62	93,092		opp	rs1052536	C	0.53	0.11	1	0.11	0.07	0.11	39,808		same
rs9892651	33	PRKCA	C	0.429	-0.74	rs9892651	c	0.428	-0.024	1	-0.024	0.051	0.65	89,355		same	rs9892651	C	0.42	0.38	1	0.38	0.07	2.2E-08	39,987	signif	opp
rs236586	34	KCNJ2	G	0.466	0.64	rs236586	g	0.460	-0.040	1	-0.040	0.053	0.48	90,833		opp	rs236586	A	0.53	0.03	-1	-0.03	0.07	0.71	36,222		opp
rs10775360	34	KCNJ2	T	0.292	-0.76	rs10775360	t	0.280	-0.004	1	-0.004	0.057	0.95	87,453		same	rs10775360	C	0.70	0.04	-1	-0.04	0.07	0.63	38,892		same
rs1396515	34	KCNJ2	C	0.521	-0.98	rs1396515	c	0.494	-0.033	1	-0.033	0.050	0.54	93,126		same	rs1396515	C	0.52	-0.07	1	-0.07	0.07	0.30	40,207		same
rs17763769	34	KCNJ2	A	0.146	0.89	rs17763769	a	0.148	-0.025	1	-0.025	0.072	0.74	86,665		opp	rs17763769	A	0.16	0.15	1	0.15	0.09	0.10	40,110		same
rs1805128	35	KCNE1	T	0.010	7.42	rs1805128	t	0.041	-0.149	1	-0.149	0.219	0.52	62,132		opp	rs1805128	C	0.95	0.29	-1	-0.29	0.23	0.21	22,167		opp
									1=same coded allele											1=same coded allele							
									-1 = alternate coded allele		-0.41	r QT-HR		opp	38					-1 = alternate coded allele		-0.16	r QT-QRS			31	opp
											0.16	r2 QT-HR		same	30							0.03	r2 QT-QRS			37	same
											0.0006	p-value		p(binomial)	0.198							0.18	p-value			0.272	p(binomial

NHGRI Strongest SNP-Risk Allele	NHGRI Trait	NHGRI First Author	NHGRI PUBMED ID	NHGRI Chr_id	NHGRI Chr_pos	NHGRI p-Value	QT-IGC proxy	QT-IGC SNP	QT-IGC gene	QT-IGC r2_proxy_sentinel	QT-IGC r2_source
rs11708996-C	PR interval	Pfeufer A	20062060	3	38633923	6.00E-26	rs11708996	rs11708996	SCN5A-SCN10A	1	1KG
rs6795970-A	PR interval	Chambers JC	20062061	3	38766675	3.00E-15	rs6795970	rs6801957	SCN5A-SCN10A	0.933	1KG
rs6795970-A	PR interval	Holm H	20062063	3	38766675	1.00E-58	rs6795970	rs6801957	SCN5A-SCN10A	0.933	1KG
rs6800541-C	PR interval	Pfeufer A	20062060	3	38774832	2.00E-74	rs6800541	rs6801957	SCN5A-SCN10A	0.966	1KG
rs174535-T	n-3 fatty acid	Lemaitre RN	21829377	11	61551356	1.00E-151	rs174535	rs174583	FADS2	1	HM22
rs174535-T	n-3 fatty acid	Lemaitre RN	21829377	11	61551356	6.00E-58	rs174535	rs174583	FADS2	1	HM22
rs174536-A	n-3 fatty acid	Lemaitre RN	21829377	11	61551927	1.00E-63	rs174536	rs174583	FADS2	1	HM22
rs102275-T	n-3 fatty acid	Lemaitre RN	21829377	11	61557803	7.00E-64	rs102275	rs174583	FADS2	1	HM22
rs102275-T	n-3 fatty acid	Lemaitre RN	21829377	11	61557803	8.00E-153	rs102275	rs174583	FADS2	1	HM22
rs102275-C	Crohn's disease	Franke A	21102463	11	61557803	2.00E-11	rs102275	rs174583	FADS2	1	HM22
rs174538-A	n-3 fatty acid	Lemaitre RN	21829377	11	61560081	5.00E-58	rs174538	rs174583	FADS2	0.896	HM22
rs4246215-T	n-3 fatty acid	Lemaitre RN	21829377	11	61564299	6.00E-55	rs4246215	rs174583	FADS2	0.899	HM22
rs4246215-T	n-3 fatty acid	Lemaitre RN	21829377	11	61564299	1.00E-139	rs4246215	rs174583	FADS2	0.899	HM22
rs4246215-T	n-3 fatty acid	Lemaitre RN	21829377	11	61564299	9.00E-60	rs4246215	rs174583	FADS2	0.899	HM22
rs174547-T	n-3 fatty acid	Lemaitre RN	21829377	11	61570783	4.00E-154	rs174547	rs174583	FADS2	1	HM22
rs174547-T	n-3 fatty acid	Lemaitre RN	21829377	11	61570783	3.00E-64	rs174547	rs174583	FADS2	1	HM22
rs174547-C	phosphotidylcholine	Illig T	20037589	11	61570783	7.00E-179	rs174547	rs174583	FADS2	1	HM22
rs174547-C	HDL	Kathiresan S	19060906	11	61570783	2.00E-12	rs174547	rs174583	FADS2	1	HM22
rs174547-C	TG	Kathiresan S	19060906	11	61570783	2.00E-14	rs174547	rs174583	FADS2	1	HM22
rs174548-G	HDL	Waterworth DM	20864672	11	61571348	1.00E-12	rs174548	rs174583	FADS2	0.835	1KG
rs174548-G	TG	Waterworth DM	20864672	11	61571348	5.00E-14	rs174548	rs174583	FADS2	0.835	1KG
rs174550-T	n-3 fatty acid	Lemaitre RN	21829377	11	61571478	1.00E-57	rs174550	rs174583	FADS2	1	HM22
rs174550-T	fasting plasma glucos	Dupuis J	20081858	11	61571478	2.00E-15	rs174550	rs174583	FADS2	1	HM22
rs174550-T	HOMA-B	Dupuis J	20081858	11	61571478	5.00E-13	rs174550	rs174583	FADS2	1	HM22
rs1535-A	n-3 fatty acid	Lemaitre RN	21829377	11	61597972	3.00E-63	rs1535	rs174583	FADS2	1	1KG
rs1535-A	n-3 fatty acid	Lemaitre RN	21829377	11	61597972	3.00E-152	rs1535	rs174583	FADS2	1	1KG
rs174574-A	n-3 fatty acid	Lemaitre RN	21829377	11	61600342	4.00E-55	rs174574	rs174583	FADS2	1	1KG
rs174601-T	alkaline phosphatase	Chambers JC	22001757	11	61623140	3.00E-09	rs174601	rs174583	FADS2	0.896	1KG
rs1659127-A	age at menarche	Elks CE	21102462	16	14388305	4.00E-09	rs1659127	rs246185	MKL2	0.837	1KG

Supplementary Table 11: Association of QT SNPs in the NHGRI GWAS Catalog. Shown are the association results for all SNPs with r2>0.80 in HapMap CEU or 1000 Genomes CEU to one of the 68 independent QT interval associated SNPs that achieve genome-wide significance (P<5x10-8) for any biomedical trait (excluding heart rate or QRS, see Supplementary Table 10) as reported in the NHGRI GWAS catalog of associations. The first author, journal, Pubmed ID and PubMed link for the publication are included. The r2 between the QT-IGC SNP and the NHGRI SNP is shown based on HapMap (release 22) or 1000 Genomes (1KG). Locus labels are reported based on the nearest gene in QT-IGC.

eQTL	eQTL	eQTL	eQTL	eQTL	eQTL	eQTL	eQTL	eQTL	eQTL	eQTL	eQTL	eQTL	QT-IGC	QT-IGC	QT-IGC	QT-IGC GWAS only	eQTL	QT-IGC GWAS only	eQTL	QT-IGC GWAS only
Transcript	eSNP	Tissue	eQTL P	chr	pos	lowest P for transcript	eSNP r2>0.8 besteSNP	ExpProbe	BestEqtl.p	BestEqtlSNP	rSqrGWASeQTLtoBesteQTL	rSqrGWASeQTLtoGWASindexSNP	top QT SNP	LOCUS	NEAREST GENE	P QT topQT SNP	eSNP	P QT for eSNP	BestEqtlSNP	P QT for bestQTLSNP
TCEA3	rs2298632	PFC:All	3.E-27	1	23,583,062	lowest	yes	10023826907	2.58E-27	rs2298632	same	same	rs2298632	2	TCEA3	6.8E-15	rs2298632	6.8E-15	rs2298632	6.8E-15
TCEA3	rs2298632	CR:All	8.E-15	1	23,583,062	no	yes	10023826907	8.49E-15	rs2298632	same	same	rs2298632	2	TCEA3	6.8E-15	rs2298632	6.8E-15	rs2298632	6.8E-15
TCEA3	rs2298632	PFC:Alzh	2.E-14	1	23,583,062	no	yes	10023826907	1.96E-14	rs2298632	same	same	rs2298632	2	TCEA3	6.8E-15	rs2298632	6.8E-15	rs2298632	6.8E-15
TCEA3	rs2298632	VC:All	3.E-12	1	23,583,062	no	yes	10023826907	2.75E-12	rs2298632	same	same	rs2298632	2	TCEA3	6.8E-15	rs2298632	6.8E-15	rs2298632	6.8E-15
TCEA3	rs2298632	Blood(Fehrmann et	2.E-08	1	23,583,062	no	no	4050491	2.00E-31	rs2077066	0.087	same	rs2298632	2	TCEA3	6.8E-15	rs2298632	6.8E-15	rs2077066	9.7E-02
ATP1B1	rs10919071	CD4+lymph	2.E-25	1	167,366,107	lowest	yes		2.40E-25	rs10919071	same	1	rs10919070	4	ATP1B1	5.9E-31	rs10919071	8.1E-31	rs10919071	8.1E-31
ATP1B1	rs2000321	CD4+lymph	4.E-25	1	167,364,087	no	yes		2.40E-25	rs10919071	0.915	0.915	rs10919070	4	ATP1B1	5.9E-31	rs2000321	6.9E-26	rs10919071	8.1E-31
ATP1B1	rs10919062	CD4+lymph	7.E-25	1	167,355,571	no	yes		2.40E-25	rs10919071	1	1	rs10919070	4	ATP1B1	5.9E-31	rs10919062	4.4E-25	rs10919071	8.1E-31
ATP1B1	rs2000321	Blood(Fehrmann et	2.E-17	1	167,364,087	no	yes	Human_RefSeq-8_v2	2.10E-17	rs2000321	same	0.915	rs10919070	4	ATP1B1	5.9E-31	rs2000321	6.9E-26	rs2000321	6.9E-26
ATP1B1	rs2000321	PaxGeneCells	5.E-12	1	167,364,087	no	yes	ILMN_1736862	4.85E-12	rs2000321	same	0.915	rs10919070	4	ATP1B1	5.9E-31	rs2000321	6.9E-26	rs2000321	6.9E-26
ATP1B1	rs2143290	pons	4.E-10	1	167,355,303	no	yes	ILMN_1736862	3.91E-10	rs2143290	same	1	rs10919070	4	ATP1B1	5.9E-31	rs2143290	5.1E-30	rs2143290	5.1E-30
ATP1B1	rs10919074	pons	5.E-10	1	167,370,578	no	yes	ILMN_1736862	3.91E-10	rs2143290	0.915	0.915	rs10919070	4	ATP1B1	5.9E-31	rs10919074	1.1E-26	rs2143290	5.1E-30
ATP1B1	rs17345156	pons	5.E-10	1	167,389,241	no	yes	ILMN_1736862	3.91E-10	rs2143290	0.831	0.831	rs10919070	4	ATP1B1	5.9E-31	rs17345156	2.0E-29	rs2143290	5.1E-30
ATP1B1	rs10919070	pons	5.E-10	1	167,365,661	no	yes	ILMN_1736862	3.91E-10	rs2143290	1	same	rs10919070	4	ATP1B1	5.9E-31	rs10919070	5.9E-31	rs2143290	5.1E-30
ATP1B1	rs10919062	pons	5.E-10	1	167,355,571	no	yes	ILMN_1736862	3.91E-10	rs2143290	1	1	rs10919070	4	ATP1B1	5.9E-31	rs10919062	4.4E-25	rs2143290	5.1E-30
ATP1B1	rs10919071	pons	5.E-10	1	167,366,107	no	yes	ILMN_1736862	3.91E-10	rs2143290	1	1	rs10919070	4	ATP1B1	5.9E-31	rs10919071	8.1E-31	rs2143290	5.1E-30
ATP1B1	rs12035622	pons	6.E-10	1	167,368,964	no	yes	ILMN_1736862	3.91E-10	rs2143290	0.915	0.915	rs10919070	4	ATP1B1	5.9E-31	rs12035622	2.3E-26	rs2143290	5.1E-30
ATP1B1	rs2000321	pons	6.E-10	1	167,364,087	no	yes	ILMN_1736862	3.91E-10	rs2143290	0.915	0.915	rs10919070	4	ATP1B1	5.9E-31	rs2000321	6.9E-26	rs2143290	5.1E-30
ATP1B1	rs10919062	Stomach	4.E-08	1	167,355,571	no	yes	100307288	4.23E-08	rs10919062	same	1	rs10919070	4	ATP1B1	5.9E-31	rs10919062	4.4E-25	rs10919062	4.4E-25
NME7	rs2000321	Blood(Fehrmann et	2.E-17	1	167,364,087	lowest	yes	Human_RefSeq-8_v2	2.10E-17	rs2000321	same	0.915	rs10919070	4	ATP1B1	5.9E-31	rs2000321	6.9E-26	rs2000321	6.9E-26
NME7	rs2000321	LCL	1.E-09	1	167,364,087	no	no	227556_at	2.80E-19	rs12741540	0.062	0.915	rs10919070	4	ATP1B1	5.9E-31	rs2000321	6.9E-26	rs12741540	8.5E-02
Hs.431200	rs10931897	Lymph	5.E-12	2	200,870,765	lowest	no	Hs.431200-S	4.62E-12	rs295114	0.526	1	rs295140	8	LOC26010	9.1E-09	rs10931897	9.3E-09	rs295114	5.1E-06
Hs.431200	rs295140	Lymph	1.E-11	2	200,868,944	no	no	Hs.431200-S	4.62E-12	rs295114	0.526	same	rs295140	8	LOC26010	9.1E-09	rs295140	9.1E-09	rs295114	5.1E-06
Hs.431200	rs3769476	Lymph	1.E-11	2	200,889,673	no	no	Hs.431200-S	4.62E-12	rs295114	0.526	1	rs295140	8	LOC26010	9.1E-09	rs3769476	1.3E-08	rs295114	5.1E-06
KLHL18	rs6780013	LCL	4.E-14	3	47,427,122	lowest	no	1557165_s_at	1.70E-24	rs10490798	0.214	0.915	rs17784882	10	C3ORF75	4.7E-08	rs6780013	3.2E-06	rs10490798	2.2E-01
KLHL18	rs2276853	LCL	7.E-13	3	47,257,307	no	no	1557165_s_at	1.70E-24	rs10490798	0.175	0.966	rs17784882	10	C3ORF75	4.7E-08	rs2276853	7.4E-07	rs10490798	2.2E-01
KLHL18	rs11130126	LCL	1.E-12	3	47,281,898	no	no	1557165_s_at	1.70E-24	rs10490798	0.193	0.868	rs17784882	10	C3ORF75	4.7E-08	rs11130126	5.8E-06	rs10490798	2.2E-01
KLHL18	rs2062278	LCL	1.E-12	3	47,391,765	no	no	1557165_s_at	1.70E-24	rs10490798	0.2	1	rs17784882	10	C3ORF75	4.7E-08	rs2062278	1.6E-07	rs10490798	2.2E-01
KLHL18	rs807936	LCL	5.E-12	3	47,297,500	no	no	1557165_s_at	1.70E-24	rs10490798	0.193	0.966	rs17784882	10	C3ORF75	4.7E-08	rs807936	7.6E-07	rs10490798	2.2E-01
KLHL18	rs295441	LCL	5.E-12	3	47,308,299	no	no	1557165_s_at	1.70E-24	rs10490798	0.163	0.966	rs17784882	10	C3ORF75	4.7E-08	rs295441	8.0E-07	rs10490798	2.2E-01
KLHL18	rs295449	LCL	6.E-12	3	47,350,959	no	no	1557165_s_at	1.70E-24	rs10490798	0.193	0.966	rs17784882	10	C3ORF75	4.7E-08	rs295449	4.7E-08	rs10490798	2.2E-01
KLHL18	rs2159400	LCL	6.E-12	3	47,350,894	no	no	1557165_s_at	1.70E-24	rs10490798	0.193	0.966	rs17784882	10	C3ORF75	4.7E-08	rs2159400	3.8E-07	rs10490798	2.2E-01
KLHL18	rs4078466	LCL	8.E-12	3	47,101,547	no	no	1557165_s_at	1.70E-24	rs10490798	0.153	0.844	rs17784882	10	C3ORF75	4.7E-08	rs4078466	3.2E-05	rs10490798	2.2E-01
KLHL18	rs295428	LCL	9.E-12	3	47,334,266	no	no	1557165_s_at	1.70E-24	rs10490798	0.193	0.966	rs17784882	10	C3ORF75	4.7E-08	rs295428	5.3E-07	rs10490798	2.2E-01
KLHL18	rs11130127	LCL	1.E-11	3	47,373,797	no	no	1557165_s_at	1.70E-24	rs10490798	0.193	0.966	rs17784882	10	C3ORF75	4.7E-08	rs11130127	2.6E-07	rs10490798	2.2E-01
KLHL18	rs4858893	LCL	1.E-11	3	47,459,801	no	no	1557165_s_at	1.70E-24	rs10490798	0.185	1	rs17784882	10	C3ORF75	4.7E-08	rs4858893	6.0E-07	rs10490798	2.2E-01
KLHL18	rs922957	LCL	2.E-11	3	47,397,156	no	no	1557165_s_at	1.70E-24	rs10490798	0.2	1	rs17784882	10	C3ORF75	4.7E-08	rs922957	8.1E-08	rs10490798	2.2E-01
KLHL18	rs3816779	LCL	2.E-11	3	47,518,393	no	no	1557165_s_at	1.70E-24	rs10490798	0.2	1	rs17784882	10	C3ORF75	4.7E-08	rs3816779	5.9E-08	rs10490798	2.2E-01
KLHL18	rs2276854	LCL	3.E-11	3	47,251,972	no	no	1557165_s_at	1.70E-24	rs10490798	0.175	0.966	rs17784882	10	C3ORF75	4.7E-08	rs2276854	4.9E-07	rs10490798	2.2E-01
KLHL18	rs11130123	LCL	3.E-11	3	47,260,916	no	no	1557165_s_at	1.70E-24	rs10490798	0.169	0.966	rs17784882	10	C3ORF75	4.7E-08	rs11130123	1.0E-07	rs10490798	2.2E-01
KLHL18	rs1079276	LCL	4.E-11	3	47,020,743	no	no	1557165_s_at	1.70E-24	rs10490798	0.148	0.873	rs17784882	10	C3ORF75	4.7E-08	rs1079276	1.9E-05	rs10490798	2.2E-01
KLHL18	rs2305638	LCL	2.E-10	3	47,021,846	no	no	1557165_s_at	1.70E-24	rs10490798	0.153	0.844	rs17784882	10	C3ORF75	4.7E-08	rs2305638	6.4E-05	rs10490798	2.2E-01
KLHL18	rs4082155	LCL	2.E-10	3	47,100,389	no	no	1557165_s_at	1.70E-24	rs10490798	0.148	0.844	rs17784882	10	C3ORF75	4.7E-08	rs4082155	6.9E-06	rs10490798	2.2E-01
KLHL18	rs2385867	LCL	2.E-10	3	47,034,327	no	no	1557165_s_at	1.70E-24	rs10490798	0.153	0.844	rs17784882	10	C3ORF75	4.7E-08	rs2385867	3.1E-05	rs10490798	2.2E-01
KLHL18	rs11130124	LCL	3.E-10	3	47,267,187	no	no	1557165_s_at	1.70E-24	rs10490798	0.175	0.966	rs17784882	10	C3ORF75	4.7E-08	rs11130124	1.1E-07	rs10490798	2.2E-01
KLHL18	rs7610636	LCL	4.E-10	3	47,039,440	no	no	1557165_s_at	1.70E-24	rs10490798	0.153	0.844	rs17784882	10	C3ORF75	4.7E-08	rs7610636	3.2E-05	rs10490798	2.2E-01
PTPN23	rs2062278	Blood(Fehrmann et	3.E-31	3	47,391,765	lowest	yes	3140382	2.70E-31	rs2062278	same	1	rs17784882	10	C3ORF75	4.7E-08	rs2062278	1.6E-07	rs2062278	1.6E-07
PTPN23	rs2276853	Blood(Fehrmann et	1.E-26	3	47,257,307	no	yes	3140382	2.70E-31	rs2062278	0.873	0.966	rs17784882	10	C3ORF75	4.7E-08	rs2276853	7.4E-07	rs2062278	1.6E-07
PTPN23	rs6780013	Blood(Fehrmann et	2.E-26	3	47,427,122	no	yes	3140382	2.70E-31	rs2062278	0.866	0.915	rs17784882	10	C3ORF75	4.7E-08	rs6780013	3.2E-06	rs2062278	1.6E-07
SCAP	rs2062278	Blood(Fehrmann et	3.E-31	3	47,391,765	lowest	yes	3140382	2.70E-31	rs2062278	same	1	rs17784882	10	C3ORF75	4.7E-08	rs2062278	1.6E-07	rs2062278	1.6E-07
SCAP	rs6780013	Blood(Fehrmann et	2.E-26	3	47,427,122	no	yes	3140382	2.70E-31	rs2062278	0.866	0.915	rs17784882	10	C3ORF75	4.7E-08	rs6780013	3.2E-06	rs2062278	1.6E-07
SETD2	rs4078466	Blood(Fehrmann et	9.E-09	3	47,101,547	lowest	yes	1260615	9.10E-09	rs4078466	same	0.844	rs17784882	10	C3ORF75	4.7E-08	rs4078466	3.2E-05	rs4078466	3.2E-05
ATXN1	rs1042391	LCL	4.E-09	6	16,398,740	lowest	no	203231_s_at	2.10E-26	rs180017	0.411	1	rs7765828	14	GMPR	4.1E-10	rs1042391	6.5E-10	rs180017	8.7E-03
ATXN1	rs7765828	PrefrontalCortex	2.E-08	6	16,402,701	no	yes	203231_s_at	2.00E-08	rs7765828	same	same	rs7765828	14	GMPR	4.1E-10	rs7765828	4.1E-10	rs7765828	4.1E-10
C11orf10	rs174556	Blood(Fehrmann et	6.E-13	11	61,337,211	lowest	no	630445	5.10E-13	rs968567	0.539	0.866	rs174583	23	FADS2	1.3E-10	rs174556	3.6E-08	rs968567	9.1E-05
C11orf10	rs174537	Blood(Fehrmann et	3.E-11	11	61,309,256	no	no	630445	5.10E-13	rs968567	0.451	1	rs174583	23	FADS2	1.3E-10	rs174537	2.3E-10	rs968567	9.1E-05
C11orf10	rs174546	Blood(Fehrmann et	4.E-11	11	61,326,406	no	no	630445	5.10E-13	rs968567	0.467	1	rs174583	23	FADS2	1.3E-10	rs174546	1.5E-10	rs968567	9.1E-05

Supplementary Table 12 (4 pages): Association of QT SNPs with tissue expression. Shown in the table are eSNP associations showing eSNPs, tissues from which eSNP associations are drawn, the p-value for association of the eSNP with a transcript, the transcript to which the eSNP is associated, the lowest p-value for any eSNP ("best") at the locus and the identification of that eSNP, the "best" eSNPs correlation to the eSNP on that row, the distance of the best eSNP to the eSNP for that row, and the correlation of the eSNP on that row to the QT SNP. Abbreviations of eQTL tissues include: CR=cerebellum or PFC=dorsolateral prefrontal cortex or VC=visual cortex from individuals with Alzh=Alzheimer's disease, Hunt=Huntington's disease, Norm=normal (non-diseased), All=combined disease and normal samples; LCL=lymphoblastoid cell line; PBMC=peripheral blood mononuclear cell.

C11orf10	rs1535	Blood(Fehrmann et	4.E-11	11	61,354,548	no	no	630445	5.10E-13	rs968567	0.467	1	rs174583	23	FADS2	1.3E-10	rs1535	2.5E-10	rs968567	9.1E-05
C11orf10	rs102275	Blood(Fehrmann et	2.E-10	11	61,314,379	no	no	630445	5.10E-13	rs968567	0.451	1	rs174583	23	FADS2	1.3E-10	rs102275	1.7E-10	rs968567	9.1E-05
FADS1	rs102275	Liver(Greenawalt)	2.E-19	11	61,314,379	lowest	yes	10025909626	1.56E-19	rs102275	same	1	rs174583	23	FADS2	1.3E-10	rs102275	1.7E-10	rs102275	1.7E-10
FADS1	rs174576	CR:All	4.E-13	11	61,360,086	no	yes	10025909626	4.13E-13	rs174576	same	1	rs174583	23	FADS2	1.3E-10	rs174576	1.7E-10	rs174576	1.7E-10
FADS1	rs174549	Brain	4.E-11	11	61,327,958	no	yes	GI_14141179-S	3.70E-11	rs174549	same	0.866	rs174583	23	FADS2	1.3E-10	rs174549	4.2E-08	rs174549	4.2E-08
FADS1	rs174556	Blood(Fehrmann et	5.E-11	11	61,337,211	no	no	2360020	2.30E-13	rs968567	0.539	0.866	rs174583	23	FADS2	1.3E-10	rs174556	3.6E-08	rs968567	9.1E-05
FADS1	rs174548	Brain	2.E-10	11	61,327,924	no	yes	GI_14141179-S	3.70E-11	rs174549	0.964	0.835	rs174583	23	FADS2	1.3E-10	rs174548	6.6E-08	rs174549	4.2E-08
FADS1	rs174556	PFC:All	2.E-10	11	61,337,211	no	yes	10025909626	2.10E-10	rs174556	same	0.866	rs174583	23	FADS2	1.3E-10	rs174556	3.6E-08	rs174556	3.6E-08
FADS1	rs174537	VC:All	3.E-10	11	61,309,256	no	yes	10025909626	3.08E-10	rs174537	same	1	rs174583	23	FADS2	1.3E-10	rs174537	2.3E-10	rs174537	2.3E-10
FADS1	rs174546	omental	3.E-09	11	61,326,406	no	yes	10025909626	2.62E-09	rs174546	same	1	rs174583	23	FADS2	1.3E-10	rs174546	1.5E-10	rs174546	1.5E-10
FADS1	rs174578	LCL	9.E-09	11	61,362,075	no	yes	208962_s_at	8.90E-09	rs174578	same	1	rs174583	23	FADS2	1.3E-10	rs174578	1.7E-09	rs174578	1.7E-09
FADS1	rs174547	Brain	9.E-09	11	61,327,359	no	yes	GI_14141179-S	3.70E-11	rs174549	0.828	1	rs174583	23	FADS2	1.3E-10	rs174547	2.8E-10	rs174549	4.2E-08
FADS1	rs174537	Lymph	1.E-08	11	61,309,256	no	yes	GI_14141179-S	1.33E-08	rs174537	same	1	rs174583	23	FADS2	1.3E-10	rs174537	2.3E-10	rs174537	2.3E-10
FADS1	rs174546	Blood(Fehrmann et	2.E-08	11	61,326,406	no	no	2360020	2.30E-13	rs968567	0.467	1	rs174583	23	FADS2	1.3E-10	rs174546	1.5E-10	rs968567	9.1E-05
FADS1	rs102275	Lymph	2.E-08	11	61,314,379	no	yes	GI_14141179-S	1.33E-08	rs174537	1	1	rs174583	23	FADS2	1.3E-10	rs102275	1.7E-10	rs174537	2.3E-10
FADS1	rs174537	Blood(Fehrmann et	2.E-08	11	61,309,256	no	no	2360020	2.30E-13	rs968567	0.451	1	rs174583	23	FADS2	1.3E-10	rs174537	2.3E-10	rs968567	9.1E-05
FADS1	rs174574	LCL	3.E-08	11	61,356,918	no	yes	208962_s_at	8.90E-09	rs174578	1	1	rs174583	23	FADS2	1.3E-10	rs174574	1.4E-09	rs174578	1.7E-09
FADS1	rs1535	Blood(Fehrmann et	5.E-08	11	61,354,548	no	no	2360020	2.30E-13	rs968567	0.467	1	rs174583	23	FADS2	1.3E-10	rs1535	2.5E-10	rs968567	9.1E-05
FADS2	rs174556	Lymph	2.E-27	11	61,337,211	lowest	no	GI_14141180-S	2.99E-57	rs968567	0.539	0.866	rs174583	23	FADS2	1.3E-10	rs174556	3.6E-08	rs968567	9.1E-05
FADS2	rs174546	Lymph	1.E-26	11	61,326,406	no	no	GI_14141180-S	2.99E-57	rs968567	0.467	1	rs174583	23	FADS2	1.3E-10	rs174546	1.5E-10	rs968567	9.1E-05
FADS2	rs174576	Lymph	7.E-25	11	61,360,086	no	no	GI_14141180-S	2.99E-57	rs968567	0.467	1	rs174583	23	FADS2	1.3E-10	rs174576	1.7E-10	rs968567	9.1E-05
FADS2	rs1535	Lymph	8.E-25	11	61,354,548	no	no	GI_14141180-S	2.99E-57	rs968567	0.467	1	rs174583	23	FADS2	1.3E-10	rs1535	2.5E-10	rs968567	9.1E-05
FADS2	rs174548	Monocytes	2.E-23	11	61,327,924	no	no		9.00E-33	rs174589	0.384	0.835	rs174583	23	FADS2	1.3E-10	rs174548	6.6E-08	rs174589	7.5E-08
FADS2	rs174549	Monocytes	1.E-22	11	61,327,958	no	no		9.00E-33	rs174589	0.368	0.866	rs174583	23	FADS2	1.3E-10	rs174549	4.2E-08	rs174589	7.5E-08
FADS2	rs174583	Monocytes	3.E-20	11	61,366,326	no	no		9.00E-33	rs174589	0.49	same	rs174583	23	FADS2	1.3E-10	rs174583	1.3E-10	rs174589	7.5E-08
FADS2	rs174577	Monocytes	5.E-20	11	61,361,390	no	no		9.00E-33	rs174589	0.49	1	rs174583	23	FADS2	1.3E-10	rs174577	1.2E-10	rs174589	7.5E-08
FADS2	rs174547	Monocytes	2.E-19	11	61,327,359	no	no		9.00E-33	rs174589	0.443	1	rs174583	23	FADS2	1.3E-10	rs174547	2.8E-10	rs174589	7.5E-08
FADS2	rs174546	Blood	3.E-16	11	61,326,406	no	yes	HSG00271634	3.28E-16	rs174546	same	1	rs174583	23	FADS2	1.3E-10	rs174546	1.5E-10	rs174546	1.5E-10
FADS2	rs174556	Blood	3.E-16	11	61,337,211	no	yes	HSG00271634	3.28E-16	rs174546	0.866	0.866	rs174583	23	FADS2	1.3E-10	rs174556	3.6E-08	rs174546	1.5E-10
FADS2	rs174576	PBMC	3.E-12	11	61,360,086	no	no	3333247	6.58E-22	rs968567	0.467	1	rs174583	23	FADS2	1.3E-10	rs174576	1.7E-10	rs968567	9.1E-05
FADS2	rs1535	PBMC	5.E-12	11	61,354,548	no	no	3333247	6.58E-22	rs968567	0.467	1	rs174583	23	FADS2	1.3E-10	rs1535	2.5E-10	rs968567	9.1E-05
FADS2	rs174556	PBMC	6.E-12	11	61,337,211	no	no	3333247	6.58E-22	rs968567	0.539	0.866	rs174583	23	FADS2	1.3E-10	rs174556	3.6E-08	rs968567	9.1E-05
FADS2	rs174537	PBMC	5.E-11	11	61,309,256	no	no	3333247	6.58E-22	rs968567	0.451	1	rs174583	23	FADS2	1.3E-10	rs174537	2.3E-10	rs968567	9.1E-05
FADS2	rs174546	PBMC	5.E-11	11	61,326,406	no	no	3333247	6.58E-22	rs968567	0.467	1	rs174583	23	FADS2	1.3E-10	rs174546	1.5E-10	rs968567	9.1E-05
FADS2	rs102275	PBMC	1.E-10	11	61,314,379	no	no	3333247	6.58E-22	rs968567	0.451	1	rs174583	23	FADS2	1.3E-10	rs102275	1.7E-10	rs968567	9.1E-05
FADS2	rs174546	Liver(Greenawalt)	2.E-08	11	61,326,406	no	yes	10023819584	2.14E-08	rs174546	same	1	rs174583	23	FADS2	1.3E-10	rs174546	1.5E-10	rs174546	1.5E-10
FADS3	rs174548	SchadtLiver	2.E-09	11	61,327,924	lowest	yes		1.60E-09	rs174548	same	0.835	rs174583	23	FADS2	1.3E-10	rs174548	6.6E-08	rs174548	6.6E-08
ANAPC7	rs1502337	Monocytes	2.E-14	12	109,547,235	lowest	no		5.51E-16	rs2339511	0.249	0.851	rs3026445	24	ATP2A2	9.8E-09	rs1502337	1.6E-07	rs2339511	7.1E-01
ANAPC7	rs4766492	Monocytes	3.E-11	12	109,413,644	no	no		5.51E-16	rs2339511	0.231	0.925	rs3026445	24	ATP2A2	9.8E-09	rs4766492	2.0E-06	rs2339511	7.1E-01
ANAPC7	rs7296679	Monocytes	8.E-11	12	109,113,875	no	no		5.51E-16	rs2339511	0.231	1	rs3026445	24	ATP2A2	9.8E-09	rs7296679	4.8E-08	rs2339511	7.1E-01
ARPC3	rs4766500	Blood(Fehrmann et	3.E-13	12	109,478,174	lowest	yes	7380193	3.10E-13	rs4766500	same	0.851	rs3026445	24	ATP2A2	9.8E-09	rs4766500	3.8E-07	rs4766500	3.8E-07
ARPC3	rs10774599	Blood(Fehrmann et	4.E-12	12	109,181,831	no	yes	7380193	3.10E-13	rs4766500	0.886	0.962	rs3026445	24	ATP2A2	9.8E-09	rs10774599	2.9E-08	rs4766500	3.8E-07
C12orf24	rs4766500	Blood(Fehrmann et	4.E-10	12	109,478,174	lowest	yes	780240	4.40E-10	rs4766500	same	0.851	rs3026445	24	ATP2A2	9.8E-09	rs4766500	3.8E-07	rs4766500	3.8E-07
C12orf24	rs4766500	Blood(Fehrmann et	5.E-10	12	109,478,174	no	yes	Human_RefSeq-8_v2	4.40E-10	rs4766500	same	0.851	rs3026445	24	ATP2A2	9.8E-09	rs4766500	3.8E-07	rs4766500	3.8E-07
C12orf24	rs10774599	Blood(Fehrmann et	4.E-09	12	109,181,831	no	yes	Human_RefSeq-8_v2	4.40E-10	rs4766500	0.886	0.962	rs3026445	24	ATP2A2	9.8E-09	rs10774599	2.9E-08	rs4766500	3.8E-07
GPN3	rs4766500	Lymph	4.E-15	12	109,478,174	lowest	yes	GI_21361522-S	3.68E-15	rs4766500	same	0.851	rs3026445	24	ATP2A2	9.8E-09	rs4766500	3.8E-07	rs4766500	3.8E-07
VPS29	rs4766497	omental	3.E-89	12	109,434,759	lowest	yes	10025904743	2.82E-89	rs4766497	same	0.887	rs3026445	24	ATP2A2	9.8E-09	rs4766497	1.9E-06	rs4766497	1.9E-06
VPS29	rs4766497	SubCutAdipose(Gre	4.E-76	12	109,434,759	no	yes	10025904743	3.66E-76	rs4766497	same	0.887	rs3026445	24	ATP2A2	9.8E-09	rs4766497	1.9E-06	rs4766497	1.9E-06
VPS29	rs4766497	PFC:All	3.E-62	12	109,434,759	no	yes	10025904743	2.82E-62	rs4766497	same	0.887	rs3026445	24	ATP2A2	9.8E-09	rs4766497	1.9E-06	rs4766497	1.9E-06
VPS29	rs4766497	Liver(Greenawalt)	1.E-59	12	109,434,759	no	yes	10025904743	1.13E-59	rs4766497	same	0.887	rs3026445	24	ATP2A2	9.8E-09	rs4766497	1.9E-06	rs4766497	1.9E-06
VPS29	rs4766497	CR:All	1.E-53	12	109,434,759	no	yes	10025904743	1.19E-53	rs4766497	same	0.887	rs3026445	24	ATP2A2	9.8E-09	rs4766497	1.9E-06	rs4766497	1.9E-06
VPS29	rs4766497	VC:All	7.E-43	12	109,434,759	no	yes	10025904743	6.57E-43	rs4766497	same	0.887	rs3026445	24	ATP2A2	9.8E-09	rs4766497	1.9E-06	rs4766497	1.9E-06
VPS29	rs4766492	SchadtLiver	3.E-39	12	109,413,644	no	yes		2.73E-39	rs4766492	same	0.925	rs3026445	24	ATP2A2	9.8E-09	rs4766492	2.0E-06	rs4766492	2.0E-06
VPS29	rs4766497	PFC:Alzh	3.E-30	12	109,434,759	no	yes	10025904743	2.63E-30	rs4766497	same	0.887	rs3026445	24	ATP2A2	9.8E-09	rs4766497	1.9E-06	rs4766497	1.9E-06
VPS29	rs4766497	CR:Alzh	5.E-26	12	109,434,759	no	yes	10025904743	4.78E-26	rs4766497	same	0.887	rs3026445	24	ATP2A2	9.8E-09	rs4766497	1.9E-06	rs4766497	1.9E-06
VPS29	rs6606686	PFC:All	1.E-25	12	109,387,763	no	yes	10025904743	2.82E-62	rs4766497	0.813	0.855	rs3026445	24	ATP2A2	9.8E-09	rs6606686	1.8E-07	rs4766497	1.9E-06
VPS29	rs6606686	CR:All	7.E-24	12	109,387,763	no	yes	10025904743	1.19E-53	rs4766497	0.813	0.855	rs3026445	24	ATP2A2	9.8E-09	rs6606686	1.8E-07	rs4766497	1.9E-06
VPS29	rs6606686	VC:All	8.E-23	12	109,387,763	no	yes	10025904743	6.57E-43	rs4766497	0.813	0.855	rs3026445	24	ATP2A2	9.8E-09	rs6606686	1.8E-07	rs4766497	1.9E-06
VPS29	rs4766497	PFC:Hunt	5.E-18	12	109,434,759	no	yes	10025904743	5.28E-18	rs4766497	same	0.887	rs3026445	24	ATP2A2	9.8E-09	rs4766497	1.9E-06	rs4766497	1.9E-06
VPS29	rs4766497	CR:Hunt	2.E-16	12	109,434,759	no	yes	10025904743	2.18E-16	rs4766497	same	0.887	rs3026445	24	ATP2A2	9.8E-09	rs4766497	1.9E-06	rs4766497	1.9E-06
VPS29	rs4766497	VC:Alzh	3.E-16	12	109,434,759	no	yes	10025904743	2.60E-16	rs4766497	same	0.887	rs3026445	24	ATP2A2	9.8E-09	rs4766497	1.9E-06	rs4766497	1.9E-06
VPS29	rs4766497	PFC:Norm	2.E-15	12	109,434,759	no	yes	10025904743	2.23E-15	rs4766497	same	0.887	rs3026445	24	ATP2A2	9.8E-09	rs4766497	1.9E-06	rs4766497	1.9E-06
VPS29	rs6606686	CR:Alzh	9.E-14	12	109,387,763	no	yes	10025904743	4.78E-26	rs4766497	0.813	0.855	rs3026445	24	ATP2A2	9.8E-09	rs6606686	1.8E-07	rs4766497	1.9E-06

