Table S1. Primers and restriction enzyme used for *SLC22A1* genotyping.

SNP	Nucleotide change	Primer sequence F: 5′-3′ R: 3′-5′	Size bp	Enzyme	RFLP pattern bp
rs12208357	C/T	F: TGATCAGATGGCCACGTGCATT R: GAGCCGGGCGTGTCATACAC	607	*HhaI*	CC: 26, 83, 87, 100 y 311 CT: 26, 83, 87, 100, 170 y 311 TT: 26, 100, 170 y 311
rs2282143	C/T	F: TGCCCCTTGTCATGGGTGTGAAGC R: AGCGTGCTGATTCTGCCTGGA	267	*ApeKI*	CC: 267 CT: 86,181 y 267 TT:86 y 181
rs34130495	G/A	F: CTCAGGTTCACGGACTCTGTGCT R: CACTGTGCACGGCCCCTCAAT	381	*Sau96I*	GG: 14, 34, 110 y 223 GA: 14, 34, 110, 223 y 257 AA: 14, 110 y 257
rs34059508	G/A	F: TGTTGCCCTGTGCTGCAAATCTC R: GCCCACTGCCGAGCTGCAAAA	870	*Bsa*XI	GG: 166, 346 y 358 GA: 166, 346, 358 y 524 AA: 346 y 524

F, forward primer; R, reverse primers; bp, base pairs.

Table S2. Minor allele frequency of *SCL22A1* gene variants among T2DM population.

Population	Minor allele frequency (MAF)							Ref
	rs622342 C	rs628031 A	rs72552763 del	rs2282143 T	rs12208357 T	rs34059508 A	rs34130495 A	
This study	0.32	0.25	0.22	0.04	0.04	0.01	0.01	
***Mexican ancestry LA**	0.41	0.11	0.37	0.02	0.02	0.04	0.01	[34]
South Mexico	0.37	0.18	-	-	-	-	-	[8]
North Mexico	-	0.15	0.38	-	0.02	-	-	[21]
South Mexico	0.36	-	0.24	-	0.02	0.004	-	[25]
South Mexico	0.41	-	0.35	-	-	-	-	[7]
South Mexico	-	0.13	-	-	-	-	-	[6]
Argentine	-	-	0.20	0.02	0.05	0.06	0.09	[27]
Javanese-Indonesia	-	-	0.98	-	-	-	-	[33]
Han Chinese	-	0.27	1	-	0.01	-	-	[19]
Jordanian	0.23	-	-	0.02	-	-	-	[24]
Soth Indian	0.54	-	-	-	-	-	-	[23]
Caucasian	0.37	0.440	-	-	-	-	-	[22]
Scotland	-	-	0.20	-	0.07	-	-	[26]

*The 1000 genome database samples are from healthy people.