

Table 1. Sample characteristics for the traits of interest

Exposure (UK biobank code)	Mean (standard deviation)	sample size	Anthropometrics-MS risk			Anthropometrics-MS severity		
			Independent genome-wide significant SNPs	Approximate variance explained (%)	mean <i>F</i> -statistic	Independent genome-wide significant SNPs	Approximate variance explained (%)	mean <i>F</i> -statistic
MS risk (as exposure)		115,803	97	19 ^a	77			
Height (50)	168.5 cm (9.3)	360,388	530	8.6	118	401	6.9	126
BMI (21,001)	27.3 kg/m ² (4.8)	359,983	266	4.2	58	168	2.9	64
Weight (21,002)	77.9 kg (15.9)	360,116	304	4.2	64	168	2.9	64
Trunk fat-mass (23,128)	13.7 kg (5.1)	354,597	261	4.1	56	176	3.1	62
Arm fat mass left (23,124)	1.3 kg (0.7)	354,673	249	3.8	57	165	2.7	62
Arm fat mass right (23,120)	1.2 kg (0.6)	354,736	253	3.9	57	162	2.7	63
Arm fat percentage left (23,123)	30.2 % (10.2)	354,707	225	2	55	151	1.4	60
Arm fat percentage right (23,119)	29.4 % (10.1)	354,760	236	2.1	55	147	1.4	60
Arm non-fat mass left (23,125)	2.9 kg (0.8)	354,668	330	2.6	69	228	1.9	75
Arm non-fat mass right (23,121)	2.9 kg (0.8)	354,732	323	2.5	71	218	1.8	77
Whole body fat mass (23,100)	24.8 kg (9.5)	354,244	258	3.8	56	168	2.8	63
Whole body fat percentage (23,099)	31.4 % (8.5)	354,628	240	2.1	54	156	1.4	58
Whole body non-fat mass (23,101)	53.1 kg (11.5)	354,808	374	3.1	76	242	2.2	84
Leg fat mass left (23,116)	4.2 kg (1.9)	354,788	249	2.5	56	155	1.7	63
Leg fat mass right (23,112)	4.3 kg (1.9)	354,807	249	2.5	57	152	1.7	64
Leg fat percentage left (23,115)	32.0 % (10.6)	354,791	228	1.2	52	144	0.8	54
Leg fat percentage right (23,111)	32.0 % (10.7)	354,811	230	1.3	52	149	0.9	54
Leg non-fat mass left (23,117)	8.8 kg (2.0)	354,771	333	2.8	72	217	1.9	78
Leg non-fat mass right (23,113)	8.9 kg (2.0)	354,798	350	2.9	71	228	2	77
Trunk fat percentage (23,127)	31.1 % (8.0)	354,619	225	2.8	54	148	2	59
Trunk non-fat mass (23,129)	29.6 kg (6.0)	354,530	353	3	79	243	2.3	86

MS: multiple sclerosis; BMI: body mass index

^a Because MS risk is a binary trait, variance explained was extracted from the original MS risk genome-wide association study. Because anthropometric measures are continuous traits that were scaled into SD units, variance is estimated from equation 2 (see supplementary).