ESM Table 2: The power to replicate the 18 novel type 1 diabetes susceptibility loci discovered in Barrett *et al.* [1]. We assumed significance levels of 0.05 and 2.8×10^{-3} (0.05 alpha level corrected for 18 independent tests using the Bonferroni approach), minor allele frequency (MAF) in 10,335 British controls samples (7,181 subjects drawn from the British 1958 Birth Cohort (www.cls.ioe.ac.uk/studies.asp?section=000100020003) and 3,154 subjects drawn from the UK Blood Services Common Control Collection [2, 3]) and odds ratio (OR) for the minor allele from the case/control component of the replication samples [1].

Region Candidate gene rsnumber Alleles	MAF OR	Power (%)			
		Barrett *et al.* 2,107 families 4,212 trios		Combined 4,366 families 7,013 trios	
		Alpha = 0.05	Alpha = 2.8×10^{-3}	Alpha = 0.05	Alpha = 2.8×10^{-3}
1q32.1 *IL10* rs3024505 C>T	0.17 0.84	98.4	87.0	100.0	99.0
4p15.2 rs10517086 G>A	0.30 1.09	73.3	34.2	91.5	63.4
6q22.32 *C6orf173* rs9388489 A>G	0.45 1.17	99.9	98.2	100.0	100.0
7p12.1 *COBL* rs4948088 C>A	0.047 0.77	92.3	65.2	99.2	91.6
7p15.2 *SKAP2* rs7804356 T>C	0.24 0.88	94.5	68.5	99.4	93.2
9p24.2 *GLIS3* rs7020673 G>C	0.50 0.88	98.6	87.6	100.0	99.1
10q23.31 *RNLS* rs10509540 T>C	0.29 0.75	100.0	100.0	100.0	100.0
12p13.31 *CD69* rs4763879 G>A	0.37 1.09	77.4	39.0	93.8	69.5
14q24.1 *ZFP36L1/C14orf181* rs1465788 G>A	0.29 0.86	99.2	91.4	100.0	99.6

14q32.2 *C14orf64* rs4900384 A>G	0.29 1.09	72.4	33.2	90.9	62.1
16p11.2 *IL27* rs4788084 G>A	0.42 0.86	99.8	96.5	100.0	99.9
16q23.1 *CTRB2* rs7202877 T>G	0.096 1.28	99.9	97.6	100.0	100.0
17q12 *GSDMB/ORMDL3* rs2290400 G>A	0.50 0.87	99.5	93.6	100.0	99.8
17q21.2 *CCR7* rs7221109 C>T	0.35 0.95	35.4	8.0	53.4	17.2
19q13.32 *PRKD2* rs425105 A>G	0.16 0.86	94.0	70.0	99.5	93.9
20p13 *SIRPG* rs2281808 C>T	0.36 0.90	90.3	60.7	98.8	88.8
22q12.2 *HORMAD2* rs5753037 C>T	0.39 1.10	85.8	51.7	97.5	82.2
Xq28 *GAB3* rs2664170 A>G	0.32 1.16	99.5	93.9	100.0	99.8

References

[1] Barrett JC, Clayton DG, Concannon P, et al. (2009) Genome-wide association study and meta-analysis find that over 40 loci affect risk of type 1 diabetes. Nat Genet 41: 703-707

[2] The Wellcome Trust Case Control Consortium (2007) Genome-wide association study of 14,000 cases of seven common diseases and 3,000 shared controls. Nature 447: 661-678

[3] Burton PR, Clayton DG, Cardon LR, et al. (2007) Association scan of 14,500 nonsynonymous SNPs in four diseases identifies autoimmunity variants. Nat Genet 39: 1329-1337