

S6 Table. Six SNP loci associated with diabetic nephropathy including microalbuminuria (Meta-analysis in Discovery Stage, $P < 5 \times 10^{-7}$) in Japanese patients with type 2 diabetes.

SNP ID		Alleles		OR(95% CI)	P-value	Phet	RAF*	
Gene	Chromosome	Effect	Non-Effect					
rs56094641		G	A	Japanese discovery set	1.18(1.12-1.25)	2.425x10 ⁻⁹	0.7535	0.173
<i>FTO</i>				Japanese all replication set	1.11(0.93-1.32)	0.2578		
Ch16				Japanese all combined set	1.18(1.12-1.24)	1.64x10 ⁻⁹		
				European replication set	1.04(0.96-1.13)	0.6416		0.434
rs78954674		A	G	Japanese discovery set	1.20(1.12-1.28)	1.107x10 ⁻⁷	0.6454	0.149
<i>WWC1</i>				Japanese all replication set	0.95(0.77-1.16)	0.6101		
Ch5				Japanese all combined set	1.17(1.10-1.25)	1.06x10 ⁻⁶		
				European replication set	1.01(0.81-1.27)	0.8084		0.046
rs16977473		G	A	Japanese discovery set	1.28(1.18-1.41)	1.6227x10 ⁻⁷	0.0887	0.096
<i>CGNLI</i>				Japanese all replication set	1.12(0.85-1.47)	0.4152		
Ch15				Japanese all combined set	1.27(1.15-1.39)	1.83x10 ⁻⁷		
				European replication set	1.19(0.81-1.75)	0.7769		0.016
rs895157		G	T	Japanese discovery set	1.23(1.14-1.32)	1.623x10 ⁻⁷	0.6195	0.139
<i>PRCD</i>				Japanese all replication set	1.04(0.83-1.30)	0.7476		
Ch17				Japanese all combined set	1.2(1.11-1.29)	1.17x10 ⁻⁶		
				European replication set	0.96(0.87-1.08)	0.4431		0.189
rs16940484		T	C	Japanese discovery set	1.14(1.09-1.21)	2.435x10 ⁻⁷	0.9865	0.322
<i>TTC39C</i>				Japanese all replication set	1.02(0.87-1.20)	0.7874		
Ch18				Japanese all combined set	1.13(1.08-1.19)	5.80x10 ⁻⁷		
				European replication set	1.04(0.82-1.33)	0.3193		0.15
rs73048515		C	T	Japanese discovery set	1.56(1.32-1.85)	4.709x10 ⁻⁷	0.4369	0.0014
<i>LOC107986400</i>				Japanese all replication set	1.23(0.78-1.96)	0.3732		
Ch5				Japanese all combined set	1.52(1.28-1.79)	4.74x10 ⁻⁷		
				European replication set	1.10(0.94-1.28)	0.2529		0.073

CI, confidence interval; OR, odds ratio; Phet, P-value for Cochran's Q-test for heterogeneity; RAF, risk allele frequency; SNP, single-nucleotide polymorphism.

*Risk allele frequency in each populations.

Data are from 1000 Genomes Project Phase 3 allele frequencies (JPT and EUR)