Web table B Details of genotypes used in the analysis showing the risk alleles and the odds ratios for type 2 diabetes from phase 3 to phase 7, excluding 103 with type 2 diabetes at phase 3.

Gene	Rs number	Genotype	Risk allele	N	No diabetic (%)	OR (95% CI)[1]	OR (95% CI)[2]
ADAMTS9	rs4607103	GG GA AA	G	2607 1677 275	155 (6.0) 102 (6.1) 19 (6.9)	1.00 1.01 (0.78-1.31) 1.15 (0.70-1.88) P=0.68	0.96 (0.79-1.18) P=0.70
BCL11A	rs10490072	AA AG GG	A	2464 1729 351	159 (6.5) 96 (5.6) 21 (6.0)	1.00 0.81 (0.62-1.06) 0.92 (0.58-1.48) P=0.29	1.12 (0.92-1.37) P=0.25
CAPN10	rs3792267	GG GA AA	G	2669 1940 346	154 (5.8) 120 (6.2) 17 (4.9)	1.00 1.15 (0.89-1.47) 0.89 (0.53-1.49) P=0.44	0.97 (0.80-1.17) P=0.72
CDC123, CAMK1D	rs12779790	AA AG GG	G	2957 1400 128	177 (6.0) 85 (6.1) 11 (8.6)	1.00 1.01 (0.77-1.32) 1.44 (0.76-2.73) P=0.53	1.06 (0.85-1.33) P=0.61
CDKALI	rs17036101	GG GA AA	G	4040 497 20	247 (6.1) 28 (5.6) 1 (5.0)	GG 1.00 A+ 0.93 (0.62-1.38) P=0.72	1.08 (0.74-1.58) P=0.68
CDKN2A/2B	rs10811661*	AA AG GG	A	3150 1298 116	205 (6.5) 63 (4.9) 8 (6.9)	AA 1.00 G+ 0.76 (0.58-1.01) P=0.06	1.22 (0.95-1.56) P=0.13
FTO	rs1421085*	TT	C	1760	100 (5.7)	1.00	1.04 (0.88-1.23)

		TC CC		2461 860	152 (6.2) 50 (5.8)	1.11 (0.85-1.45) 1.05 (0.73-1.50) P=0.73	P=0.67
HHEX	rs1111875*	GG GA AA	G	1606 2182 764	96 (6.0) 130 (6.0) 49 (6.4)	1.00 1.01 (0.77-1.33) 1.08 (0.76-1.54) P=0.70	0.94 (0.79-1.13) P=0.52
HNF1A	rs1800574	CC CT TT	T	4629 276 5	269 (5.8) 18 (6.5) 1 (20.0)	CC 1.00 T+1.29 (0.79-2.09) P=0.31	1.34 (0.84-2.13) P=0.22
IGF2BP2	rs4402960	CC AC AA	A	2155 1960 442	109 (5.1) 140 (7.1) 26 (5.9)	1.00 1.44 (1.11-1.87) 1.19 (0.76-1.85) P=0.05	1.16 (0.97-1.40) P=0.11
JAZF1	rs864745	AA AG GG	A	1137 2240 1176	81 (7.1) 139 (6.2) 56 (4.8)	1.00 0.85 (0.64-1.13) 0.63 (0.44-0.90) P=0.01	1.23 (1.03-1.46) P=0.02
KCNJ11	rs5219*	CC CT TT	T	1978 2110 612	114 (5.5) 134 (6.0) 49 (7.4)	1.00 1.11 (0.85-1.44) 1.47 (1.03-2.08) p=0.05	1.19 (1.00-1.41) P=0.05
NOTCH2	rs10923931	CC AC AA P value	A	3643 861 58	212 (5.8) 62 (7.2) 2 (3.5)	CC 1.00 A+ 1.19 (0.89-1.59) P=0.24	1.14 (0.87-1.49) P=0.34
PPAR G	rs1801282	CC CG	C	3881 1038	221 (5.7) 70 (6.7)	CG+GG vs. CC 1.00	0.90 (0.70-1.15) P=0.39

		GG P value		79	3 (3.8)	1.19 (0.90-1.57) P=0.21	
SLC30A8	rs13266634*	GG GA AA	G	2190 1967 391	131 (6.0) 117 (6.0) 25 (6.4)	1.00 0.98 (0.76-1.27) 1.05 (0.67-1.64) P=0.93	0.98 (0.81-1.19) P=0.84
TCF2 (HNF1B)	rs4430796*	AA AG GG	G	1268 2214 1041	78 (6.2) 125 (5.7) 71 (6.8)	1.00 0.91 (0.68-1.22) 1.09 (0.78-1.52) P=0.66	1.04 (0.87-1.24) P=0.65
TCF7L2	rs7901695	AA AG GG	G	2157 1943 433	116 (5.4) 121 (6.2) 37 (8.6)	1.00 1.17 (0.89-1.52) 1.65 (1.11-2.44) P=0.051	1.25 (1.04-1.50) P=0.02
THADA	rs7578597	AA AG GG	A	3592 898 69	217 (6.0) 56 (6.2) 3 (4.4)	AA 1.00 G+ 1.01 (0.75-1.36) P=0.94	0.99 (0.75-1.29) P=0.91
TSPAN8, LGR5	rs7961581	AA AG GG	G	2376 1792 368	149 (6.3) 103 (5.8) 22 (6.0)	1.00 0.92 (0.71-1.19) 0.97 (0.61-1.55) P=0.66	0.94 (0.77-1.14) P=0.54
VEGFA	rs9472138	GG GA AA	A	2369 1813 364	140 (5.9) 117 (6.5) 17 (4.7)	1.00 1.12 (0.87-1.45) 0.80 (0.48-1.35) P=0.37	0.996 (0.82-1.21) P=0.96

[1]odds ratio from logistic regression adjusted for age and gender.

[2]odds ratio for additive effect (number of risk alleles held) adjusted for age and gender.