Supplemental Information

SUPPLEMENTAL TABLE 4 Thirty-eight Published SNPs Associated With T2D at Genome-Wide Significance and Their Association With T2D in the Bogalusa Heart Study

Nearest Gene	Marker	Chr	Alleles (Risk/Other)	Published Odds Ratio Per Risk Allele	Data Included in Genotype Score	Hazard Ratio (95% CI) for T2D Per Risk Allele in the Bogalusa Heart Study[b]
KCNQ1	rs2237892[a]	11	C/T	1.40[52]	Genotyped	0.85 (0.50, 1.45)
TCF7L2	rs7903146	10	T/C	1.37[53]	Genotyped	1.42 (1.06–1.91)
CDKN2A/B	rs10811661	9	T/C	1.20[7,10,11]	Genotyped	0.73 (0.49–1.08)
IRS1[c]	rs2943641	*2*	C/T	1.19[8]	Genotyped	1.30 (0.96–1.75)
IGF2BP[c]	rs4402960	3	T/G	1.17[7,10,11]	Genotyped	1.37 (0.99–1.90)
FTO[c]	rs8050136	16	A/C	1.15[7,11]	Genotyped	1.22 (0.91–1.65)
KCNJ11[c]	rs5219	11	T/C	1.15[54]	Genotyped	0.84 (0.58–1.21)
THADA	rs7578597	2	T/C	1.15[5]	Genotyped	0.77 (0.53–1.12)
CENTD2	rs1552224	11	A/C	1.14[6]	Genotyped	0.79 (0.50–1.25)
PPARG	rs1801282	3	C/G	1.14[55]	Genotyped	1.77 (0.89–3.49)
HHEX	rs1111875	10	C/T	1.13[9]	Genotyped	0.81 (0.60–1.11)
NOTCH2	rs10923931	1	T/G	1.13[5]	Genotyped	1.12 (0.77–1.63)
WFS1[c]	rs1801214	4	G/A	1.13[6]	Imputed	0.82 (0.60–1.11)
ADCY5	rs11708067	3	A/G	1.12[56]	Imputed	1.17 (0.76–1.81)
CDKAL1	rs7754840	6	C/G	1.12[7,10,11]	Genotyped	1.48 (1.09–2.00)
HNF1B	rs757210[57,58]	17	A/G	1.12[59,60]	Genotyped	1.13 (0.84–1.51)
SLC30A8	rs13266634	8	C/T	1.12[9]	Genotyped	1.30 (0.86–1.96)
CDC123/CAMK1D	rs12779790	10	G/A	1.11[5]	Imputed	1.04 (0.70–1.54)
RBMS1/ITGB6	rs7593730	2	C/T	1.11[59]	Imputed	0.78 (0.57–1.07)
TLE4	rs13292136	9	C/T	1.11[6]	Imputed	0.83 (0.49–1.41)
HMGA2	rs1531343	12	C/G	1.10[6]	Imputed	1.16 (0.81–1.66)
JAZF1	rs864745	7	T/C	1.10[5]	Genotyped	1.26 (0.89–1.77)
ADAMSTS9	rs4607103	3	C/T	1.09[5]	Genotyped	1.46 (1.01–2.10)
MTNR1B	rs10830963	11	G/C	1.09[56]	Genotyped	0.97 (0.64–1.47)
TSPAN8/LGR5	rs7961581	12	C/T	1.09[5]	Imputed	1.25 (0.90–1.73)
BCL11A	rs243021	2	A/G	1.08[6]	Genotyped	0.89 (0.66–1.20)
KCNQ1	rs231362[a]	11	G/A	1.08[6]	Genotyped	1.16 (0.84–1.60)
DCD	rs1153188	12	A/T	1.08[5]	Imputed	1.33 (0.91–1.95)
HCCA2	rs2334499	11	T/C	1.08[60]	Genotyped	0.85 (0.59–1.23)
GCK	rs4607517	7	A/G	1.07[56]	Genotyped	0.90 (0.58–1.40)
KLF14	rs972283	7	G/A	1.07[6]	Imputed	1.02 (0.73–1.41)
OASL/HNF1A	rs7957197	12	T/A	1.07[6]	Imputed	0.93 (0.62–1.39)
PRC1	rs8042680	15	A/C	1.07[6]	Genotyped	1.41 (0.98–2.04)
PROX1	rs340874	1	C/T	1.07[56]	Genotyped	1.10 (0.79–1.53)
DGKB/TMEM195	rs2191349	7	T/G	1.06[56]	Imputed	1.19 (0.89–1.60)
GCKR	rs780094	2	C/T	1.06[56]	Genotyped	0.93 (0.66–1.31)
TP53INP1	rs896854	8	T/C	1.06[6]	Genotyped	0.98 (0.73–1.32)
VEGFA	rs9472138	6	T/C	1.06[5]	Genotyped	1.26 (0.92–1.73)

SNPs are ordered by published odds ratio for T2D from previous genome-wide association studies (cited). Chr, chromosome.

[a] These SNPs are in low linkage disequilibrium in Europeans ($r^2 = 0.01$) and likely represent independent association signals at the KCNQ1 locus.

[b] Hazard ratios from Cox proportional hazards models adjusted for gender, race, and baseline age.

[c] Genotype score in present analyses included rs7578326 (risk allele A), rs1470579 (risk allele C), rs9939609 (risk allele A), rs5215 (risk allele C), and rs10010131 (risk allele G) for the susceptibility loci near *IRS1*, *IGF2BP2*, *FTO*, *KCNJ11*, and *WFS1*, respectively.