

SUPPLEMENTARY DATA

Supplementary Table 1. Characteristics of 32 established SNPs for BMI

SNP	Nearest Gene	Chr	Allele*		Beta (SE)†	HPFS (Men)		NHS (Women)	
			Effect	Other		EAF	r ² ‡	EAF	r ² ‡
rs543874	<i>SEC16B</i>	1	G	A	0.22 (0.03)	0.19	1.00	0.19	1.00
rs1514175	<i>TNNI3K</i>	1	A	G	0.07 (0.02)	0.40	1.00	0.43	1.00
rs1555543	<i>PTBP2</i>	1	C	A	0.06 (0.02)	0.57	1.00	0.59	1.00
rs2815752	<i>NEGR1</i>	1	A	G	0.13 (0.02)	0.64	1.00	0.62	1.00
rs2890652	<i>LRP1B</i>	2	C	T	0.09 (0.03)	0.16	1.00	0.17	0.99
rs887912	<i>FANCL</i>	2	T	C	0.10 (0.02)	0.30	0.99	0.30	0.99
rs713586	<i>RBJ</i>	2	C	T	0.14 (0.02)	0.48	1.00	0.47	1.00
rs2867125	<i>TMEM18</i>	2	C	T	0.31 (0.03)	0.81	1.00	0.82	1.00
rs13078807	<i>CADM2</i>	3	G	A	0.10 (0.02)	0.22	0.98	0.20	0.98
rs9816226	<i>ETV5</i>	3	T	A	0.14 (0.03)	0.83	0.97	0.83	0.97
rs13107325	<i>SLC39A8</i>	4	T	C	0.19 (0.04)	0.11	0.69	0.09	0.67
rs10938397	<i>GNPDA2</i>	4	G	A	0.18 (0.02)	0.44	0.98	0.44	0.99
rs4836133	<i>ZNF608</i>	5	A	C	0.07 (0.02)	0.51	0.93	0.49	0.94
rs2112347	<i>FLJ35779</i>	5	T	G	0.10 (0.02)	0.63	0.98	0.64	0.97
rs987237	<i>TFAP2B</i>	6	G	A	0.13 (0.03)	0.17	1.00	0.18	1.00
rs206936	<i>NUDT3</i>	6	G	A	0.06 (0.02)	0.20	1.00	0.19	1.00
rs10968576	<i>LRRN6C</i>	9	G	A	0.11 (0.02)	0.32	1.00	0.32	1.00
rs3817334	<i>MTCH2</i>	11	T	C	0.06 (0.02)	0.42	1.00	0.42	1.00
rs4929949	<i>RPL27A</i>	11	C	T	0.06 (0.02)	0.47	0.98	0.51	0.98
rs10767664	<i>BDNF</i>	11	A	T	0.19 (0.03)	0.78	1.00	0.78	1.00
rs7138803	<i>FAIM2</i>	12	A	G	0.12 (0.02)	0.39	1.00	0.39	1.00
rs4771122	<i>MTIF3</i>	13	G	A	0.09 (0.03)	0.21	0.95	0.22	0.96
rs11847697	<i>PRKD1</i>	14	T	C	0.17 (0.05)	0.05	0.76	0.05	0.80
rs10150332	<i>NRXN3</i>	14	C	T	0.13 (0.03)	0.20	1.00	0.22	0.99
rs2241423	<i>MAP2K5</i>	15	G	A	0.13 (0.02)	0.74	1.00	0.77	1.00
rs7359397	<i>SH2B1</i>	16	T	C	0.15 (0.02)	0.37	0.96	0.39	0.97
rs1558902	<i>FTO</i>	16	A	T	0.39 (0.02)	0.45	1.00	0.42	1.00
rs12444979	<i>GPRC5B</i>	16	C	T	0.17 (0.03)	0.86	0.98	0.86	0.99
rs571312	<i>MC4R</i>	18	A	C	0.23 (0.03)	0.24	0.99	0.24	1.00
rs29941	<i>KCTD15</i>	19	G	A	0.06 (0.02)	0.68	0.99	0.68	0.99
rs3810291	<i>TMEM160</i>	19	A	G	0.09 (0.02)	0.65	0.70	0.66	0.72
rs2287019	<i>QPCTL</i>	19	C	T	0.15 (0.03)	0.80	0.60	0.81	0.60

Chr: chromosome; EAF: effect allele frequency; *Allele coding based on the forward strand; †Effect sizes in kg/m² of BMI obtained from GWAS; ‡r² refers to the measurement of SNPs imputation quality.

