

SUPPLEMENTARY DATA

Supplementary Table 1. 46 European type 2 diabetes SNPs (or proxies) genotyped in the Inter99 cohort.

Nearby gene	Odds ratios used for weighting	SNP or perfect proxy genotyped	References
<i>TCF7L2</i>	1.39	rs7903146	[1-6]
<i>KCNQ1</i>	1.08	rs231362	[6]
<i>KCNQ1</i>	1.09	rs163184	[7]
<i>CDKN2A/2B</i>	1.18	rs10811661	[4, 8, 9]
<i>MTNR1B</i>	1.10	rs10830963	[6, 10]
<i>THADA</i>	1.14	rs7578597	[11]
<i>HHEX/IDE</i>	1.11	rs1111875	[8, 9]
<i>SLC30A8</i>	1.14	rs13266634	[6]
<i>CDKAL1</i>	1.17	rs7756992	[8]
<i>KCNJ11</i>	1.07	rs5219	[8, 11]
<i>IGF2BP2</i>	1.13	rs4402960	[4, 8, 9, 11]
<i>ARAP1</i>	1.11	rs1552224	[6]
<i>WFS1</i>	1.10	rs10010131	[6]
<i>JAZF1</i>	1.11†	rs864745	[11]
<i>CDC123</i>	1.07†	rs12779790 *	[11]
<i>TSPAN8</i>	1.06†	rs7961581 *	[11]
<i>GCK</i>	1.08	rs1799884	[12]
<i>PROX1</i>	1.07	rs340874	[12]
<i>DGKB</i>	1.05	rs2191349	[12]
<i>HNF1B</i>	1.10	rs7501939	[13]
<i>BCL11A</i>	1.07	rs243083	[6]
<i>ADCY5</i>	1.11	rs11708067	[12]
<i>ANK1</i>	1.09	rs516946	[14]
<i>BCAR1</i>	1.12	rs7202877	[14]
<i>IRS1</i>	1.10†	rs2943641	[15]
<i>PPARG</i>	1.13	rs1801282	[8]
<i>ADAMTS9</i>	1.08	rs4607103	[11]
<i>GCKR</i>	1.06†	rs1260326	[12]
<i>KLF14</i>	1.04	rs972283	[6]
<i>RBMS1</i>	1.04	rs4410242	[16]
<i>C2CD4A</i>	1.06†	rs7172432 *	[17]
<i>GRB14</i>	1.07	rs13389219	[14]
<i>ANKRD55</i>	1.08	rs459193	[14]
<i>HMGA2</i>	1.12†	rs1531343 *	[6]
<i>NOTCH2</i>	1.08	rs10923931	[11]
<i>CHCHD9</i>	1.12†	rs13292136 *	[6]

SUPPLEMENTARY DATA

<i>HNFI1A</i>	1.08	rs7957197	[6]
<i>ZBED3</i>	1.10	rs4457053	[6]
<i>PRC1</i>	1.07	rs8042680	[6]
<i>TP53INP1</i>	1.05	rs896854	[6]
<i>ZFAND6</i>	1.05	rs11634397	[6]
<i>TLE1</i>	1.07	rs2796441	[14]
<i>ZMIZ1</i>	1.08	rs12571751	[14]
<i>KLHDC5</i>	1.10	rs10842994	[14]
<i>HMG20A</i>	1.08	rs7177055	[14]
<i>CILP2</i>	1.13	rs10401969	[14]

Proxy search was performed based on 1000 Genome Pilot 1 data, linkage disequilibrium was estimated using SNP annotation proxy search (SNAP, <http://www.broadinstitute.org/mpg/snap/>). *SNPs were genotyped by KBioscience, Hoddesdon. All other SNPs were genotyped in-house using the Illumina Metabochip. †proxy SNP used for weighting if the effect of genotyped SNP is not reported in [18] (all are $R^2 > 0.7$).

References

1. Grant, S.F., et al., *Variant of transcription factor 7-like 2 (TCF7L2) gene confers risk of type 2 diabetes*. *Nature genetics*, 2006. **38**(3): p. 320-3.
2. Saxena, R., et al., *Common single nucleotide polymorphisms in TCF7L2 are reproducibly associated with type 2 diabetes and reduce the insulin response to glucose in nondiabetic individuals*. *Diabetes*, 2006. **55**(10): p. 2890-5.
3. Sladek, R., et al., *A genome-wide association study identifies novel risk loci for type 2 diabetes*. *Nature*, 2007. **445**(7130): p. 881-5.
4. Scott, L.J., et al., *A genome-wide association study of type 2 diabetes in Finns detects multiple susceptibility variants*. *Science*, 2007. **316**(5829): p. 1341-5.
5. *Genome-wide association study of 14,000 cases of seven common diseases and 3,000 shared controls*. *Nature*, 2007. **447**(7145): p. 661-78.
6. Voight, B.F., et al., *Twelve type 2 diabetes susceptibility loci identified through large-scale association analysis*. *Nature genetics*, 2010. **42**(7): p. 579-89.
7. Unoki, H., et al., *SNPs in KCNQ1 are associated with susceptibility to type 2 diabetes in East Asian and European populations*. *Nat Genet*, 2008. **40**(9): p. 1098-102.
8. Zeggini, E., et al., *Replication of genome-wide association signals in UK samples reveals risk loci for type 2 diabetes*. *Science*, 2007. **316**(5829): p. 1336-41.
9. Saxena, R., et al., *Genome-wide association analysis identifies loci for type 2 diabetes and triglyceride levels*. *Science*, 2007. **316**(5829): p. 1331-6.
10. Bouatia-Naji, N., et al., *A variant near MTNR1B is associated with increased fasting plasma glucose levels and type 2 diabetes risk*. *Nature genetics*, 2009. **41**(1): p. 89-94.
11. Zeggini, E., et al., *Meta-analysis of genome-wide association data and large-scale replication identifies additional susceptibility loci for type 2 diabetes*. *Nature genetics*, 2008. **40**(5): p. 638-45.
12. Dupuis, J., et al., *New genetic loci implicated in fasting glucose homeostasis and their impact on type 2 diabetes risk*. *Nature genetics*, 2010. **42**(2): p. 105-16.
13. Gudmundsson, J., et al., *Two variants on chromosome 17 confer prostate cancer risk, and the one in TCF2 protects against type 2 diabetes*. *Nature genetics*, 2007. **39**(8): p. 977-83.
14. Morris, A.P., et al., *Large-scale association analysis provides insights into the genetic architecture and pathophysiology of type 2 diabetes*. *Nature genetics*, 2012. **44**(9): p. 981-90.
15. Rung, J., et al., *Genetic variant near IRS1 is associated with type 2 diabetes, insulin resistance and hyperinsulinemia*. *Nature genetics*, 2009. **41**(10): p. 1110-5.
16. Qi, L., et al., *Genetic variants at 2q24 are associated with susceptibility to type 2 diabetes*. *Human molecular genetics*, 2010. **19**(13): p. 2706-15.
17. Yamauchi, T., et al., *A genome-wide association study in the Japanese population identifies susceptibility loci for type 2 diabetes at UBE2E2 and C2CD4A-C2CD4B*. *Nat Genet*, 2010. **42**(10): p. 864-8.
18. Morris, A.P., et al., *Large-scale association analysis provides insights into the genetic architecture and pathophysiology of type 2 diabetes*. *Nat Genet*, 2012. **44**(9): p. 981-90.