Supplemental Materials

Supplemental Table 1 Characteristics of 32 established SNPs for BMI

SNP	Nearest Gene	Chr	Allele*		Beta (SE)†	Women (NHS)		Men (HPFS)	
			Effect	Other		EAF	r^2‡	EAF	r^2‡
rs543874	*SEC16B*	1	G	A	0.22 (0.03)	0.19	1.00	0.19	1.00
rs1514175	*TNNI3K*	1	A	G	0.07 (0.02)	0.42	1.00	0.40	1.00
rs1555543	*PTBP2*	1	C	A	0.06 (0.02)	0.59	1.00	0.58	1.00
rs2815752	*NEGR1*	1	A	G	0.13 (0.02)	0.63	1.00	0.63	1.00
rs2890652	*LRP1B*	2	C	T	0.09 (0.03)	0.17	0.99	0.17	0.99
rs887912	*FANCL*	2	T	C	0.10 (0.02)	0.30	0.99	0.30	0.99
rs713586	*RBJ*	2	C	T	0.14 (0.02)	0.47	1.00	0.48	1.00
rs2867125	*TMEM18*	2	C	T	0.31 (0.03)	0.82	1.00	0.81	1.00
rs13078807	*CADM2*	3	G	A	0.10 (0.02)	0.21	0.99	0.22	0.99
rs9816226	*ETV5*	3	T	A	0.14 (0.03)	0.82	0.97	0.82	0.97
rs13107325	*SLC39A8*	4	T	C	0.19 (0.04)	0.08	0.86	0.09	0.83
rs10938397	*GNPDA2*	4	G	A	0.18 (0.02)	0.44	0.98	0.44	0.99
rs4836133	*ZNF608*	5	A	C	0.07 (0.02)	0.48	0.94	0.52	0.93
rs2112347	*FLJ35779*	5	T	G	0.10 (0.02)	0.64	0.97	0.63	0.97
rs987237	*TFAP2B*	6	G	A	0.13 (0.03)	0.18	1.00	0.18	1.00
rs206936	*NUDT3*	6	G	A	0.06 (0.02)	0.20	1.00	0.20	1.00
rs10968576	*LRRN6C*	9	G	A	0.11 (0.02)	0.31	1.00	0.31	1.00
rs3817334	*MTCH2*	11	T	C	0.06 (0.02)	0.42	1.00	0.41	1.00
rs4929949	*RPL27A*	11	C	T	0.06 (0.02)	0.51	0.97	0.49	0.97
rs10767664	*BDNF*	11	A	T	0.19 (0.03)	0.78	1.00	0.78	1.00
rs7138803	*FAIM2*	12	A	G	0.12 (0.02)	0.38	1.00	0.39	1.00
rs4771122	*MTIF3*	13	G	A	0.09 (0.03)	0.22	0.95	0.21	0.95
rs11847697	*PRKD1*	14	T	C	0.17 (0.05)	0.05	0.85	0.05	0.80
rs10150332	*NRXN3*	14	C	T	0.13 (0.03)	0.22	1.00	0.20	1.00
rs2241423	*MAP2K5*	15	G	A	0.13 (0.02)	0.77	1.00	0.74	1.00
rs7359397	*SH2B1*	16	T	C	0.15 (0.02)	0.39	0.98	0.37	0.97
rs1558902	*FTO*	16	A	T	0.39 (0.02)	0.42	1.00	0.44	1.00
rs12444979	*GPRC5B*	16	C	T	0.17 (0.03)	0.86	0.99	0.86	0.98
rs571312	*MC4R*	18	A	C	0.23 (0.03)	0.24	1.00	0.24	1.00
rs29941	*KCTD15*	19	G	A	0.06 (0.02)	0.68	1.00	0.68	1.00
rs3810291	*TMEM160*	19	A	G	0.09 (0.02)	0.65	0.70	0.64	0.71
rs2287019	*QPCTL*	19	C	T	0.15 (0.03)	0.81	0.75	0.80	0.67

Chr: chromosome; EAF: effect allele frequency.

*Allele coding based on the forward strand. Effect allele is the one associated with a higher BMI; and other is the reference allele.

†Effect sizes in kg/m^2 of BMI obtained from GWAS.

‡r^2 refers to the measurement of SNPs imputation quality.

Supplemental Figure 1 Genetic risk score and body mass index in the NHS and HPFS

The histograms represent the percentage of participants; and the means (±SE) of BMI are plotted, with the trend lines across the genetic risk score.