Table-2: Allele frequencies and genetic association estimates of previously identified loci for type-2 diabetes

[a]SNP	Gene	[b]Minor allele frequency – HapMap GIH	[c]Minor Allele Frequency in IMS	[d]Odds ratio for Type-2 diabetes ([e]95% CI, [h]p-value) N=561 pairs	[f]Adjusted Odds ratio for Type-2 diabetes ([e]95% CI, p-value) N=561 pairs
rs1799854	*ABCC8*	0.35 (A)	0.32 (T)	0.88 (0.67-1.17, 0.39)	0.86 (0.64-1.14, 0.30)
rs2641348	*ADAM30*	0.23 (G)	0.24 (G)	1.12 (0.83-1.53, 0.45)	1.13 (0.83-1.55, 0.43)
rs10490072	*BCL11A*	0.15 (C)	0.09 (C)	1.13 (0.73-1.75, 0.59)	1.08 (0.69-1.69, 0.73)
rs12779790	*CDC123*	n/a	0.13 (G)	0.97 (0.68-1.40, 0.89)	0.97 (0.67-1.41, 0.88)
rs10811661	*CDKN2A/B*	0.09 (C)	0.15 (C)	0.84 (0.59-1.21, 0.35)	0.79 (0.55-1.14, 0.22)
rs10946398	*CDKAL1*	0.22 (C)	0.26 (C)	0.96 (0.71-1.30, 0.81)	0.99 (0.73-1.36, 0.98)
rs7754840	*CDKAL1*	0.22 (C)	0.26 (C)	0.99 (0.73-1.33, 0.93)	1.02 (0.76-1.39, 0.87)
rs7756992	*CDKAL1*	0.24 (G)	0.26 (G)	1.01 (0.75-1.36, 0.94)	1.03 (0.76-1.40, 0.85)
rs932206	*CXCR4*	0.16 (T)	0.14 (T)	1.10 (0.76-1.59, 0.61)	1.05 (0.72-1.53, 0.79)
rs1153188	*DCD*	0.17 (T)	0.19 (A)	1.24 (0.90-1.72, 0.19)	1.17 (0.90-1.54, 0.23)
rs17044137	*FLJ39370*	0.12 (A)	0.10 (A)	0.97 (0.64-1.47, 0.90)	1.02 (0.67-1.56, 0.92)
rs9939609	*FTO*	0.26 (A)	0.32 (A)	1.31 (0.99-1.73, 0.06)	1.29 (0.97-1.72, 0.08)
rs2268573	*GCK*	0.39 (G)	0.44 (G)	1.10 (0.86-1.42, 0.44)	1.11 (0.86-1.44, 0.42)
rs5015480	*HHEX*	0.44 (C)	0.45 (C)	0.90 (0.70-1.16, 0.43)	0.87 (0.67-1.13, 0.31)
rs7923837	*HHEX*	0.38 (G)	0.45 (G)	1.07 (0.83-1.38, 0.59)	1.12 (0.86-1.45, 0.38)
rs1111875	*HHEX*	0.41 (C)	0.41 (G)	1.15 (0.88-1.49, 0.30)	1.10 (0.85-1.43, 0.44)
rs2237892	*KCNQ1*	0.01 (T)	0.01 (T)	0.70 (0.26-1.89, 0.48)	0.67 (0.24-1.87, 0.45)
rs2876711	*KCTD12*	0.26 (C)	0.30 (C)	0.89 (0.67-1.17, 0.41)	0.91 (0.68-1.21, 0.51)
rs1256517	*LOC646279*	0.10 (C)	0.13 (C)	1.06 (0.72-1.55, 0.76)	1.02 (0.69-1.52, 0.91)
rs10823406	*NGN3*	0.27 (A)	0.23 (A)	1.29 (0.95-1.75, 0.10)	1.33 (0.97-1.82, 0.07)
rs10923931	*NOTCH2*	0.22 (T)	0.22 (T)	1.16 (0.85-1.59, 0.34)	1.20 (0.87-1.66, 0.26)
rs1801282	*PPARG*	0.09 (G)	0.13 (G)	0.99 (0.65-1.51, 0.96)	1.02 (0.66-1.57, 0.93)
rs3856806	*PPARG*	0.14 (T)	0.15 (T)	0.94 (0.66-1.35, 0.74)	0.94 (0.65-1.35, 0.72)
rs13266634	*SLC30A8*	0.22 (T)	0.22 (T)	0.83 (0.61-1.13, 0.23)	0.88 (0.64-1.21, 0.44)
rs757210	*TCF2*	n/a	0.28 (A)	0.97 (0.74-1.27, 0.82)	0.96 (0.73-1.26, 0.76)
rs7578597	***THADA***	0.83 ([g] T)	0.87 **([g] T)**	**1.51 (1.04-2.22, 0.03)**	**1.58 (1.07-2.3, 0.02)**
rs7903146	*TCF7L2*	0.29 (T)	0.29 (T)	1.10 (0.84-1.45, 0.47)	1.14 (0.86-1.50, 0.36)
rs12255372	*TCF7L2*	0.24 (T)	0.22 (T)	1.17 (0.87-1.57, 0.30)	1.19 (0.88-1.62, 0.25)
rs7961581	*TSPAN8*	0.35 (C)	0.33 (C)	0.80 (0.61-1.05, 0.11)	0.77 (0.58-1.01, 0.06)
rs9472138	*VEGFA*	0.23 (T)	0.16 (T)	0.97 (0.68-1.38, 0.87)	1.02 (0.71-1.46, 0.93)
rs10010131	*WFS1*	0.33 (A)	0.26 (A)	0.94 (0.69-1.27, 0.67)	0.98 (0.72-1.35, 0.94)

[a]SNP: Single nucleotide polymorphism; [b]GIH: Gujarati Indians in Houston, where, n/a=frequency is not available in HapMap data; [c]IMS: Indian Migration Study; [d]Within sib-pairs association estimate model adjusted for age, sex and location; [e]95%CI: 95% confidence interval; [f]model adjusted for body mass index; [g]T: major allele (C: minor allele); [h]Corrected overall critical p-value using false discovery rate = 0.002.