Supplementary Table 12. Combined effect of three 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	*TCF7L2* rs7903146 (C)	2–3	116 (90.6)	12 (9.4)	0.006	1	
	KCNQ1 rs2237892 (C)	4	437 (83.1)	89 (16.9)		2.37 (1.04–5.41)	0.040
	KCNQ1 rs2237897 (T)	5–6	24 (68.6)	11 (31.4)		6.90 (2.30–20.71)	0.001
2	*TCF7L2* rs7903146 (C)	1–3	93 (83.0)	19 (17.0)	0.162	1	
	TCF7L2 rs290487 (T)	4	199 (87.3)	29 (12.7)		0.74 (0.35–1.57)	0.436
	KCNQ1 rs2237892 (C)	5	206 (83.4)	41 (16.6)		0.87 (0.43–1.77)	0.704
		6	79 (77.5)	23 (22.5)		1.48 (0.66–3.31)	0.345
3	*TCF7L2* rs7903146 (C)	1–2	91 (85.0)	16 (15.0)	0.678	1	
	TCF7L2 rs290487 (T)	3	208 (85.6)	35 (14.4)		0.90 (0.41–1.95)	0.785
	KCNQ1 rs2237897 (T)	4	197 (81.7)	44 (18.3)		1.32 (0.62–2.82)	0.475
		5–6	81 (82.7)	17 (17.3)		1.09 (0.45–2.68)	0.843
4	*TCF7L2* rs290487 (T)	0–2	149 (86.1)	24 (13.9)	0.321	1	
	KCNQ1 rs2237892 (C)	3	266 (84.8)	49 (15.6)		0.96 (0.52–1.78)	0.895
	KCNQ1 rs2237897 (T)	4–6	162 (80.6)	39 (19.4)		1.35 (0.71–2.56)	0.368

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; *TCF7L2*, transcription factor 7-like 2; *KCNQ1*, potassium voltage-gated channel subfamily Q member 1.

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