VPS29	rs4766497	VC:Hunt	2.E-13	12	109,434,759	no	yes	10025904743	1.61E-13	rs4766497	same	0.887	rs3026445	24	ATP2A2	9.8E-09	rs4766497	1.9E-06	rs4766497	1.9E-06
VPS29	rs6606686	PFC:Alzh	6.E-13	12	109,387,763	no	yes	10025904743	2.63E-30	rs4766497	0.813	0.855	rs3026445	24	ATP2A2	9.8E-09	rs6606686	1.8E-07	rs4766497	1.9E-06
VPS29	rs4766497	VC:Norm	2.E-12	12	109,434,759	no	yes	10025904743	2.17E-12	rs4766497	same	0.887	rs3026445	24	ATP2A2	9.8E-09	rs4766497	1.9E-06	rs4766497	1.9E-06
VPS29	rs4766497	CR:Norm	2.E-11	12	109,434,759	no	yes	10025904743	2.33E-11	rs4766497	same	0.887	rs3026445	24	ATP2A2	9.8E-09	rs4766497	1.9E-06	rs4766497	1.9E-06
VPS29	rs6606686	VC:Alzh	2.E-09	12	109,387,763	no	yes	10025904743	2.60E-16	rs4766497	0.813	0.855	rs3026445	24	ATP2A2	9.8E-09	rs6606686	1.8E-07	rs4766497	1.9E-06
ANKRD9	rs1190554	omental	4.E-49	14	101,988,439	lowest	yes	10023819395	4.14E-49	rs1190554	same	1	rs2273905	26	ANKRD9	4.8E-11	rs1190554	1.5E-09	rs1190554	1.5E-09
ANKRD9	rs1190554	SubCutAdipose(Gre	2.E-43	14	101,988,439	no	yes	10023819395	2.39E-43	rs1190554	same	1	rs2273905	26	ANKRD9	4.8E-11	rs1190554	1.5E-09	rs1190554	1.5E-09
ANKRD9	rs1190554	Liver(Greenawalt)	4.E-33	14	101,988,439	no	yes	10023819395	4.26E-33	rs1190554	same	1	rs2273905	26	ANKRD9	4.8E-11	rs1190554	1.5E-09	rs1190554	1.5E-09
ANKRD9	rs4906205	Blood(Fehrmann et	4.E-32	14	102,002,200	no	yes	7050370	4.30E-32	rs4906205	same	1	rs2273905	26	ANKRD9	4.8E-11	rs4906205	9.9E-10	rs4906205	9.9E-10
ANKRD9	rs12586673	Blood(Fehrmann et	4.E-24	14	101,897,396	no	yes	7050370	4.30E-32	rs4906205	0.853	0.853	rs2273905	26	ANKRD9	4.8E-11	rs12586673	1.2E-07	rs4906205	9.9E-10
ANKRD9	rs4906205	PFC:All	6.E-19	14	102,002,200	no	yes	10023819395	6.44E-19	rs4906205	same	1	rs2273905	26	ANKRD9	4.8E-11	rs4906205	9.9E-10	rs4906205	9.9E-10
ANKRD9	rs1190554	PFC:Norm	9.E-11	14	101,988,439	no	yes	10023819395	9.43E-11	rs1190554	same	1	rs2273905	26	ANKRD9	4.8E-11	rs1190554	1.5E-09	rs1190554	1.5E-09
ANKRD9	rs11704	PFC:All	1.E-09	14	101,878,408	no	yes	10023819395	6.44E-19	rs4906205	0.819	0.819	rs2273905	26	ANKRD9	4.8E-11	rs11704	4.1E-08	rs4906205	9.9E-10
ANKRD9	rs1190554	VC:All	3.E-09	14	101,988,439	no	yes	10023819395	3.09E-09	rs1190554	same	1	rs2273905	26	ANKRD9	4.8E-11	rs1190554	1.5E-09	rs1190554	1.5E-09
ANKRD9	rs1190554	PFC:Alzh	3.E-08	14	101,988,439	no	yes	10023819395	3.21E-08	rs1190554	same	1	rs2273905	26	ANKRD9	4.8E-11	rs1190554	1.5E-09	rs1190554	1.5E-09
ANKRD9	rs1190554	SchadtLiver	3.E-08	14	101,988,439	no	yes		3.26E-08	rs1190554	same	1	rs2273905	26	ANKRD9	4.8E-11	rs1190554	1.5E-09	rs1190554	1.5E-09
hCT2287249	rs3105591	omental	8.E-16	15	48,656,334	lowest	yes	10025928787	8.38E-16	rs3105591	same	1	rs3105593	27	TRPM7	2.7E-12	rs3105591	1.3E-07	rs3105591	1.3E-07
hCT2287249	rs2630	PFC:All	4.E-12	15	48,636,691	no	yes	10025928787	3.82E-12	rs2630	same	1	rs3105593	27	TRPM7	2.7E-12	rs2630	2.8E-07	rs2630	2.8E-07
hCT2287249	rs2630	CR:All	7.E-10	15	48,636,691	no	yes	10025928787	7.04E-10	rs2630	same	1	rs3105593	27	TRPM7	2.7E-12	rs2630	2.8E-07	rs2630	2.8E-07
hCT2287249	rs2630	SubCutAdipose(Gre	3.E-09	15	48,636,691	no	yes	10025928787	3.18E-09	rs2630	same	1	rs3105593	27	TRPM7	2.7E-12	rs2630	2.8E-07	rs2630	2.8E-07
TRPM7	rs3105593	Lymph	6.E-15	15	48,632,310	lowest	no	GI_29893551-S	1.97E-22	rs473357	0.563	same	rs3105593	27	TRPM7	2.7E-12	rs3105593	2.7E-12	rs473357	2.6E-07
TRPM7	rs3131576	Lymph	2.E-14	15	48,650,950	no	no	GI_29893551-S	1.97E-22	rs473357	0.604	1	rs3105593	27	TRPM7	2.7E-12	rs3131576	4.0E-12	rs473357	2.6E-07
TRPM7	rs3105591	Lymph	2.E-10	15	48,656,334	no	no	GI_29893551-S	1.97E-22	rs473357	0.563	1	rs3105593	27	TRPM7	2.7E-12	rs3105591	1.3E-07	rs473357	2.6E-07
TRPM7	rs2630	Lymph	4.E-10	15	48,636,691	no	no	GI_29893551-S	1.97E-22	rs473357	0.563	1	rs3105593	27	TRPM7	2.7E-12	rs2630	2.8E-07	rs473357	2.6E-07
LITAF	rs12444261	Monocytes	7.E-78	16	11,642,143	lowest	no		6.09E-109	rs12446552	0.395	same	rs12444261	29	LITAF	1.8E-12	rs12444261	1.8E-12	rs12446552	1.2E-09
LITAF	rs933572	Monocytes	1.E-70	16	11,664,592	no	no		6.09E-109	rs12446552	0.361	0.806	rs12444261	29	LITAF	1.8E-12	rs933572	3.0E-01	rs12446552	1.2E-09
LITAF	rs7191330	Monocytes	3.E-28	16	11,600,159	no	no		6.09E-109	rs12446552	0.09	0.95	rs735951	29	LITAF	3.8E-28	rs7191330	6.5E-01	rs12446552	1.2E-09
CNOT1	rs246258	Monocytes	7.E-23	16	57,136,775	lowest	yes		6.94E-23	rs246258	same	1	rs246196	31	CNOT1	2.6E-57	rs246258	3.0E-57	rs246258	3.0E-57
CNOT1	rs37060	Monocytes	1.E-22	16	57,123,805	no	yes		6.94E-23	rs246258	1	1	rs246196	31	CNOT1	2.6E-57	rs37060	2.3E-57	rs246258	3.0E-57
CNOT1	rs7199856	Monocytes	1.E-21	16	57,142,273	no	yes		6.94E-23	rs246258	1	1	rs246196	31	CNOT1	2.6E-57	rs7199856	3.7E-57	rs246258	3.0E-57
NDRG4	rs37060	CR:All	3.E-38	16	57,123,805	lowest	yes	10025905416	2.60E-38	rs37060	same	1	rs246196	31	CNOT1	2.6E-57	rs37060	2.3E-57	rs37060	2.3E-57
NDRG4	rs37060	PFC:All	5.E-38	16	57,123,805	no	yes	10025905416	5.48E-38	rs37060	same	1	rs246196	31	CNOT1	2.6E-57	rs37060	2.3E-57	rs37060	2.3E-57
NDRG4	rs1549607	VC:All	4.E-18	16	57,141,476	no	yes	10025905416	3.55E-18	rs1549607	same	1	rs246196	31	CNOT1	2.6E-57	rs1549607	2.6E-57	rs1549607	2.6E-57
NDRG4	rs37060	CR:Alzh	1.E-15	16	57,123,805	no	yes	10025905416	9.91E-16	rs37060	same	1	rs246196	31	CNOT1	2.6E-57	rs37060	2.3E-57	rs37060	2.3E-57
NDRG4	rs37060	PFC:Norm	2.E-14	16	57,123,805	no	yes	10025905416	1.69E-14	rs37060	same	1	rs246196	31	CNOT1	2.6E-57	rs37060	2.3E-57	rs37060	2.3E-57
NDRG4	rs37060	PFC:Alzh	2.E-14	16	57,123,805	no	yes	10025905416	2.10E-14	rs37060	same	1	rs246196	31	CNOT1	2.6E-57	rs37060	2.3E-57	rs37060	2.3E-57
NDRG4	rs1549607	CR:Hunt	3.E-14	16	57,141,476	no	yes	10025905416	3.30E-14	rs1549607	same	1	rs246196	31	CNOT1	2.6E-57	rs1549607	2.6E-57	rs1549607	2.6E-57
NDRG4	rs1549607	PFC:Hunt	2.E-12	16	57,141,476	no	yes	10025905416	1.59E-12	rs1549607	same	1	rs246196	31	CNOT1	2.6E-57	rs1549607	2.6E-57	rs1549607	2.6E-57
NDRG4	rs37060	CR:Norm	5.E-09	16	57,123,805	no	yes	10025905416	5.10E-09	rs37060	same	1	rs246196	31	CNOT1	2.6E-57	rs37060	2.3E-57	rs37060	2.3E-57
SETD6	rs37060	Blood(Fehrmann et	1.E-24	16	57,123,805	lowest	no	6520382	5.10E-28	rs11866002	0.183	1	rs246196	31	CNOT1	2.6E-57	rs37060	2.3E-57	rs11866002	4.6E-10
SETD6	rs1549607	Blood(Fehrmann et	1.E-24	16	57,141,476	lowest	no	6520382	5.10E-28	rs11866002	0.183	1	rs246196	31	CNOT1	2.6E-57	rs1549607	2.6E-57	rs11866002	4.6E-10
SETD6	rs4784051	Liver(UChicago)	<1e-16	16	57,195,029	no	yes	A_23_P129358	<1e-16	rs4784051	same	1	rs246196	31	CNOT1	2.6E-57	rs4784051	6.1E-56	rs4784051	6.1E-56
CCT6B	rs12948362	Monocytes	3.E-14	17	30,356,742	lowest	no		1.43E-17	rs2074519	0.765	1	rs1052536	32	LIG3	3.0E-24	rs12948362	7.6E-24	rs2074519	1.8E-17
CCT6B	rs1052536	Monocytes	3.E-14	17	30,355,688	no	no		1.43E-17	rs2074519	0.765	same	rs1052536	32	LIG3	3.0E-24	rs1052536	3.0E-24	rs2074519	1.8E-17
LIG3	rs12948362	Monocytes	4.E-66	17	30,356,742	lowest	yes		3.57E-66	rs12948362	same	1	rs1052536	32	LIG3	3.0E-24	rs12948362	7.6E-24	rs12948362	7.6E-24
LIG3	rs1052536	Monocytes	5.E-66	17	30,355,688	no	yes		3.57E-66	rs12948362	1	same	rs1052536	32	LIG3	3.0E-24	rs1052536	3.0E-24	rs12948362	7.6E-24
LIG3	rs1634800	PFC:All	7.E-40	17	30,407,143	no	yes	10025907314	7.43E-40	rs1634800	same	0.983	rs1052536	32	LIG3	3.0E-24	rs1634800	6.4E-24	rs1634800	6.4E-24
LIG3	rs1634800	omental	2.E-37	17	30,407,143	no	yes	10025907314	1.58E-37	rs1634800	same	0.983	rs1052536	32	LIG3	3.0E-24	rs1634800	6.4E-24	rs1634800	6.4E-24
LIG3	rs797989	Blood(Fehrmann et	7.E-30	17	30,438,871	no	yes	3460431	7.10E-30	rs797989	same	1	rs1052536	32	LIG3	3.0E-24	rs797989	4.5E-23	rs797989	4.5E-23
LIG3	rs1634800	SubCutAdipose(Gre	4.E-29	17	30,407,143	no	yes	10025907314	4.44E-29	rs1634800	same	0.983	rs1052536	32	LIG3	3.0E-24	rs1634800	6.4E-24	rs1634800	6.4E-24
LIG3	rs797989	VC:All	9.E-25	17	30,438,871	no	yes	10025907314	8.94E-25	rs797989	same	1	rs1052536	32	LIG3	3.0E-24	rs797989	4.5E-23	rs797989	4.5E-23
LIG3	rs3135967	PFC:All	1.E-22	17	30,337,842	no	yes	10025907314	7.43E-40	rs1634800	0.934	0.967	rs1052536	32	LIG3	3.0E-24	rs3135967	3.7E-23	rs1634800	6.4E-24
LIG3	rs797989	CR:All	2.E-20	17	30,438,871	no	yes	10025907314	2.40E-20	rs797989	same	1	rs1052536	32	LIG3	3.0E-24	rs797989	4.5E-23	rs797989	4.5E-23
LIG3	rs1634800	PFC:Alzh	1.E-18	17	30,407,143	no	yes	10025907314	1.27E-18	rs1634800	same	0.983	rs1052536	32	LIG3	3.0E-24	rs1634800	6.4E-24	rs1634800	6.4E-24
LIG3	rs797989	Liver(Greenawalt)	2.E-14	17	30,438,871	no	yes	10025907314	2.18E-14	rs797989	same	1	rs1052536	32	LIG3	3.0E-24	rs797989	4.5E-23	rs797989	4.5E-23
LIG3	rs1634800	PFC:Norm	2.E-13	17	30,407,143	no	yes	10025907314	1.61E-13	rs1634800	same	0.983	rs1052536	32	LIG3	3.0E-24	rs1634800	6.4E-24	rs1634800	6.4E-24
LIG3	rs3135967	VC:All	1.E-12	17	30,337,842	no	yes	10025907314	8.94E-25	rs797989	0.936	0.967	rs1052536	32	LIG3	3.0E-24	rs3135967	3.7E-23	rs797989	4.5E-23
LIG3	rs3135967	PFC:Alzh	2.E-12	17	30,337,842	no	yes	10025907314	1.27E-18	rs1634800	0.934	0.967	rs1052536	32	LIG3	3.0E-24	rs3135967	3.7E-23	rs1634800	6.4E-24
LIG3	rs797989	FrontalCtx	2.E-11	17	30,438,871	no	yes	ILMN_1660582	2.28E-11	rs797989	same	1	rs1052536	32	LIG3	3.0E-24	rs797989	4.5E-23	rs797989	4.5E-23
LIG3	rs2074518	FrontalCtx	2.E-11	17	30,348,495	no	yes	ILMN_1660582	2.28E-11	rs797989	0.936	1	rs1052536	32	LIG3	3.0E-24	rs2074518	2.3E-23	rs797989	4.5E-23
LIG3	rs1052536	FrontalCtx	2.E-11	17	30,355,688	no	yes	ILMN_1660582	2.28E-11	rs797989	0.967	same	rs1052536	32	LIG3	3.0E-24	rs1052536	3.0E-24	rs797989	4.5E-23
LIG3	rs1003918	FrontalCtx	2.E-11	17	30,356,290	no	yes	ILMN_1660582	2.28E-11	rs797989	0.967	1	rs1052536	32	LIG3	3.0E-24	rs1003918	9.4E-24	rs797989	4.5E-23
LIG3	rs12948362	FrontalCtx	2.E-11	17	30,356,742	no	yes	ILMN_1660582	2.28E-11	rs797989	0.967	1	rs1052536	32	LIG3	3.0E-24	rs12948362	7.6E-24	rs797989	4.5E-23

LIG3	rs2339122	FrontalCtx	2.E-11	17	30,406,914	no	yes	ILMN_1660582	2.28E-11	rs797989	0.87	1	rs1052536	32	LIG3	3.0E-24	rs2339122	9.4E-24	rs797989	4.5E-23
LIG3	rs1634800	FrontalCtx	2.E-11	17	30,407,143	no	yes	ILMN_1660582	2.28E-11	rs797989	0.936	0.983	rs1052536	32	LIG3	3.0E-24	rs1634800	6.4E-24	rs797989	4.5E-23
LIG3	rs3135967	FrontalCtx	8.E-11	17	30,337,842	no	yes	ILMN_1660582	2.28E-11	rs797989	0.936	0.967	rs1052536	32	LIG3	3.0E-24	rs3135967	3.7E-23	rs797989	4.5E-23
LIG3	rs2074518	Cerebellum2	1.E-10	17	30,348,495	no	yes	ILMN_1660582	1.40E-10	rs1003918	0.967	1	rs1052536	32	LIG3	3.0E-24	rs2074518	2.3E-23	rs1003918	9.4E-24
LIG3	rs1052536	Cerebellum2	1.E-10	17	30,355,688	no	yes	ILMN_1660582	1.40E-10	rs1003918	1	same	rs1052536	32	LIG3	3.0E-24	rs1052536	3.0E-24	rs1003918	9.4E-24
LIG3	rs1003918	Cerebellum2	1.E-10	17	30,356,290	no	yes	ILMN_1660582	1.40E-10	rs1003918	same	1	rs1052536	32	LIG3	3.0E-24	rs1003918	9.4E-24	rs1003918	9.4E-24
LIG3	rs12948362	Cerebellum2	1.E-10	17	30,356,742	no	yes	ILMN_1660582	1.40E-10	rs1003918	1	1	rs1052536	32	LIG3	3.0E-24	rs12948362	7.6E-24	rs1003918	9.4E-24
LIG3	rs2339122	Cerebellum2	1.E-10	17	30,406,914	no	yes	ILMN_1660582	1.40E-10	rs1003918	0.905	1	rs1052536	32	LIG3	3.0E-24	rs2339122	9.4E-24	rs1003918	9.4E-24
LIG3	rs1634800	Cerebellum2	1.E-10	17	30,407,143	no	yes	ILMN_1660582	1.40E-10	rs1003918	0.967	0.983	rs1052536	32	LIG3	3.0E-24	rs1634800	6.4E-24	rs1003918	9.4E-24
LIG3	rs3135967	CR:All	2.E-10	17	30,337,842	no	yes	10025907314	2.40E-20	rs797989	0.936	0.967	rs1052536	32	LIG3	3.0E-24	rs3135967	3.7E-23	rs797989	4.5E-23
LIG3	rs1634800	VC:Alzh	2.E-10	17	30,407,143	no	yes	10025907314	1.61E-10	rs1634800	same	0.983	rs1052536	32	LIG3	3.0E-24	rs1634800	6.4E-24	rs1634800	6.4E-24
LIG3	rs10853174	FrontalCtx	2.E-10	17	30,376,030	no	yes	ILMN_1660582	2.28E-11	rs797989	0.967	1	rs1052536	32	LIG3	3.0E-24	rs10853174	1.1E-21	rs797989	4.5E-23
LIG3	rs797989	Cerebellum2	3.E-10	17	30,438,871	no	yes	ILMN_1660582	1.40E-10	rs1003918	0.967	1	rs1052536	32	LIG3	3.0E-24	rs797989	4.5E-23	rs1003918	9.4E-24
LIG3	rs3135967	Cerebellum2	1.E-09	17	30,337,842	no	yes	ILMN_1660582	1.40E-10	rs1003918	0.967	0.967	rs1052536	32	LIG3	3.0E-24	rs3135967	3.7E-23	rs1003918	9.4E-24
LIG3	rs10853174	Cerebellum2	2.E-09	17	30,376,030	no	yes	ILMN_1660582	1.40E-10	rs1003918	1	1	rs1052536	32	LIG3	3.0E-24	rs10853174	1.1E-21	rs1003918	9.4E-24
LIG3	rs1634800	VC:Norm	2.E-09	17	30,407,143	no	yes	10025907314	2.27E-09	rs1634800	same	0.983	rs1052536	32	LIG3	3.0E-24	rs1634800	6.4E-24	rs1634800	6.4E-24
LIG3	rs1634800	CR:Norm	2.E-09	17	30,407,143	no	yes	10025907314	2.47E-09	rs1634800	same	0.983	rs1052536	32	LIG3	3.0E-24	rs1634800	6.4E-24	rs1634800	6.4E-24
LIG3	rs2074518	TemporalCtx	9.E-09	17	30,348,495	no	yes	ILMN_1660582	8.85E-09	rs1003918	0.967	1	rs1052536	32	LIG3	3.0E-24	rs2074518	2.3E-23	rs1003918	9.4E-24
LIG3	rs1052536	TemporalCtx	9.E-09	17	30,355,688	no	yes	ILMN_1660582	8.85E-09	rs1003918	1	same	rs1052536	32	LIG3	3.0E-24	rs1052536	3.0E-24	rs1003918	9.4E-24
LIG3	rs1003918	TemporalCtx	9.E-09	17	30,356,290	no	yes	ILMN_1660582	8.85E-09	rs1003918	same	1	rs1052536	32	LIG3	3.0E-24	rs1003918	9.4E-24	rs1003918	9.4E-24
LIG3	rs12948362	TemporalCtx	9.E-09	17	30,356,742	no	yes	ILMN_1660582	8.85E-09	rs1003918	1	1	rs1052536	32	LIG3	3.0E-24	rs12948362	7.6E-24	rs1003918	9.4E-24
LIG3	rs2339122	TemporalCtx	9.E-09	17	30,406,914	no	yes	ILMN_1660582	8.85E-09	rs1003918	0.905	1	rs1052536	32	LIG3	3.0E-24	rs2339122	9.4E-24	rs1003918	9.4E-24
LIG3	rs1634800	TemporalCtx	9.E-09	17	30,407,143	no	yes	ILMN_1660582	8.85E-09	rs1003918	0.967	0.983	rs1052536	32	LIG3	3.0E-24	rs1634800	6.4E-24	rs1003918	9.4E-24
LIG3	rs797989	CR:Alzh	2.E-08	17	30,438,871	no	yes	10025907314	1.62E-08	rs797989	same	1	rs1052536	32	LIG3	3.0E-24	rs797989	4.5E-23	rs797989	4.5E-23
LIG3	rs797989	CR:All	2.E-08	17	30,438,871	no	yes	10023820814	2.40E-20	rs797989	same	1	rs1052536	32	LIG3	3.0E-24	rs797989	4.5E-23	rs797989	4.5E-23
LIG3	rs797989	TemporalCtx	2.E-08	17	30,438,871	no	yes	ILMN_1660582	8.85E-09	rs1003918	0.967	1	rs1052536	32	LIG3	3.0E-24	rs797989	4.5E-23	rs1003918	9.4E-24
LIG3	rs10853174	TemporalCtx	2.E-08	17	30,376,030	no	yes	ILMN_1660582	8.85E-09	rs1003918	1	1	rs1052536	32	LIG3	3.0E-24	rs10853174	1.1E-21	rs1003918	9.4E-24
LIG3	rs797989	PFC:Hunt	3.E-08	17	30,438,871	no	yes	10025907314	2.50E-08	rs797989	same	1	rs1052536	32	LIG3	3.0E-24	rs797989	4.5E-23	rs797989	4.5E-23

Supplementary Table 13 (16 pages): QT SNP relationship to left ventricular enhancers. Shown in the table are the set of 68 independent QT interval-associated SNPs (lead SNPs), as well as all SNPs in LD (r2>0.8 in 1000Genomes CEU), including their QT association p-value and the presence (1) or absence (0) of an overlying enhancer in left ventricular tissue, or secondarily, 123 non-cardiac tissues or fetal heart, right atrium or right ventricle.

LD SNP (r2 > 0.8)	lead SNP	Index/OtherSignal	Locus #	Nearest gene	QT P value	r2 (1000 Genomes, CEU Phase 1)	Left Ventricle	# Non-Cardiac Tissues Overlapped (123 non-cardiac tissues)	Fetal Heart	Right Atrium	Right Ventricle
rs11583631	rs2273042	OTHERSIGNAL	1	RNF207	-	0.98	0	3	0	0	0
rs11584419	rs2273042	OTHERSIGNAL	1	RNF207	-	0.99	0	3	0	0	0
rs11586626	rs2273042	OTHERSIGNAL	1	RNF207	-	0.86	0	7	0	0	0
rs12128870	rs2273042	OTHERSIGNAL	1	RNF207	-	0.85	0	13	0	0	0
rs200114858	rs2273042	OTHERSIGNAL	1	RNF207	-	0.83	0	0	0	0	0
rs2273042	rs2273042	OTHERSIGNAL	1	RNF207	6.7986E-09	1.00	0	0	0	0	0
rs2273043	rs2273042	OTHERSIGNAL	1	RNF207	0.90368	0.99	0	0	0	0	0
rs2281304	rs2273042	OTHERSIGNAL	1	RNF207	0.88588	0.99	0	2	0	0	0
rs2294935	rs2273042	OTHERSIGNAL	1	RNF207	0.95725	0.96	0	6	0	0	0
rs3789530	rs2273042	OTHERSIGNAL	1	RNF207	3.2947E-08	0.95	0	0	0	0	0
rs749435	rs2273042	OTHERSIGNAL	1	RNF207	0.88416	0.93	0	0	0	0	0
rs846111	rs846111	INDEX	1	RNF207	7.39E-40	1.00	0	7	0	0	0
rs2298632	rs2298632	INDEX	2	TCEA3	1.3801E-14	1.00	0	23	0	1	0
rs10753778	rs3934467	OTHERSIGNAL	3	NOS1AP	-	0.96	0	5	0	0	0
rs10800352	rs3934467	OTHERSIGNAL	3	NOS1AP	2.54E-128	0.98	0	2	0	0	0
rs10918438	rs6669543	OTHERSIGNAL	3	NOS1AP	-	0.82	0	1	0	0	0
rs10918571	rs12143842	INDEX	3	NOS1AP	-	0.86	0	0	0	0	0
rs10918856	rs3934467	OTHERSIGNAL	3	NOS1AP	0.000064368	0.99	1	20	0	1	1
rs10918859	rs3934467	OTHERSIGNAL	3	NOS1AP	9.96E-111	0.82	0	12	0	0	0
rs10918883	rs4657172	OTHERSIGNAL	3	NOS1AP	-	1.00	0	8	0	0	0
rs10918963	rs3934467	OTHERSIGNAL	3	NOS1AP	1.73E-114	0.89	0	2	0	0	0
rs10918974	rs3934467	OTHERSIGNAL	3	NOS1AP	2.47E-113	0.89	0	11	1	0	0
rs10918998	rs3934467	OTHERSIGNAL	3	NOS1AP	-	0.87	0	14	0	0	0
rs111479472	rs4657172	OTHERSIGNAL	3	NOS1AP	-	0.95	0	10	0	0	0
rs111718793	rs4657172	OTHERSIGNAL	3	NOS1AP	-	1.00	0	0	0	0	0
rs113577901	rs4657172	OTHERSIGNAL	3	NOS1AP	-	0.99	0	0	0	0	0
rs11589974	rs164133	OTHERSIGNAL	3	NOS1AP	-	0.98	0	0	0	0	0
rs12025136	rs6669543	OTHERSIGNAL	3	NOS1AP	1.44E-38	0.91	1	6	1	1	1
rs12027785	rs3934467	OTHERSIGNAL	3	NOS1AP	5.37E-129	0.99	0	11	0	0	0
rs12036340	rs12143842	INDEX	3	NOS1AP	4.01E-196	0.86	0	0	0	0	0
rs12042862	rs12143842	INDEX	3	NOS1AP	-	0.96	0	0	0	0	0
rs12064639	rs4657172	OTHERSIGNAL	3	NOS1AP	2.4258E-08	1.00	1	41	0	0	0
rs12116744	rs3934467	OTHERSIGNAL	3	NOS1AP	1.82E-128	0.99	1	13	0	1	1
rs12123267	rs3934467	OTHERSIGNAL	3	NOS1AP	1.37E-125	0.96	0	8	0	0	0
rs12124745	rs3934467	OTHERSIGNAL	3	NOS1AP	0.000040916	0.97	0	12	0	0	0
rs12143842	rs12143842	INDEX	3	NOS1AP	1.32E-213	1.00	0	2	0	0	0
rs12567315	rs3934467	OTHERSIGNAL	3	NOS1AP	3.26E-129	0.99	0	24	0	1	0
rs146475167	rs12143842	INDEX	3	NOS1AP	-	0.95	0	0	0	0	0
rs148349069	rs3934467	OTHERSIGNAL	3	NOS1AP	-	0.90	0	2	0	0	0
rs148900636	rs3934467	OTHERSIGNAL	3	NOS1AP	-	0.92	0	13	0	0	0
rs164131	rs164133	OTHERSIGNAL	3	NOS1AP	-	0.87	0	1	0	0	0
rs164133	rs164133	OTHERSIGNAL	3	NOS1AP	2.9914E-11	1.00	0	1	0	0	0
rs164134	rs164133	OTHERSIGNAL	3	NOS1AP	0.0050804	1.00	0	1	0	0	0
rs164136	rs164133	OTHERSIGNAL	3	NOS1AP	0.020599	0.89	0	1	0	0	0
rs164137	rs164133	OTHERSIGNAL	3	NOS1AP	-	1.00	0	1	0	0	0
rs164406	rs164133	OTHERSIGNAL	3	NOS1AP	-	0.99	0	1	0	0	0
rs164410	rs164133	OTHERSIGNAL	3	NOS1AP	5.3643E-10	0.87	0	2	0	0	0
rs164411	rs164133	OTHERSIGNAL	3	NOS1AP	0.01918	0.87	0	2	0	0	0
rs16847548	rs12143842	INDEX	3	NOS1AP	1.12E-168	0.84	0	15	0	1	0
rs16857031	rs16857031	OTHERSIGNAL	3	NOS1AP	6.45E-61	1.00	0	18	0	0	0
rs17457880	rs17457880	OTHERSIGNAL	3	NOS1AP	2.8067E-10	0.96	1	23	0	0	1
rs17460657	rs17460657	OTHERSIGNAL	3	NOS1AP	2.72E-16	1.00	0	6	0	0	0
rs183024	rs164133	OTHERSIGNAL	3	NOS1AP	-	0.87	0	10	0	0	0
rs2250489	rs164133	OTHERSIGNAL	3	NOS1AP	0.0050804	0.98	0	1	0	0	0
rs2265613	rs164133	OTHERSIGNAL	3	NOS1AP	-	0.87	0	2	0	0	0
rs238773	rs164133	OTHERSIGNAL	3	NOS1AP	0.025484	0.89	0	1	0	0	0
rs2632549	rs164133	OTHERSIGNAL	3	NOS1AP	1.2462E-10	0.81	0	1	0	0	0
rs3122549	rs164133	OTHERSIGNAL	3	NOS1AP	-	0.85	0	0	0	0	0
rs347272	rs347272	OTHERSIGNAL	3	NOS1AP	1.29E-37	1.00	0	4	0	0	0
rs347273	rs347272	OTHERSIGNAL	3	NOS1AP	1.87E-38	1.00	0	9	0	0	0
rs348628	rs164133	OTHERSIGNAL	3	NOS1AP	0.0050804	1.00	0	1	0	0	0
rs348629	rs164133	OTHERSIGNAL	3	NOS1AP	-	1.00	0	1	0	0	0
rs351452	rs164133	OTHERSIGNAL	3	NOS1AP	0.0050804	0.99	0	10	0	0	0
rs351453	rs164133	OTHERSIGNAL	3	NOS1AP	4.2471E-11	0.99	0	14	0	0	0
rs351454	rs164133	OTHERSIGNAL	3	NOS1AP	0.0050804	0.99	0	7	0	0	0
rs351455	rs164133	OTHERSIGNAL	3	NOS1AP	-	0.87	0	8	0	0	0
rs351456	rs164133	OTHERSIGNAL	3	NOS1AP	3.8437E-11	0.99	0	6	0	0	0
rs351457	rs164133	OTHERSIGNAL	3	NOS1AP	-	0.87	0	6	0	0	0
rs391411	rs164133	OTHERSIGNAL	3	NOS1AP	-	0.93	0	1	0	0	0
rs3934467	rs3934467	OTHERSIGNAL	3	NOS1AP	2.76E-129	1.00	1	55	1	1	1
rs4098275	rs4657172	OTHERSIGNAL	3	NOS1AP	1.2197E-07	1.00	0	16	0	0	0
rs4098276	rs4657172	OTHERSIGNAL	3	NOS1AP	0.31777	1.00	0	16	0	0	0
rs4098277	rs4657172	OTHERSIGNAL	3	NOS1AP	1.087E-07	1.00	0	12	0	0	0
rs415883	rs164133	OTHERSIGNAL	3	NOS1AP	0.0050804	0.97	0	1	0	0	0
rs4233386	rs4657172	OTHERSIGNAL	3	NOS1AP	0.60027	1.00	1	16	0	0	1
rs4306106	rs3934467	OTHERSIGNAL	3	NOS1AP	5.97E-127	0.99	0	0	0	0	0
rs4391647	rs3934467	OTHERSIGNAL	3	NOS1AP	1.79E-126	1.00	0	5	0	0	0
rs4480335	rs3934467	OTHERSIGNAL	3	NOS1AP	9.88E-128	0.99	0	4	0	0	0
rs4488007	rs4657172	OTHERSIGNAL	3	NOS1AP	1.6622E-07	1.00	0	1	0	0	0
rs4656345	rs4656345	OTHERSIGNAL	3	NOS1AP	1.03E-19	1.00	0	15	0	1	0
rs4656359	rs4657172	OTHERSIGNAL	3	NOS1AP	-	1.00	1	16	0	0	1
rs4657168	rs4657172	OTHERSIGNAL	3	NOS1AP	0.000026062	1.00	0	14	0	0	0
rs4657170	rs4657172	OTHERSIGNAL	3	NOS1AP	0.056769	1.00	0	11	0	0	0
rs4657172	rs4657172	OTHERSIGNAL	3	NOS1AP	1.2664E-08	1.00	0	4	0	0	0
rs4657173	rs3934467	OTHERSIGNAL	3	NOS1AP	5.2106E-09	1.00	1	41	0	0	0

rs4657175	rs3934467	OTHERSIGNAL	3	NOS1AP	8.68E-125	0.97	0	4	0	0	0
rs55749148	rs4657172	OTHERSIGNAL	3	NOS1AP	-	1.00	0	16	0	0	0
rs55937722	rs4657172	OTHERSIGNAL	3	NOS1AP	-	1.00	0	0	0	0	0
rs56074757	rs4657172	OTHERSIGNAL	3	NOS1AP	-	1.00	0	0	0	0	0
rs57765910	rs4657172	OTHERSIGNAL	3	NOS1AP	-	1.00	0	10	0	0	0
rs60129000	rs12143842	INDEX	3	NOS1AP	-	0.96	0	1	0	0	0
rs60709352	rs347272	OTHERSIGNAL	3	NOS1AP	-	0.80	0	18	0	0	0
rs6664632	rs4657172	OTHERSIGNAL	3	NOS1AP	4.5356E-08	1.00	0	8	0	0	0
rs6664702	rs3934467	OTHERSIGNAL	3	NOS1AP	9.11E-109	0.83	0	15	1	0	0
rs6667431	rs3934467	OTHERSIGNAL	3	NOS1AP	6.53E-123	0.98	1	32	1	0	1
rs6668457	rs4657172	OTHERSIGNAL	3	NOS1AP	7.711E-08	1.00	0	13	0	0	0
rs6669543	rs6669543	OTHERSIGNAL	3	NOS1AP	1.65E-39	1.00	1	12	1	1	1
rs6674320	rs6669543	OTHERSIGNAL	3	NOS1AP	4.98E-37	0.84	1	8	0	1	1
rs6676638	rs4657172	OTHERSIGNAL	3	NOS1AP	4.9262E-08	1.00	0	13	0	0	0
rs6676737	rs4657172	OTHERSIGNAL	3	NOS1AP	8.1945E-08	1.00	0	13	0	0	0
rs6678925	rs4657172	OTHERSIGNAL	3	NOS1AP	2.7067E-08	1.00	1	11	0	0	0
rs6692381	rs3934467	OTHERSIGNAL	3	NOS1AP	8.85E-127	0.99	1	32	1	0	1
rs6696759	rs3934467	OTHERSIGNAL	3	NOS1AP	-	0.99	0	4	0	0	0
rs73017353	rs4657172	OTHERSIGNAL	3	NOS1AP	-	1.00	0	0	0	0	0
rs73017359	rs4657172	OTHERSIGNAL	3	NOS1AP	-	1.00	1	13	0	1	1
rs7415748	rs4657172	OTHERSIGNAL	3	NOS1AP	1.9995E-07	1.00	0	5	0	0	0
rs7522678	rs3934467	OTHERSIGNAL	3	NOS1AP	6.59E-115	0.88	1	27	0	0	0
rs7536043	rs3934467	OTHERSIGNAL	3	NOS1AP	-	0.83	0	15	0	0	0
rs7541606	rs3934467	OTHERSIGNAL	3	NOS1AP	0.00026807	0.88	0	11	1	0	0
rs7545047	rs7545047	OTHERSIGNAL	3	NOS1AP	8.8924E-14	1.00	0	10	0	0	0
rs10800403	rs12079745	OTHERSIGNAL	4	ATP1B1	-	0.98	0	0	0	0	0
rs1080267	rs12079745	OTHERSIGNAL	4	ATP1B1	1.1004E-09	0.89	0	3	0	0	0
rs10919062	rs10919070	INDEX	4	ATP1B1	7.59E-26	0.96	1	31	1	0	0
rs10919070	rs10919070	INDEX	4	ATP1B1	1.11E-31	1.00	0	7	0	0	0
rs10919071	rs10919070	INDEX	4	ATP1B1	1.40E-31	0.99	0	0	0	0	0
rs10919073	rs12079745	OTHERSIGNAL	4	ATP1B1	8.3032E-11	1.00	0	7	0	0	0
rs10919074	rs10919070	INDEX	4	ATP1B1	2.01E-27	0.93	0	3	0	0	0
rs1138486	rs12079745	OTHERSIGNAL	4	ATP1B1	1.5271E-10	0.98	0	8	0	0	0
rs11801853	rs12079745	OTHERSIGNAL	4	ATP1B1	8.5022E-10	0.96	0	0	0	0	0
rs11809180	rs12079745	OTHERSIGNAL	4	ATP1B1	6.5504E-08	0.98	0	0	0	0	0
rs12035622	rs10919070	INDEX	4	ATP1B1	3.58E-27	0.93	0	7	0	0	0
rs12061601	rs12061601	OTHERSIGNAL	4	ATP1B1	3.10E-21	1.00	0	20	1	0	0
rs12066676	rs12079745	OTHERSIGNAL	4	ATP1B1	-	0.92	0	0	1	0	0
rs12070626	rs12079745	OTHERSIGNAL	4	ATP1B1	0.38041	0.92	0	2	0	0	0
rs12076510	rs12079745	OTHERSIGNAL	4	ATP1B1	-	0.96	0	1	0	0	0
rs12079745	rs12079745	OTHERSIGNAL	4	ATP1B1	1.2195E-10	1.00	0	0	0	0	0
rs12079856	rs12061601	OTHERSIGNAL	4	ATP1B1	0.0404	0.96	0	25	1	0	0
rs12084964	rs12079745	OTHERSIGNAL	4	ATP1B1	4.5529E-09	1.00	0	9	0	0	0
rs12086104	rs12079745	OTHERSIGNAL	4	ATP1B1	0.4264	1.00	0	12	0	0	0
rs12095171	rs12079745	OTHERSIGNAL	4	ATP1B1	1.2795E-09	1.00	0	10	0	0	0
rs12406341	rs10919070	INDEX	4	ATP1B1	-	0.95	0	0	0	0	0
rs12564558	rs12079745	OTHERSIGNAL	4	ATP1B1	2.2966E-10	0.96	0	0	0	0	0
rs12568473	rs10919070	INDEX	4	ATP1B1	-	0.98	0	2	1	0	0
rs12751593	rs12061601	OTHERSIGNAL	4	ATP1B1	-	0.90	0	0	0	0	0
rs1320966	rs12079745	OTHERSIGNAL	4	ATP1B1	0.0012717	1.00	0	14	0	0	0
rs1320976	rs12061601	OTHERSIGNAL	4	ATP1B1	0.0025452	0.96	0	20	1	0	0
rs1320977	rs12061601	OTHERSIGNAL	4	ATP1B1	0.040886	0.96	0	20	1	0	0
rs143475554	rs545833	OTHERSIGNAL	4	ATP1B1	-	0.99	0	0	0	0	0
rs146291410	rs12079745	OTHERSIGNAL	4	ATP1B1	-	1.00	0	0	0	0	0
rs146350925	rs12079745	OTHERSIGNAL	4	ATP1B1	-	0.92	0	0	1	0	0
rs1534984	rs12061601	OTHERSIGNAL	4	ATP1B1	0.040886	0.91	0	20	0	0	0
rs17345156	rs10919070	INDEX	4	ATP1B1	2.92E-30	0.88	0	0	0	0	0
rs1892092	rs12061601	OTHERSIGNAL	4	ATP1B1	-	0.93	0	20	1	0	0
rs1892093	rs12061601	OTHERSIGNAL	4	ATP1B1	0.040886	0.92	0	20	1	0	0
rs1983546	rs1983546	OTHERSIGNAL	4	ATP1B1	9.74E-16	1.00	0	0	0	0	0
rs199593766	rs10919070	INDEX	4	ATP1B1	-	0.89	0	0	0	0	0
rs2000321	rs10919070	INDEX	4	ATP1B1	1.17E-26	0.96	0	2	0	0	0
rs2143290	rs10919070	INDEX	4	ATP1B1	9.36E-31	0.93	1	29	1	0	0
rs28362572	rs12061601	OTHERSIGNAL	4	ATP1B1	0.043497	0.93	0	0	0	0	0
rs34605921	rs12079745	OTHERSIGNAL	4	ATP1B1	-	1.00	0	0	0	0	0
rs34645703	rs12079745	OTHERSIGNAL	4	ATP1B1	-	0.98	0	0	0	0	0
rs34847919	rs12079745	OTHERSIGNAL	4	ATP1B1	-	1.00	0	5	0	0	0
rs35037551	rs12079745	OTHERSIGNAL	4	ATP1B1	-	1.00	0	5	0	0	0
rs35742469	rs12079745	OTHERSIGNAL	4	ATP1B1	-	0.94	0	0	0	0	0
rs3766045	rs12079745	OTHERSIGNAL	4	ATP1B1	-	0.92	0	7	0	0	0
rs3766063	rs12079745	OTHERSIGNAL	4	ATP1B1	0.48633	1.00	0	5	0	0	0
rs3834008	rs10919070	INDEX	4	ATP1B1	-	0.93	0	4	0	1	0
rs3835362	rs545833	OTHERSIGNAL	4	ATP1B1	-	0.88	0	1	1	0	0
rs4656647	rs12061601	OTHERSIGNAL	4	ATP1B1	0.044959	0.92	0	7	0	0	0
rs512129	rs545833	OTHERSIGNAL	4	ATP1B1	0.14647	1.00	0	12	1	0	0
rs528953	rs545833	OTHERSIGNAL	4	ATP1B1	2.35E-16	1.00	0	0	1	0	0
rs531706	rs545833	OTHERSIGNAL	4	ATP1B1	0.055766	1.00	0	1	1	0	0
rs533619	rs545833	OTHERSIGNAL	4	ATP1B1	-	1.00	0	0	0	0	0
rs545833	rs545833	OTHERSIGNAL	4	ATP1B1	3.89E-17	1.00	0	1	1	0	0
rs553721	rs545833	OTHERSIGNAL	4	ATP1B1	-	0.90	0	4	1	0	0
rs573418	rs545833	OTHERSIGNAL	4	ATP1B1	0.055766	1.00	0	0	1	0	0
rs590875	rs545833	OTHERSIGNAL	4	ATP1B1	-	1.00	0	0	0	0	0
rs59732929	rs12061601	OTHERSIGNAL	4	ATP1B1	-	0.96	1	39	1	0	0
rs607484	rs545833	OTHERSIGNAL	4	ATP1B1	0.32961	1.00	0	15	1	1	0
rs635954	rs545833	OTHERSIGNAL	4	ATP1B1	0.060358	1.00	0	9	1	0	0
rs6672876	rs12061601	OTHERSIGNAL	4	ATP1B1	-	0.89	0	0	0	0	0
rs678629	rs545833	OTHERSIGNAL	4	ATP1B1	-	0.98	0	0	1	0	0
rs681316	rs545833	OTHERSIGNAL	4	ATP1B1	0.048572	0.90	0	4	1	0	0
rs72637225	rs12079745	OTHERSIGNAL	4	ATP1B1	-	0.96	0	6	0	0	0
rs72706963	rs10919070	INDEX	4	ATP1B1	-	0.93	0	9	0	1	0
rs72706975	rs10919070	INDEX	4	ATP1B1	-	0.89	0	11	0	0	0
rs75505858	rs12061601	OTHERSIGNAL	4	ATP1B1	-	0.94	0	37	1	0	1

