Supplementary Table 8. Association between individual SNPs and micro- and macrovascular complications in type 2 diabetes mellitus patients

SNP	DM without complications (*n*=577)	DM with complication (*n*=383)	*P* value[a]	Crude OR (95% CI)	*P* value	Adjusted OR (95% CI)	*P* value
TCF7L2 rs7903146							
Additive							
CC	526 (59.4)	359 (40.6)	0.177	1		1	
CT	51 (68.0)	24 (32.0)		0.69 (0.42–1.14)	0.148	0.65 (0.32–1.33)	0.234
Allele							
C	1,103 (59.8)	742 (40.2)	0.186	1		1	
T	51 (68.0)	24 (32.0)		0.70 (0.43–1.15)	0.156	0.58 (0.31–1.07)	0.080
TCF7L2 rs290487							
Additive							
CC	124 (57.9)	90 (42.1)	0.347	1		1	
TC	281 (62.6)	168 (37.4)		0.82 (0.59–1.15)	0.252	0.81 (0.53–1.24)	0.334
TT	172 (57.9)	125 (42.1)		1.00 (0.70–1.43)	0.994	0.93 (0.59–1.46)	0.751
Dominant							
CC	124 (57.9)	90 (42.1)	0.477	1		1	
TC+TT	453 (60.7)	293 (39.3)		0.89 (0.66–1.21)	0.464	0.86 (0.58–1.27)	0.445
Recessive							
CC+TC	405 (61.1)	258 (38.9)	0.355	1		1	
TT	172 (57.9)	125 (42.1)		1.14 (0.86–1.51)	0.353	1.07 (0.75–1.52)	0.715
Allele							
C	529 (60.3)	348 (39.7)	0.888	1		1	
T	625 (59.9)	418 (40.1)		1.02 (0.85–1.22)	0.860	0.86 (0.58–1.27)	0.445
KCNQ1 rs2237892							
Additive							
TT	37 (55.2)	30 (44.8)	0.459	1		1	
CT	240 (62.2)	146 (37.8)		0.75 (0.44–1.27)	0.282	0.76 (0.40–1.42)	0.387
CC	300 (59.2)	207 (40.8)		0.85 (0.51–1.42)	0.538	0.81 (0.43–1.50)	0.495
Dominant							
TT	37 (55.2)	30 (44.8)	0.438	1		1	
CT+CC	540 (60.5)	353 (39.5)		0.81 (0.49–1.33)	0.398	0.78 (0.43–1.43)	0.426
Recessive							
TT+CT	277 (61.1)	176 (38.9)	0.553	1		1	
CC	300 (59.2)	207 (40.8)		1.09 (0.84–1.41)	0.532	1.02 (0.73–1.42)	0.921
Allele							
T	314 (60.4)	206 (39.6)	0.916	1		1	
C	840 (60.0)	560 (40.0)		1.02 (0.83–1.25)	0.878	0.78 (0.43–1.43)	0.426

(*Continued to the next page*)

Supplementary Table 8. Continued

SNP	DM without complications (*n*=577)	DM with complication (*n*=383)	*P* value[a]	Crude OR (95% CI)	*P* value	Adjusted OR (95% CI)	*P* value
KCNQ1 rs2237897							
Additive							
TT	26 (54.2)	22 (45.8)	0.274	1		1	
CT	218 (57.8)	159 (42.2)		0.86 (0.47–1.58)	0.629	1.09 (0.51–2.34)	0.829
CC	333 (62.2)	202 (37.8)		0.72 (0.40–1.30)	0.272	0.94 (0.44–1.99)	0.863
Dominant							
TT	26 (54.2)	22 (45.8)	0.450	1		1	
CC+CT	551 (60.4)	361 (39.6)		0.77 (0.43–1.39)	0.390	1.00 (0.48–2.09)	0.994
Recessive							
TT+CT	244 (57.4)	181 (42.6)	0.144	1		1	
CC	333 (62.2)	202 (37.8)		0.82 (0.63–1.06)	0.129	0.87 (0.62–1.21)	0.405
Allele							
T	270 (57.1)	203 (42.9)	0.130	1		1	
C	884 (61.1)	563 (38.9)		0.85 (0.69–1.05)	0.122	1.00 (0.48–2.09)	0.994
KCNJ11 rs5219							
Additive							
GG	235 (60.3)	155 (39.7)	0.861	1		1	
GA	265 (59.4)	181 (40.6)		1.04 (0.79–1.37)	0.805	1.21 (0.85–1.74)	0.292
AA	77 (62.1)	47 (37.9)		0.93 (0.61–1.40)	0.715	1.12 (0.67–1.86)	0.665
Dominant							
GG	235 (60.3)	155 (39.7)	0.947	1		1	
GA+AA	342 (60.0)	228 (40.0)		1.01 (0.78–1.32)	0.936	1.19 (0.85–1.67)	0.316
Recessive							
GG+GA	500 (59.8)	336 (40.2)	0.694	1		1	
AA	77 (62.1)	47 (37.9)		0.91 (0.62–1.34)	0.627	1.01 (0.63–1.61)	0.974
Allele							
G	735 (60.0)	491 (40.0)	0.884	1		1	
A	419 (60.4)	275 (39.6)		0.98 (0.81–1.19)	0.856	1.01 (0.63–1.61)	0.974

Values are presented as number (%). OR adjusted for age, sex, hypertension, dyslipidemia, glycated hemoglobin, and body mass index.
SNP, single nucleotide polymorphism; DM, diabetes mellitus; 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.