Supplemental Tables & Figures

Table S1. Components of the Mediterranean-style Diet Score (MDS) and Alternative Healthy Eating Index (AHEI)

	MDS	AHEI
Maximum score	25	110
Vegetables	+	+
Fruits	+	+
Nuts	+	
Legumes	+	
Nuts and Legumes		+
Whole grains	+	+
Fish	+	
Red meat	-	-
MUFA/SFA ratio	+	
Alcohol	+	+
SSB and fruit juice		-
EPA and DHA		+
PUFA without EPA and DHA		+
Trans-fatty acids		-
Sodium		-

+ items: Greater consumption increased the dietary score
- items: Greater consumption decreased the dietary score
MUFA/SFA ratio=ratio of monounsaturated fatty acids to saturated fatty acids. SSB=sugar-sweetened beverages.
EPA=Eicosapentaenoic acid. DHA=Docosahexaenoic acid.
PUFA=Poly-unsaturated fatty acids

Table S2. Genetic variants included in each ectopic fat GRS.

SNP	CHR	Position	Effect Allele	Other Allele	Effect Allele Frequency	Imputation Quality
VAT GRS						
rs10060123	5	125683910	C	A	0.74	0.99
rs2842895	6	7106316	G	C	0.44	0.92
SAT GRS						
rs2123685	17	38053889	T	C	0.97	1.00
rs7185735	16	53822651	A	G	0.59	0.98
rs2237199	6	16430021	G	A	0.89	0.94
VSR GRS						
rs7374732	3	23203454	T	C	0.64	1.00
rs6689335	1	219628682	T	C	0.56	0.93
rs912056	6	6736197	T	A	0.62	0.96
PAT GRS						
rs6587515	1	150608888	G	A	0.91	0.97
rs10198628	2	12964497	G	A	0.53	1.00
rs2434264	5	158022203	T	G	0.65	1.00
rs1650505	5	158029734	G	A	0.79	0.98

Genetic variants are taken from previously published genome-wide association study meta-analysis. VAT=Visceral Adipose Tissue. SAT=Subcutaneous Adipose Tissue. VSR=Visceral to Subcutaneous Adipose Tissue Ratio. PAT=Pericardial Adipose Tissue. GRS=Genetic Risk Score. SNP=Single Nucleotide Polymorphism. CHR=Chromosome.

Table S3. Genetic variants included in the BMI GRS.

SNP	CHR	Position	Effect Allele	Other Allele	Effect Allele Frequency	Imputation Quality
rs2820292	1	201784287	A	C	0.45	0.90
rs17024393	1	110154688	T	C	0.97	0.91
rs3101336	1	72751185	C	T	0.63	0.91
rs12401738	1	78446761	G	A	0.68	0.92
rs657452	1	49589847	A	G	0.38	0.93
rs977747	1	47684677	T	G	0.40	0.99
rs11165643	1	96924097	T	C	0.57	0.99
rs11583200	1	50559820	C	T	0.37	0.99
rs543874	1	177889480	A	G	0.82	0.99
rs12566985	1	75002193	G	A	0.44	1.00
rs17203016	2	208255518	A	G	0.82	0.89
rs2121279	2	143043285	C	T	0.88	0.92
rs1016287	2	59305625	C	T	0.69	0.96
rs1528435	2	181550962	T	C	0.63	0.96
rs1460676	2	164567689	T	C	0.83	0.97
rs11688816	2	63053048	G	A	0.49	0.97
rs492400	2	219349752	T	C	0.58	0.98
rs7599312	2	213413231	G	A	0.75	1.00
rs11126666	2	26928811	G	A	0.75	1.00
rs2176040	2	227092802	G	A	0.63	1.00
rs10182181	2	25150296	G	A	0.48	1.00
rs13021737	2	632348	G	A	0.82	1.00
rs6804842	3	25106437	G	A	0.56	0.95
rs13078960	3	85807590	T	G	0.79	0.96
rs16851483	3	141275436	G	T	0.94	0.96
rs2365389	3	61236462	T	C	0.39	0.97
rs1516725	3	185824004	C	T	0.85	0.98
rs3849570	3	81792112	C	A	0.67	0.99
rs11727676	4	145659064	T	C	0.92	0.32
rs10938397	4	45182527	A	G	0.59	0.78
rs13107325	4	103188709	C	T	0.92	0.98
rs17001654	4	77129568	C	G	0.83	0.99
rs2112347	5	75015242	T	G	0.63	0.96
rs7715256	5	153537893	G	T	0.44	0.98
rs2033529	6	40348653	A	G	0.72	0.94
rs13201877	6	137675541	A	G	0.88	0.97
rs9400239	6	108977663	C	T	0.67	0.98
rs205262	6	34563164	A	G	0.71	0.98
rs9374842	6	120185665	T	C	0.76	0.99
rs13191362	6	163033350	A	G	0.88	1.00
rs2207139	6	50845490	A	G	0.83	1.00