rs77448520	rs12061601	OTHERSIGNAL	4	ATP1B1	-	0.98	0	6	1	0	0
rs79011457	rs12061601	OTHERSIGNAL	4	ATP1B1	-	0.91	1	34	1	0	1
rs79284357	rs12061601	OTHERSIGNAL	4	ATP1B1	-	0.92	0	0	0	0	0
rs10490255	rs12997023	INDEX	5	SLC8A1	5.0365E-14	1.00	0	7	0	0	0
rs1072384	rs12997023	INDEX	5	SLC8A1	-	0.86	0	0	0	0	0
rs11685090	rs6544311	OTHERSIGNAL	5	SLC8A1	3.5933E-09	0.82	0	0	1	0	0
rs12991033	rs12997023	INDEX	5	SLC8A1	0.20211	1.00	0	11	0	0	0
rs12997023	rs12997023	INDEX	5	SLC8A1	4.6674E-14	1.00	0	0	0	0	0
rs12997042	rs12997023	INDEX	5	SLC8A1	0.071102	1.00	0	0	0	0	0
rs13002045	rs12997023	INDEX	5	SLC8A1	0.071102	1.00	0	0	0	0	0
rs13010657	rs12997023	INDEX	5	SLC8A1	9.36E-14	1.00	0	0	0	0	0
rs13010889	rs12997023	INDEX	5	SLC8A1	2.4185E-11	1.00	1	1	1	0	0
rs13012895	rs12997023	INDEX	5	SLC8A1	7.2045E-14	1.00	0	0	0	0	0
rs13017279	rs12997023	INDEX	5	SLC8A1	1.5351E-13	1.00	0	0	0	0	0
rs13017846	rs12997023	INDEX	5	SLC8A1	2.6225E-13	1.00	0	0	0	0	0
rs13019501	rs12997023	INDEX	5	SLC8A1	0.071102	1.00	0	0	0	0	0
rs13020186	rs12997023	INDEX	5	SLC8A1	7.686E-14	0.93	0	0	0	0	0
rs13020198	rs12997023	INDEX	5	SLC8A1	-	1.00	0	0	0	0	0
rs13026826	rs12997023	INDEX	5	SLC8A1	8.6022E-14	1.00	0	0	0	0	0
rs13028820	rs12997023	INDEX	5	SLC8A1	8.2391E-14	1.00	0	0	0	0	0
rs13029763	rs12997023	INDEX	5	SLC8A1	0.075556	0.88	0	3	0	0	0
rs142291896	rs12997023	INDEX	5	SLC8A1	-	0.85	1	0	1	0	0
rs17026106	rs12997023	INDEX	5	SLC8A1	8.0795E-14	1.00	0	12	0	0	0
rs17026114	rs12997023	INDEX	5	SLC8A1	6.50E-14	1.00	0	0	0	0	0
rs17026131	rs12997023	INDEX	5	SLC8A1	9.5471E-14	1.00	0	0	0	0	0
rs17026148	rs12997023	INDEX	5	SLC8A1	0.059683	1.00	0	0	0	0	0
rs17026152	rs12997023	INDEX	5	SLC8A1	1.4877E-13	1.00	0	0	0	0	0
rs17026155	rs12997023	INDEX	5	SLC8A1	3.166E-13	1.00	0	3	1	0	0
rs17026156	rs12997023	INDEX	5	SLC8A1	1.4339E-13	1.00	0	2	1	0	0
rs2006286	rs6544311	OTHERSIGNAL	5	SLC8A1	-	0.83	0	0	0	0	0
rs2006287	rs6544311	OTHERSIGNAL	5	SLC8A1	-	0.83	0	0	0	0	0
rs201856023	rs6544311	OTHERSIGNAL	5	SLC8A1	-	0.80	0	0	1	0	0
rs202207867	rs12997023	INDEX	5	SLC8A1	-	0.92	1	0	1	0	0
rs2098477	rs12997023	INDEX	5	SLC8A1	8.2542E-14	1.00	0	0	0	0	0
rs2098478	rs12997023	INDEX	5	SLC8A1	7.1521E-14	1.00	0	0	0	0	0
rs2110922	rs6544311	OTHERSIGNAL	5	SLC8A1	3.878E-10	0.83	0	1	1	0	0
rs2193563	rs12997023	INDEX	5	SLC8A1	0.149	1.00	0	1	1	0	0
rs2193565	rs12997023	INDEX	5	SLC8A1	5.0165E-13	1.00	0	0	0	0	0
rs34090630	rs12997023	INDEX	5	SLC8A1	-	1.00	0	0	0	0	0
rs34549837	rs12997023	INDEX	5	SLC8A1	-	1.00	0	11	0	0	0
rs34766086	rs12997023	INDEX	5	SLC8A1	-	1.00	0	12	0	0	0
rs35014850	rs12997023	INDEX	5	SLC8A1	-	1.00	0	0	0	0	0
rs35455710	rs12997023	INDEX	5	SLC8A1	-	1.00	0	0	0	0	0
rs35537386	rs12997023	INDEX	5	SLC8A1	-	1.00	0	2	1	0	0
rs36011854	rs12997023	INDEX	5	SLC8A1	-	1.00	0	11	0	0	0
rs3796079	rs12997023	INDEX	5	SLC8A1	2.5307E-13	1.00	0	5	1	0	0
rs3796080	rs12997023	INDEX	5	SLC8A1	2.8878E-13	1.00	0	3	1	0	0
rs4952469	rs6544311	OTHERSIGNAL	5	SLC8A1	-	0.87	1	7	0	1	1
rs4952632	rs12997023	INDEX	5	SLC8A1	8.4268E-14	1.00	0	0	0	0	0
rs60079242	rs12997023	INDEX	5	SLC8A1	-	1.00	0	3	0	0	0
rs6544311	rs6544311	OTHERSIGNAL	5	SLC8A1	1.785E-10	1.00	0	10	1	0	0
rs67014132	rs12997023	INDEX	5	SLC8A1	-	1.00	0	4	1	0	0
rs70957147	rs6544311	OTHERSIGNAL	5	SLC8A1	-	0.86	0	0	1	0	0
rs70957184	rs12997023	INDEX	5	SLC8A1	-	1.00	0	1	0	0	0
rs71426871	rs12997023	INDEX	5	SLC8A1	-	1.00	0	0	0	0	0
rs71441106	rs12997023	INDEX	5	SLC8A1	-	1.00	0	2	0	0	0
rs71441107	rs12997023	INDEX	5	SLC8A1	-	1.00	0	2	0	0	0
rs72935262	rs6544311	OTHERSIGNAL	5	SLC8A1	-	0.84	0	0	0	0	0
rs7573537	rs6544311	OTHERSIGNAL	5	SLC8A1	6.0902E-10	0.82	0	0	1	0	0
rs765554	rs6544311	OTHERSIGNAL	5	SLC8A1	7.4257E-10	0.92	0	14	0	0	1
rs765555	rs6544311	OTHERSIGNAL	5	SLC8A1	2.682E-09	0.95	0	9	0	0	1
rs10084350	rs938291	INDEX	6	SP3	0.00002014	0.82	0	10	0	0	0
rs11300872	rs938291	INDEX	6	SP3	-	0.95	0	0	0	0	0
rs13010038	rs938291	INDEX	6	SP3	-	0.95	0	9	0	0	0
rs35886484	rs938291	INDEX	6	SP3	-	0.95	0	0	0	0	0
rs6707596	rs938291	INDEX	6	SP3	-	0.94	0	0	0	0	0
rs938291	rs938291	INDEX	6	SP3	5.8749E-10	1.00	0	0	0	0	0
rs12464151	rs7561149	INDEX	7	TTN-CCDC141	-	0.97	0	1	0	0	0
rs12469367	rs7561149	INDEX	7	TTN-CCDC141	2.008E-08	0.97	0	1	0	0	0
rs12471428	rs7561149	INDEX	7	TTN-CCDC141	5.2887E-07	0.94	0	0	0	0	0
rs12992014	rs7561149	INDEX	7	TTN-CCDC141	-	0.97	0	1	0	0	0
rs13006510	rs7561149	INDEX	7	TTN-CCDC141	1.0548E-06	0.93	1	0	0	0	0
rs3769858	rs7561149	INDEX	7	TTN-CCDC141	0.000007715	0.80	0	1	0	0	0
rs6729746	rs7561149	INDEX	7	TTN-CCDC141	-	0.80	0	1	0	0	0
rs7561149	rs7561149	INDEX	7	TTN-CCDC141	7.0669E-09	1.00	0	4	0	0	0
rs7591782	rs7561149	INDEX	7	TTN-CCDC141	5.2774E-08	0.94	1	14	0	0	1
rs7600330	rs7561149	INDEX	7	TTN-CCDC141	1.8134E-08	0.96	0	4	0	0	0
rs10931897	rs295140	INDEX	8	SPATS2L	8.6632E-09	0.99	0	2	0	0	0
rs10931898	rs295140	INDEX	8	SPATS2L	-	0.84	0	0	0	0	0
rs10931899	rs295140	INDEX	8	SPATS2L	1.0517E-08	0.98	1	49	1	1	0
rs10931900	rs295140	INDEX	8	SPATS2L	-	0.97	1	50	1	1	1
rs11696001	rs295140	INDEX	8	SPATS2L	8.1976E-09	0.99	0	2	0	0	0
rs11888462	rs295140	INDEX	8	SPATS2L	4.9492E-09	1.00	0	1	0	0	0
rs12469091	rs295140	INDEX	8	SPATS2L	1.4743E-06	0.82	0	10	0	0	0
rs12474914	rs295140	INDEX	8	SPATS2L	-	0.82	0	0	0	0	0
rs12614621	rs295140	INDEX	8	SPATS2L	-	0.99	0	0	0	0	0
rs12618057	rs295140	INDEX	8	SPATS2L	-	0.90	0	0	0	0	0
rs13005573	rs295140	INDEX	8	SPATS2L	-	0.99	0	7	0	0	0
rs13007517	rs295140	INDEX	8	SPATS2L	-	0.82	0	5	0	0	0
rs13026151	rs295140	INDEX	8	SPATS2L	-	0.99	0	7	0	0	0
rs13028959	rs295140	INDEX	8	SPATS2L	9.6282E-09	0.96	0	40	1	1	1
rs1367856	rs295140	INDEX	8	SPATS2L	7.4342E-09	1.00	0	1	0	0	0

rs1367857	rs295140	INDEX	8	SPATS2L	-	1.00	0	1	0	0	0
rs141893693	rs295140	INDEX	8	SPATS2L	-	0.98	1	29	0	0	0
rs1431766	rs295140	INDEX	8	SPATS2L	7.588E-09	0.98	0	0	0	0	0
rs200117095	rs295140	INDEX	8	SPATS2L	-	0.95	0	18	1	0	0
rs200281491	rs295140	INDEX	8	SPATS2L	-	0.82	0	3	0	0	0
rs295140	rs295140	INDEX	8	SPATS2L	4.4143E-13	1.00	0	1	0	0	0
rs35518740	rs295140	INDEX	8	SPATS2L	-	0.96	0	3	0	0	0
rs3739121	rs295140	INDEX	8	SPATS2L	3.2653E-07	0.99	0	0	0	0	0
rs3769476	rs295140	INDEX	8	SPATS2L	1.1872E-08	0.98	1	50	0	0	0
rs3820888	rs295140	INDEX	8	SPATS2L	-	0.84	1	33	0	1	1
rs4233994	rs295140	INDEX	8	SPATS2L	1.3267E-06	0.81	0	3	0	0	0
rs4516413	rs295140	INDEX	8	SPATS2L	-	0.99	0	7	0	0	0
rs4516415	rs295140	INDEX	8	SPATS2L	-	0.81	0	5	0	0	0
rs4673904	rs295140	INDEX	8	SPATS2L	-	0.83	0	6	0	0	0
rs4673906	rs295140	INDEX	8	SPATS2L	-	0.99	0	7	0	0	0
rs4673912	rs295140	INDEX	8	SPATS2L	3.4627E-06	0.81	0	4	0	0	0
rs55677233	rs295140	INDEX	8	SPATS2L	-	0.99	0	4	0	0	0
rs56326533	rs295140	INDEX	8	SPATS2L	-	0.84	0	4	0	0	0
rs67190025	rs295140	INDEX	8	SPATS2L	-	0.94	0	1	0	0	0
rs71022314	rs295140	INDEX	8	SPATS2L	-	0.96	0	1	0	0	0
rs74853338	rs295140	INDEX	8	SPATS2L	-	0.83	0	0	0	0	0
rs7559005	rs295140	INDEX	8	SPATS2L	-	0.99	0	1	0	0	0
rs7578220	rs295140	INDEX	8	SPATS2L	9.8942E-09	0.97	1	54	1	1	1
rs7580924	rs295140	INDEX	8	SPATS2L	-	0.98	0	2	0	0	0
rs7584810	rs295140	INDEX	8	SPATS2L	-	0.99	0	33	0	0	0
rs7599609	rs295140	INDEX	8	SPATS2L	-	0.98	1	18	1	1	0
rs7605146	rs295140	INDEX	8	SPATS2L	1.7264E-06	0.84	1	57	1	1	1
rs10428132	rs6801957	OTHERSIGNAL	9	SCN5A-SCN10A	0.00092196	0.98	0	0	0	0	0
rs11441682	rs6599234	OTHERSIGNAL	9	SCN5A-SCN10A	-	0.91	0	1	0	0	0
rs11708996	rs11708996	OTHERSIGNAL	9	SCN5A-SCN10A	2.27E-11	1.00	0	0	0	0	0
rs11710077	rs11710077	OTHERSIGNAL	9	SCN5A-SCN10A	1.4245E-13	1.00	1	11	1	0	1
rs11711941	rs6801957	OTHERSIGNAL	9	SCN5A-SCN10A	-	0.86	0	0	0	0	0
rs11720166	rs6793245	INDEX	9	SCN5A-SCN10A	-	1.00	0	0	0	0	0
rs11924846	rs6801957	OTHERSIGNAL	9	SCN5A-SCN10A	4.82E-10	0.88	0	0	0	0	0
rs12053903	rs6793245	INDEX	9	SCN5A-SCN10A	2.94E-26	0.93	0	0	0	0	0
rs141384382	rs11708996	OTHERSIGNAL	9	SCN5A-SCN10A	-	1.00	0	0	0	0	0
rs35243266	rs6793245	INDEX	9	SCN5A-SCN10A	-	0.98	0	0	0	0	0
rs4076737	rs6801957	OTHERSIGNAL	9	SCN5A-SCN10A	6.7978E-10	0.88	1	16	1	0	1
rs41312411	rs11708996	OTHERSIGNAL	9	SCN5A-SCN10A	-	0.94	1	24	1	1	1
rs4131768	rs6599234	OTHERSIGNAL	9	SCN5A-SCN10A	-	0.85	0	2	0	0	0
rs6599233	rs6599234	OTHERSIGNAL	9	SCN5A-SCN10A	-	0.97	0	0	0	0	0
rs6599234	rs6599234	OTHERSIGNAL	9	SCN5A-SCN10A	2.223E-11	1.00	0	0	0	0	0
rs6599250	rs6801957	OTHERSIGNAL	9	SCN5A-SCN10A	7.2186E-11	0.97	0	0	0	0	0
rs6599251	rs6801957	OTHERSIGNAL	9	SCN5A-SCN10A	3.1797E-09	0.80	0	0	0	0	0
rs6599254	rs6801957	OTHERSIGNAL	9	SCN5A-SCN10A	2.9793E-10	0.94	0	0	0	0	0
rs6599255	rs6801957	OTHERSIGNAL	9	SCN5A-SCN10A	1.0277E-08	0.94	0	0	0	0	0
rs6782237	rs6599234	OTHERSIGNAL	9	SCN5A-SCN10A	-	0.87	0	0	0	0	0
rs6783110	rs6801957	OTHERSIGNAL	9	SCN5A-SCN10A	0.05614	0.85	0	3	1	0	0
rs6790396	rs6801957	OTHERSIGNAL	9	SCN5A-SCN10A	2.7068E-09	0.98	0	10	0	0	0
rs6793245	rs6793245	INDEX	9	SCN5A-SCN10A	4.43E-27	1.00	0	0	0	0	0
rs6795970	rs6801957	OTHERSIGNAL	9	SCN5A-SCN10A	1.891E-10	0.98	1	16	1	0	1
rs6799868	rs6793245	INDEX	9	SCN5A-SCN10A	7.63E-27	0.99	0	0	0	0	0
rs6800541	rs6801957	OTHERSIGNAL	9	SCN5A-SCN10A	8.1443E-11	0.98	0	1	0	0	0
rs6801957	rs6801957	OTHERSIGNAL	9	SCN5A-SCN10A	1.1261E-10	1.00	0	20	1	0	0
rs6804918	rs6793245	INDEX	9	SCN5A-SCN10A	-	0.99	0	0	0	0	0
rs73070977	rs11708996	OTHERSIGNAL	9	SCN5A-SCN10A	-	1.00	0	1	0	0	0
rs73070981	rs11708996	OTHERSIGNAL	9	SCN5A-SCN10A	-	1.00	0	2	0	0	0
rs7373779	rs6793245	INDEX	9	SCN5A-SCN10A	-	0.94	0	0	0	0	0
rs7428167	rs6801957	OTHERSIGNAL	9	SCN5A-SCN10A	-	0.82	0	0	0	0	0
rs7430191	rs11710077	OTHERSIGNAL	9	SCN5A-SCN10A	-	0.92	0	0	0	0	0
rs7430391	rs6599234	OTHERSIGNAL	9	SCN5A-SCN10A	-	0.96	0	1	0	0	0
rs7433306	rs6801957	OTHERSIGNAL	9	SCN5A-SCN10A	8.1281E-11	0.98	0	0	0	0	0
rs7433723	rs6801957	OTHERSIGNAL	9	SCN5A-SCN10A	0.19314	0.95	0	0	0	0	0
rs7633988	rs6599234	OTHERSIGNAL	9	SCN5A-SCN10A	1.8901E-10	0.98	0	1	0	0	0
rs7645178	rs6793245	INDEX	9	SCN5A-SCN10A	-	0.99	0	0	0	0	0
rs9311197	rs6801957	OTHERSIGNAL	9	SCN5A-SCN10A	-	0.81	0	0	0	0	0
rs9809798	rs6801957	OTHERSIGNAL	9	SCN5A-SCN10A	-	0.82	0	1	0	0	0
rs9820042	rs6801957	OTHERSIGNAL	9	SCN5A-SCN10A	-	0.98	0	0	0	0	0
rs9844378	rs6599234	OTHERSIGNAL	9	SCN5A-SCN10A	-	0.88	0	5	1	0	0
rs9844577	rs6801957	OTHERSIGNAL	9	SCN5A-SCN10A	0.24831	0.95	0	0	0	0	0
rs9851710	rs6599234	OTHERSIGNAL	9	SCN5A-SCN10A	2.4116E-11	0.98	0	0	0	0	0
rs9851724	rs6599234	OTHERSIGNAL	9	SCN5A-SCN10A	2.6998E-11	0.98	0	0	0	0	0
rs1038394	rs17784882	INDEX	10	C3ORF75	0.00072559	0.84	1	6	1	0	0
rs10865946	rs17784882	INDEX	10	C3ORF75	1.0502E-07	0.82	0	23	0	0	0
rs11130128	rs17784882	INDEX	10	C3ORF75	4.88E-08	0.90	0	4	0	0	0
rs11130129	rs17784882	INDEX	10	C3ORF75	1.4733E-07	0.90	0	0	0	0	0
rs11130132	rs17784882	INDEX	10	C3ORF75	-	0.98	0	2	0	0	0
rs11130133	rs17784882	INDEX	10	C3ORF75	-	0.98	0	0	0	0	0
rs11130137	rs17784882	INDEX	10	C3ORF75	3.8995E-08	0.94	0	4	0	0	0
rs111378194	rs17784882	INDEX	10	C3ORF75	-	0.91	0	0	0	0	0
rs11705957	rs17784882	INDEX	10	C3ORF75	3.5455E-08	0.82	0	2	0	0	0
rs11707895	rs17784882	INDEX	10	C3ORF75	-	0.95	0	3	0	0	0
rs11711265	rs17784882	INDEX	10	C3ORF75	0.0010994	0.98	0	0	0	0	0
rs11711824	rs17784882	INDEX	10	C3ORF75	0.000000747	0.83	0	0	0	0	0
rs11712445	rs17784882	INDEX	10	C3ORF75	2.3818E-07	0.82	0	6	0	0	0
rs11713413	rs17784882	INDEX	10	C3ORF75	-	0.91	0	0	0	0	0
rs11716661	rs17784882	INDEX	10	C3ORF75	-	0.84	0	2	0	0	0
rs11716763	rs17784882	INDEX	10	C3ORF75	4.5902E-08	0.93	1	45	0	1	1
rs11719877	rs17784882	INDEX	10	C3ORF75	5.6765E-08	0.82	1	13	0	0	0
rs11914795	rs17784882	INDEX	10	C3ORF75	-	0.85	0	6	0	0	0
rs11914913	rs17784882	INDEX	10	C3ORF75	-	0.96	0	0	0	0	0
rs11914932	rs17784882	INDEX	10	C3ORF75	-	0.98	0	3	0	0	0

rs11925823	rs17784882	INDEX	10	C3ORF75	-	0.82	0	1	0	0	0
rs12486969	rs17784882	INDEX	10	C3ORF75	-	0.82	0	1	0	0	0
rs12489046	rs17784882	INDEX	10	C3ORF75	3.6105E-08	0.92	0	0	0	0	0
rs12490058	rs17784882	INDEX	10	C3ORF75	0.00071005	0.98	0	0	0	0	0
rs12492433	rs17784882	INDEX	10	C3ORF75	-	0.92	1	43	0	0	0
rs12497225	rs17784882	INDEX	10	C3ORF75	-	0.83	0	2	0	0	0
rs12630641	rs17784882	INDEX	10	C3ORF75	-	0.98	0	1	0	0	0
rs12632132	rs17784882	INDEX	10	C3ORF75	-	0.83	0	5	0	0	0
rs12636851	rs17784882	INDEX	10	C3ORF75	5.22E-08	0.84	1	21	1	1	0
rs13059519	rs17784882	INDEX	10	C3ORF75	4.0735E-08	0.99	0	0	0	0	0
rs13064843	rs17784882	INDEX	10	C3ORF75	-	0.82	0	0	0	0	0
rs13075233	rs17784882	INDEX	10	C3ORF75	1.4894E-07	0.82	0	41	0	0	0
rs13079098	rs17784882	INDEX	10	C3ORF75	-	0.81	0	0	0	0	0
rs145456175	rs17784882	INDEX	10	C3ORF75	-	0.90	0	0	0	0	0
rs1531875	rs17784882	INDEX	10	C3ORF75	0.0012038	0.83	0	1	0	0	0
rs17784882	rs17784882	INDEX	10	C3ORF75	3.2863E-08	1.00	0	0	0	0	0
rs1872164	rs17784882	INDEX	10	C3ORF75	5.7238E-08	0.83	0	1	0	0	0
rs2062278	rs17784882	INDEX	10	C3ORF75	1.1509E-07	0.83	0	0	0	0	0
rs2101247	rs17784882	INDEX	10	C3ORF75	8.989E-08	0.90	1	10	0	0	0
rs2291298	rs17784882	INDEX	10	C3ORF75	1.4494E-07	0.98	0	0	0	0	0
rs34634681	rs17784882	INDEX	10	C3ORF75	-	0.94	0	5	0	0	0
rs3736177	rs17784882	INDEX	10	C3ORF75	1.2652E-07	0.83	0	0	0	0	0
rs3816779	rs17784882	INDEX	10	C3ORF75	4.0812E-08	0.98	0	0	0	0	0
rs4599332	rs17784882	INDEX	10	C3ORF75	-	0.94	0	2	0	0	0
rs4858805	rs17784882	INDEX	10	C3ORF75	-	0.81	0	0	0	0	0
rs4858811	rs17784882	INDEX	10	C3ORF75	5.7529E-08	0.87	0	0	0	0	0
rs4858848	rs17784882	INDEX	10	C3ORF75	-	0.80	0	1	0	0	0
rs4858856	rs17784882	INDEX	10	C3ORF75	4.2651E-08	0.96	0	2	0	0	0
rs4858868	rs17784882	INDEX	10	C3ORF75	5.2098E-08	0.83	0	0	0	0	0
rs4858894	rs17784882	INDEX	10	C3ORF75	1.5885E-07	0.88	1	57	1	1	1
rs56032309	rs17784882	INDEX	10	C3ORF75	-	0.83	0	0	0	0	0
rs56351005	rs17784882	INDEX	10	C3ORF75	-	0.81	0	0	0	0	0
rs57346147	rs17784882	INDEX	10	C3ORF75	-	0.83	0	3	0	0	0
rs59586735	rs17784882	INDEX	10	C3ORF75	-	0.93	1	45	0	1	1
rs60369822	rs17784882	INDEX	10	C3ORF75	-	0.88	0	0	0	0	0
rs62248599	rs17784882	INDEX	10	C3ORF75	-	0.91	0	0	0	0	0
rs62248603	rs17784882	INDEX	10	C3ORF75	-	0.87	0	0	0	0	0
rs62248605	rs17784882	INDEX	10	C3ORF75	-	0.94	0	0	0	0	0
rs62260710	rs17784882	INDEX	10	C3ORF75	-	0.97	0	6	0	0	0
rs62260711	rs17784882	INDEX	10	C3ORF75	-	0.97	0	6	0	0	0
rs62260741	rs17784882	INDEX	10	C3ORF75	-	0.91	0	0	0	0	0
rs6765990	rs17784882	INDEX	10	C3ORF75	-	0.99	0	0	0	0	0
rs6787422	rs17784882	INDEX	10	C3ORF75	-	0.82	0	11	0	0	0
rs6790763	rs17784882	INDEX	10	C3ORF75	-	0.93	0	0	0	0	0
rs6792461	rs17784882	INDEX	10	C3ORF75	5.6506E-08	0.83	0	4	1	0	0
rs6792488	rs17784882	INDEX	10	C3ORF75	-	0.89	0	8	0	0	1
rs6800271	rs17784882	INDEX	10	C3ORF75	4.348E-08	0.83	0	1	0	0	0
rs73081205	rs17784882	INDEX	10	C3ORF75	-	0.91	0	2	0	0	0
rs7628631	rs17784882	INDEX	10	C3ORF75	3.7084E-08	0.98	0	0	0	0	0
rs7649234	rs17784882	INDEX	10	C3ORF75	-	0.90	1	10	0	0	0
rs7651194	rs17784882	INDEX	10	C3ORF75	-	0.99	0	0	0	0	0
rs7651762	rs17784882	INDEX	10	C3ORF75	7.8971E-08	0.83	0	2	0	0	0
rs79438810	rs17784882	INDEX	10	C3ORF75	-	0.84	0	2	0	0	0
rs878659	rs17784882	INDEX	10	C3ORF75	3.9069E-08	0.90	0	10	0	1	0
rs922957	rs17784882	INDEX	10	C3ORF75	5.9797E-08	0.83	0	0	0	0	0
rs9683033	rs17784882	INDEX	10	C3ORF75	0.00054819	0.90	0	0	0	0	0
rs9683177	rs17784882	INDEX	10	C3ORF75	-	0.90	0	1	0	0	0
rs1947376	rs2363719	INDEX	11	SLC4A4	1.1942E-09	1.00	0	2	0	0	0
rs1947378	rs2363719	INDEX	11	SLC4A4	3.2792E-09	1.00	0	2	0	0	0
rs2363719	rs2363719	INDEX	11	SLC4A4	7.8435E-10	1.00	0	2	0	0	0
rs55760668	rs2363719	INDEX	11	SLC4A4	-	1.00	0	2	0	0	0
rs10023582	rs3857067	INDEX	12	SMARCAD1	4.3094E-06	0.94	0	1	0	0	0
rs10034161	rs3857067	INDEX	12	SMARCAD1	-	0.95	0	0	0	0	0
rs115969971	rs3857067	INDEX	12	SMARCAD1	-	1.00	0	0	0	0	0
rs12502725	rs3857067	INDEX	12	SMARCAD1	2.0672E-07	0.85	0	0	0	0	0
rs12505694	rs3857067	INDEX	12	SMARCAD1	-	0.94	0	0	0	0	0
rs1355240	rs3857067	INDEX	12	SMARCAD1	-	1.00	0	0	0	0	0
rs138036517	rs3857067	INDEX	12	SMARCAD1	-	0.94	0	0	0	0	0
rs1397025	rs3857067	INDEX	12	SMARCAD1	-	1.00	0	0	0	0	0
rs1397026	rs3857067	INDEX	12	SMARCAD1	-	1.00	0	0	0	0	0
rs1397027	rs3857067	INDEX	12	SMARCAD1	2.133E-07	0.96	0	0	0	0	0
rs140445440	rs3857067	INDEX	12	SMARCAD1	-	0.87	0	0	0	0	0
rs1472984	rs3857067	INDEX	12	SMARCAD1	4.0906E-06	0.95	0	1	0	0	0
rs1509940	rs3857067	INDEX	12	SMARCAD1	-	1.00	0	0	0	0	0
rs1509941	rs3857067	INDEX	12	SMARCAD1	-	0.96	0	0	0	0	0
rs1509942	rs3857067	INDEX	12	SMARCAD1	-	1.00	0	0	0	0	0
rs1509943	rs3857067	INDEX	12	SMARCAD1	-	1.00	0	0	0	0	0
rs1509945	rs3857067	INDEX	12	SMARCAD1	1.2919E-06	0.82	0	0	0	0	0
rs1585652	rs3857067	INDEX	12	SMARCAD1	-	1.00	0	0	0	0	0
rs1588381	rs3857067	INDEX	12	SMARCAD1	-	1.00	0	0	0	0	0
rs1588382	rs3857067	INDEX	12	SMARCAD1	0.63271	0.98	0	0	0	0	0
rs1588384	rs3857067	INDEX	12	SMARCAD1	-	0.85	0	0	0	0	0
rs1588385	rs3857067	INDEX	12	SMARCAD1	-	1.00	0	0	0	0	0
rs1841925	rs3857067	INDEX	12	SMARCAD1	8.7672E-07	0.93	0	0	0	0	0
rs1848793	rs3857067	INDEX	12	SMARCAD1	-	0.89	0	0	0	0	0
rs1848794	rs3857067	INDEX	12	SMARCAD1	-	0.86	0	0	0	0	0
rs1904094	rs3857067	INDEX	12	SMARCAD1	-	0.98	0	0	0	0	0
rs1904095	rs3857067	INDEX	12	SMARCAD1	-	0.95	0	0	0	0	0
rs1904096	rs3857067	INDEX	12	SMARCAD1	1.0807E-07	0.95	0	0	0	0	0
rs199617535	rs3857067	INDEX	12	SMARCAD1	-	0.88	0	0	0	0	0
rs201233944	rs3857067	INDEX	12	SMARCAD1	-	0.91	0	0	0	0	0
rs2089698	rs3857067	INDEX	12	SMARCAD1	-	1.00	0	0	0	0	0

rs2100915	rs3857067	INDEX	12	SMARCAD1	-	0.95	0	0	0	0	0
rs2199603	rs3857067	INDEX	12	SMARCAD1	-	1.00	0	0	0	0	0
rs2219755	rs3857067	INDEX	12	SMARCAD1	-	1.00	0	0	0	0	0
rs2865330	rs3857067	INDEX	12	SMARCAD1	5.702E-08	0.89	0	0	0	0	0
rs2865332	rs3857067	INDEX	12	SMARCAD1	1.9022E-07	0.96	0	0	0	0	0
rs2865335	rs3857067	INDEX	12	SMARCAD1	-	0.90	0	0	0	0	0
rs2865336	rs3857067	INDEX	12	SMARCAD1	1.1888E-06	0.96	0	0	0	0	0
rs28840089	rs3857067	INDEX	12	SMARCAD1	-	0.89	0	0	0	0	0
rs28876091	rs3857067	INDEX	12	SMARCAD1	-	0.89	0	0	0	0	0
rs34368301	rs3857067	INDEX	12	SMARCAD1	-	1.00	0	0	0	0	0
rs3846291	rs3857067	INDEX	12	SMARCAD1	2.948E-07	1.00	0	0	0	0	0
rs3846292	rs3857067	INDEX	12	SMARCAD1	3.1473E-07	1.00	0	0	0	0	0
rs3857067	rs3857067	INDEX	12	SMARCAD1	1.1546E-09	1.00	0	0	0	0	0
rs3857068	rs3857067	INDEX	12	SMARCAD1	4.647E-08	0.99	0	0	0	0	0
rs3975200	rs3857067	INDEX	12	SMARCAD1	-	0.96	0	0	0	0	0
rs4324525	rs3857067	INDEX	12	SMARCAD1	-	0.99	0	0	0	0	0
rs4693364	rs3857067	INDEX	12	SMARCAD1	-	0.96	0	0	0	0	0
rs4693368	rs3857067	INDEX	12	SMARCAD1	1.3379E-06	0.92	0	1	0	0	0
rs5019896	rs3857067	INDEX	12	SMARCAD1	9.1882E-07	0.94	0	1	0	0	0
rs58319462	rs3857067	INDEX	12	SMARCAD1	-	0.83	0	0	0	0	0
rs6532454	rs3857067	INDEX	12	SMARCAD1	-	0.96	0	0	0	0	0
rs6532455	rs3857067	INDEX	12	SMARCAD1	-	0.80	0	0	0	0	0
rs6532456	rs3857067	INDEX	12	SMARCAD1	-	0.81	0	0	0	0	0
rs6532462	rs3857067	INDEX	12	SMARCAD1	-	1.00	0	0	0	0	0
rs6532463	rs3857067	INDEX	12	SMARCAD1	3.6585E-07	1.00	0	0	0	0	0
rs6815207	rs3857067	INDEX	12	SMARCAD1	1.8976E-06	0.86	0	0	0	0	0
rs6817701	rs3857067	INDEX	12	SMARCAD1	-	0.81	0	0	0	0	0
rs6837655	rs3857067	INDEX	12	SMARCAD1	0.000028991	0.87	0	0	0	0	0
rs6840942	rs3857067	INDEX	12	SMARCAD1	-	0.85	0	0	0	0	0
rs7668980	rs3857067	INDEX	12	SMARCAD1	1.5346E-06	0.95	0	1	0	0	0
rs7682116	rs3857067	INDEX	12	SMARCAD1	-	0.89	0	0	0	0	0
rs7685048	rs3857067	INDEX	12	SMARCAD1	3.4272E-07	1.00	0	0	0	0	0
rs7685601	rs3857067	INDEX	12	SMARCAD1	-	1.00	0	0	0	0	0
rs7694631	rs3857067	INDEX	12	SMARCAD1	-	1.00	0	0	0	0	0
rs7694820	rs3857067	INDEX	12	SMARCAD1	-	1.00	0	0	0	0	0
rs899132	rs3857067	INDEX	12	SMARCAD1	9.6627E-07	0.94	0	0	0	0	0
rs899133	rs3857067	INDEX	12	SMARCAD1	-	1.00	0	0	0	0	0
rs899134	rs3857067	INDEX	12	SMARCAD1	-	1.00	0	0	0	0	0
rs899135	rs3857067	INDEX	12	SMARCAD1	1.3789E-07	0.95	0	0	0	0	0
rs9307135	rs3857067	INDEX	12	SMARCAD1	-	0.95	0	0	0	0	0
rs964843	rs3857067	INDEX	12	SMARCAD1	7.9975E-07	0.96	0	0	0	0	0
rs965807	rs3857067	INDEX	12	SMARCAD1	1.2223E-06	0.92	0	0	0	0	0
rs10040989	rs10040989	INDEX	13	GFRA3	5.4089E-11	1.00	0	3	0	0	0
rs17171780	rs10040989	INDEX	13	GFRA3	4.3871E-09	0.90	0	0	0	0	0
rs185184885	rs10040989	INDEX	13	GFRA3	-	0.90	0	0	0	0	0
rs2231472	rs10040989	INDEX	13	GFRA3	0.11392	0.90	0	0	0	0	0
rs1042391	rs7765828	INDEX	14	GMPR	3.9133E-10	0.99	0	4	0	0	0
rs11400155	rs7765828	INDEX	14	GMPR	-	0.90	0	2	0	0	0
rs148303943	rs7765828	INDEX	14	GMPR	-	0.83	0	2	0	0	0
rs200027952	rs7765828	INDEX	14	GMPR	-	0.80	0	2	0	0	0
rs2327958	rs7765828	INDEX	14	GMPR	-	0.99	0	1	0	0	0
rs4716053	rs7765828	INDEX	14	GMPR	-	0.86	0	3	0	0	0
rs4716054	rs7765828	INDEX	14	GMPR	-	0.87	0	12	0	0	0
rs4716056	rs7765828	INDEX	14	GMPR	3.9501E-10	0.88	1	47	0	1	0
rs57120780	rs7765828	INDEX	14	GMPR	-	0.81	0	2	0	0	0
rs6459465	rs7765828	INDEX	14	GMPR	9.4581E-10	0.88	0	0	0	0	0
rs6459466	rs7765828	INDEX	14	GMPR	-	0.87	0	6	1	0	0
rs6459467	rs7765828	INDEX	14	GMPR	6.1566E-10	0.97	0	1	0	0	0
rs6933491	rs7765828	INDEX	14	GMPR	4.9072E-09	0.92	0	2	0	0	0
rs7742883	rs7765828	INDEX	14	GMPR	4.6049E-09	0.89	1	19	1	1	1
rs7752579	rs7765828	INDEX	14	GMPR	-	0.87	0	6	1	0	0
rs7763322	rs7765828	INDEX	14	GMPR	3.6914E-09	0.89	0	1	0	0	0
rs7765828	rs7765828	INDEX	14	GMPR	3.211E-10	1.00	0	1	0	0	0
rs9383142	rs7765828	INDEX	14	GMPR	-	0.88	1	6	0	0	0
rs9477074	rs7765828	INDEX	14	GMPR	5.7198E-09	0.90	0	1	0	0	0
rs1034247	rs457162	OTHERSIGNAL	15	SLC35F1-PLN	4.18E-17	1.00	0	2	0	0	0
rs10457327	rs12210733	OTHERSIGNAL	15	SLC35F1-PLN	2.68E-28	0.86	0	4	1	0	0
rs10485390	rs3902035	OTHERSIGNAL	15	SLC35F1-PLN	1.46E-16	0.99	0	1	0	0	0
rs11153730	rs11153730	INDEX	15	SLC35F1-PLN	2.23E-67	1.00	0	0	0	0	0
rs11153733	rs12210733	OTHERSIGNAL	15	SLC35F1-PLN	0.046791	0.80	0	1	0	0	0
rs112615743	rs457162	OTHERSIGNAL	15	SLC35F1-PLN	-	0.88	0	2	0	0	0
rs11752626	rs11153730	INDEX	15	SLC35F1-PLN	3.24E-61	0.81	0	0	0	0	0
rs118167130	rs3902035	OTHERSIGNAL	15	SLC35F1-PLN	-	1.00	0	2	0	0	0
rs11965985	rs11153730	INDEX	15	SLC35F1-PLN	-	0.81	0	4	0	0	0
rs11968293	rs11153730	INDEX	15	SLC35F1-PLN	1.35E-55	0.82	0	3	1	0	0
rs11970286	rs11153730	INDEX	15	SLC35F1-PLN	9.55E-61	0.87	0	0	0	0	0
rs12206973	rs12210733	OTHERSIGNAL	15	SLC35F1-PLN	1.75E-24	0.80	0	7	0	0	0
rs12210733	rs12210733	OTHERSIGNAL	15	SLC35F1-PLN	1.13E-22	1.00	0	1	0	0	0
rs12210810	rs12210733	OTHERSIGNAL	15	SLC35F1-PLN	2.67E-30	1.00	0	0	0	0	0
rs12212795	rs12210733	OTHERSIGNAL	15	SLC35F1-PLN	4.43E-31	1.00	0	2	0	0	0
rs12215355	rs12210733	OTHERSIGNAL	15	SLC35F1-PLN	9.13E-28	0.94	0	0	0	0	0
rs12661563	rs9489510	OTHERSIGNAL	15	SLC35F1-PLN	3.3869E-10	0.80	0	12	1	0	0
rs1334489	rs11153730	INDEX	15	SLC35F1-PLN	1.40E-54	0.83	0	18	1	0	0
rs141547617	rs457162	OTHERSIGNAL	15	SLC35F1-PLN	-	0.96	0	0	0	0	0
rs150144	rs457162	OTHERSIGNAL	15	SLC35F1-PLN	0.026818	0.98	0	1	0	0	0
rs1572226	rs11153730	INDEX	15	SLC35F1-PLN	2.58E-57	0.82	0	4	1	0	1
rs17226667	rs11153730	INDEX	15	SLC35F1-PLN	1.20E-60	0.83	0	3	0	0	0
rs17227124	rs11153730	INDEX	15	SLC35F1-PLN	3.42E-61	0.82	0	0	1	0	0
rs17349133	rs3902035	OTHERSIGNAL	15	SLC35F1-PLN	2.18E-16	1.00	0	1	0	0	0
rs17349301	rs3902035	OTHERSIGNAL	15	SLC35F1-PLN	7.53E-16	1.00	0	23	0	0	0
rs17825393	rs11153730	INDEX	15	SLC35F1-PLN	7.50E-61	0.81	0	0	0	0	0
rs17825652	rs11153730	INDEX	15	SLC35F1-PLN	-	0.81	0	0	0	0	0

