Supplementary Table 10. Combined effect of three risk alleles on diabetic nephropathy in T2DM patients

Model no.	SNPs in model (effect allele)	No.of effect allele (GRS)	Control (n=577)	DN (n=181)	P value[a]	OR (95% CI)	P value
1	*TCF7L2* rs7903146 (C)	2–3	116 (83.5)	23 (16.5)	0.029	1	
	KCNQ1 rs2237892 (C)	4	437 (75.1)	145 (24.9)		2.02 (1.11–3.68)	0.021
	KCNQ1 rs2237897 (T)	5–6	24 (64.9)	13 (35.1)		2.28 (0.82–6.35)	0.115
2	*TCF7L2* rs7903146 (C)	1–3	93 (76.9)	28 (23.1)	0.521	1	
	TCF7L2 rs290487 (T)	4	199 (75.7)	64 (24.3)		1.74 (0.92–3.29)	0.089
	KCNQ1 rs2237892 (C)	5	206 (78.3)	57 (21.7)		1.20 (0.63–2.28)	0.578
		6	79 (71.2)	32 (28.8)		1.42 (0.68–3.00)	0.354
3	*TCF7L2* rs7903146 (C)	1–2	91 (75.8)	29 (24.2)	0.678	1	
	TCF7L2 rs290487 (T)	3	208 (78.2)	58 (21.8)		0.57 (0.31–1.03)	0.062
	KCNQ1 rs2237897 (T)	4	197 (75.8)	63 (24.2)		0.68 (0.37–1.24)	0.207
		5–6	81 (72.3)	31 (27.7)		0.72 (0.36–1.43)	0.344
4	*TCF7L2* rs290487 (T)	0–2	149 (74.9)	50 (25.1)	0.102	1	
	KCNQ1 rs2237892 (C)	3	266 (79.6)	68 (20.4)		0.89 (0.54–1.45)	0.626
	KCNQ1 rs2237897 (T)	4–6	162 (72.0)	63 (28.0)		0.99 (0.59–1.66)	0.961

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.

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 permutations.