

**Supplementary Table S1.** Results of association analysis between SNP and BMI adjusting for sex, age, and recruitment area using KBA dataset of 57,110 individuals from HEXA cohort. A total of 20 lead SNPs showing genome-wide significant association were selected from about 8M SNPs used for association analysis.

CHR	SNP	BP	RA	MAF	Beta	SE	P	Candidate Gene
1	rs633715	177852580	C	0.147	0.207	0.019	$1.40 \times 10^{-26}$	<i>SEC16B</i>
16	rs55872725	53809123	T	0.166	0.255	0.025	$9.79 \times 10^{-24}$	<i>FTO</i>
18	rs476828	57852587	C	0.205	0.188	0.019	$3.87 \times 10^{-23}$	<i>MC4R</i>
11	rs6265	27679916	C	0.488	0.160	0.017	$2.67 \times 10^{-21}$	<i>BDNF-AS - BDNF</i>
19	rs35560038	46175046	A	0.468	0.130	0.017	$2.55 \times 10^{-14}$	<i>GIPR</i>
2	rs713586	25158008	C	0.478	0.122	0.017	$4.48 \times 10^{-13}$	<i>ADCY3 - DNAJC27</i>
5	rs261967	95850250	C	0.465	0.117	0.017	$4.32 \times 10^{-12}$	<i>PCSK1 - CAST</i>
2	rs7570198	648198	T	0.087	0.200	0.029	$7.41 \times 10^{-12}$	<i>LOC105373352 - TMEM18</i>
3	rs3755804	52866289	T	0.217	0.124	0.019	$2.46 \times 10^{-11}$	<i>ITIH4 - MUSTN1</i>
4	rs10938397	45182527	G	0.303	0.120	0.019	$1.57 \times 10^{-10}$	<i>PRDX4P1 - THAP12P9</i>
16	rs13329725	20257273	A	0.191	0.135	0.021	$2.18 \times 10^{-10}$	<i>SNRPEP3</i>
12	rs11066132	112468206	C	0.172	0.144	0.023	$6.07 \times 10^{-10}$	<i>NAA25</i>
2	rs7560575	54142030	T	0.012	0.496	0.080	$6.60 \times 10^{-10}$	<i>PSME4</i>
5	rs112862634	87970352	C	0.474	0.103	0.017	$1.05 \times 10^{-9}$	<i>LINC00461</i>
13	rs4883723	54084032	A	0.282	0.110	0.019	$3.44 \times 10^{-9}$	<i>ZNF646P1</i>
17	rs35867081	79047278	A	0.298	0.101	0.018	$7.31 \times 10^{-9}$	<i>BAIAP2</i>
20	rs143349795	34559849	A	0.012	0.309	0.054	$1.19 \times 10^{-8}$	<i>CNBD2</i>
16	rs2540034	4022694	T	0.313	0.098	0.018	$2.21 \times 10^{-8}$	<i>ADCY9</i>
21	rs2211691	35609354	T	0.485	0.094	0.017	$2.30 \times 10^{-8}$	<i>LINC00310</i>
6	rs4946936	109003321	C	0.284	0.111	0.020	$4.00 \times 10^{-8}$	<i>FOXO3</i>

Results of association analysis are limited to SNPs with  $P$ -value  $< 5.0 \times 10^{-8}$ . The SNP ID and chromosomal position (BP) are based on NCBI genome build 37/hg19. Abbreviations are as follows: CHR, chromosome; SNP, single nucleotide polymorphism; BP, physical position (base-pair); RA, risk allele; MAF, minor allele frequency; SE, standard error.