rs1889465	rs457162	OTHERSIGNAL	15	SLC35F1-PLN	8.16E-19	1.00	0	2	0	0	0
rs1889466	rs457162	OTHERSIGNAL	15	SLC35F1-PLN	4.57E-19	1.00	0	7	1	0	0
rs1891713	rs3902035	OTHERSIGNAL	15	SLC35F1-PLN	9.60E-16	0.99	0	0	0	0	0
rs1891714	rs3902035	OTHERSIGNAL	15	SLC35F1-PLN	-	1.00	0	0	0	0	0
rs1891715	rs3902035	OTHERSIGNAL	15	SLC35F1-PLN	1.08E-16	1.00	0	13	0	1	0
rs1931976	rs457162	OTHERSIGNAL	15	SLC35F1-PLN	0.017235	1.00	0	0	0	0	0
rs2050312	rs457162	OTHERSIGNAL	15	SLC35F1-PLN	4.09E-19	1.00	0	0	0	0	0
rs2050313	rs457162	OTHERSIGNAL	15	SLC35F1-PLN	8.23E-19	0.98	0	0	0	0	0
rs205917	rs457162	OTHERSIGNAL	15	SLC35F1-PLN	-	1.00	0	3	0	0	0
rs205918	rs457162	OTHERSIGNAL	15	SLC35F1-PLN	-	1.00	0	4	0	0	0
rs205919	rs457162	OTHERSIGNAL	15	SLC35F1-PLN	-	1.00	0	3	0	0	0
rs205920	rs457162	OTHERSIGNAL	15	SLC35F1-PLN	-	1.00	0	1	0	0	0
rs205921	rs457162	OTHERSIGNAL	15	SLC35F1-PLN	-	0.83	0	2	0	0	0
rs205922	rs457162	OTHERSIGNAL	15	SLC35F1-PLN	-	0.93	0	2	0	0	0
rs205923	rs457162	OTHERSIGNAL	15	SLC35F1-PLN	0.026818	0.98	0	1	0	0	0
rs2065707	rs457162	OTHERSIGNAL	15	SLC35F1-PLN	8.94E-21	0.81	0	0	0	0	0
rs2078383	rs11153730	INDEX	15	SLC35F1-PLN	-	0.81	0	0	0	0	0
rs2093369	rs11153730	INDEX	15	SLC35F1-PLN	-	0.83	0	4	0	0	0
rs2095406	rs457162	OTHERSIGNAL	15	SLC35F1-PLN	0.06312	1.00	0	0	0	0	0
rs2105021	rs457162	OTHERSIGNAL	15	SLC35F1-PLN	0.017235	1.00	0	0	0	0	0
rs2184365	rs457162	OTHERSIGNAL	15	SLC35F1-PLN	3.87E-19	1.00	0	0	0	0	0
rs28436726	rs12210733	OTHERSIGNAL	15	SLC35F1-PLN	0.018876	0.87	0	1	0	0	0
rs28710027	rs3902035	OTHERSIGNAL	15	SLC35F1-PLN	-	0.91	0	2	0	0	0
rs2883847	rs457162	OTHERSIGNAL	15	SLC35F1-PLN	0.019385	1.00	0	2	0	0	0
rs2883848	rs457162	OTHERSIGNAL	15	SLC35F1-PLN	3.12E-19	1.00	0	0	0	0	0
rs34367290	rs457162	OTHERSIGNAL	15	SLC35F1-PLN	-	1.00	0	1	0	0	0
rs34634569	rs457162	OTHERSIGNAL	15	SLC35F1-PLN	-	1.00	0	0	0	0	0
rs34889941	rs457162	OTHERSIGNAL	15	SLC35F1-PLN	-	0.90	0	0	0	0	0
rs36012145	rs457162	OTHERSIGNAL	15	SLC35F1-PLN	-	0.88	0	0	0	0	0
rs3902035	rs3902035	OTHERSIGNAL	15	SLC35F1-PLN	8.00E-16	1.00	0	18	0	0	0
rs4245500	rs457162	OTHERSIGNAL	15	SLC35F1-PLN	6.20E-20	0.98	0	0	0	0	0
rs455227	rs457162	OTHERSIGNAL	15	SLC35F1-PLN	0.019385	1.00	0	1	0	0	0
rs455338	rs457162	OTHERSIGNAL	15	SLC35F1-PLN	0.019385	1.00	0	0	0	0	0
rs457162	rs457162	OTHERSIGNAL	15	SLC35F1-PLN	2.49E-18	1.00	0	0	0	0	0
rs457210	rs457162	OTHERSIGNAL	15	SLC35F1-PLN	0.019385	1.00	0	0	0	0	0
rs458588	rs457162	OTHERSIGNAL	15	SLC35F1-PLN	1.72E-18	1.00	0	1	0	0	0
rs460399	rs457162	OTHERSIGNAL	15	SLC35F1-PLN	-	1.00	0	0	0	0	0
rs465226	rs457162	OTHERSIGNAL	15	SLC35F1-PLN	4.64E-19	1.00	0	0	0	0	0
rs4945614	rs457162	OTHERSIGNAL	15	SLC35F1-PLN	3.52E-19	1.00	0	3	1	0	0
rs4945615	rs457162	OTHERSIGNAL	15	SLC35F1-PLN	0.000020996	1.00	0	0	0	0	0
rs4945617	rs457162	OTHERSIGNAL	15	SLC35F1-PLN	2.93E-19	1.00	0	3	0	0	0
rs4946328	rs457162	OTHERSIGNAL	15	SLC35F1-PLN	3.98E-19	1.00	0	1	1	0	0
rs56061975	rs3902035	OTHERSIGNAL	15	SLC35F1-PLN	-	0.98	0	0	0	0	0
rs5879454	rs457162	OTHERSIGNAL	15	SLC35F1-PLN	-	0.81	0	0	0	0	0
rs59712944	rs11153730	INDEX	15	SLC35F1-PLN	-	0.81	0	14	0	0	0
rs62422253	rs3902035	OTHERSIGNAL	15	SLC35F1-PLN	-	1.00	0	4	0	0	0
rs62422254	rs3902035	OTHERSIGNAL	15	SLC35F1-PLN	-	0.99	0	11	0	0	0
rs62422258	rs3902035	OTHERSIGNAL	15	SLC35F1-PLN	-	1.00	0	10	0	0	0
rs62422259	rs3902035	OTHERSIGNAL	15	SLC35F1-PLN	-	1.00	0	8	0	0	0
rs62423960	rs3902035	OTHERSIGNAL	15	SLC35F1-PLN	-	1.00	0	9	0	0	0
rs62423961	rs3902035	OTHERSIGNAL	15	SLC35F1-PLN	-	1.00	0	2	0	0	0
rs62423962	rs3902035	OTHERSIGNAL	15	SLC35F1-PLN	-	0.99	0	2	0	0	0
rs62423963	rs3902035	OTHERSIGNAL	15	SLC35F1-PLN	-	0.99	0	3	0	0	0
rs62423965	rs3902035	OTHERSIGNAL	15	SLC35F1-PLN	-	1.00	0	2	0	0	0
rs62423966	rs3902035	OTHERSIGNAL	15	SLC35F1-PLN	-	1.00	0	1	0	0	0
rs62423967	rs3902035	OTHERSIGNAL	15	SLC35F1-PLN	-	1.00	0	2	0	0	0
rs62423968	rs3902035	OTHERSIGNAL	15	SLC35F1-PLN	-	1.00	0	2	0	0	0
rs62423969	rs3902035	OTHERSIGNAL	15	SLC35F1-PLN	-	1.00	0	2	0	0	0
rs62423970	rs3902035	OTHERSIGNAL	15	SLC35F1-PLN	-	1.00	0	1	0	0	0
rs62423993	rs3902035	OTHERSIGNAL	15	SLC35F1-PLN	-	1.00	0	1	0	0	0
rs62423994	rs3902035	OTHERSIGNAL	15	SLC35F1-PLN	-	0.99	0	1	0	0	0
rs62423995	rs3902035	OTHERSIGNAL	15	SLC35F1-PLN	-	0.99	0	3	0	0	0
rs62423996	rs3902035	OTHERSIGNAL	15	SLC35F1-PLN	-	0.87	0	0	0	0	0
rs62423997	rs3902035	OTHERSIGNAL	15	SLC35F1-PLN	-	0.99	0	0	0	0	0
rs62423999	rs3902035	OTHERSIGNAL	15	SLC35F1-PLN	-	0.99	0	4	0	0	0
rs62424000	rs3902035	OTHERSIGNAL	15	SLC35F1-PLN	-	0.98	0	5	0	0	0
rs6906332	rs11153730	INDEX	15	SLC35F1-PLN	-	0.83	0	0	0	0	0
rs6911035	rs11153730	INDEX	15	SLC35F1-PLN	-	0.83	0	0	0	0	0
rs6911094	rs457162	OTHERSIGNAL	15	SLC35F1-PLN	6.02E-19	1.00	0	2	0	0	0
rs6911339	rs11153730	INDEX	15	SLC35F1-PLN	9.58E-55	0.83	0	0	0	0	0
rs6917963	rs457162	OTHERSIGNAL	15	SLC35F1-PLN	4.65E-19	1.00	0	3	0	0	0
rs6921633	rs457162	OTHERSIGNAL	15	SLC35F1-PLN	2.61E-19	1.00	0	3	0	0	0
rs6921657	rs457162	OTHERSIGNAL	15	SLC35F1-PLN	1.83E-19	1.00	0	3	0	0	0
rs6933344	rs457162	OTHERSIGNAL	15	SLC35F1-PLN	7.63E-19	0.98	0	2	0	0	0
rs72967533	rs11153730	INDEX	15	SLC35F1-PLN	-	0.97	0	3	0	0	0
rs74640693	rs12210733	OTHERSIGNAL	15	SLC35F1-PLN	-	0.89	0	0	0	0	0
rs7748215	rs457162	OTHERSIGNAL	15	SLC35F1-PLN	-	1.00	0	0	0	0	0
rs7768436	rs457162	OTHERSIGNAL	15	SLC35F1-PLN	4.66E-19	1.00	0	2	0	0	0
rs77710920	rs12210733	OTHERSIGNAL	15	SLC35F1-PLN	-	0.86	1	0	1	0	0
rs7772845	rs11153730	INDEX	15	SLC35F1-PLN	3.42E-55	0.83	0	4	1	0	0
rs78757409	rs11153730	INDEX	15	SLC35F1-PLN	-	0.80	0	1	0	0	0
rs928598	rs457162	OTHERSIGNAL	15	SLC35F1-PLN	5.19E-20	0.81	0	0	0	0	0
rs928599	rs457162	OTHERSIGNAL	15	SLC35F1-PLN	0.017188	0.81	0	0	0	0	0
rs9320645	rs457162	OTHERSIGNAL	15	SLC35F1-PLN	0.019385	1.00	0	1	0	0	0
rs9481771	rs457162	OTHERSIGNAL	15	SLC35F1-PLN	0.035452	0.92	0	0	0	0	0
rs9481772	rs457162	OTHERSIGNAL	15	SLC35F1-PLN	2.75E-19	1.00	0	1	0	0	0
rs9489323	rs457162	OTHERSIGNAL	15	SLC35F1-PLN	-	1.00	0	0	0	0	0
rs9489324	rs457162	OTHERSIGNAL	15	SLC35F1-PLN	3.45E-19	1.00	0	0	0	0	0
rs9489325	rs457162	OTHERSIGNAL	15	SLC35F1-PLN	5.55E-20	0.81	0	0	0	0	0
rs9489510	rs9489510	OTHERSIGNAL	15	SLC35F1-PLN	1.3596E-08	1.00	0	16	0	0	0
rs980916	rs457162	OTHERSIGNAL	15	SLC35F1-PLN	3.22E-19	1.00	0	0	0	0	0
rs9920	rs9920	INDEX	16	CAV1	2.6008E-08	1.00	0	9	1	1	1

rs1805121	rs3807375	OTHERSIGNAL	17	KCNH2	7.44E-33	0.84	0	0	1	0	0
rs2072413	rs2072413	INDEX	17	KCNH2	1.32E-49	1.00	0	2	1	0	0
rs3807375	rs3807375	OTHERSIGNAL	17	KCNH2	2.88E-33	1.00	1	27	1	0	1
rs10504469	rs16936870	INDEX	18	NCOA2	2.6074E-08	0.95	1	11	1	0	0
rs10504474	rs16936870	INDEX	18	NCOA2	1.975E-09	0.98	0	24	1	0	1
rs10504476	rs16936870	INDEX	18	NCOA2	5.917E-09	0.98	0	10	0	0	0
rs10957519	rs16936870	INDEX	18	NCOA2	5.8135E-09	0.98	0	1	0	0	0
rs10957520	rs16936870	INDEX	18	NCOA2	8.4789E-09	0.98	0	48	0	1	0
rs11776287	rs16936870	INDEX	18	NCOA2	7.7381E-09	0.95	0	0	0	0	0
rs11776606	rs16936870	INDEX	18	NCOA2	0.0029361	0.95	0	0	0	0	0
rs11777095	rs16936870	INDEX	18	NCOA2	2.388E-09	0.95	0	45	0	0	0
rs11777780	rs16936870	INDEX	18	NCOA2	0.00072038	0.98	0	20	0	0	0
rs11780251	rs16936870	INDEX	18	NCOA2	6.1428E-09	0.98	0	2	0	0	0
rs11780609	rs16936870	INDEX	18	NCOA2	2.2642E-08	0.95	0	38	0	0	0
rs11780758	rs16936870	INDEX	18	NCOA2	2.4234E-09	0.94	0	53	0	0	0
rs11780994	rs16936870	INDEX	18	NCOA2	4.1213E-09	0.96	0	3	0	0	0
rs11993276	rs16936870	INDEX	18	NCOA2	1.2749E-08	0.95	0	0	0	0	0
rs11998005	rs16936870	INDEX	18	NCOA2	7.4718E-09	0.93	0	1	0	0	0
rs12675593	rs16936870	INDEX	18	NCOA2	2.0764E-09	0.95	0	11	0	0	0
rs12675772	rs16936870	INDEX	18	NCOA2	1.7554E-09	1.00	1	8	0	1	0
rs12678300	rs16936870	INDEX	18	NCOA2	4.0511E-09	0.98	0	0	0	0	0
rs12681491	rs16936870	INDEX	18	NCOA2	7.0558E-09	0.98	0	3	0	0	0
rs12682284	rs16936870	INDEX	18	NCOA2	3.186E-09	0.96	0	7	0	0	0
rs13254587	rs16936870	INDEX	18	NCOA2	-	1.00	0	2	0	0	0
rs13255359	rs16936870	INDEX	18	NCOA2	4.167E-09	0.98	0	30	0	0	0
rs13260060	rs16936870	INDEX	18	NCOA2	2.0187E-09	1.00	0	0	0	0	0
rs13266875	rs16936870	INDEX	18	NCOA2	-	0.98	0	7	0	0	0
rs13276452	rs16936870	INDEX	18	NCOA2	0.0027788	0.86	0	3	0	0	0
rs13277206	rs16936870	INDEX	18	NCOA2	2.7548E-09	1.00	0	2	0	0	0
rs142937720	rs16936870	INDEX	18	NCOA2	-	0.95	0	4	0	0	0
rs145139458	rs16936870	INDEX	18	NCOA2	-	0.93	0	8	0	0	0
rs16936749	rs16936870	INDEX	18	NCOA2	-	0.87	0	2	0	0	0
rs16936761	rs16936870	INDEX	18	NCOA2	1.8342E-08	0.88	0	3	0	0	0
rs16936861	rs16936870	INDEX	18	NCOA2	2.1933E-09	0.99	0	11	0	0	0
rs16936870	rs16936870	INDEX	18	NCOA2	1.051E-09	1.00	0	2	0	0	0
rs16936880	rs16936870	INDEX	18	NCOA2	2.157E-09	1.00	0	5	0	0	0
rs16936968	rs16936870	INDEX	18	NCOA2	6.8277E-09	0.98	1	5	0	0	0
rs16937002	rs16936870	INDEX	18	NCOA2	2.6924E-09	0.92	0	0	0	0	0
rs16937019	rs16936870	INDEX	18	NCOA2	6.4588E-09	0.91	0	2	0	0	0
rs1903343	rs16936870	INDEX	18	NCOA2	0.00068982	0.98	0	3	0	0	0
rs201613522	rs16936870	INDEX	18	NCOA2	-	0.98	0	40	0	1	0
rs28374075	rs16936870	INDEX	18	NCOA2	0.00090577	0.98	1	4	0	0	0
rs2926698	rs16936870	INDEX	18	NCOA2	2.2592E-09	0.91	0	0	0	0	0
rs2926699	rs16936870	INDEX	18	NCOA2	-	1.00	0	0	0	0	0
rs2926700	rs16936870	INDEX	18	NCOA2	2.115E-09	1.00	0	0	0	0	1
rs2926702	rs16936870	INDEX	18	NCOA2	8.3092E-08	0.80	1	12	0	1	1
rs2926705	rs16936870	INDEX	18	NCOA2	2.1109E-09	0.98	0	1	0	0	0
rs2926714	rs16936870	INDEX	18	NCOA2	3.6228E-09	0.98	0	0	0	0	0
rs2926718	rs16936870	INDEX	18	NCOA2	3.8989E-09	0.96	0	2	0	0	0
rs2958368	rs16936870	INDEX	18	NCOA2	2.4231E-09	0.98	0	5	0	0	0
rs2958370	rs16936870	INDEX	18	NCOA2	3.4756E-08	0.91	0	0	0	0	0
rs2958371	rs16936870	INDEX	18	NCOA2	3.656E-08	0.93	0	0	0	0	0
rs2977982	rs16936870	INDEX	18	NCOA2	2.0677E-09	0.98	0	4	0	0	0
rs2977984	rs16936870	INDEX	18	NCOA2	2.0063E-08	0.91	0	5	0	0	0
rs2977987	rs16936870	INDEX	18	NCOA2	2.1401E-08	0.98	0	2	0	0	0
rs2979638	rs16936870	INDEX	18	NCOA2	1.7564E-08	0.90	0	1	0	0	0
rs34220425	rs16936870	INDEX	18	NCOA2	-	0.90	0	1	0	0	0
rs34246353	rs16936870	INDEX	18	NCOA2	0.00040575	0.88	0	8	0	0	0
rs34280145	rs16936870	INDEX	18	NCOA2	0.0028243	0.92	0	0	0	0	0
rs34726915	rs16936870	INDEX	18	NCOA2	-	0.86	0	11	0	0	0
rs34738535	rs16936870	INDEX	18	NCOA2	-	0.94	0	0	0	0	0
rs34937845	rs16936870	INDEX	18	NCOA2	-	0.92	0	0	0	0	0
rs34957854	rs16936870	INDEX	18	NCOA2	-	0.98	0	8	0	1	0
rs34966562	rs16936870	INDEX	18	NCOA2	-	0.98	0	16	0	0	0
rs35006067	rs16936870	INDEX	18	NCOA2	0.00067012	0.96	0	11	0	0	0
rs35050697	rs16936870	INDEX	18	NCOA2	0.00090577	0.98	1	12	0	0	0
rs35060705	rs16936870	INDEX	18	NCOA2	-	0.98	0	13	0	0	0
rs35124548	rs16936870	INDEX	18	NCOA2	0.00067012	0.95	1	17	0	1	0
rs35168212	rs16936870	INDEX	18	NCOA2	-	0.87	0	2	0	0	0
rs35229942	rs16936870	INDEX	18	NCOA2	0.0029361	0.95	0	16	0	0	0
rs35380946	rs16936870	INDEX	18	NCOA2	-	0.92	0	0	0	0	0
rs35386521	rs16936870	INDEX	18	NCOA2	0.00072038	0.98	1	58	0	1	0
rs35395175	rs16936870	INDEX	18	NCOA2	0.000909	1.00	0	0	0	0	0
rs35607891	rs16936870	INDEX	18	NCOA2	-	0.82	0	2	0	0	0
rs35825351	rs16936870	INDEX	18	NCOA2	-	0.96	0	1	0	0	0
rs4074358	rs16936870	INDEX	18	NCOA2	2.6327E-08	0.88	0	11	0	0	0
rs4146466	rs16936870	INDEX	18	NCOA2	7.2569E-09	0.98	0	21	0	0	0
rs4236982	rs16936870	INDEX	18	NCOA2	6.6453E-09	0.95	0	0	0	0	0
rs4410938	rs16936870	INDEX	18	NCOA2	-	0.98	0	4	0	0	0
rs4483195	rs16936870	INDEX	18	NCOA2	4.9804E-09	0.98	0	50	0	0	0
rs4512408	rs16936870	INDEX	18	NCOA2	1.9401E-09	0.95	0	11	1	0	0
rs4645588	rs16936870	INDEX	18	NCOA2	0.0014207	0.95	0	4	0	0	0
rs4737300	rs16936870	INDEX	18	NCOA2	2.4571E-08	0.95	0	6	0	0	0
rs4737302	rs16936870	INDEX	18	NCOA2	0.00057709	0.98	0	0	0	0	0
rs4738079	rs16936870	INDEX	18	NCOA2	9.1126E-09	0.98	1	50	0	1	0
rs56933287	rs16936870	INDEX	18	NCOA2	-	0.88	0	7	0	0	0
rs57881093	rs16936870	INDEX	18	NCOA2	-	0.96	0	0	0	0	0
rs5892231	rs16936870	INDEX	18	NCOA2	-	0.98	0	12	0	0	0
rs60034031	rs16936870	INDEX	18	NCOA2	-	0.98	1	14	0	0	0
rs60195405	rs16936870	INDEX	18	NCOA2	-	0.94	0	7	0	0	0
rs6472512	rs16936870	INDEX	18	NCOA2	5.0938E-09	0.95	0	13	0	0	0
rs67939803	rs16936870	INDEX	18	NCOA2	-	0.95	0	17	0	0	0

rs6986625	rs16936870	INDEX	18	NCOA2	3.9952E-09	0.92	0	6	0	0	0
rs6987924	rs16936870	INDEX	18	NCOA2	3.0722E-09	0.92	1	59	1	1	1
rs7001409	rs16936870	INDEX	18	NCOA2	8.2992E-09	0.95	0	18	0	0	0
rs7003091	rs16936870	INDEX	18	NCOA2	2.7447E-09	1.00	0	1	0	0	0
rs7005564	rs16936870	INDEX	18	NCOA2	-	0.95	0	0	0	0	0
rs7006399	rs16936870	INDEX	18	NCOA2	1.7905E-07	0.86	0	0	0	0	0
rs7012908	rs16936870	INDEX	18	NCOA2	6.1003E-09	0.98	0	15	0	0	0
rs71523180	rs16936870	INDEX	18	NCOA2	-	0.98	0	7	0	0	0
rs71523181	rs16936870	INDEX	18	NCOA2	-	0.98	0	2	0	0	0
rs71558586	rs16936870	INDEX	18	NCOA2	-	0.96	0	54	0	0	0
rs726285	rs16936870	INDEX	18	NCOA2	1.9662E-08	0.92	0	3	0	0	0
rs74783055	rs16936870	INDEX	18	NCOA2	-	0.94	0	18	0	0	0
rs78167479	rs16936870	INDEX	18	NCOA2	-	0.94	0	18	0	0	0
rs9918828	rs16936870	INDEX	18	NCOA2	0.0012079	0.94	0	1	0	0	0
rs10504980	rs11779860	INDEX	19	LAPTM4B	6.0542E-10	0.98	0	1	0	0	0
rs10504981	rs11779860	INDEX	19	LAPTM4B	7E-10	0.98	0	1	0	0	0
rs11779860	rs11779860	INDEX	19	LAPTM4B	1.6869E-10	1.00	0	1	0	0	0
rs13256148	rs11779860	INDEX	19	LAPTM4B	-	0.84	0	1	0	0	0
rs17827449	rs11779860	INDEX	19	LAPTM4B	-	0.98	0	1	0	0	0
rs17827519	rs11779860	INDEX	19	LAPTM4B	2.3177E-09	0.98	0	1	0	0	0
rs1872015	rs11779860	INDEX	19	LAPTM4B	5.5136E-09	0.84	1	19	1	0	1
rs1872016	rs11779860	INDEX	19	LAPTM4B	6.4768E-09	0.83	1	19	1	0	1
rs1872017	rs11779860	INDEX	19	LAPTM4B	7.8932E-09	0.84	1	19	1	0	1
rs2449530	rs11779860	INDEX	19	LAPTM4B	-	0.83	0	1	0	0	0
rs2449541	rs11779860	INDEX	19	LAPTM4B	2.0161E-09	0.84	1	8	1	0	0
rs2449550	rs11779860	INDEX	19	LAPTM4B	6.3579E-09	0.83	0	2	0	0	0
rs2512057	rs11779860	INDEX	19	LAPTM4B	5.4831E-09	0.83	0	3	0	0	0
rs2512058	rs11779860	INDEX	19	LAPTM4B	-	0.83	1	7	0	0	0
rs2512061	rs11779860	INDEX	19	LAPTM4B	5.9207E-09	0.84	0	23	1	0	0
rs2513967	rs11779860	INDEX	19	LAPTM4B	5.2778E-09	0.83	0	3	0	0	0
rs2513968	rs11779860	INDEX	19	LAPTM4B	7.9414E-09	0.84	0	21	1	0	0
rs34039147	rs11779860	INDEX	19	LAPTM4B	-	0.90	0	1	0	0	0
rs34567914	rs11779860	INDEX	19	LAPTM4B	-	0.85	0	0	0	0	0
rs34673051	rs11779860	INDEX	19	LAPTM4B	-	0.98	0	3	0	0	0
rs4410873	rs11779860	INDEX	19	LAPTM4B	-	0.90	0	0	0	0	0
rs55987368	rs11779860	INDEX	19	LAPTM4B	-	0.90	0	3	0	0	0
rs67764958	rs11779860	INDEX	19	LAPTM4B	-	0.97	0	15	0	0	0
rs6983263	rs11779860	INDEX	19	LAPTM4B	-	0.84	0	0	0	0	0
rs6986429	rs11779860	INDEX	19	LAPTM4B	4.9263E-10	0.97	0	15	0	0	0
rs6986810	rs11779860	INDEX	19	LAPTM4B	4.7785E-10	0.98	0	14	0	0	0
rs6992805	rs11779860	INDEX	19	LAPTM4B	-	0.98	0	1	0	0	0
rs6994620	rs11779860	INDEX	19	LAPTM4B	3.0971E-10	0.97	1	7	0	0	0
rs7004556	rs11779860	INDEX	19	LAPTM4B	3.9937E-10	0.97	0	15	0	0	0
rs7004748	rs11779860	INDEX	19	LAPTM4B	4.6943E-10	0.98	0	14	0	0	0
rs7014909	rs11779860	INDEX	19	LAPTM4B	9.4616E-10	0.98	0	1	0	0	0
rs7015672	rs11779860	INDEX	19	LAPTM4B	-	0.94	0	1	0	0	0
rs1961102	rs1961102	INDEX	20	AZIN1	3.4067E-09	1.00	0	32	1	1	0
rs2679744	rs1961102	INDEX	20	AZIN1	-	0.86	0	7	0	0	0
rs606335	rs1961102	INDEX	20	AZIN1	-	0.89	0	9	0	0	0
rs10786665	rs2485376	INDEX	21	GBF1	-	0.95	0	0	0	0	0
rs1081655	rs2485376	INDEX	21	GBF1	-	0.99	0	1	0	0	0
rs11191245	rs2485376	INDEX	21	GBF1	-	0.98	0	0	0	0	0
rs11191267	rs2485376	INDEX	21	GBF1	3.9695E-08	0.95	0	0	0	0	0
rs11312135	rs2485376	INDEX	21	GBF1	-	0.97	0	6	0	0	0
rs11814894	rs2485376	INDEX	21	GBF1	-	0.95	0	0	0	0	0
rs146574493	rs2485376	INDEX	21	GBF1	-	0.90	0	0	0	0	0
rs148921436	rs2485376	INDEX	21	GBF1	-	0.99	0	1	0	0	0
rs1541046	rs2485376	INDEX	21	GBF1	4.9269E-08	0.97	0	0	0	0	0
rs1541047	rs2485376	INDEX	21	GBF1	0.0078094	0.84	0	5	0	0	0
rs1541048	rs2485376	INDEX	21	GBF1	-	0.97	0	5	0	0	0
rs1541049	rs2485376	INDEX	21	GBF1	-	0.97	0	6	0	0	0
rs1796765	rs2485376	INDEX	21	GBF1	3.5146E-08	0.97	0	37	1	0	1
rs1854291	rs2485376	INDEX	21	GBF1	0.014535	0.96	0	0	0	0	0
rs202032433	rs2485376	INDEX	21	GBF1	-	0.88	0	5	0	0	0
rs2246775	rs2485376	INDEX	21	GBF1	3.6788E-08	0.98	0	2	0	0	0
rs2273555	rs2485376	INDEX	21	GBF1	6.8418E-08	0.88	0	0	0	0	0
rs2281983	rs2485376	INDEX	21	GBF1	-	0.96	1	5	1	0	0
rs2479548	rs2485376	INDEX	21	GBF1	-	0.97	0	0	0	0	0
rs2479551	rs2485376	INDEX	21	GBF1	4.2515E-08	0.99	0	1	0	0	0
rs2479552	rs2485376	INDEX	21	GBF1	-	0.98	1	36	1	1	1
rs2479555	rs2485376	INDEX	21	GBF1	-	0.98	0	3	0	1	1
rs2485371	rs2485376	INDEX	21	GBF1	0.0030816	0.99	1	22	1	0	1
rs2485374	rs2485376	INDEX	21	GBF1	3.6783E-08	1.00	0	5	0	0	0
rs2485375	rs2485376	INDEX	21	GBF1	-	1.00	0	1	0	1	0
rs2485376	rs2485376	INDEX	21	GBF1	2.6914E-08	1.00	0	1	0	1	0
rs2485378	rs2485376	INDEX	21	GBF1	3.2351E-08	0.97	1	14	0	1	1
rs2993089	rs2485376	INDEX	21	GBF1	-	0.96	0	1	0	0	0
rs3061705	rs2485376	INDEX	21	GBF1	-	0.99	0	5	0	0	0
rs3758551	rs2485376	INDEX	21	GBF1	-	0.94	0	26	0	0	0
rs3758552	rs2485376	INDEX	21	GBF1	-	0.96	0	0	0	0	0
rs3758553	rs2485376	INDEX	21	GBF1	1.6277E-07	0.96	0	0	0	0	0
rs3781295	rs2485376	INDEX	21	GBF1	-	0.88	0	0	0	0	0
rs3802681	rs2485376	INDEX	21	GBF1	3.5016E-08	0.95	0	0	0	0	0
rs3808938	rs2485376	INDEX	21	GBF1	6.4749E-08	0.96	0	0	0	0	0
rs4244350	rs2485376	INDEX	21	GBF1	4.1253E-08	0.97	0	32	0	1	0
rs4244351	rs2485376	INDEX	21	GBF1	4.3316E-08	0.97	0	25	0	1	0
rs4331020	rs2485376	INDEX	21	GBF1	3.6355E-08	0.95	0	28	0	0	0
rs4919620	rs2485376	INDEX	21	GBF1	0.012283	0.97	0	4	0	0	0
rs4919621	rs2485376	INDEX	21	GBF1	1.557E-07	0.97	0	4	0	0	0
rs4919622	rs2485376	INDEX	21	GBF1	0.0043929	0.98	0	0	0	0	0
rs4919623	rs2485376	INDEX	21	GBF1	4.5771E-08	0.97	0	1	0	0	0
rs56115161	rs2485376	INDEX	21	GBF1	-	0.96	0	0	0	0	0

rs58626853	rs2485376	INDEX	21	GBF1	-	0.96	1	32	0	1	0
rs7080055	rs2485376	INDEX	21	GBF1	5.2645E-08	0.97	0	38	0	1	0
rs72490587	rs2485376	INDEX	21	GBF1	-	0.95	1	3	0	0	0
rs72845663	rs2485376	INDEX	21	GBF1	-	0.93	0	1	0	0	0
rs72845670	rs2485376	INDEX	21	GBF1	-	0.89	0	0	0	0	0
rs733283	rs2485376	INDEX	21	GBF1	7.2381E-08	0.97	0	4	0	0	0
rs74309119	rs2485376	INDEX	21	GBF1	-	0.92	0	0	0	0	0
rs772008	rs2485376	INDEX	21	GBF1	0.0067139	0.97	0	4	0	0	0
rs772010	rs2485376	INDEX	21	GBF1	-	0.97	0	1	0	0	0
rs772012	rs2485376	INDEX	21	GBF1	4.9753E-08	0.97	1	2	0	0	0
rs772014	rs2485376	INDEX	21	GBF1	4.5923E-08	0.91	0	6	0	0	0
rs772015	rs2485376	INDEX	21	GBF1	-	0.96	0	0	0	0	0
rs772016	rs2485376	INDEX	21	GBF1	3.4774E-08	0.90	0	5	0	0	0
rs772018	rs2485376	INDEX	21	GBF1	-	0.98	0	1	0	0	0
rs772019	rs2485376	INDEX	21	GBF1	-	0.97	0	5	0	0	0
rs772021	rs2485376	INDEX	21	GBF1	1.1365E-07	0.99	0	1	0	0	0
rs772022	rs2485376	INDEX	21	GBF1	-	0.99	0	0	0	0	0
rs772023	rs2485376	INDEX	21	GBF1	-	0.97	0	1	0	0	0
rs772024	rs2485376	INDEX	21	GBF1	-	0.93	0	1	0	0	0
rs772025	rs2485376	INDEX	21	GBF1	3.3681E-08	0.97	0	1	0	0	0
rs772026	rs2485376	INDEX	21	GBF1	-	0.97	1	3	0	0	0
rs772027	rs2485376	INDEX	21	GBF1	4.7659E-08	0.97	1	4	1	0	0
rs772028	rs2485376	INDEX	21	GBF1	-	0.83	1	6	1	0	0
rs772029	rs2485376	INDEX	21	GBF1	3.5903E-08	0.97	1	40	1	1	1
rs772030	rs2485376	INDEX	21	GBF1	1.5511E-07	0.93	0	6	0	0	0
rs772032	rs2485376	INDEX	21	GBF1	-	0.98	0	0	0	0	0
rs772033	rs2485376	INDEX	21	GBF1	-	0.97	0	0	0	0	0
rs7916262	rs2485376	INDEX	21	GBF1	-	0.98	0	4	0	0	0
rs7923183	rs2485376	INDEX	21	GBF1	-	0.96	0	0	0	0	0
rs796427	rs2485376	INDEX	21	GBF1	3.648E-08	0.97	0	5	0	0	0
rs812799	rs2485376	INDEX	21	GBF1	2.7191E-08	0.99	0	1	0	0	0
rs9664049	rs2485376	INDEX	21	GBF1	0.015089	0.97	0	7	1	0	0
rs11821100	rs7122937	INDEX	22	KCNQ1	-	0.91	0	0	0	0	0
rs12280952	rs7122937	INDEX	22	KCNQ1	0.000011774	0.94	0	26	0	1	1
rs12296050	rs7122937	INDEX	22	KCNQ1	4.38E-48	0.96	0	21	0	0	0
rs16928285	rs7122937	INDEX	22	KCNQ1	2.57E-52	0.84	1	20	1	0	1
rs16928297	rs7122937	INDEX	22	KCNQ1	2.09E-53	0.99	1	14	1	0	1
rs2074238	rs2074238	OTHERSIGNAL	22	KCNQ1	1.86E-28	1.00	0	24	1	0	1
rs2074239	rs7122937	INDEX	22	KCNQ1	5.32E-51	0.96	0	23	1	0	0
rs2301696	rs2301696	OTHERSIGNAL	22	KCNQ1	4.2589E-10	1.00	0	2	0	0	0
rs3864884	rs7122937	INDEX	22	KCNQ1	1.03E-52	0.83	1	19	1	1	1
rs58558735	rs7122937	INDEX	22	KCNQ1	-	0.94	0	0	0	0	0
rs7122937	rs7122937	INDEX	22	KCNQ1	1.24E-54	1.00	1	16	1	0	1
rs7939542	rs7122937	INDEX	22	KCNQ1	1.50E-50	0.96	1	14	1	0	1
rs7948689	rs7122937	INDEX	22	KCNQ1	-	0.81	1	21	1	1	1
rs7948693	rs7122937	INDEX	22	KCNQ1	0.000014241	0.82	1	21	1	1	1
rs7951832	rs7122937	INDEX	22	KCNQ1	1.06E-51	0.80	1	22	1	1	1
rs102274	rs174583	INDEX	23	FADS2	-	0.82	0	1	0	0	0
rs102275	rs174583	INDEX	23	FADS2	1.899E-10	0.86	0	1	0	0	0
rs1535	rs174583	INDEX	23	FADS2	2.222E-10	0.85	0	26	1	1	0
rs174533	rs174583	INDEX	23	FADS2	-	0.81	0	5	1	0	0
rs174535	rs174583	INDEX	23	FADS2	1.449E-10	0.80	0	5	0	0	0
rs174536	rs174583	INDEX	23	FADS2	1.3582E-10	0.81	0	4	0	0	0
rs174537	rs174583	INDEX	23	FADS2	2.0363E-10	0.81	0	1	0	0	0
rs174545	rs174583	INDEX	23	FADS2	1.714E-10	0.82	0	0	0	0	0
rs174546	rs174583	INDEX	23	FADS2	1.5244E-10	0.82	0	0	0	0	0
rs174547	rs174583	INDEX	23	FADS2	2.9193E-10	0.82	0	0	0	0	0
rs174550	rs174583	INDEX	23	FADS2	1.5079E-10	0.82	0	0	0	0	0
rs174553	rs174583	INDEX	23	FADS2	-	0.82	0	0	0	0	0
rs174554	rs174583	INDEX	23	FADS2	-	0.82	0	1	0	0	0
rs174562	rs174583	INDEX	23	FADS2	-	0.82	0	23	1	0	0
rs174564	rs174583	INDEX	23	FADS2	-	0.83	0	24	0	0	0
rs174566	rs174583	INDEX	23	FADS2	0.033673	0.86	0	1	0	0	0
rs174567	rs174583	INDEX	23	FADS2	-	0.85	0	0	0	0	0
rs174568	rs174583	INDEX	23	FADS2	0.033673	0.83	0	25	0	0	0
rs174574	rs174583	INDEX	23	FADS2	1.5317E-09	0.89	0	18	1	1	1
rs174576	rs174583	INDEX	23	FADS2	1.7591E-10	0.94	0	12	0	0	0
rs174577	rs174583	INDEX	23	FADS2	1.2964E-10	0.94	0	2	0	0	0
rs174578	rs174583	INDEX	23	FADS2	1.7373E-09	1.00	0	0	0	0	0
rs174580	rs174583	INDEX	23	FADS2	-	0.96	0	0	0	0	0
rs174581	rs174583	INDEX	23	FADS2	-	0.96	0	0	0	0	0
rs174583	rs174583	INDEX	23	FADS2	8.2073E-11	1.00	0	0	1	0	0
rs174584	rs174583	INDEX	23	FADS2	-	0.96	0	1	0	0	0
rs174592	rs174583	INDEX	23	FADS2	-	0.90	1	8	1	1	1
rs174594	rs174583	INDEX	23	FADS2	-	0.88	1	0	0	0	0
rs174599	rs174583	INDEX	23	FADS2	-	0.86	1	6	1	0	0
rs174601	rs174583	INDEX	23	FADS2	2.9326E-10	0.87	0	7	0	0	0
rs3834458	rs174583	INDEX	23	FADS2	-	0.83	0	7	0	0	0
rs5792235	rs174583	INDEX	23	FADS2	-	0.84	0	0	0	0	0
rs72381599	rs174583	INDEX	23	FADS2	-	0.82	0	0	0	0	0
rs97384	rs174583	INDEX	23	FADS2	-	0.83	0	0	0	0	0
rs99780	rs174583	INDEX	23	FADS2	-	0.86	0	1	0	0	0
rs10774599	rs3026445	INDEX	24	ATP2A2	2.2303E-08	0.94	0	0	0	0	0
rs11065628	rs3026445	INDEX	24	ATP2A2	-	0.90	0	0	0	0	0
rs12300631	rs3026445	INDEX	24	ATP2A2	-	0.83	0	7	0	0	0
rs1986123	rs3026445	INDEX	24	ATP2A2	-	0.93	1	19	0	0	0
rs199567377	rs3026445	INDEX	24	ATP2A2	-	0.84	0	1	0	0	0
rs3026427	rs3026445	INDEX	24	ATP2A2	1.6157E-08	0.89	1	9	1	1	0
rs3026445	rs3026445	INDEX	24	ATP2A2	2.9213E-12	1.00	0	24	0	0	0
rs4630352	rs3026445	INDEX	24	ATP2A2	1.0896E-08	0.94	0	4	1	1	0
rs57897915	rs3026445	INDEX	24	ATP2A2	-	0.80	0	1	0	0	0
rs58356085	rs3026445	INDEX	24	ATP2A2	-	0.86	0	1	0	0	0

rs7296679	rs3026445	INDEX	24	ATP2A2	4.0863E-08	0.88	0	0	0	0	0
rs17061696	rs728926	INDEX	25	KLF12	2.5022E-08	0.99	0	25	0	0	0
rs1886512	rs728926	INDEX	25	KLF12	4.2965E-08	0.99	1	49	1	1	0
rs728926	rs728926	INDEX	25	KLF12	2.0558E-08	1.00	0	41	0	0	0
rs7992314	rs728926	INDEX	25	KLF12	-	0.99	0	12	0	0	0
rs9573330	rs728926	INDEX	25	KLF12	7.6616E-08	1.00	0	21	1	0	0
rs1046651	rs2273905	INDEX	26	ANKRD9	-	0.84	1	6	1	1	1
rs10665540	rs2273905	INDEX	26	ANKRD9	-	0.87	0	0	0	0	0
rs11160691	rs2273905	INDEX	26	ANKRD9	-	0.95	0	16	0	0	0
rs1190544	rs2273905	INDEX	26	ANKRD9	-	0.90	0	0	0	0	0
rs1190547	rs2273905	INDEX	26	ANKRD9	2.2729E-09	0.90	0	20	0	0	1
rs1190549	rs2273905	INDEX	26	ANKRD9	-	0.91	0	0	0	0	0
rs1190551	rs2273905	INDEX	26	ANKRD9	1.0144E-09	0.90	0	0	0	0	0
rs1190553	rs2273905	INDEX	26	ANKRD9	-	0.91	0	0	0	0	0
rs1190554	rs2273905	INDEX	26	ANKRD9	1.8774E-09	0.91	0	0	0	0	0
rs12894354	rs2273905	INDEX	26	ANKRD9	-	0.97	0	0	0	0	0
rs1885708	rs2273905	INDEX	26	ANKRD9	-	0.96	0	0	0	0	0
rs1998422	rs2273905	INDEX	26	ANKRD9	-	1.00	0	1	0	0	0
rs200222508	rs2273905	INDEX	26	ANKRD9	-	0.88	0	14	0	0	0
rs200622845	rs2273905	INDEX	26	ANKRD9	-	0.80	0	9	0	0	0
rs200795901	rs2273905	INDEX	26	ANKRD9	-	0.80	0	0	0	0	0
rs2273905	rs2273905	INDEX	26	ANKRD9	4.0385E-11	1.00	0	23	0	0	0
rs2403058	rs2273905	INDEX	26	ANKRD9	-	0.90	0	1	1	0	0
rs3742444	rs2273905	INDEX	26	ANKRD9	-	0.84	1	6	1	1	1
rs4906205	rs2273905	INDEX	26	ANKRD9	1.2787E-09	0.90	0	1	0	0	0
rs4906208	rs2273905	INDEX	26	ANKRD9	7.5636E-10	0.96	0	6	0	0	0
rs8005804	rs2273905	INDEX	26	ANKRD9	-	0.94	0	8	0	0	0
rs8017980	rs2273905	INDEX	26	ANKRD9	-	0.96	0	0	0	0	0
rs942023	rs2273905	INDEX	26	ANKRD9	-	1.00	0	1	1	0	0
rs9743854	rs2273905	INDEX	26	ANKRD9	-	0.90	0	1	0	0	0
rs11070798	rs3105593	INDEX	27	USP50-TRPM7	1.5055E-07	0.84	0	0	0	0	0
rs11070799	rs3105593	INDEX	27	USP50-TRPM7	-	0.81	0	0	0	0	0
rs11070805	rs3105593	INDEX	27	USP50-TRPM7	-	0.81	0	5	0	0	0
rs11633404	rs3105593	INDEX	27	USP50-TRPM7	-	0.94	0	0	0	0	0
rs11634746	rs3105593	INDEX	27	USP50-TRPM7	-	0.81	0	0	1	0	0
rs11636964	rs3105593	INDEX	27	USP50-TRPM7	1.2532E-07	0.81	0	1	0	0	0
rs11637228	rs3105593	INDEX	27	USP50-TRPM7	-	0.81	0	1	0	0	0
rs12438305	rs3105593	INDEX	27	USP50-TRPM7	9.9412E-08	0.81	0	0	0	0	0
rs12439744	rs3105593	INDEX	27	USP50-TRPM7	1.7224E-07	0.81	0	0	0	0	0
rs12442787	rs3105593	INDEX	27	USP50-TRPM7	1.0329E-07	0.81	0	0	0	0	0
rs12595151	rs3105593	INDEX	27	USP50-TRPM7	-	0.83	0	0	0	0	0
rs137968959	rs3105593	INDEX	27	USP50-TRPM7	-	0.80	0	0	0	0	0
rs141987042	rs3105593	INDEX	27	USP50-TRPM7	-	0.81	0	0	0	0	0
rs146180371	rs3105593	INDEX	27	USP50-TRPM7	-	0.83	0	0	0	0	0
rs150820626	rs3105593	INDEX	27	USP50-TRPM7	-	0.92	0	0	0	0	0
rs17645523	rs3105593	INDEX	27	USP50-TRPM7	1.8647E-07	0.84	0	0	0	0	0
rs17645649	rs3105593	INDEX	27	USP50-TRPM7	-	0.81	0	1	0	0	0
rs17645826	rs3105593	INDEX	27	USP50-TRPM7	-	0.82	0	0	0	0	0
rs1986074	rs3105593	INDEX	27	USP50-TRPM7	-	0.83	0	0	0	0	0
rs1986075	rs3105593	INDEX	27	USP50-TRPM7	-	0.96	0	0	0	0	0
rs2003359	rs3105593	INDEX	27	USP50-TRPM7	-	0.96	0	0	0	0	0
rs2011064	rs3105593	INDEX	27	USP50-TRPM7	1.5191E-07	0.80	0	1	0	0	0
rs2063010	rs3105593	INDEX	27	USP50-TRPM7	-	0.81	0	0	0	0	0
rs2115671	rs3105593	INDEX	27	USP50-TRPM7	0.00001953	0.81	0	0	0	0	0
rs2292174	rs3105593	INDEX	27	USP50-TRPM7	1.0258E-07	0.81	0	0	0	0	0
rs2414059	rs3105593	INDEX	27	USP50-TRPM7	7.6888E-11	0.97	0	0	0	0	0
rs2414060	rs3105593	INDEX	27	USP50-TRPM7	1.557E-07	0.84	0	0	0	0	0
rs2414072	rs3105593	INDEX	27	USP50-TRPM7	-	0.97	0	1	0	0	0
rs2414073	rs3105593	INDEX	27	USP50-TRPM7	-	0.97	0	1	0	0	0
rs2630	rs3105593	INDEX	27	USP50-TRPM7	3.1586E-07	0.86	0	12	0	0	0
rs28718130	rs3105593	INDEX	27	USP50-TRPM7	-	0.80	0	0	0	0	0
rs2899462	rs3105593	INDEX	27	USP50-TRPM7	-	0.81	0	0	0	0	0
rs3098200	rs3105593	INDEX	27	USP50-TRPM7	-	0.89	0	0	0	0	0
rs3098202	rs3105593	INDEX	27	USP50-TRPM7	-	0.97	0	1	0	0	0
rs3101850	rs3105593	INDEX	27	USP50-TRPM7	-	0.99	0	1	0	0	0
rs3101852	rs3105593	INDEX	27	USP50-TRPM7	2.7999E-07	0.86	0	0	0	0	0
rs3101853	rs3105593	INDEX	27	USP50-TRPM7	2.6142E-07	0.84	0	0	0	0	0
rs3101854	rs3105593	INDEX	27	USP50-TRPM7	-	0.85	0	0	0	0	0
rs3101855	rs3105593	INDEX	27	USP50-TRPM7	-	0.84	0	0	0	0	0
rs3105590	rs3105593	INDEX	27	USP50-TRPM7	2.2115E-07	0.84	0	1	0	0	0
rs3105591	rs3105593	INDEX	27	USP50-TRPM7	1.4558E-07	0.84	0	1	0	0	0
rs3105592	rs3105593	INDEX	27	USP50-TRPM7	6.8025E-12	0.94	0	1	0	0	0
rs3105593	rs3105593	INDEX	27	USP50-TRPM7	3.0585E-12	1.00	0	1	0	0	0
rs3105598	rs3105593	INDEX	27	USP50-TRPM7	-	0.92	0	0	0	0	0
rs3109878	rs3105593	INDEX	27	USP50-TRPM7	-	0.95	0	3	0	0	0
rs3109879	rs3105593	INDEX	27	USP50-TRPM7	-	0.84	0	0	0	0	0
rs3109880	rs3105593	INDEX	27	USP50-TRPM7	-	0.83	0	0	0	0	0
rs3109881	rs3105593	INDEX	27	USP50-TRPM7	3.1815E-07	0.84	0	5	0	0	0
rs3109882	rs3105593	INDEX	27	USP50-TRPM7	-	0.97	0	1	0	0	0
rs3109884	rs3105593	INDEX	27	USP50-TRPM7	-	0.84	0	0	0	0	0
rs3109888	rs3105593	INDEX	27	USP50-TRPM7	2.5944E-07	0.84	0	0	0	0	0
rs3109891	rs3105593	INDEX	27	USP50-TRPM7	1.9845E-07	0.84	0	0	0	0	0
rs3109892	rs3105593	INDEX	27	USP50-TRPM7	1.5695E-07	0.83	0	0	0	0	0
rs3109894	rs3105593	INDEX	27	USP50-TRPM7	1.9335E-07	0.84	0	0	0	0	0
rs3109895	rs3105593	INDEX	27	USP50-TRPM7	1.5492E-07	0.84	0	0	0	0	0
rs3131573	rs3105593	INDEX	27	USP50-TRPM7	-	0.84	0	1	0	0	0
rs3131576	rs3105593	INDEX	27	USP50-TRPM7	4.4052E-12	0.97	0	1	0	0	0
rs3131577	rs3105593	INDEX	27	USP50-TRPM7	4.4293E-07	0.84	0	1	0	0	0
rs3131578	rs3105593	INDEX	27	USP50-TRPM7	2.8107E-07	0.84	0	1	0	0	0
rs3131580	rs3105593	INDEX	27	USP50-TRPM7	2.5611E-07	0.86	0	0	0	0	0
rs3131581	rs3105593	INDEX	27	USP50-TRPM7	-	0.85	0	0	0	0	0
rs3131582	rs3105593	INDEX	27	USP50-TRPM7	-	0.83	0	0	0	0	0

