

Table-3: Comparison of effect size of tested SNPs on type 2 diabetes in Indian and European populations

^a SNP	Gene	Minor Allele in Europeans	Minor Allele Frequency in ^b IMS sample (Minor allele)	^c Odds ratio for type-2 diabetes (^d 95% CI, p-value)	Odds ratio in European population (95% CI)	Test of Heterogeneity Q (p-value)
rs10490072	<i>BCL11A</i>	C	0.09 (C)	1.13 (0.73-1.75, 0.59)	0.96 (0.91-1.02) (Saxena et al. 2007)	0.02 (0.88)
rs10811661	<i>CDKN2A/B</i>	C	0.15 (C)	0.84 (0.59-1.21, 0.35)	1.20 (1.14-1.25) (Scott et al. 2007)	0.07 (0.77)
rs10946398	<i>CDKAL1</i>	C	0.26 (C)	0.96 (0.71-1.30, 0.81)	1.12 (1.02-1.22) (Scott et al. 2007)	0.01 (0.89)
rs12779790	<i>CDC123</i>	G	0.13 (G)	0.97 (0.68-1.40, 0.89)	1.14 (1.05-1.24) (Voight et al. 2010)	0.01 (0.89)
rs932206	<i>CXCR4</i>	T	0.14 (T)	1.10 (0.76-1.59, 0.61)	1.18 (0.92-1.51) (Cauchi et al. 2008)	0.004 (0.94)
rs17044137	<i>FLJ39370</i>	A	0.10 (A)	0.97 (0.64-1.47, 0.90)	1.09 (1.03-1.17) (Saxena et al. 2007)	0.01 (0.92)
rs9939609	<i>FTO</i>	A	0.32 (A)	1.31 (0.99-1.73, 0.06)	1.04 (0.98-1.10) (Voight et al. 2010)	0.03 (0.84)
rs5015480	<i>HHEX</i>	C	0.45 (C)	0.90 (0.70-1.16, 0.43)	1.20 (1.12-1.29) (Voight et al. 2010)	0.05 (0.82)
rs1111875	<i>HHEX</i>	G	0.41 (G)	1.15 (0.88-1.49, 0.30)	1.13 (1.09-1.17) (Scott et al. 2007)	0.00 (0.98)
rs2237892	<i>KCNQ1</i>	T	0.01 (T)	0.70 (0.26-1.89, 0.48)	1.18 (1.03-1.34) (Dupuis et al. 2010)	0.20 (0.65)
rs2876711	<i>KCTD12</i>	C	0.30 (C)	0.89 (0.67-1.17, 0.41)	1.34 (1.21-1.48) (Scott et al. 2007)	0.10 (0.74)
rs1256517	<i>LOC646279</i>	C	0.13 (C)	1.06 (0.72-1.55, 0.76)	1.11 (^e het) (Sladek et a. 2007)	–
rs10823406	<i>NGN3</i>	A	0.23 (A)	1.29 (0.95-1.75, 0.10)	1.19 (^e het) (Sladek et al. 2007)	–
rs10923931	<i>NOTCH2</i>	T	0.22 (T)	1.16 (0.85-1.59, 0.34)	1.17 (1.09-1.26) (Voight et al. 2010)	0.00 (0.99)
rs1801282	<i>PPARG2</i>	G	0.13 (G)	0.99 (0.65-1.51, 0.96)	1.14 (1.08-1.20) (Scott et al. 2007)	0.01 (0.90)
rs13266634	<i>SLC30A8</i>	T	0.22 (T)	0.83 (0.61-1.13, 0.23)	1.12 (1.07-1.16) (Scott et al. 2007)	0.05 (0.81)
rs7903146	<i>TCF7L2</i>	T	0.29 (T)	1.10 (0.84-1.45, 0.47)	1.55 (1.49-1.61) (Voight et al. 2010)	5.94 (0.01)
rs12255372	<i>TCF7L2</i>	T	0.22 (T)	1.17 (0.87-1.57, 0.30)	1.52 (1.38, 1.68) (Grant et al. 2006)	0.04 (0.83)
rs7578597	<i>THADA</i>	^f T	0.87 (^f T)	1.51 (1.04-2.22, 0.03)	1.15 (1.10-1.20) (Zeggini et al. 2008)	0.05 (0.81)
rs7961581	<i>TSPAN8</i>	C	0.33 (C)	0.80 (0.61-1.05, 0.11)	1.09 (1.06-1.12) (Zeggini et al. 2008)	0.05 (0.81)
rs9472138	<i>VEGFA</i>	T	0.16 (T)	0.97 (0.68-1.38, 0.87)	1.05 (0.96-1.14) (Scott et al. 2007)	0.005 (0.91)
rs10010131	<i>WFS1</i>	A	0.26 (A)	0.94 (0.69-1.27, 0.67)	0.84 (0.77-0.92) (Sandhu et al. 2007)	0.009 (0.92)

^aSNP: Single nucleotide polymorphism; ^bIMS: Indian Migration Study; ^cBased on within sib-pair effect of minor allele with age, sex and location as covariates; ^d95%CI: 95% confidence interval; ^ehet: heterozygous; ^fT: major allele (C: minor allele); ^gheterogeneity between IMS and European studies (using meta package in STATA 10).

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