Table S3 continued.

SNP	CHR	Position	Effect Allele	Other Allele	Effect Allele Frequency	Imputation Quality
rs2245368	7	76608143	T	C	0.80	0.89
rs6465468	7	95169514	G	T	0.72	0.90
rs9641123	7	93197732	G	C	0.60	0.94
rs16907751	8	81375457	C	T	0.90	0.68
rs2033732	8	85079709	C	T	0.76	0.95
rs17405819	8	76806584	T	C	0.71	1.00
rs10733682	9	129460914	A	G	0.46	0.68
rs10968576	9	28414339	A	G	0.71	0.99
rs4740619	9	15634326	C	T	0.47	0.99
rs6477694	9	111932342	T	C	0.66	1.00
rs1928295	9	120378483	T	C	0.56	1.00
rs7903146	10	114758349	C	T	0.69	0.94
rs11191560	10	104869038	T	C	0.91	0.98
rs17094222	10	102395440	T	C	0.76	0.99
rs7899106	10	87410904	A	G	0.96	1.00
rs2176598	11	43864278	C	T	0.73	0.99
rs4256980	11	8673939	G	C	0.64	0.99
rs12286929	11	115022404	A	G	0.49	1.00
rs11030104	11	27684517	A	G	0.79	1.00
rs3817334	11	47650993	C	T	0.59	1.00
rs7138803	12	50247468	G	A	0.64	0.92
rs12429545	13	54102206	G	A	0.87	0.50
rs1441264	13	79580919	A	G	0.60	0.89
rs12016871	13	28017782	C	T	0.83	0.95
rs9540493	13	66205704	A	G	0.44	1.00
rs11847697	14	30515112	C	T	0.95	0.76
rs10132280	14	25928179	C	A	0.69	0.91
rs7141420	14	79899454	T	C	0.52	1.00
rs12885454	14	29736838	C	A	0.67	1.00
rs3736485	15	51748610	A	G	0.51	0.91
rs7164727	15	73093991	C	T	0.33	0.98
rs16951275	15	68077168	T	C	0.78	1.00
rs758747	16	3627358	C	T	0.70	0.60
rs2080454	16	49062590	A	C	0.62	0.66
rs4787491	16	30015337	A	G	0.49	0.77
rs9925964	16	31129895	A	G	0.61	0.83
rs12446632	16	19935389	G	A	0.85	0.99
rs2650492	16	28333411	G	A	0.74	0.99
rs1558902	16	53803574	T	A	0.58	1.00
rs1000940	17	5283252	A	G	0.70	0.98
rs12940622	17	78615571	G	A	0.56	1.00
rs9914578	17	2005136	C	G	0.81	1.00

Table S3 continued.

SNP	CHR	Position	Effect Allele	Other Allele	Effect Allele Frequency	Imputation Quality
rs7243357	18	56883319	T	G	0.82	0.95
rs1808579	18	21104888	T	C	0.47	0.96
rs6567160	18	57829135	T	C	0.78	0.97
rs7239883	18	40147671	A	G	0.60	1.00
rs3810291	19	47569003	G	A	0.38	0.49
rs2287019	19	46202172	C	T	0.82	0.78
rs29941	19	34309532	G	A	0.67	0.93
rs17724992	19	18454825	A	G	0.72	0.95
rs6091540	20	51087862	C	T	0.70	1.00
rs2836754	21	40291740	T	C	0.38	1.00

Genetic variants are taken from previously published genome-wide association study meta-analysis. BMI=Body Mass Index. GRS=Genetic Risk Score. SNP=Single Nucleotide Polymorphism. CHR=Chromosome.