rs3131584	rs3105593	INDEX	27	USP50-TRPM7	0.80315	0.86	0	0	0	0	0
rs3131585	rs3105593	INDEX	27	USP50-TRPM7	-	0.86	0	0	0	0	0
rs3131586	rs3105593	INDEX	27	USP50-TRPM7	-	0.81	0	1	0	0	0
rs3131587	rs3105593	INDEX	27	USP50-TRPM7	2.2267E-07	0.86	0	1	0	0	0
rs3131588	rs3105593	INDEX	27	USP50-TRPM7	0.50387	0.99	0	0	0	0	0
rs3131589	rs3105593	INDEX	27	USP50-TRPM7	-	0.84	0	0	0	0	0
rs3131590	rs3105593	INDEX	27	USP50-TRPM7	-	0.84	0	0	0	0	0
rs3131595	rs3105593	INDEX	27	USP50-TRPM7	-	0.97	0	0	0	0	0
rs3131596	rs3105593	INDEX	27	USP50-TRPM7	-	0.84	0	0	0	0	0
rs3131597	rs3105593	INDEX	27	USP50-TRPM7	5.9233E-12	0.93	0	0	0	0	0
rs3131598	rs3105593	INDEX	27	USP50-TRPM7	-	0.92	0	0	0	0	0
rs3131599	rs3105593	INDEX	27	USP50-TRPM7	-	0.85	0	0	0	0	0
rs3131600	rs3105593	INDEX	27	USP50-TRPM7	-	0.85	0	0	0	0	0
rs3131601	rs3105593	INDEX	27	USP50-TRPM7	-	0.97	0	0	0	0	0
rs34386878	rs3105593	INDEX	27	USP50-TRPM7	-	0.81	0	0	0	0	0
rs3848129	rs3105593	INDEX	27	USP50-TRPM7	1.9869E-07	0.81	0	0	0	0	0
rs3848130	rs3105593	INDEX	27	USP50-TRPM7	1.392E-07	0.81	0	0	0	0	0
rs4509958	rs3105593	INDEX	27	USP50-TRPM7	-	0.80	0	0	0	0	0
rs4775893	rs3105593	INDEX	27	USP50-TRPM7	-	0.81	0	0	0	0	0
rs4775894	rs3105593	INDEX	27	USP50-TRPM7	8.0227E-12	0.93	0	0	0	0	0
rs4775897	rs3105593	INDEX	27	USP50-TRPM7	-	0.81	0	0	0	0	0
rs56015830	rs3105593	INDEX	27	USP50-TRPM7	-	0.81	0	0	0	0	0
rs56069965	rs3105593	INDEX	27	USP50-TRPM7	-	0.81	0	1	0	0	0
rs56080544	rs3105593	INDEX	27	USP50-TRPM7	-	0.82	0	0	0	0	0
rs56118429	rs3105593	INDEX	27	USP50-TRPM7	-	0.80	0	0	0	0	0
rs56944208	rs3105593	INDEX	27	USP50-TRPM7	-	0.81	0	0	0	0	0
rs57002197	rs3105593	INDEX	27	USP50-TRPM7	-	0.84	0	0	0	0	0
rs62017189	rs3105593	INDEX	27	USP50-TRPM7	-	0.81	0	0	0	0	0
rs62017197	rs3105593	INDEX	27	USP50-TRPM7	-	0.81	0	0	0	0	0
rs62017203	rs3105593	INDEX	27	USP50-TRPM7	-	0.81	0	0	0	0	0
rs62017204	rs3105593	INDEX	27	USP50-TRPM7	-	0.81	0	0	0	0	0
rs62017206	rs3105593	INDEX	27	USP50-TRPM7	-	0.81	0	0	0	0	0
rs62017210	rs3105593	INDEX	27	USP50-TRPM7	-	0.81	0	0	0	0	0
rs62017243	rs3105593	INDEX	27	USP50-TRPM7	-	0.81	1	27	0	0	1
rs7167138	rs3105593	INDEX	27	USP50-TRPM7	-	0.80	0	0	0	0	0
rs7174839	rs3105593	INDEX	27	USP50-TRPM7	4.1431E-12	0.94	0	0	0	0	0
rs7176874	rs3105593	INDEX	27	USP50-TRPM7	-	0.93	0	0	0	0	0
rs72527399	rs3105593	INDEX	27	USP50-TRPM7	-	0.82	0	0	0	0	0
rs74334968	rs3105593	INDEX	27	USP50-TRPM7	-	0.81	0	0	0	0	0
rs74728887	rs3105593	INDEX	27	USP50-TRPM7	-	0.81	0	0	0	0	0
rs76365099	rs3105593	INDEX	27	USP50-TRPM7	-	0.80	0	0	0	0	0
rs8023644	rs3105593	INDEX	27	USP50-TRPM7	6.1394E-07	0.81	0	0	0	0	0
rs8029073	rs3105593	INDEX	27	USP50-TRPM7	-	0.80	0	0	0	0	0
rs8033256	rs3105593	INDEX	27	USP50-TRPM7	-	0.80	1	0	0	0	0
rs8036588	rs3105593	INDEX	27	USP50-TRPM7	-	0.81	0	0	0	0	0
rs874665	rs3105593	INDEX	27	USP50-TRPM7	4.5285E-12	0.97	0	0	0	0	0
rs934624	rs3105593	INDEX	27	USP50-TRPM7	-	0.81	0	20	0	0	0
rs934625	rs3105593	INDEX	27	USP50-TRPM7	-	0.81	0	15	0	0	0
rs1296720	rs1296720	INDEX	28	CREBBP	3.5687E-10	1.00	1	91	1	1	1
rs12443744	rs12930096	OTHERSIGNAL	29	LITAF	-	0.99	0	38	0	0	0
rs12444261	rs12444261	OTHERSIGNAL	29	LITAF	2.1438E-12	1.00	1	86	1	1	1
rs12444280	rs12930096	OTHERSIGNAL	29	LITAF	0.66356	1.00	0	15	0	0	1
rs12444633	rs12930096	OTHERSIGNAL	29	LITAF	2.7487E-13	0.98	0	30	0	0	0
rs12444653	rs12930096	OTHERSIGNAL	29	LITAF	-	0.99	0	30	0	0	0
rs12445222	rs12930096	OTHERSIGNAL	29	LITAF	0.60034	0.99	0	35	0	0	0
rs12445902	rs12930096	OTHERSIGNAL	29	LITAF	-	0.83	0	21	0	0	0
rs12446514	rs12930096	OTHERSIGNAL	29	LITAF	0.65295	0.99	0	21	0	0	0
rs12446567	rs12930096	OTHERSIGNAL	29	LITAF	0.65295	0.99	0	23	0	0	0
rs12446730	rs12444261	OTHERSIGNAL	29	LITAF	4.7041E-12	0.82	0	0	0	0	0
rs12447508	rs12930096	OTHERSIGNAL	29	LITAF	-	0.94	0	11	0	0	1
rs12447546	rs12930096	OTHERSIGNAL	29	LITAF	0.66356	0.91	0	5	0	0	0
rs12447658	rs12930096	OTHERSIGNAL	29	LITAF	-	0.94	0	11	0	0	1
rs12447714	rs12930096	OTHERSIGNAL	29	LITAF	-	0.93	0	5	0	0	0
rs12448294	rs12930096	OTHERSIGNAL	29	LITAF	-	0.99	0	46	0	0	0
rs12448494	rs12930096	OTHERSIGNAL	29	LITAF	0.64063	0.83	0	21	0	0	0
rs12917676	rs12930096	OTHERSIGNAL	29	LITAF	-	0.93	0	0	0	0	0
rs12921437	rs12930096	OTHERSIGNAL	29	LITAF	0.59059	0.92	0	0	0	0	0
rs12927050	rs12930096	OTHERSIGNAL	29	LITAF	1.1715E-13	0.98	0	9	0	0	0
rs12927097	rs12930096	OTHERSIGNAL	29	LITAF	0.66896	0.99	0	9	0	0	0
rs12929430	rs12930096	OTHERSIGNAL	29	LITAF	9.6318E-13	0.98	1	6	0	0	0
rs12930096	rs12930096	OTHERSIGNAL	29	LITAF	2.9187E-13	1.00	1	44	0	0	0
rs1814273	rs12444261	OTHERSIGNAL	29	LITAF	-	0.96	0	0	0	0	0
rs202166128	rs12444261	OTHERSIGNAL	29	LITAF	-	0.99	0	7	0	0	0
rs2080512	rs735951	INDEX	29	LITAF	-	0.97	0	42	0	0	1
rs28439748	rs12930096	OTHERSIGNAL	29	LITAF	0.66356	1.00	0	16	0	0	1
rs34096091	rs12930096	OTHERSIGNAL	29	LITAF	-	0.97	0	45	0	0	0
rs35592815	rs12930096	OTHERSIGNAL	29	LITAF	0.60034	0.99	1	44	0	0	0
rs35901585	rs12930096	OTHERSIGNAL	29	LITAF	0.67084	0.99	0	33	0	0	0
rs36020240	rs12930096	OTHERSIGNAL	29	LITAF	0.64688	0.99	0	21	0	0	0
rs4510029	rs12444261	OTHERSIGNAL	29	LITAF	3.4858E-12	0.98	0	0	0	0	0
rs55693174	rs12444261	OTHERSIGNAL	29	LITAF	-	0.96	0	0	0	0	0
rs55947021	rs12930096	OTHERSIGNAL	29	LITAF	-	0.98	0	19	0	0	0
rs56021873	rs12444261	OTHERSIGNAL	29	LITAF	-	0.81	0	0	0	0	0
rs57439922	rs12444261	OTHERSIGNAL	29	LITAF	-	0.89	0	0	0	0	0
rs59642881	rs12930096	OTHERSIGNAL	29	LITAF	-	0.86	0	23	0	0	0
rs60493856	rs12444261	OTHERSIGNAL	29	LITAF	-	0.89	0	0	0	0	0
rs61541101	rs12444261	OTHERSIGNAL	29	LITAF	-	0.98	0	0	0	0	0
rs67188060	rs12930096	OTHERSIGNAL	29	LITAF	-	0.98	1	6	0	0	0
rs67188401	rs12444261	OTHERSIGNAL	29	LITAF	-	0.86	0	4	0	0	0
rs67445581	rs12444261	OTHERSIGNAL	29	LITAF	-	0.98	0	0	0	0	0
rs67850232	rs12444261	OTHERSIGNAL	29	LITAF	-	0.95	0	0	0	0	0
rs67918820	rs12444261	OTHERSIGNAL	29	LITAF	-	0.98	0	0	0	0	0

rs71388711	rs12930096	OTHERSIGNAL	29	LITAF	-	0.87	0	0	0	0	0
rs7187498	rs735951	INDEX	29	LITAF	-	0.93	0	5	0	0	0
rs7191330	rs735951	INDEX	29	LITAF	0.65053	0.97	0	13	0	0	0
rs7195296	rs12444261	OTHERSIGNAL	29	LITAF	9.62E-12	0.83	0	3	0	0	0
rs72779183	rs12930096	OTHERSIGNAL	29	LITAF	-	0.99	0	33	0	0	0
rs72781065	rs12444261	OTHERSIGNAL	29	LITAF	-	0.90	0	17	0	0	0
rs72781086	rs12444261	OTHERSIGNAL	29	LITAF	-	0.81	1	31	0	0	0
rs735951	rs735951	INDEX	29	LITAF	2.29E-28	1.00	0	11	0	0	0
rs8048558	rs12930096	OTHERSIGNAL	29	LITAF	0.42749	0.99	0	21	0	0	0
rs8049607	rs735951	INDEX	29	LITAF	3.40E-28	0.85	0	62	0	0	1
rs8050192	rs12930096	OTHERSIGNAL	29	LITAF	-	0.99	1	16	0	0	0
rs8050461	rs12930096	OTHERSIGNAL	29	LITAF	5.4085E-15	0.98	0	9	0	0	0
rs8050641	rs12930096	OTHERSIGNAL	29	LITAF	-	0.98	0	9	0	0	0
rs8052020	rs12930096	OTHERSIGNAL	29	LITAF	0.65295	0.99	0	14	0	0	0
rs8052255	rs12930096	OTHERSIGNAL	29	LITAF	-	0.98	0	9	0	0	0
rs8052262	rs12930096	OTHERSIGNAL	29	LITAF	-	0.98	0	9	0	0	0
rs8052803	rs12930096	OTHERSIGNAL	29	LITAF	0.65295	0.99	0	14	0	0	0
rs8056062	rs12930096	OTHERSIGNAL	29	LITAF	-	0.99	0	17	0	0	0
rs8063949	rs12444261	OTHERSIGNAL	29	LITAF	3.1273E-11	0.99	0	15	0	0	0
rs9929603	rs12930096	OTHERSIGNAL	29	LITAF	0.66356	1.00	0	39	0	0	0
rs9930359	rs12444261	OTHERSIGNAL	29	LITAF	-	0.81	0	1	0	0	0
rs1659127	rs246185	INDEX	30	MKL2	6.38E-11	0.87	0	1	0	0	0
rs1704528	rs246185	INDEX	30	MKL2	-	0.88	0	0	0	0	0
rs1704529	rs246185	INDEX	30	MKL2	-	0.87	0	0	0	0	0
rs181766	rs246185	INDEX	30	MKL2	-	1.00	0	32	0	0	0
rs193536	rs246185	INDEX	30	MKL2	-	0.98	0	32	0	0	0
rs246180	rs246185	INDEX	30	MKL2	-	0.93	0	0	0	0	0
rs246185	rs246185	INDEX	30	MKL2	2.6393E-13	1.00	0	5	1	0	0
rs30152	rs246185	INDEX	30	MKL2	-	0.81	0	0	0	0	0
rs30153	rs246185	INDEX	30	MKL2	-	0.81	0	0	0	0	0
rs10719000	rs4784934	OTHERSIGNAL	31	CNOT1	-	0.82	1	13	0	1	1
rs11364517	rs246196	INDEX	31	CNOT1	-	0.91	0	4	0	0	0
rs11859781	rs246196	INDEX	31	CNOT1	0.049714	0.81	0	0	0	0	0
rs11860728	rs246196	INDEX	31	CNOT1	-	0.86	0	0	0	0	0
rs11862156	rs246196	INDEX	31	CNOT1	0.022633	0.98	0	0	0	0	0
rs12102473	rs246196	INDEX	31	CNOT1	0.048234	0.85	0	0	0	0	0
rs12149484	rs246196	INDEX	31	CNOT1	0.024903	0.91	0	4	0	0	0
rs12149850	rs246196	INDEX	31	CNOT1	-	0.96	0	0	0	0	0
rs12232402	rs246196	INDEX	31	CNOT1	-	0.93	0	5	0	0	0
rs12232436	rs246196	INDEX	31	CNOT1	0.031186	0.93	0	4	0	0	0
rs12445577	rs246196	INDEX	31	CNOT1	0.014925	0.88	0	0	0	0	0
rs12446307	rs246196	INDEX	31	CNOT1	3.44E-56	0.93	0	0	0	0	0
rs12597246	rs246196	INDEX	31	CNOT1	-	0.93	0	0	0	0	0
rs12925702	rs246196	INDEX	31	CNOT1	6.46E-51	0.93	0	0	0	0	0
rs13339147	rs246196	INDEX	31	CNOT1	-	0.85	0	1	0	0	0
rs1424077	rs4784934	OTHERSIGNAL	31	CNOT1	3.0326E-08	0.98	1	5	0	0	0
rs151812	rs246196	INDEX	31	CNOT1	-	0.90	0	0	0	0	0
rs151814	rs246196	INDEX	31	CNOT1	-	0.93	0	10	0	0	0
rs151816	rs246196	INDEX	31	CNOT1	-	0.86	0	1	0	0	0
rs154431	rs246196	INDEX	31	CNOT1	-	0.93	0	41	1	0	0
rs154434	rs246196	INDEX	31	CNOT1	0.068956	0.93	0	0	0	0	0
rs1549607	rs246196	INDEX	31	CNOT1	2.16E-57	0.98	0	0	0	0	0
rs1646010	rs246196	INDEX	31	CNOT1	0.020653	1.00	0	0	0	0	0
rs173475	rs246196	INDEX	31	CNOT1	0.02001	1.00	0	0	0	0	0
rs181951	rs246196	INDEX	31	CNOT1	0.050527	0.93	0	0	0	0	0
rs1895522	rs4784934	OTHERSIGNAL	31	CNOT1	1.6808E-07	0.85	1	9	0	0	0
rs1971073	rs246196	INDEX	31	CNOT1	0.026818	0.93	0	1	0	0	0
rs1981960	rs246196	INDEX	31	CNOT1	0.036239	0.98	0	6	0	0	0
rs1981961	rs246196	INDEX	31	CNOT1	0.023108	0.98	0	6	0	0	0
rs199630654	rs246196	INDEX	31	CNOT1	-	0.90	0	1	0	0	0
rs2015185	rs246196	INDEX	31	CNOT1	-	0.93	0	0	0	0	0
rs2042401	rs4784934	OTHERSIGNAL	31	CNOT1	3.6835E-08	0.97	1	0	0	0	0
rs2067207	rs246196	INDEX	31	CNOT1	-	0.97	0	0	0	0	0
rs2067270	rs246196	INDEX	31	CNOT1	-	0.97	0	0	0	0	0
rs2090727	rs246196	INDEX	31	CNOT1	5.64E-57	0.97	0	0	0	0	0
rs2243463	rs246196	INDEX	31	CNOT1	0.015381	1.00	0	0	0	0	0
rs2405860	rs246196	INDEX	31	CNOT1	0.026818	0.93	0	0	0	0	0
rs244915	rs246196	INDEX	31	CNOT1	1.17E-52	0.88	0	0	0	0	0
rs246194	rs246196	INDEX	31	CNOT1	0.013972	1.00	0	0	0	0	0
rs246196	rs246196	INDEX	31	CNOT1	2.03E-57	1.00	0	0	0	0	0
rs246258	rs246196	INDEX	31	CNOT1	2.33E-57	1.00	0	0	0	0	0
rs27097	rs246196	INDEX	31	CNOT1	2.65E-53	0.91	0	0	0	0	0
rs28307	rs246196	INDEX	31	CNOT1	0.015381	1.00	0	0	0	0	0
rs28479997	rs246196	INDEX	31	CNOT1	-	0.97	0	0	0	0	0
rs28627526	rs4784934	OTHERSIGNAL	31	CNOT1	0.40965	0.83	1	11	0	1	1
rs28667004	rs246196	INDEX	31	CNOT1	-	0.93	0	0	0	0	0
rs2897253	rs246196	INDEX	31	CNOT1	0.025812	0.93	0	0	0	0	0
rs34716647	rs246196	INDEX	31	CNOT1	-	0.91	0	0	0	0	0
rs35239829	rs246196	INDEX	31	CNOT1	-	0.97	0	0	0	0	0
rs37034	rs246196	INDEX	31	CNOT1	0.015806	1.00	0	0	0	0	0
rs37036	rs246196	INDEX	31	CNOT1	2.36E-52	1.00	0	0	0	0	0
rs37039	rs246196	INDEX	31	CNOT1	0.015381	1.00	0	0	0	0	0
rs37040	rs246196	INDEX	31	CNOT1	-	1.00	0	0	0	0	0
rs37041	rs246196	INDEX	31	CNOT1	-	1.00	0	0	0	0	0
rs37051	rs246196	INDEX	31	CNOT1	0.015381	1.00	0	0	0	0	0
rs37053	rs246196	INDEX	31	CNOT1	2.09E-57	1.00	0	0	0	0	0
rs37054	rs246196	INDEX	31	CNOT1	5.47E-53	1.00	0	0	0	0	0
rs37055	rs246196	INDEX	31	CNOT1	2.20E-57	0.98	0	0	0	0	0
rs37056	rs246196	INDEX	31	CNOT1	-	0.96	0	0	0	0	0
rs37057	rs246196	INDEX	31	CNOT1	0.015381	0.97	0	1	0	0	0
rs37060	rs246196	INDEX	31	CNOT1	2.89E-57	0.97	0	0	0	0	0
rs37061	rs246196	INDEX	31	CNOT1	-	0.97	0	0	0	0	0

rs37062	rs246196	INDEX	31	CNOT1	1.88E-55	0.95	0	0	0	0	0
rs37063	rs246196	INDEX	31	CNOT1	-	0.95	0	0	0	0	0
rs37064	rs246196	INDEX	31	CNOT1	-	0.96	0	0	0	0	0
rs40187	rs246196	INDEX	31	CNOT1	-	1.00	0	0	0	0	0
rs40188	rs246196	INDEX	31	CNOT1	0.015381	0.97	0	0	0	0	0
rs42947	rs246196	INDEX	31	CNOT1	0.03485	1.00	0	0	0	0	0
rs4471670	rs246196	INDEX	31	CNOT1	-	0.97	0	0	0	0	0
rs4485352	rs246196	INDEX	31	CNOT1	5.26E-57	0.96	0	0	0	0	0
rs4496133	rs246196	INDEX	31	CNOT1	-	0.93	0	5	0	0	0
rs4784051	rs246196	INDEX	31	CNOT1	7.22E-56	0.93	0	46	1	1	0
rs4784052	rs246196	INDEX	31	CNOT1	-	0.92	0	3	0	0	0
rs4784934	rs4784934	OTHERSIGNAL	31	CNOT1	5.5462E-09	1.00	1	24	1	0	1
rs4784935	rs4784934	OTHERSIGNAL	31	CNOT1	0.50463	1.00	1	25	1	0	0
rs4784938	rs4784934	OTHERSIGNAL	31	CNOT1	6.2376E-08	0.91	1	13	0	1	1
rs4784956	rs246196	INDEX	31	CNOT1	0.08443	0.96	0	0	0	0	0
rs4784960	rs246196	INDEX	31	CNOT1	3.23E-56	0.93	0	0	0	0	0
rs60415374	rs4784934	OTHERSIGNAL	31	CNOT1	-	0.90	0	0	0	0	1
rs6499956	rs4784934	OTHERSIGNAL	31	CNOT1	-	0.85	0	1	0	0	0
rs6499962	rs246196	INDEX	31	CNOT1	7.43E-57	0.97	0	1	0	0	0
rs7186158	rs4784934	OTHERSIGNAL	31	CNOT1	0.39566	0.81	0	0	1	0	0
rs7186997	rs246196	INDEX	31	CNOT1	0.023108	0.97	0	0	0	0	0
rs7188697	rs246196	INDEX	31	CNOT1	6.96E-53	0.87	0	0	0	0	0
rs7189568	rs246196	INDEX	31	CNOT1	4.43E-56	0.93	0	0	0	0	0
rs7190613	rs246196	INDEX	31	CNOT1	-	0.93	1	7	0	0	0
rs7196236	rs246196	INDEX	31	CNOT1	-	0.91	0	1	0	0	0
rs7197786	rs246196	INDEX	31	CNOT1	0.04391	0.92	0	0	0	0	0
rs7198329	rs246196	INDEX	31	CNOT1	-	0.93	0	0	0	0	0
rs7199856	rs246196	INDEX	31	CNOT1	3.09E-57	0.99	0	0	0	0	0
rs7203887	rs246196	INDEX	31	CNOT1	1.02E-55	0.93	0	2	0	0	0
rs7205071	rs246196	INDEX	31	CNOT1	3.45E-52	0.93	0	16	0	0	0
rs78143441	rs246196	INDEX	31	CNOT1	-	0.85	0	0	0	0	0
rs78202261	rs246196	INDEX	31	CNOT1	-	0.93	0	0	0	0	0
rs78512818	rs246196	INDEX	31	CNOT1	-	0.93	0	0	0	0	0
rs8043716	rs246196	INDEX	31	CNOT1	-	0.92	0	0	0	0	0
rs8043726	rs246196	INDEX	31	CNOT1	-	0.88	0	0	0	0	0
rs8047769	rs246196	INDEX	31	CNOT1	-	0.99	0	0	0	0	0
rs8049393	rs246196	INDEX	31	CNOT1	1.72E-56	0.93	0	0	0	0	0
rs8051650	rs246196	INDEX	31	CNOT1	3.61E-56	0.93	0	1	0	0	0
rs8053455	rs246196	INDEX	31	CNOT1	-	0.99	0	0	0	0	0
rs8056620	rs246196	INDEX	31	CNOT1	0.022051	0.89	0	0	0	0	0
rs8061326	rs246196	INDEX	31	CNOT1	0.026818	0.93	0	1	0	0	0
rs8062272	rs246196	INDEX	31	CNOT1	-	0.91	0	2	0	0	0
rs863433	rs246196	INDEX	31	CNOT1	1.58E-55	0.87	0	0	0	0	0
rs9302700	rs246196	INDEX	31	CNOT1	-	0.93	0	2	0	0	0
rs9302701	rs246196	INDEX	31	CNOT1	0.040789	0.93	0	2	0	0	0
rs950843	rs246196	INDEX	31	CNOT1	1.44E-52	0.93	0	0	0	0	0
rs9921370	rs246196	INDEX	31	CNOT1	-	0.97	0	0	0	0	0
rs9923491	rs246196	INDEX	31	CNOT1	4.75E-57	0.97	0	0	0	0	0
rs9924724	rs246196	INDEX	31	CNOT1	0.027646	0.84	0	0	0	0	0
rs9924805	rs246196	INDEX	31	CNOT1	-	0.97	0	0	0	0	0
rs9926577	rs246196	INDEX	31	CNOT1	0.023108	0.97	0	0	0	0	0
rs9927443	rs246196	INDEX	31	CNOT1	0.043394	0.93	0	0	0	0	0
rs9928581	rs4784934	OTHERSIGNAL	31	CNOT1	-	0.99	0	7	1	0	0
rs9931547	rs4784934	OTHERSIGNAL	31	CNOT1	0.47119	0.97	1	6	0	1	1
rs9932944	rs246196	INDEX	31	CNOT1	0.014442	0.97	0	0	0	0	0
rs9935054	rs246196	INDEX	31	CNOT1	2.78E-56	0.93	0	0	0	0	0
rs9941290	rs246196	INDEX	31	CNOT1	2.53E-54	0.92	0	0	0	0	0
rs1003918	rs1052536	INDEX	32	LIG3	1.97E-24	0.99	0	0	0	0	0
rs1052536	rs1052536	INDEX	32	LIG3	6.21E-25	1.00	0	0	0	0	0
rs10853174	rs1052536	INDEX	32	LIG3	2.78E-22	0.96	0	9	0	0	0
rs1088450	rs1052536	INDEX	32	LIG3	-	0.89	0	25	0	0	0
rs12945428	rs1052536	INDEX	32	LIG3	-	0.88	0	0	0	0	0
rs12948362	rs1052536	INDEX	32	LIG3	1.61E-24	0.99	0	0	0	0	0
rs1634800	rs1052536	INDEX	32	LIG3	1.72E-24	0.93	0	24	0	0	0
rs1634802	rs1052536	INDEX	32	LIG3	-	0.93	0	9	0	0	0
rs2074518	rs1052536	INDEX	32	LIG3	4.65E-24	0.99	1	15	1	1	1
rs2339122	rs1052536	INDEX	32	LIG3	2.54E-24	0.93	0	16	0	0	0
rs2339123	rs1052536	INDEX	32	LIG3	-	0.93	0	7	0	0	0
rs3135967	rs1052536	INDEX	32	LIG3	8.84E-24	0.94	0	0	0	0	0
rs797989	rs1052536	INDEX	32	LIG3	1.22E-23	0.91	0	49	0	0	0
rs797990	rs1052536	INDEX	32	LIG3	-	0.91	0	53	0	0	0
rs810042	rs1052536	INDEX	32	LIG3	-	0.94	0	7	0	0	0
rs978202	rs1052536	INDEX	32	LIG3	-	0.81	0	3	0	0	0
rs11079650	rs9892651	INDEX	33	PRKCA	-	0.96	0	10	0	0	0
rs11658550	rs9892651	INDEX	33	PRKCA	-	0.97	0	4	0	0	0
rs11658630	rs9892651	INDEX	33	PRKCA	-	0.97	0	4	0	0	0
rs11867573	rs9892651	INDEX	33	PRKCA	-	0.97	0	7	0	0	0
rs12601850	rs9892651	INDEX	33	PRKCA	5.171E-11	0.83	0	36	0	0	0
rs12938407	rs9892651	INDEX	33	PRKCA	-	0.80	0	14	0	0	0
rs12940610	rs9892651	INDEX	33	PRKCA	6.214E-14	0.97	0	2	0	0	0
rs12944131	rs9892651	INDEX	33	PRKCA	-	0.83	0	10	0	0	0
rs12945138	rs9892651	INDEX	33	PRKCA	-	0.80	0	8	0	0	0
rs17633401	rs9892651	INDEX	33	PRKCA	4.4716E-11	0.83	0	6	1	0	0
rs17633437	rs9892651	INDEX	33	PRKCA	-	0.83	0	24	0	0	0
rs17706845	rs9892651	INDEX	33	PRKCA	8.873E-11	0.81	0	17	0	0	0
rs35105653	rs9892651	INDEX	33	PRKCA	-	0.80	0	8	0	0	0
rs35183571	rs9892651	INDEX	33	PRKCA	-	0.80	0	17	0	0	0
rs35433169	rs9892651	INDEX	33	PRKCA	-	0.80	0	10	0	0	0
rs35512343	rs9892651	INDEX	33	PRKCA	-	0.81	0	17	0	0	0
rs35687884	rs9892651	INDEX	33	PRKCA	-	0.80	0	11	0	0	0
rs4328478	rs9892651	INDEX	33	PRKCA	4.8561E-14	0.96	0	11	0	0	0
rs4335805	rs9892651	INDEX	33	PRKCA	-	0.96	0	10	0	0	0

rs4433842	rs9892651	INDEX	33	PRKCA	3.8041E-11	0.80	0	12	0	0	0
rs4577128	rs9892651	INDEX	33	PRKCA	1.1262E-13	0.97	0	15	0	0	0
rs67675584	rs9892651	INDEX	33	PRKCA	-	0.80	0	14	0	0	0
rs67700546	rs9892651	INDEX	33	PRKCA	-	0.83	0	9	1	0	0
rs67828405	rs9892651	INDEX	33	PRKCA	-	0.80	0	12	0	0	0
rs7210446	rs9892651	INDEX	33	PRKCA	7.5294E-14	0.99	0	15	0	0	0
rs7406054	rs9892651	INDEX	33	PRKCA	-	0.95	0	2	0	0	0
rs7406066	rs9892651	INDEX	33	PRKCA	-	0.96	0	2	0	0	0
rs8071250	rs9892651	INDEX	33	PRKCA	-	0.96	0	8	0	0	0
rs9303504	rs9892651	INDEX	33	PRKCA	8.6568E-14	0.97	1	2	0	1	0
rs9890911	rs9892651	INDEX	33	PRKCA	8.5512E-14	0.97	0	1	0	0	0
rs9892651	rs9892651	INDEX	33	PRKCA	2.705E-14	1.00	0	8	0	0	0
rs9893075	rs9892651	INDEX	33	PRKCA	4.5709E-14	0.97	0	4	0	0	0
rs9909004	rs9892651	INDEX	33	PRKCA	-	0.99	0	41	0	0	0
rs9910355	rs9892651	INDEX	33	PRKCA	5.6163E-14	0.96	1	2	0	1	0
rs9910577	rs9892651	INDEX	33	PRKCA	6.6581E-14	0.96	0	9	0	0	0
rs9912468	rs9892651	INDEX	33	PRKCA	4.0585E-14	0.97	0	0	0	0	0
rs10221267	rs1396515	INDEX	34	KCNJ2	-	0.90	0	1	0	0	0
rs10445231	rs17763769	OTHERSIGNAL	34	KCNJ2	0.026886	0.84	0	0	0	0	0
rs10775360	rs10775360	OTHERSIGNAL	34	KCNJ2	1.0739E-12	1.00	0	1	0	0	0
rs10852724	rs10775360	OTHERSIGNAL	34	KCNJ2	-	1.00	0	0	0	0	0
rs1120297	rs1396515	INDEX	34	KCNJ2	1.13E-23	0.99	0	0	0	0	0
rs11654387	rs1396515	INDEX	34	KCNJ2	1.32E-21	0.95	0	0	0	0	0
rs11868103	rs17763769	OTHERSIGNAL	34	KCNJ2	-	0.98	0	0	0	0	0
rs12103465	rs1396515	INDEX	34	KCNJ2	9.43E-23	0.88	0	1	0	0	0
rs12103757	rs1396515	INDEX	34	KCNJ2	-	0.88	0	1	0	0	0
rs1396513	rs1396515	INDEX	34	KCNJ2	-	0.97	0	0	1	0	0
rs1396514	rs1396515	INDEX	34	KCNJ2	1.64E-23	1.00	0	1	1	0	0
rs1396515	rs1396515	INDEX	34	KCNJ2	2.01E-25	1.00	0	1	1	0	0
rs1396517	rs1396515	INDEX	34	KCNJ2	1.89E-23	0.97	0	0	1	0	0
rs140229087	rs17763769	OTHERSIGNAL	34	KCNJ2	-	0.94	0	0	0	0	0
rs143379259	rs17763769	OTHERSIGNAL	34	KCNJ2	-	1.00	0	0	1	0	0
rs146789811	rs17763769	OTHERSIGNAL	34	KCNJ2	-	0.87	0	0	0	0	0
rs148491234	rs1396515	INDEX	34	KCNJ2	-	0.80	0	0	1	0	0
rs149316268	rs17763769	OTHERSIGNAL	34	KCNJ2	-	0.84	0	0	0	0	0
rs150310449	rs1396515	INDEX	34	KCNJ2	-	0.85	0	1	0	0	0
rs151082794	rs17763769	OTHERSIGNAL	34	KCNJ2	-	0.94	0	0	0	0	0
rs1588278	rs1396515	INDEX	34	KCNJ2	8.30E-23	0.88	0	0	1	0	0
rs1605749	rs1396515	INDEX	34	KCNJ2	7.13E-23	0.89	0	2	0	0	0
rs1605750	rs1396515	INDEX	34	KCNJ2	2.97E-23	0.90	0	0	0	0	0
rs17715938	rs10775360	OTHERSIGNAL	34	KCNJ2	9.819E-12	1.00	0	2	1	0	0
rs17763769	rs17763769	OTHERSIGNAL	34	KCNJ2	4.7729E-11	1.00	0	5	1	0	0
rs17778418	rs10775360	OTHERSIGNAL	34	KCNJ2	0.28177	1.00	0	1	0	0	0
rs17780198	rs17763769	OTHERSIGNAL	34	KCNJ2	3.5241E-11	0.95	0	0	0	0	0
rs1911970	rs1396515	INDEX	34	KCNJ2	-	0.86	0	0	0	0	0
rs2024186	rs1396515	INDEX	34	KCNJ2	3.1291E-06	0.96	0	0	0	0	0
rs2035582	rs17763769	OTHERSIGNAL	34	KCNJ2	0.040014	0.93	0	0	0	0	0
rs2159437	rs1396515	INDEX	34	KCNJ2	1.22E-24	0.94	0	0	0	0	0
rs236521	rs236586	OTHERSIGNAL	34	KCNJ2	-	0.98	0	0	0	0	0
rs236523	rs236586	OTHERSIGNAL	34	KCNJ2	4.7693E-11	0.97	0	3	0	0	0
rs236586	rs236586	OTHERSIGNAL	34	KCNJ2	6.0138E-11	1.00	0	7	0	0	0
rs236591	rs236586	OTHERSIGNAL	34	KCNJ2	0.072509	0.99	0	0	0	0	0
rs236595	rs236586	OTHERSIGNAL	34	KCNJ2	7.9529E-11	0.98	0	0	0	0	0
rs35813361	rs17763769	OTHERSIGNAL	34	KCNJ2	-	0.98	0	1	1	0	0
rs41408048	rs17763769	OTHERSIGNAL	34	KCNJ2	-	0.86	0	5	0	0	0
rs41459950	rs17763769	OTHERSIGNAL	34	KCNJ2	-	0.88	0	2	0	0	0
rs4436818	rs1396515	INDEX	34	KCNJ2	9.33E-22	0.90	0	0	0	0	0
rs4519367	rs1396515	INDEX	34	KCNJ2	-	0.84	0	0	0	0	0
rs4603601	rs1396515	INDEX	34	KCNJ2	3.74E-23	0.89	0	0	0	0	0
rs4640232	rs1396515	INDEX	34	KCNJ2	2.74E-23	0.90	0	0	0	0	0
rs4793370	rs1396515	INDEX	34	KCNJ2	-	0.89	0	0	0	0	0
rs4793394	rs1396515	INDEX	34	KCNJ2	1.49E-20	0.83	0	0	0	0	0
rs4793395	rs1396515	INDEX	34	KCNJ2	1.37E-20	0.84	0	0	0	0	0
rs6501392	rs1396515	INDEX	34	KCNJ2	6.65E-24	0.99	0	3	0	0	0
rs71357754	rs1396515	INDEX	34	KCNJ2	-	0.88	0	0	0	0	0
rs717118	rs1396515	INDEX	34	KCNJ2	3.37E-23	0.91	0	2	0	0	0
rs7211586	rs1396515	INDEX	34	KCNJ2	-	0.85	0	0	0	0	0
rs7213968	rs1396515	INDEX	34	KCNJ2	-	0.86	0	0	0	0	0
rs72529845	rs1396515	INDEX	34	KCNJ2	-	0.92	0	5	0	0	0
rs72855754	rs17763769	OTHERSIGNAL	34	KCNJ2	-	0.95	0	1	0	0	0
rs72855903	rs17763769	OTHERSIGNAL	34	KCNJ2	-	0.88	0	1	0	0	0
rs72855940	rs17763769	OTHERSIGNAL	34	KCNJ2	-	0.99	0	0	0	0	0
rs72868952	rs17763769	OTHERSIGNAL	34	KCNJ2	-	0.88	0	5	1	0	0
rs72868953	rs17763769	OTHERSIGNAL	34	KCNJ2	-	0.88	1	15	0	0	0
rs76665103	rs17763769	OTHERSIGNAL	34	KCNJ2	-	0.89	0	0	0	0	0
rs766752	rs1396515	INDEX	34	KCNJ2	-	0.97	0	0	0	0	0
rs78014203	rs17763769	OTHERSIGNAL	34	KCNJ2	-	0.98	0	0	0	0	0
rs8066985	rs1396515	INDEX	34	KCNJ2	2.17E-23	0.95	0	0	0	0	0
rs8070093	rs1396515	INDEX	34	KCNJ2	3.37E-23	0.90	0	1	0	0	0
rs8072275	rs1396515	INDEX	34	KCNJ2	1.61E-21	0.86	0	0	0	0	0
rs8073911	rs1396515	INDEX	34	KCNJ2	-	0.86	0	1	0	0	0
rs9302917	rs1396515	INDEX	34	KCNJ2	7.94E-22	0.86	0	0	0	0	0
rs981106	rs1396515	INDEX	34	KCNJ2	7.79E-23	0.89	0	1	1	0	0
rs9890689	rs1396515	INDEX	34	KCNJ2	2.74E-21	0.96	0	0	1	0	0
rs9894256	rs1396515	INDEX	34	KCNJ2	1.06E-20	0.83	0	0	0	0	0
rs9896031	rs1396515	INDEX	34	KCNJ2	-	0.86	0	0	0	0	0
rs9897538	rs1396515	INDEX	34	KCNJ2	3.30E-22	0.99	0	2	0	0	0
rs9899335	rs1396515	INDEX	34	KCNJ2	1.21E-21	0.86	0	13	0	0	0
rs9899840	rs1396515	INDEX	34	KCNJ2	4.03E-23	0.89	0	0	0	0	0
rs9904355	rs1396515	INDEX	34	KCNJ2	0.019643	0.94	0	0	0	0	0
rs9904480	rs1396515	INDEX	34	KCNJ2	-	0.94	0	0	0	0	0
rs9912702	rs1396515	INDEX	34	KCNJ2	9.48E-24	0.95	0	0	0	0	0

rs9913332	rs1396515	INDEX	34	KCNJ2	4.85E-21	0.88	0	0	0	0	0
rs9916380	rs1396515	INDEX	34	KCNJ2	-	0.97	0	0	0	0	0
rs1805128	rs1805128	INDEX	35	KCNE1	0.0037693	1.00	0	1	0	0	0

Supplementary Table 14 (3 pages): Magenta analyses. Shown are the Gene Set Enrichment Analysis p-values testing for association of QT-interval associated SNPs with pathways in GO, INGENUITY, KEGG and PANTHER databases.

