ESM Table 5: A summary of replication evidence in case/control and family collections for the 18 type 1 diabetes susceptibility loci discovered and replicated in Barrett *et al.* [1]. The case/control data mainly consist of the case/control component of the replication samples analysed in Barrett *et al.* [1], however, as 192 case samples were no longer available for analysis, we included available case and control samples not previously analysed in discovery or replication for the 18 susceptibility loci. We note that two-tailed *P*-values are reported for the case/control analyses and, as we attempted to replicate the evidence from the case/control component of the replication samples (Methods; ESM Table 2), one-tailed *P*-values for the family analyses. The reported odds ratios (ORs) and relative risks (RRs) are for the minor allele and the minor allele frequency (MAF) for rs2664170/*GAB3*/Xq28 is based on female samples. MAF –in controls and in unaffected parents from Great Britain, df – degree(s) of freedom and CI – confidence interval.

Region Candidate gene rsnumber Alleles	Independent cases and controls*		**Current study**
			4,429 independent families
	Sample size	MAF OR (95% CI) for minor allele two-tailed *P*-value	MAF RR (95% CI) for minor allele one-tailed *P*-value
1q32.1 *IL10* rs3024505 C>T	4,260 cases, 6,159 controls	0.17 0.87 (0.86-0.93) $P = 3.9\text{x}10^{-4}$	0.15 0.89 (0.83-0.96) $P = 9.5\text{x}10^{-4}$
4p15.2 rs10517086 G>A	4,172 cases, 6,462 controls	0.30 1.08 (1.02-1.15) $P = 0.016$	0.32 1.07 (1.02-1.13) $P = 8.5\text{x}10^{-3}$
6q22.32 *C6orf173* rs9388489 A>G	4,249 cases, 6,115 controls	0.45 1.18 (1.11-1.25) $P = 9.2\text{x}10^{-9}$	0.47 1.06 (1.01-1.12) $P = 0.010$
7p12.1 *COBL* rs4948088 C>A	4,300 cases, 6,293 controls	0.047 0.84 (0.73-0.97) $P = 0.021$	0.043 0.87 (0.76-1.01) $P = 0.046$
7p15.2 *SKAP2* rs7804356 T>C	4,278 cases, 6,608 controls	0.24 0.89 (0.84-0.96) $P = 1.2\text{x}10^{-3}$	0.23 0.94 (0.89-1.00) $P = 0.021$

9p24.2 *GLIS3* rs7020673 G>C	4,303 cases, 6,261 controls	0.50 0.91 (0.86-0.96) $P = 7.1\mathrm{x}10^{-4}$	0.49 0.95 (0.90-1.00) $P = 0.017$
10q23.31 *RNLS* rs10509540 T>C	[$]2,513 cases, 4,668 controls from Great Britain	0.29 0.73 (0.67-0.79) $P = 1.8\mathrm{x}10^{-14}$	0.25 0.80 (0.75-0.84) $P = 9.0\mathrm{x}10^{-15}$
12p13.31 *CD69* rs4763879 G>A	4,229 cases, 6,009 controls	0.37 1.08 (1.02-1.15) $P = 9.6\mathrm{x}10^{-3}$	0.36 1.11 (1.05-1.17) $P = 5.0\mathrm{x}10^{-5}$
14q24.1 *ZFP36L1/C14orf181* rs1465788 G>A	4,287 cases, 6,089 controls	0.29 0.87 (0.81-0.93) $P = 2.0\mathrm{x}10^{-5}$	0.28 0.95 (0.90-1.01) $P = 0.055$
14q32.2 *C14orf64* rs4900384 A>G	4,246 cases, 6,164 controls	0.29 1.08 (1.02-1.15) $P = 0.010$	0.28 1.08 (1.02-1.14) $P = 1.4\mathrm{x}10^{-3}$
16p11.2 *IL27* rs4788084 G>A	4,271 cases, 6,593 controls	0.42 0.87 (0.82-0.92) $P = 3.0\mathrm{x}10^{-6}$	0.43 0.92 (0.88-0.97) $P = 4.6\mathrm{x}10^{-4}$
16q23.1 *CTRB2* rs7202877 T>G	4,266 cases, 6,566 controls	0.096 1.28 (1.17-1.40) $P = 6.5\mathrm{x}10^{-8}$	0.11 1.09 (1.01-1.18) $P = 6.5\mathrm{x}10^{-3}$
17q12 *GSDMB/ORMDL3* rs2290400 G>A	4,192 cases, 5,891 controls	0.50 0.88 (0.83-0.93) $P = 1.4\mathrm{x}10^{-5}$	0.48 0.89 (0.85-0.94) $P = 1.8\mathrm{x}10^{-6}$
17q21.2 *CCR7* rs7221109 C>T	4,337 cases, 6,343 controls	0.35 0.96 (0.90-1.02) $P = 0.14$	0.34 0.91 (0.86-0.96) $P = 1.8\mathrm{x}10^{-4}$
19q13.32 *PRKD2* rs425105 A>G	3,955 cases, 6,187 controls	0.16 0.84 (0.78-0.91) $P =3.0\mathrm{x}10^{-5}$	0.15 0.88 (0.82-0.95) $P = 4.0\ \mathrm{x}10^{-4}$
20p13 *SIRPG* rs2281808 C>T	4,317 cases, 6,333 controls	0.36 0.90 (0.85-0.96) $P = 4.7\mathrm{x}10^{-4}$	0.36 0.89 (0.85-0.94) $P = 2.6\mathrm{x}10^{-5}$
22q12.2 *HORMAD2* rs5753037 C>T	4,254 cases, 6,480 controls	rs5753037 C>T 0.39 1.13 (1.07-1.20) $P = 2.9\mathrm{x}10^{-5}$	rs5753037 C>T 0.40 1.10 (1.05-1.16) $P = 7.0\mathrm{x}10^{-5}$
Xq28 *GAB3* rs2664170 A>G	4,714 cases, 7,438 controls	0.32 1.10 (1.04-1.15) $P = 1.9\mathrm{x}10^{-5}$	0.33 1.04 (1.00-1.09) $P = 0.025$

[*] Cases and controls are from Great Britain and Denmark unless otherwise stated.

[$] Cases and controls from Denmark dropped for rs10509540/*RNLS*/10q23.31 because of population heterogeneity in disease association between British and Danish case/control collections ($P = 4.1\mathrm{x}10^{-3}$).

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