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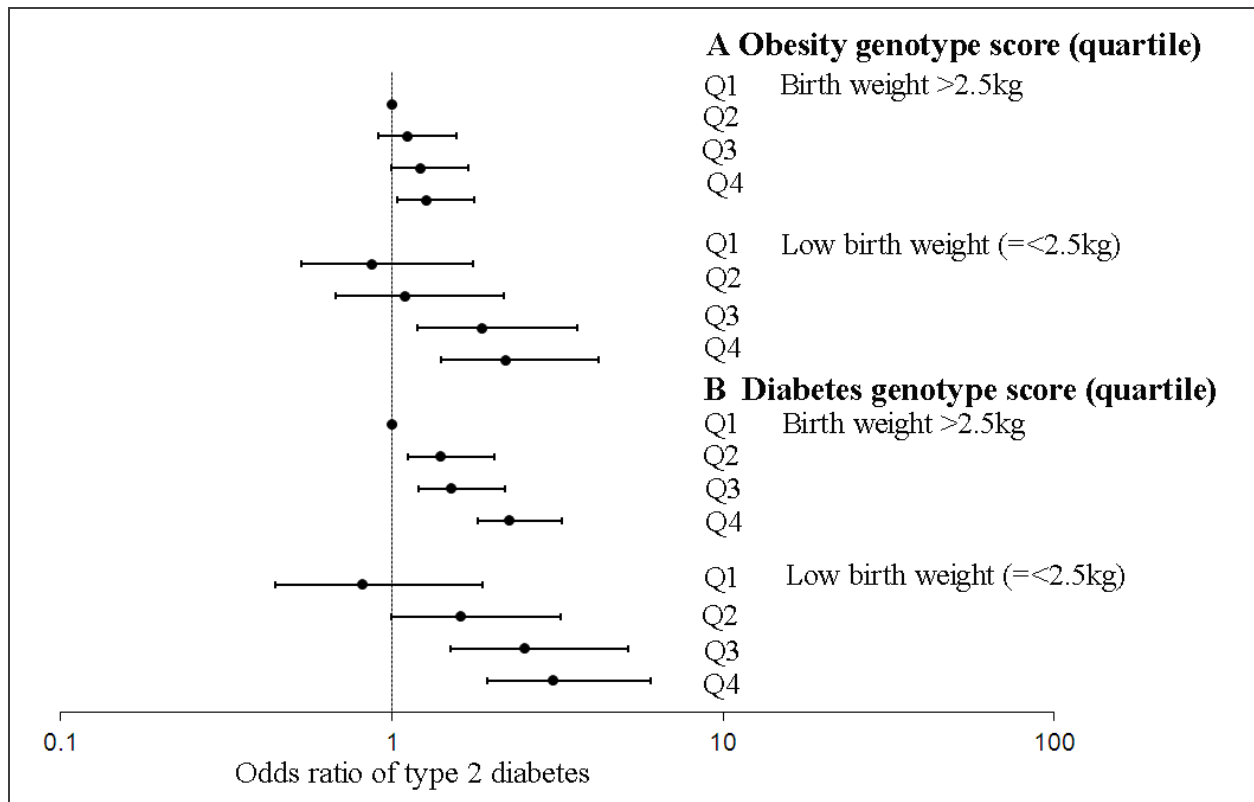
Supplementary Table 2. Characteristics of 35 established SNPs for diabetes