Gene set	NOMINAL GSEA PVAL 95PERC CUTOFF	FDR 95PERC CUTOFF	EXP # GENES ABOVE 95PERC CUTOFF	OBS # GENES ABOVE 95PERC CUTOFF
regulation of the force of heart contraction	1.00E-04	6.00E-03	1	6
inorganic anion exchanger activity	1.67E-04	3.14E-02	1	5
voltage-gated ion channel activity	2.00E-04	3.58E-01	7	17
Voltage-gated_potassium_channel	4.00E-04	2.19E-01	4	12
anion transmembrane transporter activity	4.00E-04	2.29E-02	1	5
blood circulation	5.00E-04	2.62E-01	2	9
Cation_transport	5.25E-04	3.89E-01	22	37
anion transport	1.20E-03	2.14E-01	1	5
cellular calcium ion homeostasis	1.40E-03	2.70E-01	3	9
transcription repressor activity	1.60E-03	3.66E-01	8	17
Extracellular_transport_and_import	2.40E-03	2.04E-01	4	10
cAMP biosynthetic process	2.70E-03	2.55E-01	1	4
Nucleic_acid_binding	3.10E-03	2.40E-01	31	45
potassium ion transport	3.10E-03	4.02E-01	7	16
chromatin modification	3.40E-03	3.90E-01	10	19
protein localization	4.20E-03	3.71E-01	3	8
ATP binding	4.50E-03	5.03E-01	65	83
membrane depolarization	4.50E-03	2.48E-01	1	4
Meiosis	4.70E-03	2.56E-01	3	9
transcription factor activity	5.90E-03	5.34E-01	41	56
nucleotide metabolic process	6.70E-03	3.95E-01	1	5
VEGF.Signaling	6.90E-03	1.06E-01	1	4
Cation_transporter	6.90E-03	3.16E-01	5	12
Transporter	7.20E-03	3.45E-01	4	9
KEGG_MELANOGENESIS	7.50E-03	1.00E+00	5	11
Homeostasis	7.80E-03	2.26E-01	3	8
nucleoside diphosphate kinase activity	8.00E-03	3.34E-01	0	3
GABA-B_receptor_II_signaling	8.30E-03	2.41E-01	0	3
cellular response to oxidative stress	8.30E-03	2.89E-01	0	3
response to hypoxia	8.40E-03	5.22E-01	6	13
UTP biosynthetic process	8.40E-03	3.18E-01	0	3
GTP biosynthetic process	8.40E-03	2.40E-01	0	3
regulation of transcription from RNA polymerase II p	9.00E-03	5.31E-01	10	18
activation of protein kinase A activity	9.40E-03	3.84E-01	1	4
regulation of gene expression by genetic imprinting	9.50E-03	2.80E-01	1	3
regulation of ARF GTPase activity	9.60E-03	3.95E-01	1	5
Protein_phosphorylation	1.04E-02	3.65E-01	29	41
G1 phase of mitotic cell cycle	1.07E-02	3.07E-01	1	3
KEGG_DILATED_CARDIOMYOPATHY	1.12E-02	7.05E-01	4	10
ARF GTPase activator activity	1.15E-02	3.95E-01	1	5

Nitric.Oxide.Signaling.in.the.Cardiovascular.System	1.16E-02	2.06E-01	1	3
Protein_phosphatase	1.23E-02	2.63E-01	6	13
Ras protein signal transduction	1.24E-02	5.39E-01	3	8
CTP biosynthetic process	1.24E-02	3.78E-01	1	3
Transmembrane_receptor_regulatory/adaptor_prot	1.31E-02	2.50E-01	3	8
Adenylate_cyclase	1.35E-02	2.38E-01	1	3
muscle myosin complex	1.35E-02	3.58E-01	1	3
Action_potential_propagation	1.36E-02	2.15E-01	1	4
protein self-association	1.36E-02	3.57E-01	1	3
transcription factor binding	1.37E-02	5.56E-01	7	14
Kinase	1.42E-02	2.76E-01	2	5
trophectodermal cell differentiation	1.50E-02	3.62E-01	1	3
learning or memory	1.50E-02	4.78E-01	2	5
regulation of G-protein coupled receptor protein sig	1.53E-02	4.43E-01	1	5
Chromatin_packaging_and_remodeling	1.55E-02	3.67E-01	8	14
histone-lysine N-methyltransferase activity	1.55E-02	4.04E-01	1	4
Spermatogenesis_and_motility	1.58E-02	3.88E-01	5	10
regulation of heart contraction	1.69E-02	4.83E-01	2	5
RNA polymerase II transcription factor activity	1.73E-02	6.01E-01	6	12
Heart_development	1.73E-02	3.17E-01	2	6
cation channel activity	1.75E-02	3.89E-01	1	3
basolateral plasma membrane	1.81E-02	6.04E-01	5	10
adenylate cyclase activity	1.85E-02	3.81E-01	1	3
positive regulation of vasodilation	1.89E-02	3.87E-01	1	3
delayed rectifier potassium channel activity	1.95E-02	4.01E-01	1	3
KEGG_OOCYTE_MEIOSIS	2.03E-02	7.10E-01	6	11
methyltransferase activity	2.06E-02	5.94E-01	6	11
caveola	2.10E-02	5.26E-01	2	6
KEGG_VEGF_SIGNALING_PATHWAY	2.10E-02	7.37E-01	4	8
cardiac muscle tissue development	2.16E-02	3.93E-01	1	3
Angiotensin_II-stimulated_signaling_through_G_pro	2.17E-02	1.89E-01	0	2
calcium-dependent phospholipid binding	2.26E-02	4.91E-01	1	4
KEGG_VASCULAR_SMOOTH_MUSCLE_CONTRACTIO	2.28E-02	5.60E-01	6	11
nucleotide binding	2.33E-02	6.40E-01	85	98
KEGG_WNT_SIGNALING_PATHWAY	2.39E-02	5.54E-01	7	13
nucleoside-triphosphatase activity	2.46E-02	5.96E-01	3	7
Z disc	2.50E-02	5.76E-01	2	6
oligodendrocyte development	2.61E-02	4.68E-01	1	3
multicellular organismal development	2.79E-02	6.33E-01	40	51
phosphoprotein phosphatase activity	2.80E-02	6.12E-01	2	5
aging	2.82E-02	6.06E-01	3	7
De_novo_purine_biosynthesis	2.85E-02	6.43E-01	1	4
biosynthetic process	2.91E-02	5.98E-01	2	6
cell-cell signaling	3.01E-02	6.22E-01	11	18
ubiquitin-dependent protein catabolic process	3.16E-02	6.13E-01	7	12

protein complex	3.17E-02	6.47E-01	7	12
Immunoglobulin	3.20E-02	3.65E-01	0	2
Actin_binding_cytoskeletal_protein	3.24E-02	4.73E-01	4	8
Chromatin/chromatin-binding_protein	3.27E-02	4.83E-01	6	11
Other_transcription_factor	3.51E-02	4.80E-01	16	23
nucleoplasm	3.54E-02	6.42E-01	21	30
negative regulation of endothelial cell proliferation	3.57E-02	5.33E-01	1	3
2-oxoglutarate metabolic process	3.61E-02	5.65E-01	1	3
receptor-mediated endocytosis	3.71E-02	6.22E-01	2	5
manganese ion binding	3.72E-02	5.85E-01	1	4
ubiquitin thiolesterase activity	3.79E-02	6.33E-01	3	7
Basic_helix-loop-helix_transcription_factor	3.95E-02	4.69E-01	5	9
KEGG_ALPHA_LINOLENIC_ACID_METABOLISM	4.03E-02	8.28E-01	1	3
DNA_methyltransferase	4.10E-02	3.12E-01	1	3
cation transport	4.11E-02	6.41E-01	3	7
ion transport	4.13E-02	6.85E-01	24	32
attachment of GPI anchor to protein	4.21E-02	4.79E-01	0	2
muscle contraction	4.29E-02	6.37E-01	5	9
histone binding	4.41E-02	6.49E-01	2	5
KEGG_VIBRIO_CHOLERAE_INFECTION	4.47E-02	6.10E-01	3	6
KEGG_FC_GAMMA_R_MEDIATED_PHAGOCYTOSIS	4.49E-02	6.01E-01	5	9
sarcoplasmic reticulum membrane	4.56E-02	6.06E-01	1	3
protein tyrosine phosphatase activity	4.60E-02	6.47E-01	4	8
ER to Golgi vesicle-mediated transport	4.61E-02	6.50E-01	2	5
oxidoreductase activity, acting on paired donors, wit	4.63E-02	6.10E-01	1	3
intracellular protein transport	4.75E-02	6.75E-01	9	14
structural constituent of muscle	4.79E-02	6.26E-01	2	5
regulation of fatty acid oxidation	4.83E-02	6.05E-01	1	3
KEGG_PHENYLALANINE_METABOLISM	4.87E-02	6.35E-01	1	3
transcriptional repressor complex	4.94E-02	6.52E-01	1	4

R2 increment for genome-wide significant SNPs in explaining age-, sex-, RR-adjusted QT interval

	35 SNPs	68 SNPs	60 SNPs from GWiS
ARIC	5.5%	7.6%	7.4%
FHS	5.8%	8.3%	NA
ERGO	7.0%	9.9%	NA

Supplementary Table 15: Proportion variance explained by QT SNPs. Shown is the proportion of variance in QT (adjusted for age, sex and RR interval) explained by the 35 sentinel QT interval SNPs at 35 loci, as well as by 68 independent ($r2<0.05$) SNPs at 35 loci compared to a model without the SNPs in 3 large cohort studies. In addition, 60 independent SNPs selected by GWiS (see Supplementary Table 15) were tested in one cohort.

Supplementary Table 16 (2 pages): GWiS analysis. Shown are SNPs selected by GWiS (see Methods for details) as independent QT-associated SNPs at 35 loci that achieved genome-wide significance in association of GWAS+replication samples. Loci are indicated by GeneID with multiple SNPs at some loci. The estimated variance explained is shown per SNP and per locus (which may include more than one SNP). The GWiS analysis incorporates LD information from ARIC and association information from the GWAS meta-analysis (without replication results incorporated).

Supplementary Table 16a: **Results for all SNPs at genome-wide significant loci**

Chr	GeneID	Name	Start	End	Length	SNPs	Tests	SNP.name	SNP.pos	SNP.MAF	SNP.R2	K	SSM	VarExp	BIC	f.stat	R2
1	GeneID:1	RNF207	6,071,709	6,245,523	173815	834	96.1617	rs846111	6201957	0.281	1	1	0.726131	0.00213568	71.2677	163.078	0
1	GeneID:1	RNF207	6,071,709	6,245,523	173815	834	96.1617	SUMMARY	-	-	-	1	0.726131	0.00213568	71.2677	163.078	-
1	GeneID:2	TCEA3	23,491,293	23,625,485	134193	517	50.19	rs2298632	23583062	0.4988	1	1	0.270607	0.000795902	20.7988	60.6928	0
1	GeneID:2	TCEA3	23,491,293	23,625,485	134193	517	50.19	rs946267	23620290	0.1403	1	2	0.349358	0.000231618	20.8083	34.9414	0.0549715
1	GeneID:2	TCEA3	23,491,293	23,625,485	134193	517	50.19	SUMMARY	-	-	-	2	0.349358	0.00102752	20.8083	39.1863	-
1	GeneID:3	NOS1AP	160,240,600	160,705,156	464557	1596	131.26	rs12143842	#########	0.2443	1	1	4.20778	0.0123758	463.951	954.805	0
1	GeneID:3	NOS1AP	160,240,600	160,705,156	464557	1596	131.26	rs3934467	#########	0.2232	1	2	5.37438	0.0034312	586.746	584.317	0.0775377
1	GeneID:3	NOS1AP	160,240,600	160,705,156	464557	1596	131.26	rs12090201	#########	0.0964	1	3	5.74192	0.001081	619.233	180.899	0.0190682
1	GeneID:3	NOS1AP	160,240,600	160,705,156	464557	1596	131.26	rs12025136	#########	0.7438	1	4	5.85197	0.0003237	622.69	164.698	0.0591093
1	GeneID:3	NOS1AP	160,240,600	160,705,156	464557	1596	131.26	rs4657166	#########	0.7028	1	5	5.95865	0.0003137	625.998	461.562	0.297037
1	GeneID:3	NOS1AP	160,240,600	160,705,156	464557	1596	131.26	rs2655732	#########	0.4243	1	6	6.03706	0.0002307	626.275	32.9139	0.0052209
1	GeneID:3	NOS1AP	160,240,600	160,705,156	464557	1596	131.26	SUMMARY	-	-	-	6	6.03706	0.0177561	626.275	229.551	-
1	GeneID:4	DPT_ATP1E	166,929,898	167,778,502	848605	2125	150.888	rs10919070	#########	0.8726	1	1	0.596612	0.00175474	56.2755	133.939	0
1	GeneID:4	DPT_ATP1E	166,929,898	167,778,502	848605	2125	150.888	rs12061601	#########	0.8825	1	2	0.972088	0.00110434	88.5098	84.6155	0.0044386
1	GeneID:4	DPT_ATP1E	166,929,898	167,778,502	848605	2125	150.888	rs17502733	#########	0.0518	1	3	1.24557	0.00080437	109.731	62.952	0.0001288
1	GeneID:4	DPT_ATP1E	166,929,898	167,778,502	848605	2125	150.888	rs545833	#########	0.2673	1	4	1.34623	0.00029605	111.822	63.1373	0.166901
1	GeneID:4	DPT_ATP1E	166,929,898	167,778,502	848605	2125	150.888	rs12564558	#########	0.9405	1	5	1.43696	0.00026685	113.03	39.4824	0.045542
1	GeneID:4	DPT_ATP1E	166,929,898	167,778,502	848605	2125	150.888	rs17349138	#########	0.5532	1	6	1.52326	0.00025384	113.931	68.4349	0.114986
1	GeneID:4	DPT_ATP1E	166,929,898	167,778,502	848605	2125	150.888	SUMMARY	-	-	-	6	1.52326	0.00448019	113.931	57.1477	-
2	GeneID:5	SLC8A1	40,193,490	40,635,501	442012	1808	103.789	rs12997023	40606486	0.9502	1	1	0.252463	0.000742538	18.0375	56.6204	0
2	GeneID:5	SLC8A1	40,193,490	40,635,501	442012	1808	103.789	rs6544311	40206781	0.3808	1	2	0.433748	0.000533192	28.8121	40.7517	0.0025257
2	GeneID:5	SLC8A1	40,193,490	40,635,501	442012	1808	103.789	SUMMARY	-	-	-	2	0.433748	0.00127573	28.8121	48.6642	-
2	GeneID:6	SP3	174,447,598	174,452,072	4475	887	89.1393	rs13002675	#########	0.186	1	1	0.147055	0.000432514	6.37118	32.9701	0
2	GeneID:6	SP3	174,447,598	174,452,072	4475	887	89.1393	SUMMARY	-	-	-	1	0.147055	0.000432514	6.37118	32.9701	-
2	GeneID:7	CCDC141	179,398,101	179,399,915	1815	784	52.9721	rs7600330	#########	0.5829	1	1	0.136362	0.000401065	5.69291	30.5718	0
2	GeneID:7	CCDC141	179,398,101	179,399,915	1815	784	52.9721	SUMMARY	-	-	-	1	0.136362	0.000401065	5.69291	30.5718	-
2	GeneID:8	LOC26010	200,868,744	200,899,279	30536	926	60.5995	rs11888462	#########	0.4192	1	1	0.15186	0.000446647	7.29579	34.048	0
2	GeneID:8	LOC26010	200,868,744	200,899,279	30536	926	60.5995	SUMMARY	-	-	-	1	0.15186	0.000446647	7.29579	34.048	-
3	GeneID:9	SCN5A_SCN	38,392,349	38,773,840	381492	976	84.3762	rs6793245	38574041	0.3208	1	1	0.502789	0.00147879	46.3263	112.845	0
3	GeneID:9	SCN5A_SCN	38,392,349	38,773,840	381492	976	84.3762	rs3922843	38599347	0.2568	1	2	0.71445	0.00062253	60.736	49.8789	0.0002682
3	GeneID:9	SCN5A_SCN	38,392,349	38,773,840	381492	976	84.3762	rs6800541	38749836	0.5949	1	3	0.883459	0.00049709	70.7858	40.4217	0.00026
3	GeneID:9	SCN5A_SCN	38,392,349	38,773,840	381492	976	84.3762	rs6599234	38690304	0.3249	1	4	1.04364	0.00047113	80.1532	40.0629	0.0032239
3	GeneID:9	SCN5A_SCN	38,392,349	38,773,840	381492	976	84.3762	SUMMARY	-	-	-	4	1.04364	0.00306954	80.1532	58.6494	-
3	GeneID:10	C3orf75	47,350,959	47,553,842	202884	315	28.7103	rs17784882	47519007	0.399	1	1	0.133178	0.000391699	5.94848	29.8576	0
3	GeneID:10	C3orf75	47,350,959	47,553,842	202884	315	28.7103	SUMMARY	-	-	-	1	0.133178	0.000391699	5.94848	29.8576	-
4	GeneID:11	SLC4A4	72,240,018	72,357,080	117063	683	46.4592	rs2363719	72357080	0.1104	1	1	0.163143	0.000479832	8.82637	36.5788	0
4	GeneID:11	SLC4A4	72,240,018	72,357,080	117063	683	46.4592	SUMMARY	-	-	-	1	0.163143	0.000479832	8.82637	36.5788	-
4	GeneID:12	SMARCAD1	95,245,457	95,473,753	228297	1024	75.2791	rs183993	95349048	0.5792	1	1	0.147664	0.000434306	6.60846	33.1067	0
4	GeneID:12	SMARCAD1	95,245,457	95,473,753	228297	1024	75.2791	SUMMARY	-	-	-	1	0.147664	0.000434306	6.60846	33.1067	-
5	GeneID:13	PKD2L2	137,031,668	137,821,115	789448	1092	75.6065	rs13355516	#########	0.8267	1	1	0.183234	0.000538924	10.5919	41.086	0
5	GeneID:13	PKD2L2	137,031,668	137,821,115	789448	1092	75.6065	SUMMARY	-	-	-	1	0.183234	0.000538924	10.5919	41.086	-
6	GeneID:14	GMPR	16,356,109	16,402,701	46593	1265	128.208	rs4716056	16386369	0.613	1	1	0.17443	0.000513028	9.07669	39.1108	0
6	GeneID:14	GMPR	16,356,109	16,402,701	46593	1265	128.208	SUMMARY	-	-	-	1	0.17443	0.000513028	9.07669	39.1108	-
6	GeneID:15	SLC35F1_PI	118,545,211	119,153,843	608633	1388	85.6662	rs11153730	#########	0.5011	1	1	1.32803	0.00390596	139.034	298.786	0
6	GeneID:15	SLC35F1_PI	118,545,211	119,153,843	608633	1388	85.6662	rs12212795	#########	0.0545	1	2	1.58337	0.00075102	158.404	132.435	0.0580396
6	GeneID:15	SLC35F1_PI	118,545,211	119,153,843	608633	1388	85.6662	rs1771756	#########	0.4424	1	3	1.68597	0.00030177	161.007	215.5	0.403238
6	GeneID:15	SLC35F1_PI	118,545,211	119,153,843	608633	1388	85.6662	SUMMARY	-	-	-	3	1.68597	0.00495875	161.007	126.57	-
7	GeneID:16	CAV1	115,987,328	115,987,328	1	734	47.6158	rs9920	#########	0.9055	1	1	0.108442	0.000318946	2.66974	24.3101	0
7	GeneID:16	CAV1	115,987,328	115,987,328	1	734	47.6158	SUMMARY	-	-	-	1	0.108442	0.000318946	2.66974	24.3101	-
7	GeneID:17	KCNH2	150,127,461	150,320,876	193416	960	103.954	rs2968863	#########	0.2392	1	1	0.830752	0.00244339	82.9401	186.632	0
7	GeneID:17	KCNH2	150,127,461	150,320,876	193416	960	103.954	rs6972137	#########	0.8096	1	2	1.22624	0.0011632	117.83	167.85	0.0827454
7	GeneID:17	KCNH2	150,127,461	150,320,876	193416	960	103.954	SUMMARY	-	-	-	2	1.22624	0.00360659	117.83	137.899	-
8	GeneID:18	NCOA2	71,208,737	71,513,712	304976	957	72.8754	rs16936870	71351896	0.0986	1	1	0.158539	0.000466291	7.86008	35.5461	0
8	GeneID:18	NCOA2	71,208,737	71,513,712	304976	957	72.8754	SUMMARY	-	-	-	1	0.158539	0.000466291	7.86008	35.5461	-
8	GeneID:19	LAPTM4B	98,872,905	98,933,499	60595	971	85.6488	rs6995436	98880310	0.5212	1	1	0.16734	0.000492175	8.68521	37.5203	0
8	GeneID:19	LAPTM4B	98,872,905	98,933,499	60595	971	85.6488	SUMMARY	-	-	-	1	0.16734	0.000492175	8.68521	37.5203	-
8	GeneID:20	AZIN1	103,916,575	104,002,021	85447	1150	101.012	rs2916558	#########	0.3684	1	1	0.134251	0.000394856	4.8108	30.0983	0
8	GeneID:20	AZIN1	103,916,575	104,002,021	85447	1150	101.012	SUMMARY	-	-	-	1	0.134251	0.000394856	4.8108	30.0983	-
10	GeneID:21	GBF1	103,995,376	104,104,318	108943	463	33.8115	rs2485376	#########	0.3887	1	1	0.137998	0.000405876	6.32525	30.9387	0
10	GeneID:21	GBF1	103,995,376	104,104,318	108943	463	33.8115	SUMMARY	-	-	-	1	0.137998	0.000405876	6.32525	30.9387	-
11	GeneID:22	KCNQ1	2,288,613	2,484,900	196288	986	130.642	rs7122937	2443126	0.1916	1	1	1.06536	0.00313342	109.074	239.504	0
11	GeneID:22	KCNQ1	2,288,613	2,484,900	196288	986	130.642	rs739677	2430556	0.7657	1	2	1.31975	0.00074819	127.888	57.0919	0.0006925
11	GeneID:22	KCNQ1	2,288,613	2,484,900	196288	986	130.642	rs2074238	2441379	0.0532	1	3	1.49918	0.00052774	138.699	116.633	0.0760608
11	GeneID:22	KCNQ1	2,288,613	2,484,900	196288	986	130.642	rs800138	2352867	0.2341	1	4	1.60414	0.00030871	141.431	28.8631	0.0019987
11	GeneID:22	KCNQ1	2,288,613	2,484,900	196288	986	130.642	SUMMARY	-	-	-	4	1.60414	0.00471806	141.431	90.2968	-
11	GeneID:23	FEN1	61,300,075	61,379,716	79642	639	67.8047	rs174577	61361390	0.3449	1	1	0.184699	0.000543232	10.8651	41.4146	0
11	GeneID:23	FEN1	61,300,075	61,379,716	79642	639	67.8047	SUMMARY	-	-	-	1	0.184699	0.000543232	10.8651	41.4146	-

12	GeneID:24	ATP2A2	109,113,875	109,567,467	453593	481	51.9027	rs4630352	#########	0.3528	1	1	0.146736	0.000431577	6.8763	32.8987	0
12	GeneID:24	ATP2A2	109,113,875	109,567,467	453593	481	51.9027	SUMMARY	-	-	-	1	0.146736	0.000431577	6.8763	32.8987	-
13	GeneID:25	KLF12	73,409,992	73,418,187	8196	1210	113.814	rs728926	73411123	0.364	1	1	0.140443	0.000413066	5.38555	31.487	0
13	GeneID:25	KLF12	73,409,992	73,418,187	8196	1210	113.814	SUMMARY	-	-	-	1	0.140443	0.000413066	5.38555	31.487	-
14	GeneID:26	ANKRD9	101,878,083	102,044,752	166670	608	51.7251	rs4906208	#########	0.6481	1	1	0.171069	0.000503144	9.60763	38.3569	0
14	GeneID:26	ANKRD9	101,878,083	102,044,752	166670	608	51.7251	SUMMARY	-	-	-	1	0.171069	0.000503144	9.60763	38.3569	-
15	GeneID:27	TRPM7	48,538,342	48,690,892	152551	858	51.0794	rs3105593	48632310	0.4416	1	1	0.217985	0.000641134	14.8805	48.8832	0
15	GeneID:27	TRPM7	48,538,342	48,690,892	152551	858	51.0794	SUMMARY	-	-	-	1	0.217985	0.000641134	14.8805	48.8832	-
16	GeneID:28	CREBBP	3,792,777	3,813,643	20867	655	82.6529	rs1296720	3813643	0.8003	1	1	0.17559	0.000516442	9.64581	39.3711	0
16	GeneID:28	CREBBP	3,792,777	3,813,643	20867	655	82.6529	rs889807	4198174	0.4823	1	2	0.298008	0.000360053	14.0432	27.4471	9.58E-05
16	GeneID:28	CREBBP	3,792,777	3,813,643	20867	655	82.6529	SUMMARY	-	-	-	2	0.298008	0.000876495	14.0432	33.4216	-
16	GeneID:29	LITAF	11,574,706	11,658,516	83811	995	97.8788	rs735951	11601037	0.458	1	1	0.53916	0.00158577	50.2598	121.021	0
16	GeneID:29	LITAF	11,574,706	11,658,516	83811	995	97.8788	SUMMARY	-	-	-	1	0.53916	0.00158577	50.2598	121.021	-
16	GeneID:30	MKL2	14,285,074	14,302,933	17860	591	70.702	rs1659127	14295806	0.336	1	1	0.191709	0.00056385	11.6092	42.9873	0
16	GeneID:30	MKL2	14,285,074	14,302,933	17860	591	70.702	SUMMARY	-	-	-	1	0.191709	0.00056385	11.6092	42.9873	-
16	GeneID:31	GINS3_CNC	57,017,427	57,273,249	255823	972	103.157	rs37055	57118276	0.2568	1	1	1.13576	0.00334047	117.225	255.383	0
16	GeneID:31	GINS3_CNC	57,017,427	57,273,249	255823	972	103.157	rs4784934	57017427	0.2635	1	2	1.28803	0.00044785	124.795	34.1413	4.20E-05
16	GeneID:31	GINS3_CNC	57,017,427	57,273,249	255823	972	103.157	SUMMARY	-	-	-	2	1.28803	0.00378832	124.795	144.874	-
17	GeneID:32	RFFL	30,165,268	30,464,279	299012	1247	120.119	rs1052536	30355688	0.4681	1	1	0.460086	0.00135319	41.1812	103.248	0
17	GeneID:32	RFFL	30,165,268	30,464,279	299012	1247	120.119	SUMMARY	-	-	-	1	0.460086	0.00135319	41.1812	103.248	-
17	GeneID:33	PRKCA	61,630,703	61,761,499	130797	1146	78.1473	rs9892651	61734255	0.5773	1	1	0.251356	0.000739282	18.1972	56.372	0
17	GeneID:33	PRKCA	61,630,703	61,761,499	130797	1146	78.1473	SUMMARY	-	-	-	1	0.251356	0.000739282	18.1972	56.372	-
17	GeneID:34	KCNJ2	65,715,141	66,125,360	410220	1472	115.689	rs1396515	65942588	0.5192	1	1	0.472405	0.00138943	42.6012	106.016	0
17	GeneID:34	KCNJ2	65,715,141	66,125,360	410220	1472	115.689	rs236523	65724237	0.5268	1	2	0.592022	0.00035181	46.3562	41.8045	0.0167027
17	GeneID:34	KCNJ2	65,715,141	66,125,360	410220	1472	115.689	rs4793397	66031984	0.4828	1	3	0.701791	0.00032285	49.4246	76.0242	0.154314
17	GeneID:34	KCNJ2	65,715,141	66,125,360	410220	1472	115.689	SUMMARY	-	-	-	3	0.701791	0.00206409	49.4246	52.5322	-
21	GeneID:35	KCNE1	34,743,550	34,743,550	1	877	94.8299	rs2070359	34748646	0.1793	1	1	0.103345	0.000303955	1.4095	23.1672	0
21	GeneID:35	KCNE1	34,743,550	34,743,550	1	877	94.8299	SUMMARY	-	-	-	1	0.103345	0.000303955	1.4095	23.1672	-

Supplementary Table 16b: Summary by locus

Chr	GeneID	Name	Start	End	Length	SNPs	Tests	SNP.name	K	SSM	VarExp	BIC	f.stat	R2	indexSNP	VarExpTopSNP
1	GeneID:1	RNF207	6,071,709	6,245,523	173815	834	96.1617	SUMMARY	1	0.726131	0.0021357	71.2677	163.078	-	rs846111	0.0021357
1	GeneID:2	TCEA3	23,491,293	23,625,485	134193	517	50.19	SUMMARY	2	0.349358	0.0010275	20.8083	39.1863	-	rs2298632	0.0007959
1	GeneID:3	NOS1AP	160,240,600	160,705,156	464557	1596	131.26	SUMMARY	6	6.03706	0.0177561	626.275	229.551	-	rs12143842	0.0123758
1	GeneID:4	DPT_ATP1	166,929,898	167,778,502	848605	2125	150.888	SUMMARY	6	1.52326	0.0044802	113.931	57.1477	-	rs1091907	0.0017547
2	GeneID:5	SLC8A1	40,193,490	40,635,501	442012	1808	103.789	SUMMARY	2	0.433748	0.0012757	28.8121	48.6642	-	rs12997023	0.0007425
2	GeneID:6	SP3	174,447,598	174,452,072	4475	887	89.1393	SUMMARY	1	0.147055	0.0004325	6.37118	32.9701	-	rs13002675	0.0004325
2	GeneID:7	CCDC141	179,398,101	179,399,915	1815	784	52.9721	SUMMARY	1	0.136362	0.0004011	5.69291	30.5718	-	rs7600330	0.0004011
2	GeneID:8	LOC26010	200,868,744	200,899,279	30536	926	60.5995	SUMMARY	1	0.15186	0.0004466	7.29579	34.048	-	rs11888462	0.0004466
3	GeneID:9	SCN5A_SC	38,392,349	38,773,840	381492	976	84.3762	SUMMARY	4	1.04364	0.0030695	80.1532	58.6494	-	rs6793245	0.0014788
3	GeneID:10	C3orf75	47,350,959	47,553,842	202884	315	28.7103	SUMMARY	1	0.133178	0.0003917	5.94848	29.8576	-	rs17784882	0.0003917
4	GeneID:11	SLC4A4	72,240,018	72,357,080	117063	683	46.4592	SUMMARY	1	0.163143	0.0004798	8.82637	36.5788	-	rs2363719	0.0004798
4	GeneID:12	SMARCAD1	95,245,457	95,473,753	228297	1024	75.2791	SUMMARY	1	0.147664	0.0004343	6.60846	33.1067	-	rs183993	0.0004343
5	GeneID:13	PKD2L2	137,031,668	137,821,115	789448	1092	75.6065	SUMMARY	1	0.183234	0.0005389	10.5919	41.086	-	rs13355516	0.0005389
6	GeneID:14	GMPR	16,356,109	16,402,701	46593	1265	128.208	SUMMARY	1	0.17443	0.000513	9.07669	39.1108	-	rs4716056	0.000513
6	GeneID:15	SLC35F1_P	118,545,211	119,153,843	608633	1388	85.6662	SUMMARY	3	1.68597	0.0049588	161.007	126.57	-	rs1115373	0.003906
7	GeneID:16	CAV1	115,987,328	115,987,328	1	734	47.6158	SUMMARY	1	0.108442	0.0003189	2.66974	24.3101	-	rs9920	0.0003189
7	GeneID:17	KCNH2	150,127,461	150,320,876	193416	960	103.954	SUMMARY	2	1.22624	0.0036066	117.83	137.899	-	rs2968863	0.0024434
8	GeneID:18	NCOA2	71,208,737	71,513,712	304976	957	72.8754	SUMMARY	1	0.158539	0.0004663	7.86008	35.5461	-	rs1693687	0.0004663
8	GeneID:19	LAPTM4B	98,872,905	98,933,499	60595	971	85.6488	SUMMARY	1	0.16734	0.0004922	8.68521	37.5203	-	rs6995436	0.0004922
8	GeneID:20	AZIN1	103,916,575	104,002,021	85447	1150	101.012	SUMMARY	1	0.134251	0.0003949	4.8108	30.0983	-	rs2916558	0.0003949
10	GeneID:21	GBF1	103,995,376	104,104,318	108943	463	33.8115	SUMMARY	1	0.137998	0.0004059	6.32525	30.9387	-	rs2485376	0.0004059
11	GeneID:22	KCNQ1	2,288,613	2,484,900	196288	986	130.642	SUMMARY	4	1.60414	0.0047181	141.431	90.2968	-	rs7122937	0.0031334
11	GeneID:23	FEN1	61,300,075	61,379,716	79642	639	67.8047	SUMMARY	1	0.184699	0.0005432	10.8651	41.4146	-	rs174577	0.0005432
12	GeneID:24	ATP2A2	109,113,875	109,567,467	453593	481	51.9027	SUMMARY	1	0.146736	0.0004316	6.8763	32.8987	-	rs4630352	0.0004316
13	GeneID:25	KLF12	73,409,992	73,418,187	8196	1210	113.814	SUMMARY	1	0.140443	0.0004131	5.38555	31.487	-	rs728926	0.0004131
14	GeneID:26	ANKRD9	101,878,083	102,044,752	166670	608	51.7251	SUMMARY	1	0.171069	0.0005031	9.60763	38.3569	-	rs4906208	0.0005031
15	GeneID:27	TRPM7	48,538,342	48,690,892	152551	858	51.0794	SUMMARY	1	0.217985	0.0006411	14.8805	48.8832	-	rs3105593	0.0006411
16	GeneID:28	CREBBP	3,792,777	3,813,643	20867	655	82.6529	SUMMARY	2	0.298008	0.0008765	14.0432	33.4216	-	rs1296720	0.0005164
16	GeneID:29	LITAF	11,574,706	11,658,516	83811	995	97.8788	SUMMARY	1	0.53916	0.0015858	50.2598	121.021	-	rs735951	0.0015858
16	GeneID:30	MKL2	14,285,074	14,302,933	17860	591	70.702	SUMMARY	1	0.191709	0.0005639	11.6092	42.9873	-	rs1659127	0.0005639
16	GeneID:31	GINS3_CNC	57,017,427	57,273,249	255823	972	103.157	SUMMARY	2	1.28803	0.0037883	124.795	144.874	-	rs37055	0.0033405
17	GeneID:32	RFFL	30,165,268	30,464,279	299012	1247	120.119	SUMMARY	1	0.460086	0.0013532	41.1812	103.248	-	rs1052536	0.0013532
17	GeneID:33	PRKCA	61,630,703	61,761,499	130797	1146	78.1473	SUMMARY	1	0.251356	0.0007393	18.1972	56.372	-	rs9892651	0.0007393
17	GeneID:34	KCNJ2	65,715,141	66,125,360	410220	1472	115.689	SUMMARY	3	0.701791	0.0020641	49.4246	52.5322	-	rs1396515	0.0013894
21	GeneID:35	KCNE1	34,743,550	34,743,550	1	877	94.8299	SUMMARY	1	0.103345	0.000304	1.4095	23.1672	-	rs2070359	0.000304
Total									**60**		**0.0625514**					**0.0468069**

Supplementary Table 17 (4 pages): Long QT Syndrome proband phenotypes. Shown are the sex, age, QTc and presence of any LQTS-related cardiac event (cardiac arrest or syncope) for the 298 unrelated individuals with phenotype-positive LQTS but without mutations in LQT1, LQT2, LQT3 genes, who underwent open reading frame mutational analysis of six genes at novel QT interval loci.

CaseNo	Gender	Age at Diagnosis (yrs)	QTc (ms)	LQTS-related cardiac events (yes or no)	Comments
Nantes_1	M	38	552	yes	
Nantes_2	M	12	539	no	
Nantes_3	M	10	655	not available	
Nantes_4	F	12	612	yes	
Nantes_5	F	23	481	yes	
Nantes_6	F	78	616	yes	
Nantes_7	M	14	516	no	
Nantes_8	M	34	621	not available	
Nantes_9	M	16	631	no	
Nantes_10	F	16	613	yes	
Nantes_11	F	29	559	yes	
Nantes_12	F	12	633	yes	
Nantes_13	F	12	505	yes	
Nantes_14	F	23	534	yes	
Nantes_15	F	47	511	yes	
Nantes_16	M	42	539	yes	
Nantes_17	M	52	492	yes	
Nantes_18	F	24	618	not available	
Nantes_19	F	8	558	yes	
Nantes_20	F	79	669	yes	
Nantes_21	F	18	480	not available	
Nantes_22	M	11	641	yes	
Nantes_23	F	31	552	yes	
Nantes_24	F	49	622	yes	
Nantes_25	M	22	647	yes	
Nantes_26	M	6	505	no	
Nantes_27	F	63	536	not available	
Nantes_28	F	23	582	yes	
Nantes_29	F	46	511	no	
Nantes_30	F	70	647	yes	
Nantes_31	M	68	537	no	
Nantes_32	M	13	640	no	
Nantes_33	F	26	715	yes	
Nantes_34	F	49	463	yes	syncope, TdP/VF, no family history Schwartz score >3
Nantes_35	F	18	460	yes	syncope, no family history Schwartz score>3
Nantes_36	F	37	486	yes	
Nantes_37	M	18	600	no	
Nantes_38	M	2	604	yes	
Nantes_39	M	23	531	no	
Nantes_40	M	61	563	not available	
Nantes_41	M	19	485	yes	
Nantes_42	M	15	541	yes	
Nantes_43	F	54	529	yes	
Nantes_44	F	53	602	yes	
Nantes_45	M	26	574	no	
Nantes_46	F	41	611	yes	
Nantes_47	F	2	483	no	
Nantes_48	M	35	480	yes	
Nantes_49	F	18	546	yes	
Nantes_50	F	49	486	yes	
Nantes_51	F	42	600	yes	
Nantes_52	M	15	548	yes	
Nantes_53	F	30	492	no	
Nantes_54	F	72	632	no	
Nantes_55	F	40	646	not available	
Nantes_56	M	2	560	yes	
Nantes_57	F	34	521	yes	
Nantes_58	M	14	534	yes	
Nantes_59	F	69	598	yes	
Nantes_60	F	15	520	yes	
Nantes_61	F	35	480	yes	
Nantes_62	M	64	583	no	
Nantes_63	M	50	471	yes	
Nantes_64	F	15	473	yes	
Nantes_65	F	22	516	yes	
Nantes_66	M	35	474	no	
Nantes_67	F	57	539	no	
Nantes_68	M	9	491	no	
Nantes_69	M	15	543	no	
Nantes_70	F	44	561	yes	
Nantes_71	F	58	475	no	
Nantes_72	M	26	546	no	
Nantes_73	M	12	539	yes	
Nantes_74	M	36	554	yes	
Nantes_75	F	49	557	yes	
Nantes_76	F	68	474	yes	
Nantes_77	F	84	508	yes	
Nantes_78	F	28	457	yes	syncope, SCD, TdV/VF, ICD, family history, Schwartz score >3
Nantes_79	M	47	567	yes	
Nantes_80	F	47	592	yes	
Nantes_81	F	71	604	yes	
Nantes_82	F	30	578	yes	
Nantes_83	F	34	626	no	
Nantes_84	F	75	555	yes	
Nantes_85	F	11	503	yes	
Nantes_86	F	27	605	yes	
Nantes_87	F	34	518	yes	

Nantes_88	F	76	621	no	
Nantes_89	F	29	500	yes	
Nantes_90	F	50	466	yes	syncope, SCD, TdV/VF, Schwartz score >3
Nantes_91	M	18	655	yes	
UnivLondon_1	F	60	492	yes	
UnivLondon_2	F	4	500	no	
UnivLondon_3	M	39	611	no	
UnivLondon_4	F	40	481	no	
UnivLondon_5	F	21	510	yes	
UnivLondon_6	F	30	500	yes	
UnivLondon_7	F	21	503	yes	
UnivLondon_8	F	55	490	yes	
UnivLondon_9	F	26	507	yes	
UnivLondon_10	F	38	460	yes	
UnivLondon_11	M	12	489	yes	
UnivLondon_12	F	59	621	no	
UnivLondon_13	F	49	506	no	
UnivLondon_14	M	4	480	yes	
UnivLondon_15	M	69	450	yes	
UnivLondon_16	F	36	600	yes	
UnivLondon_17	F	44	500	no	
UnivLondon_18	F	0	600	no	0 (Neonate)
UnivLondon_19	F	21	548	yes	
UnivLondon_20	F	55	520	no	
Toronto_1	F	15	553	yes	syncope (also anorexia)
Toronto_2	M	13.5	497	yes	syncope
Toronto_3	F	13	480	yes	exertional syncope
Toronto_4	F	0	517		bradycardia 2° to 2:1 AV block
Toronto_5	F	0	685		bradycardia
Toronto_6	F	12	565	no	No
Toronto_7	F	14	580	yes	syncope
Toronto_8	M	7	604	yes	VT following epinephrine for anaphylaxis
Toronto_9	F	12.5	607	yes	syncope
Toronto_10	M	0	573		bradycardia
Toronto_11	M	12	565	yes	exertional syncope
Toronto_12	F	0	623		bradycardia 2° to 2:1 AV block
Toronto_13	M	5	698	yes	syncope (with spont heart block & QT prolongation)
Toronto_14	M	13	522		palpitations, presynope
Toronto_15	F	12	553	no	No
Toronto_16	F	14	636	no	No
Toronto_17	F	14	501	yes	syncope
Toronto_18	M	15	502	yes	syncope
Toronto_19	M	15	566	yes	sudden cardiac arrest
Toronto_20	F	8	528	yes	syncope
Toronto_21	F	0	531		bradycardia 2° to 2:1 AV block, methylmalonic acidemia
Toronto_22	M	5	597	yes	syncope with 'a few breaths of CPR', LVNC
Toronto_23	M	9	480		presyncope
Toronto_24	M	6	604		torsades' on monitor during meningitis Rx
Pavia_1	M	9	602	yes	
Pavia_2	M	12	569	no	
Pavia_3	M	23	566	no	
Pavia_4	M	39	546	yes	
Pavia_5	M	14	516	no	
Pavia_6	F	20	510	yes	
Pavia_7	F	19	510	yes	
Pavia_8	M	15	509	no	
Pavia_9	M	14	507	no	
Pavia_10	F	8	506	no	
Pavia_11	M	38	500	no	
Pavia_12	M	9	500	no	
Pavia_13	F	27	498	yes	
Pavia_14	F	78	498	yes	
Pavia_15	F	44	498	no	
Pavia_16	M	66	497	no	
Pavia_17	F	54	496	yes	
Pavia_18	M	26	495	yes	
Pavia_19	F	36	494	yes	
Pavia_20	M	42	494	no	
Pavia_21	M	17	493	no	
Pavia_22	F	6	492	no	
Pavia_23	F	27	490	no	
Pavia_24	F	51	488	yes	
Pavia_25	F	14	483	no	
Pavia_26	F	43	482	no	
Pavia_27	F	34	480	no	
Pavia_28	F	47	480	yes	
Pavia_29	M	15	490	no	
Pavia_30	M	21	480	yes	
Pavia_31	M	12	532	no	
Pavia_32	M	19	506	no	
Pavia_33	M	13	600	yes	
Pavia_34	M	12	480	no	
Pavia_35	M	14	500	no	
Pavia_36	F	0.25	482	no	
Pavia_37	M	12	510	no	
Pavia_38	F	24	522	no	
Amsterdam_1	F	3	554	yes	
Amsterdam_2	F	4	484	yes	

