Supplementary Table 14. Combined effect of three 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	*TCF7L2* rs7903146 (C)	2–3	116 (76.8)	35 (23.2)	0.002	1	
	KCNQ1 rs2237892 (C)	4	437 (66.0)	225 (34.0)		2.13 (1.28–3.53)	0.003
	KCNQ1 rs2237897 (T)	5–6	24 (51.1)	23 (48.9)		3.92 (1.75–8.76)	0.001
2	*TCF7L2* rs7903146 (C)	1–3	93 (66.4)	47 (33.6)	0.458	1	
	TCF7L2 rs290487 (T)	4	199 (68.9)	90 (31.1)		1.16 (0.70–1.93)	0.573
	KCNQ1 rs2237892 (C)	5	206 (68.2)	96 (31.8)		1.09 (0.66–1.81)	0.741
		6	79 (61.2)	50 (38.8)		1.46 (0.80–2.64)	0.218
3	*TCF7L2* rs7903146 (C)	1–2	91 (67.9)	43 (32.1)	0.600	1	
	TCF7L2 rs290487 (T)	3	208 (69.3)	92 (30.7)		0.88 (0.53–1.45)	0.604
	KCNQ1 rs2237897 (T)	4	197 (66.3)	100 (33.7)		1.04 (0.63–1.72)	0.886
		5–6	81 (62.8)	48 (37.2)		1.16 (0.64–2.07)	0.629
4	*TCF7L2* rs290487 (T)	0–2	149 (67.4)	72 (32.6)	0.181	1	
	KCNQ1 rs2237892 (C)	3	266 (69.8)	115 (30.2)		0.92 (0.61–1.39)	0.691
	KCNQ1 rs2237897 (T)	4–6	162 (62.8)	96 (37.2)		1.21 (0.78–1.87)	0.397

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

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