Gene region	SNP	Chr	Allele*		Men (HPFS)		Women (NHS)	
			Risk	Other	RAF	r†	RAF	r†
<i>NOTCH2</i>	rs10923931	1	T	G	0.09	1.00	0.10	1.00
<i>PROX1</i>	rs340874	1	C	T	0.54	0.96	0.54	0.96
<i>BCL11A</i>	rs243021	2	A	G	0.48	0.98	0.47	0.99
<i>GCKR</i>	rs780094	2	C	T	0.58	1.00	0.60	1.00
<i>IRS1</i>	rs2943641	2	C	T	0.65	1.00	0.65	1.00
<i>RBMS1-ITGB6</i>	rs7593730	2	C	T	0.77	1.00	0.79	1.00
<i>THADA</i>	rs7578597	2	T	C	0.90	0.98	0.90	0.99
<i>IGF2BP2</i>	rs4402960	3	T	G	0.34	1.00	0.32	1.00
<i>ADAMTS9</i>	rs4607103	3	C	T	0.72	1.00	0.75	1.00
<i>ADCY5</i>	rs11708067	3	A	G	0.79	1.00	0.78	1.00
<i>PPARG</i>	rs1801282	3	C	G	0.89	1.00	0.88	1.00
<i>WFS1</i>	rs10010131	4	G	A	0.62	1.00	0.62	1.00
<i>ZBED3</i>	rs4457053	5	G	A	0.31	0.63	0.30	0.62
<i>CDKAL1</i>	rs10946398	6	C	A	0.32	1.00	0.32	1.00
<i>GCK</i>	rs4607517	7	A	G	0.17	0.99	0.17	0.99
<i>JAZF1</i>	rs864745	7	T	C	0.51	1.00	0.50	1.00
<i>DGKB-TMEM195</i>	rs2191349	7	T	G	0.56	0.99	0.55	0.99
<i>KLF14</i>	rs972283	7	G	A	0.54	0.95	0.52	0.96
<i>TP53INP1</i>	rs896854	8	T	C	0.48	1.00	0.49	1.00
<i>SLC30A8</i>	rs13266634	8	C	T	0.71	0.93	0.71	0.92
<i>CDKN2A/B</i>	rs10811661	9	T	C	0.84	1.00	0.83	1.00
<i>CHCHD9</i>	rs13292136	9	C	T	0.94	1.00	0.94	1.00
<i>CDC123-CAMK1D</i>	rs12779790	10	G	A	0.19	0.91	0.19	0.92
<i>TCF7L2</i>	rs7901695	10	C	T	0.33	1.00	0.32	1.00
<i>HHEX/IDE</i>	rs1111875	10	C	T	0.61	1.00	0.60	1.00
<i>MTNR1B</i>	rs10830963	11	G	C	0.27	1.00	0.28	0.82
<i>KCNJ11</i>	rs5215	11	C	T	0.37	1.00	0.37	1.00
<i>KCNQ1</i>	rs231362	11	G	A	0.50	0.79	0.50	0.76
<i>CENTD2</i>	rs1552224	11	A	C	0.86	0.96	0.86	0.96
<i>HMG2</i>	rs1531343	12	C	G	0.13	1.00	0.10	1.00
<i>TSPAN8-LGR5</i>	rs7961581	12	C	T	0.29	1.00	0.29	1.00
<i>HNF1A</i>	rs7957197	12	T	A	0.80	0.99	0.81	0.98
<i>PRC1</i>	rs8042680	15	A	C	0.33	1.00	0.31	1.00
<i>ZFAND6</i>	rs11634397	15	G	A	0.65	1.00	0.66	1.00
<i>HNF1B (TCF2)</i>	rs4430796	17	A	G	0.49	0.44	0.49	0.42

Chr: chromosome; RAF: risk allele frequency; *Allele coding based on the forward strand; †r² refers to the measurement of SNPs imputation quality.

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Supplementary Figure 1. Joint effects of low birth weight and genotype score on risk of diabetes for pooled data from men and women



A: obesity genotype score; B: diabetes genotype score, adjusted for age, sex, smoking (never, past or current), alcohol intake (0, 0.1-4.9, 5.0-9.9 10.0-14.9 or ≥ 15.0 g/day), menopausal status (women only), physical activity (quintiles) and adult BMI (for diabetes gene scores only).