Amsterdam_3	M	13	510	yes	
Amsterdam_4	M	9	490	yes	
Amsterdam_5	F	56	510	yes	
Amsterdam_6	F	36	492	yes	
Amsterdam_7	M	39	593	yes	
Amsterdam_8	F	65	600	yes	
Amsterdam_9	F	32	600	yes	
Amsterdam_10	M	26	478	yes	
Amsterdam_11	M	11	513	no	
Amsterdam_12	F	13	486	yes	448 (holter: 486, positive epinephrine test)
Amsterdam_13	F	51	557	yes	
Amsterdam_14	M	9	482	yes	
Amsterdam_15	M	14	540	no	
Amsterdam_16	F	2	460	yes	
Amsterdam_17	M	10	460	yes	460 (positive epinephrine test)
Amsterdam_18	F	64	500	no	
Amsterdam_19	F	32	496	yes	
Amsterdam_20	F	1	463	yes	
Amsterdam_21	F	43	480	yes	
Amsterdam_22	F	71	480	no	
Amsterdam_23	F	26	510	yes	
Amsterdam_24	M	12	490	no	
Amsterdam_25	M	76	519	no	
Amsterdam_26	M	0	471	yes	471 (total AV-block)
Amsterdam_27	M	1	560	no	
Amsterdam_28	F	77	503	yes	
Amsterdam_29	F	61	630	no	
Amsterdam_30	M	63	490	no	
Mayo_1	F	not available	504	not available	
Mayo_2	F	18	480	yes	
Mayo_3	F	16	509	not available	
Mayo_4	F	30	620	No	
Mayo_5	F	34	480	not available	
Mayo_6	M	17	550	No	
Mayo_7	F	13	480	yes	
Mayo_8	F	2	570	no	
Mayo_9	F	16	480	not available	
Mayo_10	F	39	499	not available	
Mayo_11	F	34	480	yes	
Mayo_12	F	59	499	no	
Mayo_13	M	22	523	not available	
Mayo_14	F	12	492	yes	
Mayo_15	F	37	NA	yes	
Mayo_16	F	31	660	yes	
Mayo_17	M	11	540	no	
Mayo_18	F	14	518	yes	
Mayo_19	M	38	656	yes	
Mayo_20	F	46	493	yes	
Mayo_21	F	13	489	yes	
Mayo_22	F	45	590	yes	
Mayo_23	M	15	480	yes	
Mayo_24	F	50	480	no	
Mayo_25	M	7	473	not available	Prolonged QT considering age
Mayo_26	F	21	480	no	
Mayo_27	F	28	513	yes	
Mayo_28	F	27	515	yes	
Mayo_29	F	8	480	no	
Mayo_30	M	6	520	no	
Mayo_31	M	18	510	yes	
Mayo_32	M	26	488	no	
Mayo_33	F	29	580	yes	
Mayo_34	F	28	487	not available	
Mayo_35	M	14	497	yes	
Mayo_36	M	15	540	no	
Mayo_37	F	18	486	yes	
Mayo_38	M	1	563	no	
Mayo_39	M	14	570	yes	
Mayo_40	M	20	529	yes	
Mayo_41	F	17	558	yes	
Mayo_42	F	15	536	yes	
Mayo_43	F	14	490	yes	
Mayo_44	F	15	498	yes	
Mayo_45	F	17	575	yes	
Mayo_46	F	22	500	yes	
Mayo_47	M	1	510	no	
Mayo_48	F	14	520	no	
Mayo_49	F	40	501	no	
Mayo_50	F	10	456	yes	
Mayo_51	F	34	485	not available	
Mayo_52	F	42	500	yes	
Mayo_53	F	26	496	no	
Mayo_54	F	18	600	yes	
Mayo_55	M	18	480	not available	
Mayo_56	M	17	499	no	
Mayo_57	M	11	535	yes	
Mayo_58	F	13	507	no	
Mayo_59	F	27	759	yes	
Mayo_60	M	65	496	yes	

Mayo_61	F	12	480	yes
Mayo_62	F	43	565	yes
Mayo_63	F	50	475	not available
Mayo_64	F	36	500	no
Mayo_65	F	51	510	no
Mayo_66	M	13	503	not available
Mayo_67	M	0.1	760	not available
Mayo_68	F	14	527	not available
Mayo_69	F	19	442	yes
Mayo_70	F	4	521	not available
Mayo_71	M	1	525	not available
Mayo_72	F	33	474	yes
Munich_1	F	6	446	yes
Munich_2	F	46	500	yes
Munich_3	F	28	470	yes
Munich_4	F	20	470	yes
Munich_5	F	9	440	yes
Munich_6	F	8	440	yes
Munich_7	F	65	500	yes
Munich_8	F	25	540	yes
Munich_9	F	26	460	yes
Munich_10	F	30	460	yes
Munich_11	F	14	480	no
Munich_12	F	9	475	yes
Munich_13	M	1	500	yes
Munich_14	F	9	467	yes
Munich_15	F	10	460	yes
Munich_16	F	-	500	not available
Munich_17	F	-	507	no
Munich_18	F	.	490	no
Munich_19	F	27	500	yes
Munich_20	F	-	450	yes
Munich_21	M	8	450	yes
Munich_22	F	36	440	yes
Munich_23	F	6	467	yes

SNP	CHR	POS	Genes in InWeb High-Confidence Database	Genes NOT in InWeb High-Confidence Database
Previously discovered loci				
rs12143842	1	160,300,514	NOS1AP,ATF6,C1orf111,SH2D1B,UHMK1	OLFML2B,C1orf226
rs10919070	1	167,365,661	C1orf114,BLZF1,F5,ATP1B1,NME7,DPT	SLC19A2
rs6793245	3	38,574,041	SCN5A	
rs11153730	6	118,774,215	PLN	SLC35F1,C6orf204
rs2072413	7	150,278,902	KCNH2	
rs7122937	11	2,443,126	KCNQ1	
rs735951	16	11,601,037	LITAF,TXNDC11	SNN
rs246196	16	57,131,754	CNOT1,SETD6,GINS3	NDRG4,SLC38A7
rs1052536	17	30,355,688	RAD51L3,RFFL,NLE1,UNC45B,CCT6B,LIG3	ZNF830,FNDC8
rs236586	17	65,715,141	KCNJ2	
rs1805128	21	34,743,550	KCNE2,KCNE1	
Novel loci				
rs2298632	1	23,583,062	HNRNPR	TCEA3,ZNF436,C1orf213,ASAP3
rs12997023	2	40,606,486	SLC8A1	
rs938291	2	174,450,854	SP3	
rs7561149	2	179,398,101	CCDC141,FKBP7,TTN,PLEKHA3	
rs295140	2	200,868,944	C2orf47,C2orf69,SGOL2	ENSG00000196141,KCTD18,C2orf60
rs17784882	3	47,519,007	CSPG5,PTPN23,SMARCC1,SCAP,KLHL18,MYL3,CCDC12,PTH1R,SET	TESSP2,NBEAL2,KIF9,C3orf75
rs2363719	4	72,357,080	SLC4A4	
rs3857067	4	95,245,457	PGDS,SMARCAD1	
rs10040989	5	137,601,624	CDC25C,BRD8,FAM53C,KIF20A,REEP2,GFRA3,EGR1,CDC23,NME5,ETF1,WNT8A,KDM3B	
rs7765828	6	16,402,701	GMPR,ATXN1	
rs9920	7	115,987,328	CAV1,CAV2	
rs16936870	8	71,351,896	NCOA2,TRAM1	PRDM14,ENSG00000213002
rs11779860	8	98,919,506	MATN2	LAPTM4B
rs1961102	8	104,002,021	AZIN1	
rs2485376	10	104,039,996	CUEDC2,NOLC1,PPRC1,ACTR1A,HPS6,NFKB2,PSD,GBF1,LDB1	ELOVL3,PITX3,FBXL15,C10orf95,TMEM180
rs174583	11	61,366,326	FADS1,FEN1,DAGLA,RAB3IL1	FADS2,C11orf9,ENSG00000124915,ENSG00000214780,C11orf10,ENSG00000221968
rs3026445	12	109,207,586	ANAPC7,ENSG00000139433,RAD9B,PPP1CC,ARPC3,PPTC7,GIT2,TC	IFT81,C12orf34,HVCN1,C12orf76,ENSG00000214159,C12orf24,TCTN1
rs728926	13	73,411,123	KLF12	
rs2273905	14	102,044,752	RAGE,CINP,TECPR2	ZNF839,ANKRD9
rs3105593	15	48,632,310	SPPL2A,USP8,TRPM7	USP50
rs1296720	16	3,813,643	TRAP1,CREBBP,DNASE1	
rs246185	16	14,302,933	MKL2	
rs9892651	17	61,734,255	APOH,PRKCA	CCDC46

Supplementary Table 18: Genes at known or novel loci found in the InWeb database. Shown are the genes at previously known or novel loci harboring at least one common variant associated with QT interval with and without data in the InWeb database of protein-protein interactions.

Supplementary note

Genetic association study of QT interval highlights role for calcium signaling pathways in myocardial repolarization

The QT Interval - International GWAS Consortium (QT-IGC)

Study cohort description for QT GWAS and replication

Reported below are general descriptions of the various study cohorts, as well as the method for QT interval measurement and any additional covariates used in association analyses. All participants provided written informed consent and studies were approved by their local research ethics committees or institutional review boards. Mandatory exclusions of individuals included presence of atrial fibrillation or atrial flutter AND (QRS duration >120 msec OR presence of left/right bundle branch block). Optional exclusions included use of digitalis or QT-prolonging medication, presence of a pacemaker or implantable cardioverter defibrillator, or pregnancy. Summary demographic characteristics for all cohorts are provided in Supplementary Table 1. All GWAS studies used genome-wide genotyping arrays and filtered on quality control such as low per sample call rate or low per SNP call rate or deviation from Hardy-Weinberg equilibrium as described in Supplementary Table 2. Replication genotyping was performed on up to 35 SNPs using various platforms as described in Supplementary Table 2.

GWAS cohorts

AGES

The Reykjavik Study cohort originally comprised a random sample of 30,795 men and women born in 1907–1935 and living in Reykjavik in 1967[1]. A total of 19381 attended, resulting in 71% recruitment rate. Between 2002 and 2006, the AGES-Reykjavik study re-examined 5764 survivors of the original cohort who had participated before in the Reykjavik Study. A total of 3,219 randomly selected individuals from the study were genotyped, of which 2,522 were included in analysis for the QT-interval. Association analysis was run with age, sex, and the resting heart beat interval as covariates in a linear model for genetic association. ECG reports were obtained using a Marquette / MAC 5000 Resting ECG (GE Medical Systems, U.S.A. Software Version 006A, PN 2000657-033, Revision A). The QT interval and heart rate corrected QTc are generated by the Marquette 12SL ECG Analysis program, measured across all 12 leads from earliest onset to latest offset.

Amish studies

The Old Order Amish individuals included in this study were participants of several ongoing studies of cardiovascular health carried out at the University of Maryland. Participants were relatively healthy volunteers from the Old Order Amish community of Lancaster County, Pennsylvania and their family members[2,3]. Examinations were conducted at the Amish Research Clinic in Strasburg, PA. The Institutional Review Board at the University of Maryland approved all protocols and informed consent was obtained, including permission to use their DNA for genetic studies. Study participants were enrolled within the 2000-2008 time period. Of the total phenotyped participants, a total of 1420 had ECG measures and genotype information (Affymetrix 500K or 6.0). 12-lead electrocardiograms (ECG) were acquired using standard methods with a GE Marquette digital recording system. The QT measurements were calculated by the Marquette computer system using 12 'median beats' across all 12 leads. The clinical protocol used for Genetic association analysis was performed adjusting for centrally defined covariates and pedigree structure using Mixed models Analysis for Pedigrees and Populations (MMAP) software developed by J. O'Connell (http://edn.som.umaryland.edu/mmap/index.php).

ARIC

The ARIC study is a population-based prospective cohort study of cardiovascular disease and includes 15,792 persons aged 45-64 years at baseline (1987-89), chosen by probability sampling from four US communities[4]. Cohort members completed four clinic examinations, conducted approximately three years apart between 1987 and 1998. Clinic examinations for ARIC included assessment of cardiovascular risk factors, self-reported medical family history, employment status, educational status, diet, physical activity, co-morbidity, clinical and laboratory measurements. For assessment of QT interval at baseline, participants were asked not to smoke or ingest caffeine for at least 1 hour prior to the electrocardiogram being obtained. After resting for 5-10 minutes while the electrodes were being placed, a standard supine 12-lead electrocardiogram and a 2-minute paper recording of a three-lead (leads V1, II, and V5) rhythm strip were made. The ECGs were recorded digitally, and identical methods (MAC personal computer, Marquette Electronics, Milwaukee, Wisconsin) were used in all clinical centers. The QT interval from the digital 12-lead ECG was determined by identifying Q-onset and T-wave offset in all three leads. T-wave offset was defined as the point of maximum change of slope as the T-wave merges with the baseline as implemented in the Novacode ECG measurement and classification program as has been described in detail[5] and used in prior ARIC studies of the QT interval[6]. U-waves were not detected by the Novacode algorithm.

BLSA

The Baltimore longitudinal study on Aging (BLSA) study is a population-based study aimed to evaluate contributors of healthy aging in the older population residing predominantly in the Baltimore-Washington DC area[7]. Starting in 1958, participants are examined every one to four years depending on their age. Currently there are approximately 1100 active participants enrolled in the study. Blood samples were collected for DNA extraction, and genome-wide genotyping was completed for 1231 subjects using Illumina 550K. This analysis was done on a subset of the participants (N=477) of European ancestry with ECG data. 12 lead ECGs were recorded with using standard electrode placements using MAC5000. QT interval duration was measured electronically using a Marquette 12SL algorithm. The BLSA has continuing approval from the Institutional Review Board (IRB) of Medstar Research Institute.

BRIGHT

Two thousand unrelated white European hypertensive individuals from the BRIGHT study (www.brightstudy.ac.uk) were genotyped with the GeneChip Human Mapping 500K Array Set (Affymetrix). Twelve-lead ECG recordings (Siemens-Sicard 440; http://www.brightstudy.ac.uk/info/sop04.html), which produces an automated measurement of the QT interval, were available for all subjects. All data were transferred from each recruitment centre by electronic modem to electrophysiologists from the West of Scotland Primary Prevention Study (Professor Peter MacFarlane) for central reporting. Thirteen hundred and ninety two individuals remained in the analysis after exclusion of those having ischemic disease, stroke, or bypass, atrial fibrillation, or QRS duration >120 ms and having full covariate information.

CARLANTINO

INGI-Carlantino consisted of 900 subjects who were drawn from Carlantino, an isolated village of southern Italy. Ethics approval was obtained from the Ethics Committee of the "Burlo Garofolo children hospital" in Trieste. Written informed consent was obtained from every participant of the study. The study population had undergone clinical and instrumental evaluations between 1998 and 2005. For all subjects, anthropometrics variables (such as height, weight, etc) were taken and a structured questionnaire about lifestyle and medical history was filled out. In addiction, blood pressure and body-mass index were measured. ECG and cardiovascular evaluation was available in 679 subjects. All samples were typed with illumina 370k CNV chip (Illumina, San Diego, USA). Imputation of genotypes was carried out using the software MACH. Digital caliper measurements were made on scanned paper ECGs recorded at 25 mm/sec. Mortara instrument ELI 250 was used to obtain ECG measurements. QT was calculated as length in milliseconds and QTc was with Bazett's correction.

CHS

The CHS is a population-based cohort study of risk factors for coronary heart disease and stroke in adults ≥65 years conducted across four field centers[8]. The original predominantly European ancestry cohort of 5,201 persons was recruited in 1989-1990 from random samples of the Medicare eligibility lists; subsequently, an additional predominantly African-American cohort of 687 persons were enrolled for a total sample of 5,888. DNA was extracted from blood samples drawn on all participants at their baseline examination in 1989-90. In 2007-2008, genotyping was performed at the General Clinical Research Center's Phenotyping/Genotyping Laboratory at Cedars-Sinai using the Illumina 370CNV BeadChip system on 3980 CHS participants who were free of CVD at baseline, consented to genetic testing, and had DNA available for genotyping. A total of 1908 persons were excluded from the GWAS study sample due to the presence at study baseline of coronary heart disease, congestive heart failure, peripheral vascular disease, valvular heart disease, stroke or transient ischemic attack or lack of available DNA. Because the other cohorts were predominantly white, the African American participants were excluded from this analysis to reduce the possibility of confounding by population structure. The African American participants were analyzed separately as part of the CARe-COGENT analysis of QT interval among African Americans. Participants were excluded if they had a genotyping call rate<=95%. To date, genotyping has been successful among 3,271 of 3,373 European ancestry participants on whom genotyping was attempted; those with successful genotyping and available ECG data constitute the sample for this study. Data on QT interval and covariates came from the baseline examination. The ECGs were recorded on MAC PC-DT ECG recorder (Marquette Electronics) machines and measurements of QT interval made using the Marquette 12SL algorithm.

Croatia – Korcula

The Croatia-Korcula study is a family-based, cross-sectional study in the isolated island of Korcula. Digital ECGs were recorded using Mortara ELI 350. Genetic association was performed after adjusting for centrally defined covariates. Population stratification was accounted for using the first 3 principal components obtained from the population-specific identity-by-state (IBS) derived distances matrix generated by the "ibs" function of GenABEL and pedigree structure was accounted for the "mmscore" function of GenABEL.

Croatia - Split

The Croatia-Split study is a population-based, cross-sectional study in the Dalmatian City of Split. Digital ECGs were recorded using Mortara ELI 350. Genetic association was performed after adjusting for centrally defined covariates. Population stratification was accounted for using the first 3 principal components obtained from the population-specific identity-by-state (IBS) derived distances matrix generated by the "ibs" function of GenABEL and pedigree structure was accounted for the "mmscore" function of GenABEL.

DCCT-EDIC

The Diabetes Control and Complications Trial (DCCT)/Epidemiology of Diabetes Interventions and Complications (EDIC) study was a clinical trial and follow-up of subjects with type 1 diabetes. Fourteen hundred forty one patients with type 1 diabetes were recruited for the DCCT[9] and followed-up in EDIC[10]. To reduce the possibility of population stratification, we limited the analysis to individuals who self-identified as white, and excluded individuals who were determined to be admixed between Caucasian and other ethnic groups through population genetic approaches, using Eigenstrat seeding with genotype data from the three major populations genotyped in HapMap Phase II. Twelve-lead resting ECGs were obtained by a certified technician or research nurse at 29 clinics, measured digitally and read according to the revised Minnesota Code at the Central ECG Reading Unit (University of Minnesota, under the direction of Dr. Richard S. Crow)[11]. In brief, at least 1 full min of ECG tracing was obtained consisting of 5 s of each of the leads (I, II, III, aVR, aVL, aVF, and V1–V6). Additionally, individuals having ischemic disease, stroke, or bypass, atrial fibrillation, or QRS duration >0.120 ms were excluded, therefore in total 323 individuals were excluded from the analysis.

deCODE

The deCODE Study included all ECGs obtained and digitally stored between 2004 and 2008 at the Landspitali University Hospital, Reykjavik, the largest medical center and only tertiary referral center in Iceland. The ECGs were recorded digitally with the Philips PageWriter Trim III and PageWriter 200 cardiographs and stored in the Philips TraceMasterVue ECG Management System. These ECGs were obtained in all hospital departments, from both inpatients and outpatients. Digitally measured ECG waveforms and parameters were extracted from the database for analysis. The Philips PageWriter Trim III QT interval measurement algorithm has been described previously and shown to fulfill industrial ECG measurement accuracy standards[12].

EMERGE

The eMERGE (Electronic Medical Records and Genomics) network included 5 sites with DNA repositories linked to electronic medical record (EMR) systems: Group Health Research Institute, Marshfield Clinic, Mayo Clinic, Northwestern University, Vanderbilt University[13]. Each site identified a phenotype of choice, and developed electronic phenotyping algorithms to identify subjects with the target phenotype. Samples from ~3,000 subjects/site were then genotyped at the Center for Genotyping and Analysis at the Broad Institute and the Center for Inherited Disease Research (CIDR) at Johns Hopkins University, and cleaned using the quality control pipeline developed by the eMERGE Genomics Working Group[14]. This study included only individuals of European Americans, as designated in the EMR, and were genotyped on the Illumina Human660W-Quadv1_A platform.

The normal electrocardiogram phenotype definition developed at the Vanderbilt site identified individuals from the EMR with normal ECGs and without any cardiac disease or abnormal electrolyte values[15]. The algorithm was validated to a positive predictive value of 97%, and details are available on PheKB (http://phekb.org/). Deploying the algorithm across the five eMERGE-1 sites identified 5,272 European Americans (2,488 males and 2,784 females), who are the eMERGE-I set contributed to this meta-analysis[15].

ERF

The Erasmus Rucphen Family study (http://www.erasmusmc.nl/klinische_genetica/research/genepi/?lang=en) is comprised of a family-based cohort embedded in the Genetic Research in Isolated Populations (GRIP) program in the southwest of the Netherlands. The aim of this program is to identify genetic risk factors for the development of complex disorders. In ERF, twenty-two families that had a minimum of six children baptized in the community church between 1850 and 1900 were identified with the help of detailed genealogical records. All living descendants of these couples, and their spouses, were invited to take part in the study. Comprehensive interviews, questionnaires, and examinations were completed at a research center in the area; approximately 3,200 individuals participated. Examinations included 12 lead ECGs, which were recorded on ACTA electrocardiographs (ESAOTE, Florence, Italy) and digital measurements of the QT intervals were made using the Modular ECG Analysis System (MEANS)[16]. Data collection started in June 2002 and was completed in February 2005. In the current analyses, 1481 participants for whom complete phenotypic, genotypic and genealogical information was available were studied.

Framingham Heart Study (FHS)

The Framingham Heart Study (FHS) is a community-based, longitudinal cohort study comprising three generations of individuals in multigenerational pedigrees and additional unrelated individuals. The current study included individuals from generation 1 (eleventh examination)[17], generation 2 (first examination)[18] and generation 3 (first examination)[19]. Paper ECGs were scanned and digital caliper measurements were made using proprietary software[20]. The QT interval trait analyzed was the average of the lead-specific QT interval (from QRS onset to T-wave offset) in leads II, V2 and V5. Genetic association testing was performed adjusting for centrally defined covariates and additionally dummy variables for generation.

FVG

The INGI-FVG cohort consisted of 1700 subjects drawn from the project “Genetic Park of Friuli Venezia Giulia”. This study examined 6 isolated villages in the North-east of Italy between 2008 and 2009. Ethics approval was obtained from the Ethics Committee of the “Burlo Garofolo children hospital” in Trieste. Written informed consent was obtained from every participant of the study. The study population had undergone clinical and instrumental evaluations. For all subjects, anthropometrics variables (such as height, weight, etc) were taken and a structured questionnaire about lifestyle and medical history was filled out. In addition, blood pressure and body-mass index were measured. ECG was available in 1413 subjects. All samples were typed with Illumina 370k CNV chip (Illumina, San Diego, USA). Imputation of genotypes was carried out using the software MACH.

Digital caliper measurements were made on scanned paper ECGs recorded at 25 mm/sec. Mortara instrument ELI 250 was used to obtain ECG measurements. QT was calculated as length in milliseconds and QTc was with Bazett's correction.

HEALTH2000

The Health 2000 study was based on a stratified two-stage cluster sampling from the National Population Register to represent the total Finnish population aged 30 years and over. The survey included an interview on medical history, health-related lifestyle habits, and a clinical examination where a blood sample was drawn. In total, 6,200 persons participated and gave written informed consent. A detailed Methodology Report is available (http://www.terveys2000.fi/doc/methodologyrep.pdf). GWAS was performed on participants having metabolic syndrome according to the definition of the International Diabetes Federation, excluding diabetic individuals, and an equal number of controls free of metabolic syndrome and diabetes. After appropriate exclusions, altogether 1,921 persons with GWAS were available for analysis in the QT-IGC. The rest of the Health 2000 participants (n=3,128) was used for targeted replication analyses and genotyped with Sequenom for 35 SNPs. Digital standard resting ECGs were recorded using MAC 5000 electrocardiograph (GE Marquette Medical Systems, Milwaukee, WI, USA) and QT intervals were measured and visually reviewed from median complexes using a custom-made software, as previously described in detail[21].

Health ABC Study

The Health Aging and Body Composition (Health ABC) Study is a NIA-sponsored cohort study of the factors that contribute to incident disability and the decline in function of healthier older persons, with a particular emphasis on changes in body composition in old age[22]. Between 4/15/97 and 6/5/98 the Health ABC study recruited 3,075 70-79 year old community-dwelling adults (41% African-American), who were initially free of mobility and activities of daily living disability. ECG recordings used in the present study and blood samples used for DNA extraction were performed at the baseline visit from 1997 to 1998. Ten-second, resting, standard 12-lead electrocardiograms were recorded using the Marquette MAC PC (GE Healthcare, Milwaukee, WI, USA). The QT interval was measured electronically using the Marquette 12SL algorithm.

Heinz Nixdorf Recall (HNR)

The Heinz Nixdorf Recall (Risk Factors, Evaluation of Coronary Calcium and Lifestyle, HNR) Study is an ongoing population-based, prospective cohort study of the comparative value of modern risk stratification methods with myocardial infarction and cardiac death being primary endpoints[23]. The study base is the general German population, randomly selected from statutory lists of residence, living in the three adjacent cities of Bochum, Essen and Mülheim in Western Rhine area of Germany. For all participants, standardized digital 12-lead resting surface EKGs were sampled at 250 Hz, recorded on a MAC 5000 EKG recorder (GE Healthcare, Freiburg, Germany), and interpreted automatically using the integrated 12SL-Code[24].

KORA-F3 / KORA-S4

The KORA Study is a series of population-based epidemiological surveys of persons living in or near the city of Augsburg, Germany. All survey participants are residents of German nationality identified through the registration office and between 25 and 75 years old at the time of enrollment. Survey S3 was conducted between 1994 and 1995 and survey S4 between 1999 and 2001. KORA F3, a 10-year follow up of S3, occurred in 2004 and 2005. In KORA F3 and S4 12-lead resting ECGs were recorded with digital recording systems (F3: Mortara Portrait, Mortara Inc., Milwaukee, USA, S4: Hörmann Bioset 9000, Hörmann Medizinelektronik, Germany). The Mortara portrait ECG machine determines QT interval by the proprietary XL-ECG algorithm which has not been fully published but has shown to be in good accordance with other published ECG measurement algorithms[25]; QT intervals from Hörmann Bioset were determined using the Hannover ECG analysis software (HES-Version 3.22-12) by computerized analysis of an averaged cycle computed from all leads and all cycles of the 10 second recording after exclusion of ectopic beats as described earlier[26]. The QT interval determined by this algorithm represents the earliest beginning of depolarization until the latest deflection of repolarization between any two leads.

LIFELINES

The LifeLines Cohort Study is a multi-disciplinary prospective population-based cohort study examining in a unique three-generation design the health and health-related behaviors of 165,000 persons living in the North East region of The Netherlands. It employs a broad range of investigative procedures in assessing the biomedical, socio-demographic, behavioral, physical and psychological factors which contribute to the health and disease of the general population, with a special focus on multimorbidity. In addition, the LifeLines project comprises a number of cross-sectional sub-studies, which investigate specific age-related conditions. These include investigations into metabolic and hormonal diseases, including obesity, cardiovascular and renal diseases, pulmonary diseases and allergy, cognitive function and depression, and musculoskeletal conditions. All survey participants are between 18 and 90 years old at the time of enrollment. Recruitment has been going on since the end of 2006, and in August 2010 more than 30,000 participants had been included.

During the screening a 12-lead resting ECG was recorded with digital recording systems (Cardioperfect software, Welch-Allyn, Delft, The Netherlands). All ECGs were processed by the Modular ECG Analysis System (MEANS)[27] to obtain Minnesota Codes[28]. The MEANS program has been validated extensively[29-31]. The first series of whole genome analyses included 3,367 individuals of Caucasian origin, for which we selected the oldest participant of each family who participated in the screening between December 1, 2006 and December 1, 2009.

MICROS

The MICROS study is an ongoing, comprehensive genetic and health care survey conducted in South Tyrol (Italy), from which the present probands were sampled. They were volunteers from three Alpine, isolated, German-speaking villages located in Val Venosta, a region enclosed within the Austria and Switzerland borders[32]. An extensive genealogy spanning 12 generations was constructed and information on participants' health status was collected through a standardized questionnaire and clinical examinations, including digitized ECG measurements (Mortara Portrait, Mortara Inc., Milwaukee, USA). Individuals with identified U-waves were excluded from analysis. The Mortara portrait determines QT interval by a proprietary algorithm[25].

ORCADES

The Orkney Complex Disease Study (ORCADES) is an ongoing family-based, cross-sectional study in the isolated Scottish archipelago of Orkney. Genetic diversity in this population is decreased compared to Mainland Scotland, consistent with the high levels of endogamy historically. Data for participants aged 18-100 years, from a subgroup of ten islands, were used for this analysis. Fasting blood samples were collected and over 200 health-related phenotypes and environmental exposures were measured in each individual. All participants gave informed consent and the study was approved by Research Ethics Committees in Orkney and Aberdeen. Digital 10-second ECGs were taken after at least 10 minutes of supine rest, using a PC link with QT and RR intervals calculated using CardioView software (NUMED cardiac diagnostics; Sheffield, United Kingdom).

PopGen

DNA samples of 1,204 unrelated individuals were obtained from the PopGen biobank[33]. All individuals had white skin color and were of German descent, i.e. declared that they, their parents and their grandparents were born in Germany. 12-lead resting ECGs were recorded digitally on the General Electric MAC 1600 system (GE Healthcare, Munich, Germany). QT intervals were measured automatically with GE Marquette 12SL ECG analysis program and scrutinized by experienced cardiologists.

PREVEND

The Prevention of REnal and Vascular ENd stage Disease (PREVEND) study is an ongoing prospective study investigating the natural course of increased levels of urinary albumin excretion and its relation to renal and cardiovascular disease. Inhabitants 28 to 75 years of age (n=85,421) in the city of Groningen, The Netherlands, were asked to complete a short questionnaire, 47% responded, and individuals were then selected with a urinary albumin concentration of at least 10 mg/L (n = 7,768) and a randomly selected control group with a urinary albumin concentration less than 10 mg/L (n = 3,395). Details of the protocol have been described elsewhere (www.prevend.org). Standard 12-lead electrocardiograms were recorded with CardioPerfect equipment (Cardio Control; currently Welch Allyn, Delft, The Netherlands) and digital measurements of the QT intervals were made using the Modular ECG Analysis System (MEANS). The QT detector of MEANS operates on multiple simultaneously recorded leads, which are transformed to a detection function that brings out the QT complexes among the other parts of the signal.

Rotterdam Study

The Erasmus Rotterdam Health Study (RS-I), begun in 1990, is a prospective population-based cohort study of chronic diseases[34,35]. In 2000-2001, additional individuals (RS-II) were recruited into ERGO-II (also known as the Rotterdam Study-II)[36]. The current study sample included data from one of four (RS-I) or two (RS-II) examination cycles at which the first eligible electrocardiogram was available for each individual. In RS, digital measurements of the QT interval were made using the Modular ECG Analysis System (MEANS)[27].

SARDINIA

The SardiNIA study examined a total of 4,305 related individuals participating in a longitudinal study of aging-related quantitative traits in the Ogliastra province of the Sardinia region, Italy[37]. The SardiNIA GWAS has been described in detail previously[38]. Genotyped individuals had four Sardinian grandparents and were selected without regard to their phenotypes. QT interval has been measured with a ruler (ECG Machine: Cardiette 600) on the resting ECG tracing: three consecutive beats were considered on lead DII. The QT interval was taken from the beginning of the QRS complex to the end of the downslope of the T wave (crossing of the isoelectric line). When a U wave was present, the QT interval was measured to the nadir of the curve between the T and U waves.

SHIP

The Study of Health in Pomerania (SHIP) is a cross-sectional survey in West Pomerania, the north-east area of Germany[39,40]. A sample from the population aged 20 to 79 years was drawn from population registries. First, the three cities of the region (with 17,076 to 65,977 inhabitants) and the 12 towns (with 1,516 to 3,044 inhabitants) were selected, and then 17 out of 97 smaller towns (with less than 1,500 inhabitants), were drawn at random. Second, from each of the selected communities, subjects were drawn at random, proportional to the population size of each community and stratified by age and gender. Only individuals with German citizenship and main residency in the study area were included. Finally, 7,008 subjects were sampled, with 292 persons of each gender in each of the twelve five-year age strata. In order to minimize drop-outs by migration or death, subjects were selected in two waves. The net sample (without migrated or deceased persons) comprised 6,267 eligible subjects. Selected persons received a maximum of three written invitations. In case of non-response, letters were followed by a phone call or by home visits if contact by phone was not possible. The SHIP population finally comprised 4,308 participants (corresponding to a final response of 68.8%). QT intervals in SHIP were measured from digitally stored 12-lead resting ECGs (Personal 120LD, Esaote, Genova, Italy) using the Modular ECG Analysis System (MEANS)[16].

TWINS UK

Samples from the TwinsUK cohort were genotyped with the Infinium assay (Illumina, San Diego, USA) across three fully compatible SNP arrays, the Hap300 Duo, Hap300, and Hap550. This resulted in GWAS data being available on 305,912 SNPs for 2,256 individuals from 595 dizygotic (DZ) twin pairs and 1066 singletons (among them twins from monozygotic (MZ) twin pairs) from the TwinsUK cohort. This cohort was shown previously to be representative of the general (singleton) UK population[41]. ECG data were available on 1,104 of these individuals. Eight hundred and sixty had automated measurements of the QT interval by the Cardiofax ECG-9020K (Nihon Kohden UK Ltd., Middlesex, UK) and 244 were scored manually using a high-resolution digitizing board (GTCO CalComp Peripherals, USA). Fifty six individuals were removed from the data set because of atrial fibrillation, QRS duration >120 ms or presence of a heart condition (i.e. ischemic heart disease, stroke or bypass surgery). None of the genotyped twins had a pacemaker or used anti-arrhythmic drugs. The dataset for analyses consequently included 1,048 individuals, of which 588 were DZ twins (i.e. 294 pairs) and 460 singletons. These singletons included 235 MZ twins of which the mean QT interval of both twins was used to optimize information.

YOUNGFINNS

The Cardiovascular Risk in Young Finns (YFS) is a population-based 27 year follow up-study[42]. The first cross-sectional survey was conducted in 1980, when 3,596 Caucasian subjects aged 3-18 years participated. In adulthood, the latest 27-year follow-up study was conducted in 2007 (ages 30-45 years) with 2,204 participants. Genotyping was done for 2556 samples using custom build Illumina Human 670k BeadChip in 2009 at Welcome Trust Sanger Institute. Genotypes were called using Illumina's clustering algorithm. Applied QC filters were: sample and SNP call rate < 0.95, MAF < 0.01, HWE-P < 1-e6, possible relatedness (pi-hat > 0.2), gender check. After quality control there were 2,442 samples and 546,677 genotyped SNPs available. Genotype imputation was performed using MACH 1.0 and HapMap II CEU (release 22) samples as reference. After imputation there were 2,543,887 imputed SNPs available. In 2001, a single channel ECG was recorded during a 3-minute period. The ECG signal was collected after the participants had remained comfortably in a supine position for at least 15 minutes. The three ECG leads were positioned diagonally as follows: 1) above sternum, 2) below sternum 3) above umbilicus. The resulting QRS complex corresponds to leads V1-V2. All ECG signals were examined visually by one operator. The ECG recordings that included more than two ectopic beats were excluded. The average QT interval duration from the ECG recording was computed using a commercially available program for analysis of physiological data (WinCPRS, Absolute Aliens, Turku, Finland). All ECGs were reviewed visually to ensure that the computer program had correctly recognized Q- and T-waves. In 115 subjects, the computer program did not recognize the correct timing of the Q- or T-waves. In these subjects, the QT interval was computed manually[43].

Replication cohorts

BRHS

British Regional Heart Study (BRHS): The British Regional Heart Study recruited 7735 men aged 40-59. Full details are reported elsewhere[44]. Men were recruited from 24 medium sized British towns between 1978 and 1980. Twenty years later, when aged 60-79, 4252 participants were re-measured. Of these, 3927 underwent application of 12-lead ECG, and provided a whole blood sample with consent for DNA analysis.

BRUNECK

The Bruneck Study is an ongoing prospective, population-based survey on the epidemiology, pathophysiology and prevention of cardiovascular and cerebrovascular disease. The study protocol was approved by the pertinent ethics committee, and all participants gave their written informed consent. In 1990, 1000 individuals aged 40-79 years were randomly chosen from the inhabitants of the town of Bruneck (South Tyrol, Italy) on the basis of an age- and sex-stratified strategy (125 persons per sex and decade). The population of Bruneck is exclusively Caucasian and of heterogeneous geographic origin with sizeable segments of Austro-German or Italian background. Population mobility within the survey area was low at 0.2% per year. Follow-up examinations were performed in 1995, 2000 and 2005 with participation rates exceeding 90%. Analyses for the current investigation focused on the 1995 evaluation and included 821 men and women with DNA samples available. After exclusion of patients with atrial fibrillation, pacemakers, QRS duration > 120 ms, and QT-shortening or QT-prolonging drugs 629 subjects remained for the current analysis.

CARLA

The CARLA study is an ongoing cohort study of a representative sample of the inhabitants of the city of Halle, eastern Germany, comprising 1,779 participants aged 45–83 years at baseline (812 women, 967 men)[45]. The baseline examination took place between December 2002 and January 2006. A multi-step recruitment strategy aimed to achieve a high response rate. The final response rate after subtracting exclusions (individuals who were deceased prior to the invitation, had moved away, or were unable to participate due to illness) was 64.1%. The study was approved by the Ethics Committee of Martin-Luther-University Halle-Wittenberg and conforms to the Declaration of Helsinki. A standardized, computer-assisted interview was performed to collect information on socio-demographic and socioeconomic variables, behavioral, biomedical and psychosocial factors, medical history, and use of medication within the preceding 7 days. The medical examination included the recording of sitting blood pressure, sitting and lying heart rate (HR), waist and hip circumference, weight and height, a venous blood sample, an echocardiogram, and a 20-minute 12-lead resting ECG, recorded on a CardioControl Working Station (Welch Allyn, Delft, Netherlands). Digital measurements of the QT interval were made using the Modular ECG Analysis System (MEANS)[27]. Genotyping of the single nucleotide polymorphisms rs174583, rs2273905, rs295140, rs3026445, rs3857067, rs4493911, rs7765828, rs938291, and rs9920 was performed using pre-developed, and custom-made (rs3857067 and rs404321, primer and probe sequence see table) and validated TaqMan®SNP Genotyping Assays (Applied Biosystems, Germany) following the manufacturer’s instructions. Polymerase chain reaction conditions were as follows: initial denaturation at 95°C for 10 min, followed by 45 cycles of denaturation (92°C for 15 sec) and annealing and extension in 1 step (60°C for 60 s). The post PCR generated fluorescence intensity was quantified using an ABI 7900 Sequence Detector System Software ® version 2.3 (Applied Biosystems).

CYPRUS

The Cyprus Study is a prospectively designed study on cardiovascular disease in community-dwellers aged 40 or more (40-89). Part I consists of a pilot study of 500 subjects, part II extended this to 1100 subjects and part III will provide a minimum of 5 year follow-up. Baseline data have been collected from Pedoulas, a village in the Troodos Mountains of Cyprus (n=273), their relatives who live in any one of the main towns (n=479) and from a section of Nissou ten kilometers south of the capital, Nicosia (n=245); a total of 997. Inhabitants were identified through the population list held at the Mayor's office.The overall participation rate of those invited was 95%. The Ethics Committee of the Cyprus Institute of Neurology and Genetics approved the study. All participants provided written informed consent. Twelve-lead ECGs were acquired using standard methods with Nihon Kohden 9120K digital recording system. The QT interval was measured electronically using the Nihon Kohden algorithm and verified by independent measurement by a cardiologist.

Czech Post-MONICA

The Czech Post-Monica study in Prague study sample were selected according to the criteria used in the original MONICA (MONItoring of CArdiovascular risk factors) study[46]. The Prague-MONICA sample includes individuals collected in the district Litomerice and Prague-east. Examination by twelve lead ECG recordings was performed using a MAC 5500 (GE Healthcare). The MAC 5500 is designed for high volume ECG environment. The examination was carried out on the supine individuals after 10 minutes of rest.

MIDSPAN Family Study

This is one of the four MIDSPAN population cohort studies based in Scotland. The three original studies took place between 1964 and 1976[47,48]. Twenty years later, in 1996, the next generation was studied when offspring of couples in the original Renfrew/Paisley Study were recruited into the Family Study. This latter group is the subject of the present analysis. The offspring were ascertained (by self-report) to be from full-sibling families with no step children, adoptees or half-siblings. All were white and living in the west of Scotland. Details of the study have been described previously. Digital ECG data were in all cases transferred to the University of Glasgow ECG Core Laboratory based in Glasgow Royal Infirmary, and the University of Glasgow ECG analysis program analyzed all ECGs[49]. This software meets all of the required specifications in terms of measurement accuracy and is used widely in various commercial products and clinical trials. All ECGs were reviewed manually and checked for technical problems that would have interfered with analysis, and technically unsatisfactory ECGs were excluded. In the MIDSPAN study, which includes related individuals, associations between QT interval and SNP genotype were investigated using linear mixed effects regression models. Family structure among the MIDSPAN offspring generation was accounted for by fitting random intercepts within sibships.

Galicia

The Galicia Study is a series of population-based epidemiological surveys of persons living in Galicia, Northwestern Spain. The cohort includes 911 individuals between 18 and 92 years old at the time of enrollment. For targeted replication analyses 35 SNPs where genotyped with Sequenom Mass Array. Twelve-lead ECGs were acquired using standard methods with GE Marquette digital recording system. The QT interval was measured electronically using the Marquette 12SL algorithm.

Health 2000

Health 2000 was based on a stratified two-stage cluster sampling from the National Population Register to represent the total Finnish population aged 30 years and over. The survey included an interview on medical history, health-related lifestyle habits, and a clinical examination where a blood sample was drawn. In total, 6,200 persons participated and gave written informed consent. A detailed Methodology Report is available (http://www.terveys2000.fi/doc/methodologyrep.pdf). GWAS was performed on participants having metabolic syndrome according to the definition of the International Diabetes Federation, excluding diabetic individuals, and an equal number of controls free of metabolic syndrome and diabetes. After appropriate exclusions, altogether 1,921 persons with GWAS were available for analysis in the QT-IGC. The rest of the Health 2000 participants (n=3,128) was used for targeted replication analyses and genotyped with Sequenom for 35 SNPs. Digital standard resting ECGs were recorded using MAC 5000 electrocardiograph (GE Marquette Medical Systems, Milwaukee, WI, USA) and QT intervals were measured and reviewed visually from median complexes using a custom-made software, as previously described in detail[21].

