Electronic supplementary material

ESM Table 2 Association analysis of recently reported type 2 diabetes loci with type 1 diabetes

Gene region	SNP	r^2	Type 2 diabetes[a]			Type 1 diabetes meta-analysis[b]				
			MAF	OR	Ref.	Cases	Controls	OR (95% CI)	*p* value	Power, %
JAZF1	rs864745 (T>C)		0.50	0.91	[1]	3,562	4,650	1.00 (0.94–1.06)	0.943	53
CDC123–CAMKID	rs12779790 (A>G)		0.18	1.11	[1]	–	–	–	–	
	rs4747969 (T>C)	0.83	–	–	–	3,560	4,641	0.99 (0.91–1.08)	0.834	34
TSPAN8–LGR5	rs7961581 (T>C)		0.27	1.09	[1]	3,555	4,647	1.04 (0.97–1.12)	0.273	30
THADA	rs7578597 (T>C)		0.10	0.87	[1]	–	–	–	–	
	rs17031005 (A>G)	1.0	–	–	–	3,564	4,655	0.81 (0.73–0.89)	4.79×10^{-5}	35
ADAMTS9	rs4607103 (C>T)		0.24	0.92	[1]	3,563	4,651	0.99 (0.92–1.07)	0.858	25
NOTCH2	rs10923931 (G>T)		0.11	1.13	[1]	–	–	–	–	
	rs2793831 (T>C)	1.0	–	–	–	3,557	4,649	1.03 (0.93–1.13)	0.620	30
PPARG	rs1801282 (C>G)		0.18	0.88	[2]	3,563	4,651	0.97 (0.88–1.07)	0.523	56
CDKN2A–CDKN2B	rs10811661 (T>C)		0.15	0.83	[2]	3,565	4,656	1.06 (0.97–1.15)	0.213	85
FTO	rs9939609 (T>A)		0.40	1.15	[3]	3,564	4,657	0.97 (0.91–1.03)	0.291	91

[a]Results are taken from the listed publications for type 2 diabetes associations and the MAF from their control group. The ORs are for the minor allele

[b]Results from the meta-analysis reported by Cooper et al. [4], who used a genotype call rate ≥99%, a subject call rate ≥95% and a MAF ≥0.05 as quality control measures. They calculated *p* values using a Wald test. The SNPs with the most convincing evidence of association with type 2 diabetes in three gene regions were not included in the study by Cooper et al. However, tags SNPs (SNPs in high linkage disequilibrium with these SNPs) were included: SNPs rs4747969, rs17031005, and rs2793831 were used as tags for rs12779790, rs7578597, and rs10923931, respectively. Power was calculated for the number of cases and controls included in the Cooper et al. type 1 diabetes meta-analysis [4] for the given MAF and effect size in type 2 diabetes, at an α level of 0.003. The power loss as a result of combining the data sets into a meta-analysis was minimal (0.679%)

References

1. Zeggini E, Scott LJ, Saxena R, et al. (2008) Meta-analysis of genome-wide association data and large-scale replication identifies additional susceptibility loci for type 2 diabetes. Nat Genet 40:638–645
2. Scott LJ, Mohlke KL, Bonnycastle LL, et al. (2007) A genome-wide association study of type 2 diabetes in Finns detects multiple susceptibility variants. Science 316:1341–1345
3. Frayling TM, Timpson NJ, Weedon MN, et al. (2007) A common variant in the FTO gene is associated with body mass index and predisposes to childhood and adult obesity. Science 316:889–894
4. Cooper JD, Smyth DJ, Smiles AM et al. (2008) Meta-analysis of genome-wide association study data identifies additional type 1 diabetes risk loci. Nat Genet 40:1399–1401