TABLE 1S. Allele and genotype frequencies of tag-SNPs in the *IL6R* gene (GOOD)

			Allele frequency		Genotype frequency			
Marker	Gene	Localization	1 %	2 %	11 n (%)	12 n (%)	22 n (%)	P_{HWE}
rs952146	*IL6R*	5’ near gene	62 (A)	38 (G)	431 (40)	469 (44)	148 (14)	0.26
rs1386821	*IL6R*	intron 1	84 (T)	16 (G)	738 (69)	278 (26)	33 (3)	0.28
rs4075015	*IL6R*	intron 1	56 (A)	44 (T)	346 (32)	507 (47)	193 (18)	0.76
rs6684439	*IL6R*	intron 1	95 (C)	41 (T)	378 (35)	507 (47)	164 (15)	0.78
rs4553185	*IL6R*	intron 6	57 (T)	43 (C)	327 (31)	531 (50)	191 (18)	0.34
rs4129267	*IL6R*	intron 8	59 (C)	41 (T)	378 (35)	501 (47)	170 (16)	0.85
rs2228145*	*IL6R*	3' near gene	59 (A)	41 (C)	378 (35)	498 (47)	168 (16)	0.85
rs11265618	*IL6R*	3' near gene	81 (C)	19 (T)	718 (67)	302 (28)	27 (3)	0.47
rs4240872	*IL6R*	3' near gene	76 (T)	24 (C)	592 (55)	397 (37)	60 (6)	0.54
rs2229238	*IL6R*	3' near gene	79 (C)	21 (T)	667 (62)	343 (32)	39 (4)	0.53

Table 1S. 1 = major allele; 2 = minor allele; n = number of subjects carrying the genotype; 11 = homozygotes for major allele; 22 = homozygotes for minor allele; HWE = Hardy-Weinberg equilibrium; IL = interleukin; R = receptor; *rs2228145 is also known as rs8192284.

TABLE 2S. Associations with total fat mass and the covariates used for adjustments with fat parameters in the three cohorts

Cohort	Covariates	Effect size*	*P*
GOOD	Current physical activity (h/week)	-0.021 ± 0.006	0.0003
	Total body lean mass (kg)	0.046 ± 0.006	1×10^{-13}
MrOS Sweden	Age (yr)	0.002 ± 0.005	0.15
	Current physical activity (km/day)	-0.033 ± 0.005	0.0004
	Current smoking status	-0.261 ± 0.060	1×10^{-05}
	Height (cm)	-0.009 ± 0.003	0.006
	Total body lean mass (kg)	0.064 ± 0.003	8×10^{-79}
MrOS US	Age (yr)	0.006 ± 0.002	0.14
	Current physical activity (km/day)	-0.027 ± 0.003	0.0004
	Current smoking status	-0.187 ± 0.061	0.002
	Height (cm)	-0.015 ± 0.002	1×10^{-13}
	Total body lean mass (kg)	0.077 ± 0.002	1×10^{-99}

Table 2S. Linear regression analysis of total fat mass and covariates that then were used for adjustments of associations between SNPs and fat parameters in the three cohorts. *P*-values are calculated on log-transformed response (tissue fat mass measured by DXA) using linear regression, and are adjusted for site. *Effect size (regression coefficient) and SEM values are expressed in change in SD units of total fat mass for each covariate.

TABLE 3S: SNPs in the *IL6R* gene in relation to total fat mass in the GOOD cohort

		MODEL I	MODEL II		
Marker	**Minor allele**	***P***	**Effect size***	***P***	**P_c**
rs952146	G	0.87	-0.002 (0.043)	0.97	1
rs1386821	G	0.10	-0.069 (0.056)	0.22	0.73
rs4075015	T	0.02	-0.092 (0.042)	0.03	0.17
rs6684439	T	0.71	0.022 (0.043)	0.61	1
rs4553185	C	0.24	-0.053 (0.043)	0.22	0.82
rs4129267	T	0.40	0.039 (0.043)	0.36	0.9
rs2228145*	C	0.41	0.040 (0.043)	0.35	0.9
rs11265618	T	0.82	0.004 (0.057)	0.94	1
rs4240872	C	0.32	-0.062 (0.049)	0.21	0.81
rs2229238	T	0.47	0.057 (0.053)	0.28	0.91

Table 3S. *P*-values are calculated on log-transformed response (tissue fat mass measured by DXA) using linear regression under an additive model, corrected for race, tissue lean mass and present physical activity (hours per week). Model I is adjusted for race and Model II is adjusted for race, tissue lean mass and present physical activity (hours per week). *Effect size (regression coefficient) and SEM values are expressed as change in SD units per additional minor allele and presented for the model II. P_c is corrected for multiple testing by permutation test. *rs2228145 is also known as rs8192284.