HNR

The Heinz Nixdorf Recall (Risk Factors, Evaluation of Coronary Calcium and Lifestyle, HNR) Study is an ongoing population-based, prospective cohort study of the comparative value of modern risk stratification methods with myocardial infarction and cardiac death being primary endpoints[23]. The study base is the general German population, randomly selected from statutory lists of residence, living in the three adjacent cities of Bochum, Essen and Mülheim in Western Rhine area of Germany. For all participants, standardized digital 12-lead resting surface ECGs were sampled at 250 Hz, recorded on a MAC 5000 ECG recorder (GE Healthcare, Freiburg, Germany), and interpreted automatically using the integrated 12SL-Code[24].

INTERGENE

INTERGENE is a population based research program to assess the INTERplay between GENEtic susceptibility and environmental factors for the risk of chronic diseases in western Sweden[50,51]. The survey started in April 2001 and continued until December 2004. Randomly sampled women and men aged 25–74 years and living in the Västra Götaland region at the time of sampling were invited to participate. Of the invited cohort, 3610 (42%) responded and provided data, and were included in the study population. For the purpose of the present study, 153 non-European subjects were excluded, genotyping data were unavailable for a further 597 subjects, and relevant ECG data were missing for 43 additional subjects who had genotyping data, leaving 2817 subjects. After excluding 38 additional subjects with QRS>120 ms, 2779 subjects remained for analysis; 1509 women (54.3%) and 1270 men (45.7%), with mean age 50.6 years. All subjects provided extensive questionnaire information on risk factors, medication and diseases, and were invited for a clinical examination by a team of trained research nurses. This included spirometry, blood sampling for genetic studies, as well as anthropometric and blood pressure measurements. In addition, all participants underwent standard 12-lead ECG registration using either the Megacart R 9657578 or the Megacart RE 9657578 model (Siemens).

KORA-F3 / KORA-S4

The KORA Study is a series of population-based epidemiological surveys of persons living in or near the city of Augsburg, Germany. All survey participants are residents of German nationality identified through the registration office and between 25 and 75 years old at the time of enrollment. Survey S3 was conducted between 1994 and 1995 and survey S4 between 1999 and 2001. KORA F3, a 10-year follow up of S3, occurred in 2004 and 2005. In KORA F3 and S4 12-lead resting ECGs were recorded with digital recording systems (F3: Mortara Portrait, Mortara Inc., Milwaukee, USA, S4: Hörmann Bioset 9000, Hörmann Medizinelektronik, Germany). The Mortara portrait ECG machine determines QT interval by the proprietary XL-ECG algorithm which has not been fully published but has shown to be in good accordance with other published ECG measurement algorithms[25]; QT intervals from Hörmann Bioset were determined using the Hannover EKG analysis software (HES-Version 3.22-12) by computerized analysis of an averaged cycle computed from all leads and all cycles of the 10 second recording after exclusion of ectopic beats as described earlier[26]. The QT interval determined by this algorithm represents the earliest beginning of depolarization until the latest deflection of repolarization between any two leads.

PIVUS

The participants were randomly sampled from all men and women at age 70 living in Uppsala County in 2001 (www.medsci.uu.se/PIVUS). Of the 2025 individuals invited, 1016 participated. The participants underwent a medical examination including a detailed questionnaire on lifestyle and socioeconomic factors, fasting blood sampling, blood pressure measurement and anthropometric measurements, as previously described[52]. Blood and plasma samples have been frozen until analysis, and blood tests performed include a wide variety of traditional and more recent CVD risk factors, along with DNA extraction. In addition, the extent of subclinical cardiovascular disease has been assessed extensively by echocardiography, carotid sonography, endothelial function and arterial compliance measurements, and whole-body angiography. Cardiovascular morbidity and mortality has been recorded using the Swedish Hospital discharge registry and Cause of death registry. A standard 12-lead ECG was recorded at 50 mm/s and 10 mm/mV and evaluated according to the Minnesota code[53] and in revised form[28] by one experienced physician who was unaware of other data of the subjects.

PREVEND

The Prevention of REnal and Vascular ENd stage Disease (PREVEND) study is an ongoing prospective study investigating the natural course of increased levels of urinary albumin excretion and its relation to renal and cardiovascular disease. Inhabitants 28 to 75 years of age (n=85,421) in the city of Groningen, The Netherlands, were asked to complete a short questionnaire, 47% responded, and individuals were then selected with a urinary albumin concentration of at least 10 mg/L (n = 7,768) and a randomly selected control group with a urinary albumin concentration less than 10 mg/L (n = 3,395). Details of the protocol have been described elsewhere (www.prevend.org). Standard 12-lead electrocardiograms were recorded with CardioPerfect equipment (Cardio Control; currently Welch Allyn, Delft, The Netherlands) and digital measurements of the QT intervals were made using the Modular ECG Analysis System (MEANS). The QT detector of MEANS operates on multiple simultaneously recorded leads, which are transformed to a detection function that brings out the QT complexes among the other parts of the signal.

SAPHIR

The SAPHIR (Salzburg Atherosclerosis Prevention Program in subjects at High Individual Risk) study has been initiated in the year 1999 as a population-based prospective study that investigates genetic and environmental factors contributing to atherosclerotic vascular disease. Study participants were recruited by health screening programs in large companies in and around the city of Salzburg. All study subjects provided informed consent. The study comprises 1770 healthy unrelated subjects (663 females and 1107 males aged 39-67 years). All study participants were of Caucasian origin and were subjected to a comprehensive physical and instrumental examination. All individuals underwent standard 12-lead ECG registration using MAC-1200 ST EKG recorder (GE Healthcare, Freiburg, Germany) and data were interpreted automatically using the GE Marquette 12SL TM ECG Analysis Program (GE Medical systems, Menomonee Falls, WI, USA). Relevant ECG data were missing for 41 subjects.

ULSAM

All men born in 1920 to 1924 who were residents of Uppsala County were invited to participate in a health examination carried out 1970-73 (http://www.pubcare.uu.se/ULSAM). Of 2841 men invited, 2322 (82%) participated in the investigation at age fifty[54]. The men were invited to re-examinations at age 60 (n=1860), age 70 (n=1221), age 77 (n=839) and age 82 (n=530), and the data has been annually updated on mortality and in-hospital morbidity using national registers. The data collection in the ULSAM cohort has been focused on CVD risk factors and endpoints, including but not restricted to blood pressure, glucose metabolism, anthropometry, diet, physical activity, socioeconomic factors, and blood tests including a wide variety of traditional and more recent CVD biomarkers, together with DNA extraction. At age 70, participants also underwent a euglycemic hyperinsulinemic clamp and had muscle biopsies showing capillary density and morphology taken. A standard 12-lead ECG was recorded at 50 mm/s and 10 mm/mV and evaluated according to the Minnesota code[53] and in revised form[28] by one experienced physician who was unaware of other data of the subjects.

WHITEHALL II

The Whitehall II study recruited 10,308 participants (70% men) between 1985 and 1989 from 20 London-based Civil service departments. Clinical measurements are taken every 5 years. Blood samples for DNA were collected in phase 7 (2002–2004) from over 6000 white-European participants. ECG measurements and other phenotypeinformation from phase 7 were used in this study since this phase had the largest number of ECG measurements. Informed consent was obtained from all participants and the study was approved by UK NHS local ethics committees. Standard 12 lead ECGs were recorded on the Burdick Eclipse 850 ECG recorder. Digital ECG data were transferred to the University of Glasgow ECG Core Lab based in Glasgow Royal Infirmary and analysed by the University of Glasgow ECG analysis program[55]. This software meets all of the required specifications in terms of measurement accuracy and is used widely in various commercial products. All ECGs were reviewed manually and checked for technical problems which would have interfered with analysis, e.g. reversed limb lead connections, excessive artefact etc. Technically unsatisfactory ECGs were excluded.

QT interval association analyses (GWAS, validation, meta-analysis)

All studies used hidden Markov model approaches to impute genotypes at unmeasured HapMap SNPs so that a common set of 2.5M SNPs were available across the discovery samples[56]. Cohort-specific genome-wide association analysis was performed after exclusions with mandatory adjustment for age, sex and RR interval. Additional covariates such as principal components, study center or generation were included as available and appropriate for individual cohorts.

GWAS data quality control

Regression results from each cohort were cleaned to remove any poorly behaving SNPs. Monomorphic SNPs and SNPs with betas larger than 100,000 were removed from all results. Additionally, imputation quality score distributions were examined for systemic low imputation quality. Quality control steps were applied to specific summary results if quantile-quantile distributions of SNPs, stratified by minor allele frequency and imputation quality, showed test statistic inflation (Supplementary Table 3). Genomic control was performed on cohort-specific results after QC exclusions.

GWAS meta-analysis

The regression results were meta-analyzed using inverse variance weighted-fixed effects models. Two independent analysts conducted the meta-analysis with two different software packages: MANTEL[20] and METAL[57]. The results of the independent meta-analyses were completely concordant, indicating the robustness of the analysis. Meta-analysis test statistic inflation was low and further genomic control was not performed (λ=1.076). Significant associations were declared for SNPs with P < 5x10, a threshold reflecting an estimated testing burden of one million independent SNPs in samples of European descent[58].

To determine top independent SNPs, particularly in those regions that contained more than one statistically significant SNP, we employed an LD-based binning (“clumping”) algorithm using the software PLINK[59]. The procedure set a SNP with the most significant P value as an index SNP. Then any SNP 500kb upstream or downstream of the index SNP (regardless of P value) is added to a bin if it has a pairwise r > 0.05 to the index SNP for that bin, using LD patterns from the CEU samples in HapMap (release 27). This procedure is then repeated starting with the most significant SNP remaining, until each SNP is clustered into a “clump”. Given the liberal LD cutoff (r>0.05) to define a clump of correlated SNPs, index SNPs are in extremely weak LD with each other, determining suggestive independent association signals.

Interim validation SNP selection

At an interim stage at which GWAS results on 48,997 individuals were available from 21 cohorts, a meta-analysis was performed to select SNPs for 1) targeted SNP genotyping in validation samples and 2) nomination for inclusion on the metabochip genotyping array (Voight et al, manuscript submitted). 35 SNPs were selected for targeted genotyping on a variety of single- and low-complexity-multiplex arrays (Supplementary Table 2). SNPs were clumped according to linkage disequilibrium (r>0.05, see above) such that only the SNP with the lowest p-value per clump was eligible for targeted SNP genotyping. SNPs at loci already established to harbor common variants influencing QT interval were not considered for targeted SNP genotyping[20,60]. Up to 35 SNPs (with r in HapMap CEU to each other and to previously established QT loci) were selected for attempted genotyping in validation cohorts. Cohorts that could only genotype a smaller number of SNPs were asked to preferentially genotype SNPs that were nearly but not yet genome-wide significant, to maximize the power to identify novel loci. In parallel, a SNP previously reported to be associated with QT interval in a GWAS that included its direct genotyping on a custom gene-focused supplementary array (rs1805128 at *KCNE1*)[20] was also selected for genotyping in several of the GWAS cohort samples in which it was poorly imputed.

For the metabochip array content, SNPs were selected for "replication" or "finemapping". For replication content, the top SNPs were LD pruned such that no SNP had an $r>0.20$ to another more significant SNP based on LD in HapMap CEU. The most significant 5,000 replication SNPs were chosen for QT interval, solely on the basis of increasing ascending p-value (Supplementary Table 4). In addition, loci that had genome-wide significant associations were eligible for inclusion in the finemapping content. Finemapping loci were selected to fine map a single association signal ("signal finemapping"), for which SNPs partially correlated to the top SNP at the locus were selected (Supplementary Tables 4 and 5). Additional finemapping loci were selected for "locus finemapping", largely on the basis of preliminary evidence of >1 independent signal or strong effects on QT interval (which would presumably increase the power to resolve the association signal given finite replication resources), involving testing of SNPs within a defined genomic span regardless of correlation to the top SNP. LD-based pruning was used in both signal finemapping and locus finemapping SNP selection according to loci deemed high (GOLD), medium (SILVER) and lower (BRONZE) priority by the QT-IGC consortium on the basis of biologic interest, strengths of effect and apparent presence of multiple signals of association (Supplementary Tables 4 and 5).

Validation genotyping and meta-analysis with GWAS

To ensure compatibility between the replication data sets and the discovery GWAS data, alleles were aligned to the positive strand of NCBI 35, allele frequencies were examined, and where allele coding was ambiguous (e.g. A/T or C/G SNPs with high MAF), blatting of primers/probes performed to confirm strand assignment. Meta-analysis of discovery GWAS and replication data was run by two independent analysts using MANTEL and METAL, genome-wide significant loci were visualized using regional association plots, and the PLINK clumping algorithm was applied to determine a list of suggestive independent associations.

Regional association plots

Genomic regions containing statistically significant SNPs were visualized using regional association plots that included linkage disequilibrium information for neighboring SNPs within 0.5 Mb of the sentinel SNP, using HapMap 2 CEU samples (release 27) as a reference (Supplementary Figure 2). Because loci were declared significant on the basis of GWAS+replication genotyping, the SNP with the lowest p-value may have a larger sample size than nearby SNPs not selected for replication genotyping. We, therefore, plotted regional association results based on a GWAS-only meta-analysis to ensure a uniform sample size (although variation in imputation among neighboring SNPs still exists). Some loci therefore show evidence of a SNP with stronger evidence of association in the GWAS-only analysis than the SNP with which genome-wide significance was declared and results presented throughout the manuscript (e.g., the loci including *GFRA3*, *SMARCAD1*, *SP3*, Supplementary Figure 2).

Association of QT SNPs in African ancestry cohorts

The association of 68 independent SNPs was examined in a meta-analysis of QT interval GWAS in 13,105 individuals of African Ancestry as part of the CARe and COGENT consortia[61]. One SNP (rs12930096) was not found in HapMap YRI (and was therefore not imputed), so a proxy was selected (rs8050461). One SNP was filtered due to poor imputation due to very low frequency (rs1805128). QT interval was adjusted for age, sex, and RR interval, along with principal components for axes of genetically-defined ancestry and study site for multi-center cohorts. Effects were compared after ensuring the same coded allele using ACGT coding and coded allele frequency. Significant replication was claimed for SNPs with effects in the same direction as in QT-IGC and with 2-sided $P<0.0007$ (=0.05/67). Correlation and directional consistency were assessed using Pearson correlation coefficient and reference to a binomial distribution, respectively.

Pleiotropic effects of QT SNPs

QT SNP association with heart rate

The HRGEN consortium included data from 92,355 individuals of European or Indian Asian ancestry drawn from 36 studies[62]. Genotype-phenotype associations of heart rate (on the beats per minute scale) were adjusted for age, age and body mass index, as well as for study-specific covariates when appropriate (eg principal components) in sex- and case-status specific analyses (in samples ascertained for diseases). Summary statistics were meta-analyzed for ~2.55m directly genotyped or imputed SNPs using inverse variance-weighted fixed-effects meta-analysis, applying genomic control at the study and meta-analysis level. We examined 68 SNPs at 35 QT loci (Supplementary Table 4) in the HRGEN dataset (Supplementary Table 10).

QT SNP association with QRS duration

The QRS GWAS consortium included data from 40,407 individuals of European ancestry in whom QRS duration had been measured[63]. Genotype-phenotype associations of QRS duration on the millisecond scale were adjusted for age, sex, height, and body mass index, as well as study-specific covariates. Summary statistics were meta-analyzed for 2.5m directly genotyped or imputed SNPs using inverse variance-weighted fixed-effects meta-analysis, after applying genomic control to study-specific results. We examined 68 SNPs at 35 QT loci (Supplementary Table 4) in the QRS GWAS dataset (Supplementary Table 10).

QT SNP association with other traits

We examined the NHGRI Catalog of Published Genome-Wide Association Studies (http://www.genome.gov/gwastudies accessed December 30, 2011)[64]. We used SNAP (http://www.broadinstitute.org/mpg/snap) to identify all SNPs in HapMap CEU with r>0.8 to any of the 68 independent SNPs at 35 QT loci (Supplementary Table 4) in HapMap 2 (release 22), HapMap 3 or 1000 Genomes Pilot 1. We then looked up all SNPs in the NHGRI GWAS catalog and removed all SNPs previously related to QT interval, as well as heart rate or QRS duration as these results are presented elsewhere (Supplementary Table 11).

Non-synonymous SNPs

We used the SNP Annotation and Proxy Search (SNAP)[65] tool to examine the correlation of 35 sentinel SNPs (Table 1) and 68 putatively independent SNPs at 35 QT loci (Supplementary Table 8). We searched HapMap 2 release 22, HapMap 3 release 2 and 1000 Genomes Phase 1 data (all CEU) for any SNP within 500kb of each SNP at r>0.8 to the target SNP to identify any SNPs that are associated with an amino acid change. Four of the 68 SNPs were missense--rs846111 in *RNF207*; rs1805128 in *KCNE1*; rs1042391 in *GMPR*--or highly correlated to a missense SNP--rs6795970 in *SCN10A* with r to rs6801957 0.97 (Supplementary Table 8).

Expression analyses in non-cardiac tissues

For each of the 68 independent SNPs at 35 genome-wide significant QT loci, all proxy SNPs with *r*>0.8 were identified in HapMap CEU (releases 21, 22, and HapMap 3 release 2) using SNAP[65]. All sentinel SNPs and their proxies were then searched for in a set of expression SNP (eSNP) results including the following tissues: fresh lymphocytes[66], fresh leukocytes[67], leukocyte samples in individuals with Celiac disease[68], lymphoblastoid cell lines (LCL) derived from asthmatic children[69], HapMap LCL from 3 populations[70], a separate study on HapMap CEU LCL[71], peripheral blood monocytes[72,73], omental and subcutaneous adipose[74,75], stomach[75], and whole blood samples[74,76], endometrial carcinomas[77], brain cortex[72,78], 3 large studies of brain regions including prefrontal cortex, visual cortex and cerebellum (Emilsson, personal communication), liver[75,79,80], osteoblasts[81], skin[82] and additional fibroblast, T cell and LCL samples[83].

A strong expression association signal will be associated with a penumbra of associated nearby SNPs due to partial correlation, which may still have quite low p-values. Thus, the top QT-associated SNP appear significantly associated with expression of a nearby transcript even though a much stronger eSNP association may exist (best eQTL). In Table 1, we show only expression association results for cis transcripts in which 1) the index (top signal) QT SNPs or proxies (*r*>0.8 between eSNP and QT index) is an eSNP with *P*<5x10 in eQTL analysis and 2) the index QT SNP is highly correlated (r>0.8) to the best eSNP at the locus for that transcript. All results, including additionally those with lesser correlation between eSNP and QT SNP or best eSNP and QT SNP, association of transcripts with non-index QT SNP (i.e. additional signals of QT association), or transcript associations with *P* > 5x10 but meeting eQTL study-specific significance thresholds are shown in Supplementary Table 12. There are clear examples where the expression and QT association signals do not coincide, as evidenced by much lower QT association for the best eSNP at the locus, e.g. association of *TRPM7* (eSNP = rs3105593), *c11orf10* (eSNP = rs174556) or *FADS2* (eSNP = rs174556) transcripts, where the GWAS-only QT association (to ensure uniform sample size) for the top eSNP is orders of magnitude less significant than the top QT SNP (Supplementary Table 12).

We sought evidence of enrichment of gene expression in specific cell types among the set of genes in QT-interval associated loci, as has previously been applied to loci associated with autoimmune diseases[84]. We tested for over-representation of QT-associated genes with expression in each individual cell-type in the Novartis mouse-human gene expression atlas (containing 79 specific cell types)[85], and assessed statistical significance in a permutation-based framework[84]. We found no cell-type to be over-represented among the QT loci at p<0.01.

Expression analyses in cardiac tissue

Samples of cardiac tissue (n=313) were acquired from patients from the Myocardial Applied Genomics Network (MAGNet; www.med.upenn.edu/magnet). Left ventricular free-wall tissue was harvested at the time of cardiac surgery from subjects with heart failure undergoing transplantation and from unused donor hearts. The heart was perfused with cold cardioplegia prior to cardiectomy to arrest contraction and prevent ischemic damage. Tissue specimens were then obtained and frozen in liquid nitrogen. Genomic DNA was extracted using the Gentra Puregene Tissue Kit (Qiagen, CA) according to manufacturer's instructions. Total RNA was extracted using the miRNeasy Kit (Qiagen) including DNAse treatment. RNA concentration and quality was determined using the NanoVue Plus™ spectrophotometer (GE Healthcare) and the Agilent 2100 RNA Nano Chip (Agilent).

DNA samples were genotyped using Affymetrix Genome Wide SNP Array 6.0. We applied quality control (QC) filters to exclude unreliable samples, samples with cryptic relatedness and samples that were not genetically inferred Caucasian. For the analysis reported here, we eliminated SNPs with genotype call rate < 95%, with minor allele frequency (MAF) < 15%, or if there was significant departure from Hardy-Weinberg equilibrium ($p < 10$). A total of 360,046 SNPs passed QC and were available for analysis. To improve cross study comparisons, genotype imputation was performed using the Minimac (v 2012.11.16)[86] program. Imputation results were filtered at an imputation quality threshold of 0.5 and a MAF threshold of 0.15. For imputed genotypes, we used dosage value as genotype. To assess gene expression, RNA was hybridized with Affymetrix Genechip ST1.1 arrays using manufacturer instructions. CEL files were normalized with robust multiarray analysis (RMA) using Bioconductor[87]. To remove potential batch effects, expression values were further adjusted using ComBat[88].

There were a total of 68 independent QT-interval associated SNPs considered, of which 63 SNPs had data in the LV expression imputed genotype association results (5 SNPs were not well imputed). The 63 SNPs were tested for association with any transcript within 1 Mb. We used the combined genotype and expression data to test whether the 63 QT interval SNPs, considered individually, showed *cis* eQTL association with nearby genes found within the interval +/- 1Mb of each QT interval SNP (total of 1,146 SNP-transcript association tests examined). Our analysis used a joint-effects model that allowed for different strengths of association in comparatively healthy hearts from unused donors versus those with end-stage heart failure. Specifically, we fit linear regression models, $Y = \text{age} + \text{sex} + \text{study site} + D + \beta 1(g) + \beta 2(g \times D)$, where Y is the $\log_2$ transformed expression level of a given expression trait, g is the dosage value of the test SNP, and D is the patient group ($D = 1$ for heart failure and $D = 0$ for unused donors). Association between Y and g was assessed by testing H_0: $\beta 1 = \beta 2 = 0$ using a likelihood ratio test. Significance of the test statistic was evaluated by comparing with a Chi-squared distribution with two degrees of freedom. We considered $P < 4.36 \times 10$ (0.05/1,146 tests) to be statistically significant (Table 2). To test whether statistically significant associations were likely to be mediated through the strongest eSNPs in the region, we fit analogous models that conditioned on genotypes for the strongest observed *cis* eSNP for each expression trait. QT interval SNPs that showed substantial attenuation of the strength of association with a specific transcript upon adjustment for the best eSNP for that transcript suggest that the QT association is mediated by influence of the causal variant (not necessarily the SNP identified) on expression of that gene with the following caveats: a) some genetic variants are associated with expression of multiple genes of which the mediator of the QT effect may be a subset of one or more genes, b) some *cis* genes may have had noisier expression measurements on the array and therefore not been adequately assayed for association. For SNPs that showed minimal attenuation of association in models adjusting for the best eSNP, the myocardial repolarization effect manifest in the QT association is unlikely to be mediated by the association of the best eSNP with expression of that gene.

Left Ventricular Enhancer Roadmap Analyses

Enhancer annotations were generated by integrating combinations of histone modifications obtained from the Roadmap Epigenomics project using ChromHMM[89,90]. We identified SNPs in LD ($r > 0.8$) with each of the 68 QT interval-associated loci using genotype data from the 1000 Genomes Project (CEU population) and computed overlap with ChromHMM-annotated enhancer elements in the left ventricle tissue sample (BC Left Ventricle N41) in the NIH Roadmap Epigenomics Program[91] using the intersectBED command in BEDTools (v2.12.0, Supplementary Table 13). To assess significance of the overlap, we compared the set of SNPs at 68 QT interval-associated loci against 100,000 sets of randomly sampled control SNPs. Control SNPs were chosen from the Affymetrix 660W genotyping array and were matched for size of the LD block (+/- 5 SNPs), minor allele frequency of the lead SNP (+/- 0.1) and distance to the nearest gene (+/- 25 kb if outside a gene).

Gene-set enrichment analysis

We ran MAGENTA (Meta-Analysis Gene-set Enrichment of variaNT Associations, http://www.broadinstitute.org/mpg/magenta/) to perform pathway analysis on the results from the QT-IGC meta-analysis of 76,061 individuals. MAGENTA uses meta-analysis results to test for enrichment of genetic associations in predefined sets of related genes. These predefined biological processes and gene sets are drawn from the following databases: Gene Ontology (GO), Ingenuity, Kyoto Encyclopedia of Genes and Genomes (KEGG, versions from 2008 and 2010), and Protein ANalysis THrough Evolutionary Relationships (PANTHER). The chromosome, position, z-score, and p-value for each SNP in the meta-analysis were used as input to MAGENTA. We ranked the results by the 95 percentile gene set enrichment analysis (GSEA) p-values and searched for pathways enriched in our QT interval-associated SNPs.

We sought evidence that genes in QT interval-associated loci are over-represented among knockout mouse models with cardiac phenotypes by a systematic search in the international database resource for the laboratory mouse (MGI-Mouse Genome Informatics; www.informatics.jax.org). Each associated SNP implicates a set of nearby genes. To determine the set of genes, each SNP is assigned to a genomic interval by finding the furthest HapMap2 CEU neighboring SNP within 200 Kb with $r > 0.5$. The interval is extended up- and down-stream to the nearest recombination hotspot. All genes overlapping the interval are implicated by the given SNP, and if there are no genes overlapping the interval then the interval is extended further by 250 kb up- and downstream. To test for enrichment, random SNP sets matched to the QT interval-associated SNPs on the number of implicated genes were sampled from a list of 56,890 SNPs in linkage equilibrium covering the whole genome. We generated 100,000 random SNP sets and counted how many times a SNP set implicates at least as many genes of interest as the QT interval-associated SNPs, from which we derived an empirical p-value.

Variance explained

To determine the proportion of variance explained by the SNPs associated with QT interval, we constructed multivariable regression models. We tested the ability of 35 SNPs (one most strongly associated SNP per locus) and 68 SNPs (including all index SNPs with $r<0.05$ based on HapMap CEU to any other index SNP at the 35 loci) to explain variation in the age-, sex- and RR-interval-adjusted QT interval. Because HapMap CEU correlation patterns based on 120 independent chromosomes are somewhat imprecise, correlation among multiple SNPs at a single locus could make a genotype score (weighted by meta-analysis beta estimates) over- or under-count the influence of a locus. We therefore used individual terms in a multivariable regression framework for each SNP's genotype dosage, by which collinearity would effectively downweight partially correlated SNPs. This was applied to the FHS, ARIC and ERGO study samples (Supplementary Table 15).

As an alternate approach we implemented the GWiS method, which aggregates the statistical support for multiple independent effects at a locus using a reference linkage disequilibrium matrix[92]. A locus is defined as the genomic region flanked by the 5' and 3' most genome-wide significant signal, plus 500KB of flanking sequence on each end. For each locus, GWiS uses Bayesian model selection to find the number of independent effects and the SNPs that best tag them, choosing the SNPs that maximize the posterior probability in a greedy search. In each step, the SNP that gives the greatest increase in the posterior probability is added into the model, and this step is repeated until no more SNPs increase the posterior probability. This posterior probability is calculated as the product of three terms: the multivariable regression likelihood term, the Bayesian penalty term for model size, and the multiple testing correction term for the locus size. The first term addresses the collinearity among correlated SNPs and only allows independent association signals into the model. The second term is essentially a regularization term to prevent model over-fitting, such as the L1 norm in Lasso. It has been shown previously that the Bayesian penalty term has much better performance than the L1 norm used in Lasso[92]. The third term gives each locus the same weight to have association signals regardless of its size.

The SNPs selected by the Bayesian model selection are then used in a multivariate linear regression to calculate the variance explained. We modified the original implementation of GWiS to use the meta-analysis results as input. For a single SNP, if the sample size is large, variance explained is approximately z/N, in which z is the z-score of the SNP and N is the sample size. For multiple SNPs, however, the summation of z/N of all SNPs is not the total variance explained because SNPs can be correlated. Gram-Schmidt Ortho-normalization provides an iterative procedure to adjust for the correlations among SNPs in the summation. For each iteration, the SNP that has the best z score is selected (denoted as m). We then add its explained variance ($V_m = z_m^2/N$) to the total variance explained ($V=V+V_m$) and adjust the z scores of the remaining SNPs using the following update equations

$$\mathrm{cov}(Y,X_i) \leftarrow \mathrm{cov}(Y,X_i) - \mathrm{cov}(X_m,X_i)\frac{\mathrm{cov}(Y,X_m)}{\mathrm{cov}(X_m,X_m)}$$

$$\mathrm{cov}(X_i,X_j) \leftarrow \mathrm{cov}(X_i,X_j) - \mathrm{cov}(X_m,X_i)\frac{\mathrm{cov}(X_j,X_m)}{\mathrm{cov}(X_m,X_m)}$$

$$z_i = \frac{\mathrm{cov}(Y,X_i)\sqrt{N}}{\sqrt{\mathrm{cov}(Y,Y)\mathrm{cov}(X_i,X_i)}},$$

in which *Y* is the phenotype, *X* is the genotype, *i* and *j* are the index of the SNPs, and cov() is the covariance. The iterations are repeated until all SNPs are added into the total variance explained. Initial inputs to the iterations are the covariance between the phenotype and the SNP genotype, and the LD matrix among all SNPs. The former was calculated from the *z* score using

$$\mathrm{cov}(Y,X_i) = z_i\sqrt{\mathrm{cov}(X_i,X_i)\mathrm{cov}(Y,Y)/N},$$

and the latter was pre-calculated using genotypes from the ARIC cohort.

GWiS was applied to the GWAS meta-analysis, forcing in loci which reached genome-wide significance after joint analysis of GWAS and replication results, making use of pairwise SNP r estimates from the ARIC study. GWiS estimated 60 independent signals of association at the 35 genome-wide significant loci (Supplementary Table 16).

LQTS cohort mutation analysis

LQTS cohorts

A cohort of 298 unrelated, LQT1-3 mutation negative patients with LQTS [191 females (64%), average age= 27 ± 20 years, average QTc = 529 ± 58 ms], who satisfied the case inclusion criteria of QTc $\geq$ 480 msec (n= 261, 86%) or Schwartz score[93] $\geq$3.0. (n=298, 100%), was derived from 7 international congenital LQTS recruitment centers [l'Institut du Thorax, Nantes, France (n=91), Mayo Clinic, Rochester, Minnesota, United States (n=72), University of Pavia, Pavia, Italy (n=38), Academic Medical Centre, Amsterdam, Netherlands (n=30), The Hospital for Sick Children, Toronto, Ontario, Canada (n=24), Munich Medical International GmbH, München, Germany (n=23), and St. George's Hospital, London, England (n=20)]. Of the 265 patients with a documented clinical history, 175 (66%) were symptomatic with $\geq$ 1 LQTS-related cardiac event (i.e. syncope or cardiac arrest). All study subjects provided written informed consent and protocols were approved by local institutional review boards.

Candidate gene mutational analysis

Six genes (*ATP2A2*, *CAV1*, *CAV2*, *SLC8A1, SRL*, *TRPM7*), derived from 5 genome-wide significant novel loci, were selected for comprehensive open-reading frame/splice-site mutation analysis. These 6 candidate genes were chosen based on nominal statistical significance, proximity to the signal of association, absence of multiple nearby genes in the associated interval, and known cardiac expression or involvement in ion channel macromolecular complexes. All 298 genomic DNA samples were distributed among 5 mutation screening centers: Academic Medical Centre (*SLC8A1*), Mayo Clinic (*TRPM7*), Munich Medical International GmbH (*CAV1*/*CAV2*), l'Institut du Thorax (*ATP2A2*) and University of Pavia (*SRL*). For each gene, mutational analysis was performed using either direct Sanger-based DNA sequencing of all patient samples or using an intermediate mutation detection platform (i.e. denaturing high performance liquid chromatography [DHPLC]) followed by direct DNA sequencing of only samples showing an aberrant DHPLC elution profile.

To be considered as a potential LQTS-associated mutation, the variant must have disrupted either the open reading frame (i.e., missense, nonsense, insertion/deletion, or frameshift mutations) or the canonical splice site (splice acceptor or splice donor recognition sequences). Hence, single nucleotide substitutions that did not change the open reading frame (i.e., synonymous single nucleotide polymorphisms/variants) and intronic nucleotide substitutions located outside of the canonical splice site recognition sequence were excluded from consideration. Additionally, the candidate mutation must have been absent in at least 400 reference alleles derived from ethnically matched ostensibly healthy controls. The presence or absence of each candidate mutation among the 12,000+ individuals of European, African or Hispanic ancestry that comprise the ExomeChip was also assessed. The ExomeChip design required at least two copies of the alternate allele be observed for inclusion on the array. In addition, the presence of any alternate alleles (including singletons) was determined in the NHLBI-sponsored Exome Sequencing Project, which includes up to 5,379 individuals of European or African ancestry (http://evs.gs.washington.edu/EVS/). In-silico analysis of the identified rare variants was performed using Alamut (Interactive Biosoftware), as well as freely available software at SIFT (Sorting Intolerant From Tolerant; http://sift.jcvi.org/) and PolyPhen (Polymorphism

Phenotyping; http://genetics.bwh.harvard.edu/pph/). UniProtKB entries included Q86TD4 (*SRL*), P32418 (*SLC8A1*), Q96QT4 (*TRPM7*) and P16615 (*ATP2A2*).

DAPPLE protein-protein interaction analysis

InWeb database

The protein-protein interaction database we used is called InWeb and is described in Rossin et al. 2011; we briefly summarize that description here[94]. We used a public database of protein-protein interactions described in 2007 by Lage et al[95]. This database contains 428,430 interactions, 169,810 of which are high-confidence interactions across 12,793 proteins. High-confidence is defined by a rigorously tested signal to noise threshold as determined by comparison to well-established interactions. InWeb combines reported protein interactions from MINT, BIND, IntAct, KEGG annotated protein-protein interactions (PPrel), KEGG Enzymes involved in neighboring steps (ECrel), Reactome, and others[96-100]. All human interactions were pooled and interactions in orthologous protein pairs passing a strict threshold for orthology were included. Each interaction was assigned a probabilistic score based on the neighborhood of the interaction, the scale of the experiment in which the interaction was reported and the number of different publications in which the interaction had been sited. The data we used is available at www.broadinstitute.org/mpg/dapple.

In silico network analysis

We wanted to test whether genes previously reported to be associated with QT-interval variation assembled into a protein-protein interaction network with known Mendelian long-QT syndrome (LQTS) genes and whether the new associations discovered through the QTIGC meta-analysis fell non-randomly into this network. There were 7 loci in total that were associated previously and did not contain a known Mendelian-LQTS gene.

First, we translated the 7 previously published loci into genes as follows. We defined the wingspan of a SNP as the region containing SNPs with $r>0.5$ to the associated SNP; this region was then extended to the nearest recombination hotspot as defined by The HapMap Project[101]. We downloaded the Ensembl human gene list from UCSC Genome Browser and collapsed isoforms into single genes[102]. We converted gene IDs from Ensembl to InWeb IDs. A gene's residence in a locus was defined by whether 50kb upstream and 50kb downstream (to include regulatory DNA) of the coding region overlapped the SNP wingspan. We found 43 genes in total, 32 of which participated in high-confidence interactions according to the InWeb database (Supplementary Table 18)[20,60].

We used a published algorithm called DAPPLE (Disease Association Protein-Protein Link Evaluator) to build and analyze a network of seed genes[94]. We seeded the network with 12 known Mendelian LQTS proteins (KCNQ1, KCNH2, SCN5A, KCNE1, KCNE2, CAV3, SNTA1, KCNJ2, CACNA1C, ANK2, AKAP9, SCN4B) as well as the genes from the 7 previously associated loci. We considered direct connections among the seed proteins as well as indirect connections through other proteins, filtering on connections between proteins from different loci. DAPPLE evaluates the significance of the network and individual proteins within it by comparing it to 10,000 random, matched networks that are generated using a within-degree node-label permutation[94]. It then prioritizes the highest scoring proteins in multi-genic loci according to their propensity to interact with the rest of the network. We found the network to be significantly interconnected (direct connection $p=0.0006$, indirect connection $p=0.008$) and could prioritize ATP1B1 based on its connections to other proteins (ATP1B1 connected indirectly to 6 LQTS proteins and 1 associated protein), unlike the other proteins in the same locus.

Analysis of proteins connecting to the network

We considered the ability of protein-protein interactions to identify proteins newly associated in the QT-IGC meta-analysis. We translated the novel loci into genes, identifying 124 genes in total, 85 of which were in the InWeb database (**Supplementary Table 18**). We identified 606 other proteins interacting directly with the seeds used as inputs in the described network, 8 (from 5 loci) of which were among the 85 newly associated proteins. Note that to increase coverage, we considered any input seed regardless of its connectivity, except those not prioritized in a multi-genic locus. Using a hypergeometric test (given that the database has 12,793 proteins), this represents an enrichment beyond expectation at p=0.029. We show this network in Supplemental Figure 3.

For those other proteins that were not among the set of 85 genome-wide significant ones, we tested them for enrichment in association, following the gene-scoring procedure described in Rossin et al. Briefly, we assigned recombination hotspot-bounded linkage-disequilibrium blocks in the genome the maximum Z score in each block. Since the maximum Z score is correlated to the number of SNPs genotyped in that block, we removed this effect via linear regression in R: the original Z score was regressed onto the number of SNPs in the LD block, and the residuals from this regression were used as the corrected association score for each block. Genes were then assigned association scores based on the blocks they overlap.

We scored the other 606 proteins for association and compared their distribution of scores to all scored sub-genome-wide significant proteins in the genome. Via a one-tailed rank-sum test (since our alternative hypothesis is that they are more associated), we identified an enrichment in association at P = 0.00012 in those 606 proteins.

Description of genes of interest at novel loci associated with QT interval

Six novel loci coding for calcium handling proteins

- *ATP2A2* – encodes the Ca transporting slow twitch ATPase2 (SERCA2). The SERCA2a isoform from cardiac muscle sarcoplasmic reticulum and the ubiquitously expressed SERCA2b isoform both help to maintain low cytoplasmic Ca concentrations. Serca2 (+/-) heterozygous mice show deficits in relaxation, contractility, and a reduced Ca cycling. Defects in SERCA function have been implicated in a wide array of pathologies including heart failure, diabetes, skin diseases and cardiac hypertension and hypertrophy[103].

- *SRL* encodes sarcalumenin a Ca-binding protein localized in the sarcoplasmic reticulum (SR) of striated and cardiac muscle[104-106]. SRL physically interacts with SERCA2 enhancing its protein stability, facilitating Ca uptake into the SR and improving Ca cycling in the SR. Knockout mice develop progressive heart failure in response to pressure overload[105].

- *PRKCA* encodes the protein kinase C alpha that is a fundamental integrator of cardiac contractility. PRKCA senses intracellular Ca and influences the phosphorylation status of phospholamban (PLN), an inhibitor of the sarcoplasmic reticulum Ca ATPase-2 (SERCA-2) pump, thus altering sarcoplasmic reticulum Ca loading and intracellular Ca cycling[107].

- *CAV1* – encodes caveolin 1, a scaffolding protein of the caveolae plasma membranes found in most cell types. The CAV1 scaffold domain interacts with TRPC1 and IP3R3 to regulate Ca store release-induced Ca entry in endothelial cells[108]. CAV1 has also been shown to physically interact with KCNH2 and to participate in KCNH2 internalization under conditions of low extracellular K+[109]. Cav1 ablation in mice leads to contractile dysfunction, cardiac hypertrophy and SERCA3 upregulation[110]

- *TRPM7* encodes the ubiquitous Mg and Ca permeable transient receptor channel melastatin 7 protein with a role in intracellular ion homeostasis. It has an additional serine/threonine protein kinase function, which is essential for its channel function. TRPM7 is involved in adjusting plasma membrane divalent cation fluxes according to the metabolic and mechanical state of the cell[111-115].

- *SLC8A1*, the solute carrier family 8, encodes the cytoplasmic sodium/calcium exchanger NCX1 responsible for preventing overloading of intracellular Ca stores and maintaining an even Ca balance counteracting the Ca that enters the cardiomyocyte across the sarcolemma. The exchanger is a dominant mechanism in returning the cardiac myocyte to its resting state following excitation. Mice overexpressing NCX1 develop cardiac hypertrophy and heart failure[116]. Since original submission this locus has been reported to be associated with QT interval.

Six novel loci containing genes that encode proteins involved in transcription control

- *TCEA3* encodes the transcription elongation factor A (SII) a protein necessary for efficient RNA polymerase II transcription elongation past template-encoded arresting sites. Upregulation of TCEA3 has recently been determined to be part of a characteristic molecular signature of hESC derived cardiomyocytes[117].

- *MKL2* encoding myocardin-like 2, is a strong transcriptional coactivator of promoters containing serum response elements (SRE), the targets of serum response factor (SRF). It has an essential role in cardiovascular development and skeletal myogenic differentiation[118].

- *SP3* codes for the SP3 zinc finger transcription factor binding to consensus GC- and GT-box regulatory elements in target genes and functions as a bifunctional transcription factor. SP3 participates in the regulation of lipid metabolism in myocardial energy generation and hypertrophy response[119]. SP3 knockout mice develop a set of cardiac malformations leading to death before birth[120].

- *SMARCAD1* codes for the SWI/SNF-related, matrix-associated actin-dependent regulator of chromatin subfamily a containing DEAD/H box 1 protein. SMARCAD1 is a member of the SNF subfamily of the helicase protein superfamily that binds to transcriptional start sites of many genes involved in transcriptional regulation, most of them transcription factors or histone modifiers[121].

- *SPATS2L* (LOC26010) encodes the spermatogenesis associated, serine-rich 2-like also known as DNA polymerase-transactivated protein 6 (DNAPTP6) with no known function in the heart.

- *CREBBP* encodes the cAMP response element binding (CREB) binding protein[122]. This protein is involved in the transcriptional co-activation of many different transcription factors, and it has intrinsic histone deactyltransferase activity[123]. Mutations in CREBBP cause Rubenstein-Taybi syndrome[124]. Targeted knock in mice with an amino acid substitution in crebbp affecting acetyltransferase activity leads to cardiac malformations in heterozygotes[125].

Three novel loci that contain genes that encode proteins involved in other cellular processes

- *FADS2* encodes the delta(6) fatty acid desaturase which catalyzes biosynthesis of highly unsaturated fatty acids (HUFA) from polyunsaturated fatty acids (PUFA) linoleic and alpha-linolenic acid. The ratio of these fatty acids plays a pivotal role in membrane biology and other biological processes[126].

- *MATN2* encodes matrilin 2, a member of the von Willebrand factor A domain containing family of extracellular matrix (ECM) proteins involved in the formation of filamentous networks in the extracellular matrices of various tissues. MATN2 is expressed in the heart[127] and thought to participate in wound healing and regenerative processes of different tissues[128]

- *LAPTM4B* encodes lysosome-associated transmembrane protein 4-beta, a protein with high expression levels in uterus, heart and skeletal muscle which is up-regulated in various cancers[129]. Its function in the heart is unknown.

Structural proteins

- TTN encodes titin, a sarcomeric protein highly expressed in both cardiac and skeletal muscle. One single molecule of titin spans half a sarcomere from the Z-disc to the M-line[130]. Titin has multiple functions including: stabilizing the myosin filament; maintaining the integrity of the sarcomere; providing elasticity, and altering contractile properties of sarcomere[131]. Mutations in TTN cause familial hypertrophic type 9[132], dilated type 1G[133,134] and other inherited myopathies and dystrophies[135].

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MAGNet left ventricle eSNP

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