Supplementary File

Progressive influence of BMI-associated genetic markers in rural Gambians

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Supplementary Table 1. Summary statistics of Gambian study population

A. Demographics	Females	Males	All
Age [1], adults			
N	930	496	1426
mean	26.3 y	28.9 y	
(range)	(20.0, 82.8 y)	(20.0, 82.6 y)	
Village			
Keneba	844	625	1469
Manduar	330	241	571
Kanton Kunda	294	201	495
Ethnicity, all (N, %)			
Mandinka	1418	1003	2421
Fula	36	44	80
Other	13	21	34
B. Anthropometry at specific ages	**Females**	**Males**	**All**
Birth			
N	730	673	1403
WT mean	2.87	3.03	
(range)	(1.40, 4.02)	(1.44, 4.41)	
zWT(UK)	-1.22	-1.12	
(range)	(-4.98, 1.31)	(-4.75, 1.71)	
2 years [2]			
N	1044	776	1820
WT mean	9.64	9.64	
(range)	(5.17, 14.64)	(5.71 , 13.89)	
HT mean	-2.14	-2.55	
(range)	(-8.33, 1.79)	(-7.55, 0.96)	
zWT(UK)	80.13	80.13	
(range)	(60.82, 99.09)	(60.34, 97.12)	
zHT(UK)	-1.83	-2.16	
(range)	(-8.05, 4.27)	(-8.57, 3.34)	
Adult [3]			
N	929	497	1426
WT mean	54.65	59.68	
(range)	(33.74, 100.02)	(35.92, 115.42)	
HT mean	-0.59	-1.39	
(range)	(-4.55, 3.28)	(-6.09, 3.25)	
zWT(UK)	159.10	170.57	
(range)	(137.40 179.40)	(148.60, 197.10)	
zHT(UK)	-0.75	-0.97	
(range)	(-4.35, 2.61)	(-4.12, 2.84)	
BMI mean	21.56	20.47	
(range)	(12.64, 37.16)	(11.67, 36.84)	

BW, birthweight; LG, length; HT, height; zHT(UK), height-for-age z-score; WT, weight; zWT(UK), weight-for-age z-score. **A.** [1] Analyses other than those of adults involved at least two age points from each individual, age across the whole study population (N=2535) is thus not shown. Further details on numbers per age group are shown in Table 1. **B.** zHT(UK) and zWT(UK) refer to z-scores derived from UK standards for comparative purposes (Freeman JV *et al.* Cross sectional stature and weight reference curves for the UK, 1990. Arch Dis Child 1995;73:17– 24). [2] nearest observation to 2 years of age (>1.5 and <2.5 y); [3] first measurement at adult age (>20 y).

Supplementary Table 2. Details of polymorphisms genotyped in Gambian study population

SNP ID	Gene	Effect allele	Other allele	Homo-zygotes for effect allele [N]	Hetero-zygotes [N]	Homo-zygotes for other allele [N]	Imputed genotypes [N]
rs10146997	*NRXN3*	G	A	610	1302	640	3
rs10838738	*MTCH2*	G	A	2467	86	2	0
rs10913469	*SEC16B*	C	T	1309	1042	197	7
rs11847697	*PRKD1*	T	C	914	1228	412	1
rs12016871	*MTIF3*	T	C	2373	172	6	4
rs12488483	*CADM2*	G	A	200	1071	1275	9
rs1514175	*TNNI3K*	A	G	169	1005	1364	17
rs1555543	*PTBP2*	C	A	737	1337	423	58
rs17782313	*MC4R*	C	T	1502	815	204	34
rs206936	*NUDT3*	G	A	389	1255	900	11
rs2112347	*FLJ35779*	T	G	587	1251	688	29
rs2241423	*MAP2K5*	G	A	470	1306	774	5
rs2287019	*QPCTL*	C	T	42	493	1946	74
rs2568958	*NEGR1*	A	G	427	1253	867	8
rs2890652	*LRP1B*	C	T	931	1230	373	21
rs3810291	*TMEM160*	A	G	2237	296	11	11
rs4929949	*RPL27A*	C	T	877	1224	451	3
rs6548238	*TMEM18*	C	T	50	532	1972	1
rs713586	*RBJ_POMC*	C	T	14	328	2181	32
rs7138803	*BCDIN3D_FAIM2*	A	G	1976	524	52	3
rs7640855	*CADM2*	A	G	2441	106	4	4
rs7647305	*TRA2B_ETV5*	C	T	459	1250	835	11
rs887912	*FANCL*	T	C	2287	257	9	2
rs925946	*BDNF*	T	G	1578	835	140	2
rs987237	*TFAP2B*	G	A	2010	509	29	7
rs989139	*GPRC5B*	C	T	503	1213	832	7
rs9941349	*FTO*	T	C	1920	578	52	5
rs4836133	*ZNF608*	A	C/G	31	516	2007	1
rs13107325	*SLC39A8*	T	C	2494	0	0	NA
rs10938397	*GNPDA2*	G	A	2538	0	0	NA

SNPs associated with BMI by Speliotes and colleagues (2010) or surrogate markers to the original SNPs, locating within the same haplotype block in HapMap Yoruba and Caucasians (r^2>0.8), were screened in our Gambian population (N=). Note: No suitable surrogate SNP was identified for KCTD15 rs11084753, LRRN6C rs2183825 and SH2B1 rs7498665.