Supplementary Table 6. Association between SNPs and hypertension in all subjects

SNP	Non-HT (*n*=467)	HT (*n*=1,233)	*P* value[a]	Crude OR (95% CI)	*P* value	Adjusted OR (95% CI)	*P* value
TCF7L2 rs7903146							
Additive							
CT	47 (10.1)	92 (7.5)	0.092	1		1	
CC	420 (89.9)	1,141 (92.5)		1.39 (0.96–2.01)	0.082	1.56 (1.05–2.32)	0.030
Allele							
T	47 (5.0)	92 (3.7)	0.099	1		1	
C	887 (95.0)	2,374 (96.3)		1.37 (0.95–1.96)	0.088	1.52 (1.03–2.25)	0.034
TCF7L2 rs290487							
Additive							
TT	142 (29.3)	342 (70.7)	0.542	1		1	
TC	223 (26.9)	605 (73.1)		1.13 (0.88–1.45)	0.348	1.27 (0.97–1.67)	0.081
CC	102 (26.3)	286 (73.7)		1.16 (0.86–1.57)	0.319	1.33 (0.96–1.84)	0.087
Dominant							
TT	142 (29.3)	342 (70.7)	0.279	1		1	
TC+CC	325 (26.7)	891 (73.3)		1.14 (0.90–1.44)	0.276	1.29 (1.00–1.66)	0.050
Recessive							
TT+TC	365 (27.8)	947 (72.2)	0.561	1		1	
CC	102 (26.3)	286 (73.7)		1.08 (0.84–1.40)	0.553	1.14 (0.86–1.50)	0.354
Allele							
T	507 (28.2)	1289 (71.8)	0.299	1		1	
C	427 (26.6)	1,177 (73.4)		1.08 (0.93–1.26)	0.294	1.14 (0.86–1.50)	0.354
KCNQ1 rs2237892							
Additive							
CC	247 (52.9)	620 (50.3)	0.539	1		1	
CT	186 (39.8)	508 (41.2)		1.09 (0.87–1.36)	0.459	1.08 (0.85–1.38)	0.518
TT	34 (7.3)	105 (8.5)		1.23 (0.81–1.86)	0.326	1.30 (0.83–2.02)	0.252
Dominant							
CC	247 (52.9)	620 (50.3)	0.356	1		1	
CT+TT	220 (47.1)	613 (49.7)		1.11 (0.90–1.37)	0.337	1.12 (0.89–1.40)	0.353
Recessive							
CC+CT	433 (92.7)	1,128 (91.5)	0.429	1		1	
TT	34 (7.3)	105 (8.5)		1.19 (0.79–1.77)	0.407	1.25 (0.81–1.92)	0.309
Allele							
C	680 (72.8)	1,748 (70.9)	0.269	1		1	
T	254 (27.2)	718 (29.1)		1.10 (0.93–1.30)	0.269	1.25 (0.81–1.92)	0.309
KCNQ1 rs2237897							
Additive							
CC	261 (55.9)	659 (53.4)	0.527	1		1	
CT	181 (38.8)	493 (40.0)		1.08 (0.86–1.35)	0.505	1.10 (0.87–1.40)	0.436
TT	25 (5.4)	81 (6.1)		1.28 (0.80–2.06)	0.299	1.41 (0.85–2.33)	0.182

(*Continued to the next page*)

Supplementary Table 6. Continued

SNP	Non-HT (*n*=467)	HT (*n*=1,233)	*P* value[a]	Crude OR (95% CI)	*P* value	Adjusted OR (95% CI)	*P* value
Dominant							
CC	261 (55.9)	659 (53.4)	0.383	1		1	
CT+TT	206 (44.1)	574 (46.6)		1.10 (0.89–1.37)	0.367	1.14 (0.90–1.43)	0.276
Recessive							
CC+CT	442 (94.6)	1,152 (93.4)	0.372	1		1	
TT	25 (5.4)	81 (6.1)		1.24 (0.78–1.97)	0.355	1.35 (0.83–2.21)	0.229
Allele							
C	703 (75.3)	1,811 (73.4)	0.294	1		1	
T	231 (24.7)	655 (26.6)		1.10 (0.93–1.31)	0.278	1.35 (0.83–2.21)	0.229
KCNJ11 rs5219							
Additive							
GG	191 (26.6)	528 (73.4)	0.736	1		1	
GA	214 (28.4)	540 (71.6)		0.91 (0.73–1.15)	0.435	0.87 (0.68–1.11)	0.267
AA	62 (27.3)	165 (72.7)		0.96 (0.69–1.35)	0.824	1.06 (0.74–1.52)	0.768
Dominant							
GG	191 (26.6)	528 (73.4)	0.475	1		1	
AA+GA	276 (28.1)	705 (71.9)		0.92 (0.74–1.15)	0.474	0.91 (0.72–1.15)	0.425
Recessive							
GA+GG	405 (27.5)	1,068 (72.5)	1.000	1		1	
AA	62 (27.3)	165 (72.7)		1.01 (0.74–1.38)	0.954	1.14 (0.81–1.59)	0.463
Allele							
G	338 (28.0)	870 (72.0)	0.630	1		1	
A	596 (27.2)	1,596 (72.8)		0.96 (0.82–1.13)	0.621	1.14 (0.81–1.59)	0.463

Values are presented as number (%). OR adjusted for age, sex, BMI, type 2 diabetes mellitus, and dyslipidemia.
SNP, single nucleotide polymorphism; HT, hypertension; OR, odds ratio; CI, confidence interval; *TCF7L2*, transcription factor 7-like 2; *KCNQ1*, potassium voltage-gated channel subfamily Q member 1; *KCNJ11*, inwardly-rectifying potassium channel, subfamily J, member 11 gene.
[a]*P* value after 100,000 permutations.