Supplementary Table 13. Combined effect of two risk alleles on nephropathy and/or CAD in T2DM patients

Model no.	SNPs in model (effect allele)	No. of effect allele (GRS)	Control (*n*=577)	DN+CAD (*n*=283)	*P* value[a]	OR (95% CI)	*P* value
1	*KCNQ1* rs2237892 (C)	0-1	70 (76.1)	22 (23.9)	0.006	1	
	KCNQ1 rs2237897 (T)	2	481 (67.2)	235 (32.8)		1.78 (0.99–3.21)	0.056
		3–4	26 (50.0)	26 (50.0)		3.49 (1.49–8.15)	0.004
2	*TCF7L2* rs7903146 (C)	1–2	153 (66.5)	77 (33.5)	0.588	1	
	TCF7L2 rs290487 (T)	3	263 (68.8)	119 (31.2)		0.95 (0.63–1.42)	0.800
		4	161 (64.9)	87 (35.1)		1.08 (0.70–1.69)	0.721
3	*TCF7L2* rs7903146 (C)	1–2	59 (67.8)	28 (32.2)	0.271	1	
	KCNQ1 rs2237892 (C)	3	243 (70.0)	104 (30.0)		0.94 (0.51–1.70)	0.825
		4	275 (64.6)	151 (35.4)		1.32 (0.74–2.35)	0.350
4	*TCF7L2* rs7903146 (C)	1	25 (75.8)	8 (24.2)	0.290	1	
	KCNQ1 rs2237897 (T)	2	331 (68.5)	152 (31.5)		2.63 (0.75–9.23)	0.132
		3	198 (65.1)	106 (34.9)		3.04 (0.86–10.80)	0.086
		4	23 (57.5)	17 (42.5)		4.18 (1.01–17.34)	0.049
5	*TCF7L2* rs290487 (T)	0–1	73 (64.0)	41 (36.0)	0.248	1	
	KCNQ1 rs2237892 (C)	2	197 (68.4)	91 (31.6)		0.98 (0.57–1.66)	0.931
		3	225 (69.7)	98 (30.3)		0.85 (0.50–1.44)	0.546
		4	82 (60.7)	53 (39.3)		1.25 (0.68–2.29)	0.474
6	*TCF7L2* rs290487 (T)	0	74 (65.5)	39 (34.5)	0.614	1	
	KCNQ1 rs2237897 (T)	1	210 (69.8)	91 (30.2)		0.76 (0.45–1.28)	0.297
		2	201 (66.6)	101 (33.4)		0.87 (0.51–1.46)	0.592
		3–4	92 (63.9)	52 (36.1)		0.96 (0.53–1.72)	0.886

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; DN, diabetic nephropathy; 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 permutation.