

Supplementary Table 9. Combined effect of two 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	<i>KCNQ1</i> rs2237892 (C)	0–1	70 (81.4)	16 (18.6)	0.050	1	
		2	481 (76.3)	149 (23.7)		1.82 (0.92–3.60)	0.084
		3–4	26 (61.9)	16 (38.1)		2.26 (0.79–6.43)	0.127
2	<i>TCF7L2</i> rs7903146 (C)	1–2	153 (75.0)	51 (25.0)	0.532	1	
		3	263 (78.0)	74 (22.0)		0.75 (0.46–1.22)	0.238
		4	161 (74.2)	56 (25.8)		0.82 (0.48–1.39)	0.454
3	<i>TCF7L2</i> rs7903146 (C)	1–2	59 (77.6)	17 (22.4)	0.536	1	
		3	243 (77.9)	69 (22.1)		1.15 (0.55–2.39)	0.712
		4	275 (74.3)	95 (25.7)		1.47 (0.72–2.99)	0.291
4	<i>TCF7L2</i> rs7903146 (C)	1	25 (86.2)	4 (13.8)	0.445	1	
		2	331 (77.0)	99 (23.0)		1.59 (0.42–6.08)	0.497
		3	198 (74.2)	69 (25.8)		1.77 (0.46–6.86)	0.411
		4	23 (71.9)	9 (28.1)		1.68 (0.34–8.32)	0.524
5	<i>TCF7L2</i> rs290487 (T)	0–1	73 (74.5)	25 (25.5)	0.232	1	
		2	197 (75.8)	63 (24.2)		1.26 (0.65–2.42)	0.495
		3	225 (79.5)	58 (20.5)		0.94 (0.49–1.80)	0.845
		4	82 (70.1)	35 (29.9)		1.18 (0.56–2.50)	0.658
6	<i>TCF7L2</i> rs290487 (T)	0	74 (73.3)	27 (26.70)	0.519	1	
		1	210 (78.9)	56 (21.1)		0.57 (0.31–1.05)	0.070
		2	201 (75.8)	64 (24.2)		0.63 (0.34–1.18)	0.149
		3–4	92 (73.0)	34 (27.0)		0.67 (0.34–1.33)	0.252

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

^aP value after 100,000 permutations.