

SUPPLEMENTAL MATERIAL

Supplementary Table 1: List of 43 independent SNPs nominally associated with BMI and their highest ENCODE ChipSeq binding score. List is sorted by meta-analysis P-value (P column)

rs-number	Position	EA	NEA	EAF	P	ENCODE TFBS	Experiment Score ^{cj}	TFBS Start Position	TFBS End Position
rs186019316 ^{a)}	611740	A	G	0.02	0.000494	NRSF	118	611562	611818
rs17042288 ^{b)}	657954	T	C	0.28	0.000862	FOXA1	275	657815	658085
rs6548248	659544	T	C	0.29	0.000945				
rs6548245	659218	G	A	0.24	0.00108				
rs12714411	608411	G	T	0.16	0.00148				
rs60715336	658149	C	T	0.29	0.00178				
rs7591067	642846	A	G	0.18	0.00221				
rs73908142	602824	A	G	0.14	0.0028	Max	402	602678	602954
rs17042292	658157	C	T	0.29	0.00352				
rs35640204	681475	C	T	0.26	0.00419				
rs13007080	630024	C	A	0.18	0.00429				
rs35941143	646159	A	G	0.15	0.00556				
rs115124376	620455	T	C	0.01	0.00644				
rs4854339	623212	C	T	0.26	0.00802				
rs11127488	646061	C	T	0.17	0.00825				
rs61360200	599281	T	C	0.14	0.00954				
rs10865551	641863	A	T	0.18	0.00969				
rs7567710	645372	G	T	0.18	0.00976				
rs10172769	646345	A	G	0.17	0.0105				
rs12714413	642253	C	T	0.18	0.0121				
rs13027828	632379	G	T	0.18	0.0127				
rs188490283	622439	G	A	0.01	0.0137				
rs79882802	644356	C	A	0.16	0.0145				
rs5017301	631096	A	G	0.19	0.0155				
rs4241323	674297	G	A	0.16	0.0155	GATA-2	190	673982	674362
rs7596985	659384	G	A	0.26	0.0156				
rs13387091	650980	A	G	0.16	0.0161				
rs7570993	652565	G	A	0.12	0.0187				
rs2903489	649638	T	C	0.16	0.0193				
rs76847828	666466	G	A	0.06	0.0203				
rs6739303	628749	T	C	0.17	0.0205	Pol2	453	628694	629238
rs17729386	666343	T	C	0.30	0.0215				
rs7559447	645646	T	C	0.17	0.0224				
rs11127487	639900	T	C	0.17	0.0225				
rs35628463	653581	A	G	0.17	0.0245				
rs10865550	641718	G	T	0.18	0.0246	USF-1	90	641590	641840
rs11127489	646081	T	C	0.17	0.0252				
rs11687052	623740	G	A	0.19	0.0288				
rs2867119	662275	A	G	0.01	0.0334				
rs62103593	674054	C	T	0.14	0.0383	c-Fos	436	673942	674286
rs35913461	653575	T	C	0.17	0.0384				
rs12995666	629959	C	T	0.18	0.0408				
rs4241325	679959	C	T	0.30	0.0422				

Abbreviations: EA = effect allele, NEA = non-effect allele, EAF = Effect allele frequency, P = P-value, TBFS = transcription factor binding site

a) Variant yielded by conditional analysis on rs6548238.

b) In perfect LD with reported variant rs7596758.

c) ENCODE experiment scores have values from 0 to 1000. Higher ChipSeq binding scores indicate a higher potential evidence for transcription factor binding. In case multiple TBFS were found, only the site with the highest score was selected.

Supplementary Table 2. Cohort specific association results and random effect results for two reported variants

rs7596758 (from Table2)

Association Result of rs7596758

-cohort-specific results

Cohort	SNP	CHR	POS	EA	Non_EA	BETA	SE
ARIC	chr2:648595	2	648595	G	T	0.700	0.237
CHS	chr2:648595	2	648595	G	T	-0.148	0.293
FHS	chr2:648595	2	648595	G	T	0.536	0.227

-GWAMA random effect meta-analysis

rs_number	EA	Non_EA	beta	se	beta_95L	beta_95U	z	p-value
chr2:648595	G	T	0.392	0.238	-0.074	0.858	2.022	0.043

rs186019316 (from Table 3)

Association Result of rs186019316 Conditional on rs6548238

-cohort-specific results

Cohort	SNP	CHR	POS	EA	Non_EA	BETA	SE
ARIC	chr2:601740	2	601740	A	G	-1.935	0.638
CHS	chr2:601740	2	601740	A	G	1.303	1.390
FHS	chr2:601740	2	601740	A	G	-0.207	0.527

-GWAMA random effect meta-analysis

rs_number	EA	Non_EA	beta	se	beta_95L	beta_95U	z	p-value
chr2:601740	A	G	-0.565	0.806	-2.145	1.015	-0.595	0.552

Association Result of rs186019316 Conditional on rs2867125

-cohort-specific results

Cohort	SNP	CHR	POS	EA	Non_EA	BETA	SE
ARIC	chr2:601740	2	601740	A	G	-2.010	0.644
CHS	chr2:601740	2	601740	A	G	1.316	1.370
FHS	chr2:601740	2	601740	A	G	-0.177	0.529

-GWAMA random effect meta-analysis

rs_number	EA	Non_EA	beta	se	beta_95L	beta_95U	z	p-value
chr2:601740	A	G	-0.554	0.842	-2.204	1.096	-0.573	0.566

Note: the effect and SE were obtained from analysis with sampling weight adjustment