Web table A Genes associated with type 2 diabetes: Odds ratios from Whitehall II and the odds ratios from published meta-analysis (where possible), providing weighted odds ratios for the genetic risk function.

Gene	rs number	Genotype in WHII	OR (95% CI)‡ From WHII	Risk allele freq from meta-analysis	Odds ratio from meta-analysis	Comparison	Weight
ADAMTS9	rs4607103	GG GA AA	0.96 (0.79-1.18) P=0.70	0.76	1.09 (1.06-1.12)[1]	Per allele	0.09
BCL11A	rs10490072	AA AG GG	1.12 (0.92-1.37) P=0.25	0.72	1.05 (1.03-1.08)[1]	Per allele	0.049
CALPN10	rs3792267	GG GA AA	0.90 (0.71-1.15) P=0.42	0.27	1.18 (1.05-1.32)[2]	GG vs. GA+AA	0.166
CDC123/ CAMK1D	rs12779790	AA AG GG	1.06 (0.85-1.33) P=0.61	0.18	1.11 (1.07-1.14)[1]	Per allele	0.10
CDKALI	rs17036101	GG GA AA	1.08 (0.74-1.58) P=0.68	0.93	1.15 (1.10-1.21)[3]	Per allele	0.140
CDKN2A/2B	rs10811661	AA AG GG	1.22 (0.95-1.56) P=0.13	0.83	1.20 (1.14-1.25)[3]	Per allele	0.18
FTO	rs8050136 *	TT TC CC	1.04 (0.88-1.23) 0.67	0.47	1.17 (1.12-1.22)[4]	Per allele	0.157
HHEX	rs1111875	GG	0.94 (0.79-1.13)	0.65	1.15 (1.10-1.19)[3]	Per allele	0.12

		GA AA	P=0.52				
HNF1A	rs1800574	CC CT TT	1.29 (0.79-2.09) P=0.31	0.03	1.31 (1.08-1.57)[5]	AV+VV vs. AA	0.270
IGF2BP2	rs4402960	CC AC AA	1.16 (0.97-1.40) P=0.11	0.32	1.14 (1.11-1.18)[1]	Per allele	0.13
JAZF1	rs864745	AA AG GG	1.23 (1.03-1.46) P=0.02	0.50	1.10(1.07-1.13)[1]	Per allele	0.095
KCNJ11	rs5215	CC CT TT	1.19 (1.00-1.41) P=0.05	0.56	1.14 (1.10-1.19)[3]	Per allele	0.131
NOTCH2	rs10923931	CC AC AA	1.14 (0.87-1.49) P=0.34	0.11	1.13(1.08-1.17)[3]	Per allele	0.12
PPARG	rs1801282	CC CG GG	0.90 (0.70-1.15) P=0.39	0.08	1.14 (1.08-1.20)[3]	Per allele	0.131
SLC30A8	rs13266634	GG GA AA	0.98 (0.81-1.19) P=0.84	0.69	1.12(1.12-1.19)[3]	Per allele	0.11
TCF2 / HNF1B	rs4430796	AA AG GG	1.04 (0.87-1.24) P=0.65	0.47	1.10 (1.07-1.14)[3]	Per allele	0.095
TCF7L2	rs7901695	GG GT TT	1.25 (1.04-1.50) P=0.02	0.18	1.37 (1.31-1.43)[1]	Per allele	0.315
THADA	rs7578597	AA	0.99 (0.75-1.29)	0.90	1.15 (1.10-1.20)[3]	Per allele	0.14

		AG	P=0.91				
		GG					
TSPAN8/ LGR5	rs7961581	AA AG GG	0.94 (0.77-1.14) P=0.54	0.27	1.09(1.06-1.12)[1]	Per allele	0.09
VEGFA	rs9472138	GG GA AA	0.996 (0.82-1.21) P=0.96	0.28	1.06 (1.04-1.09)[1]	Per allele	0.058

[‡]from logistic regression adjusted for age and gender.

*LD between rs8050136 and rs9930506 = 0.93

References

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(2) Song Y, Niu T, Manson JE, Kwiatkowski DJ, Liu S. Are variants in the CAPN10 gene related to risk of type 2 diabetes? A quantitative assessment of population and family-based association studies. Am J Hum Genet 2004; 74:208-222.

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(4) Zeggini E, Weedon MN, Lindgren CM, Frayling TM, Elliott KS, Lango H et al. Replication of Genome-Wide Association Signals in U.K. Samples Reveals Risk Loci for Type 2 Diabetes. Science 2007; 316:1336-1341.

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