Supplementary Table 11. Combined effect of two risk alleles on CAD in T2DM patients

Model no.	SNPs in model (effect allele)	No. of effect allele (GRS)	Control (n=577)	CAD (n=112)	P value[a]	OR (95% CI)	P value
1	*KCNQ1* rs2237892 (C)	0–1	70 (92.1)	6 (7.9)	0.012	1	
	KCNQ1 rs2237897 (T)	2	481 (83.5)	95 (16.5)		2.51 (0.87–7.24)	0.088
		3–4	26 (70.3)	11 (29.7)		7.31 (2.03–26.35)	0.002
2	*TCF7L2* rs7903146 (C)	1–2	153 (84.5)	28 (15.5)	0.675	1	
	TCF7L2 rs290487 (T)	3	263 (84.6)	48 (15.4)		0.94 (0.52–1.72)	0.845
		4	161 (81.7)	36 (18.3)		1.12 (0.59–2.12)	0.738
3	*TCF7L2* rs7903146 (C)	1–2	59 (84.3)	11 (15.7)	0.113	1	
	KCNQ1 rs2237892 (C)	3	243 (87.1)	36 (12.9)		0.69 (0.29–1.65)	0.399
		4	275 (80.9)	65 (19.1)		1.25 (0.55–2.86)	0.596
4	*TCF7L2* rs7903146 (C)	1	25 (86.2)	4 (13.8)	0.502	1	
	KCNQ1 rs2237897 (T)	2	331 (84.4)	61 (15.6)		3.16 (0.40–25.11)	0.276
		3	198 (83.5)	39 (16.5)		3.49 (0.43–28.04)	0.241
		4	23 (74.2)	8 (25.8)		7.35 (0.79–68.37)	0.080
5	*TCF7L2* rs290487 (T)	0–1	73 (82.0)	16 (18.0)	0.273	1	
	KCNQ1 rs2237892 (C)	2	197 (86.4)	31 (13.6)		0.70 (0.32–1.52)	0.368
		3	225 (84.3)	42 (15.7)		0.72 (0.35–1.50)	0.381
		4	82 (78.1)	23 (21.9)		1.23 (0.54–2.84)	0.620
6	*TCF7L2* rs290487 (T)	0	74 (84.1)	14 (15.9)	0.796	1	
	KCNQ1 rs2237897 (T)	1	210 (85.4)	36 (14.6)		0.85 (0.38–1.89)	0.682
		2	201 (82.0)	44 (18.0)		1.12 (0.51–2.49)	0.776
		3–4	92 (83.6)	18 (16.4)		0.96 (0.39–2.37)	0.925

Values are presented as number (%). $P \leq 0.05$ indicated statistical significance. Control, T2DM without complication. OR adjusted for age, sex, hypertension, dyslipidemia, glycated hemoglobin, and body mass index.

CAD, coronary artery disease; T2DM, type 2 diabetes mellitus; SNP, single nucleotide polymorphism; GRS, genetic risk score; OR, odds ratio; CI, confidence interval; *KCNQ1*, potassium voltage-gated channel subfamily Q member 1; *TCF7L2*, transcription factor 7-like 2.

[a]*P* value after 100,000 permutations.