Table S4. Genetic variants included in the WHR GRS.

SNP	CHR	Position	Effect Allele	Other Allele	Effect Allele Frequency	Imputation Quality
rs10919388	1	170372503	C	A	0.71	0.99
rs2645294	1	119574587	T	C	0.55	1.00
rs2820443	1	219753509	T	C	0.71	0.99
rs714515	1	172352990	A	G	0.57	1.00
rs905938	1	154991389	T	C	0.74	0.79
rs10195252	2	165513091	T	C	0.61	0.98
rs1385167	2	66200648	A	G	0.88	1.00
rs1569135	2	188115398	A	G	0.54	0.97
rs10804591	3	129334233	A	C	0.78	0.97
rs17451107	3	156797609	T	C	0.58	0.65
rs17819328	3	12489342	T	G	0.59	0.88
rs2276824	3	52637486	G	C	0.56	0.81
rs2371767	3	64718258	G	C	0.69	0.97
rs303084	4	124066948	A	G	0.77	0.98
rs3805389	4	56482750	G	A	0.76	0.99
rs9991328	4	89713121	T	C	0.49	0.96
rs1045241	5	118729286	C	T	0.74	1.00
rs6556301	5	176527577	G	T	0.63	0.39
rs7705502	5	173320815	G	A	0.72	0.99
rs9687846	5	55861894	G	A	0.79	0.96
rs1294410	6	6738752	C	T	0.61	0.96
rs1358980	6	43764551	C	T	0.52	0.69
rs1776897	6	34195011	T	G	0.91	0.98
rs1936805	6	127452116	T	C	0.49	1.00
rs10245353	7	25858614	C	A	0.81	0.97
rs1534696	7	26397239	A	C	0.56	0.97
rs7801581	7	27223771	C	T	0.76	0.91
rs12679556	8	72514228	G	T	0.27	1.00
rs7830933	8	23603324	A	G	0.75	0.91
rs10991437	9	107735920	C	A	0.89	1.00
rs7917772	10	104487443	A	G	0.63	0.91
rs11231693	11	63862612	G	A	0.94	0.99
rs10842707	12	26471364	C	T	0.80	0.98
rs1443512	12	54342684	C	A	0.76	0.99
rs4765219	12	124440110	C	A	0.65	1.00
rs1440372	15	67033151	C	T	0.73	1.00
rs8030605	15	56504598	G	A	0.87	1.00
rs8042543	15	31708263	C	T	0.79	0.90
rs2925979	16	81534790	C	T	0.70	0.84
rs4646404	17	17420199	G	A	0.63	0.75
rs8066985	17	68453345	G	A	0.54	0.98

Table S4 continued.

SNP	CHR	Position	Effect Allele	Other Allele	Effect Allele Frequency	Imputation Quality
rs12608504	19	18389135	G	A	0.63	0.96
rs4081724	19	33824946	G	A	0.85	0.82
rs224333	20	34023962	G	A	0.61	0.89
rs6090583	20	45558831	A	G	0.49	1.00
rs979012	20	6623374	C	T	0.64	0.82
rs2294239	22	29449477	A	G	0.57	0.94

WHR adjusted for BMI. Genetic variants are taken from previously published genome-wide association study meta-analysis. WHR=Waist to Hip Ratio. BMI=Body Mass Index. GRS=Genetic Risk Score. SNP=Single Nucleotide Polymorphism. CHR=Chromosome.

Table S5. Intakes of dietary components of the MDS according quartile categories of ΔMDS

		ΔMDS			
		Q1	Q2	Q3	Q4
Median ΔMDS		-4	-1	1	5
		Baseline			
MDS		15±4	13±4	12±4	10±4
Vegetable	servings/d	2.8±1.8	2.6±1.8	2.4±1.6	2.2±1.5
Fruit	servings/d	2.4±1.4	2.2±1.6	1.9±1.4	1.9±1.4
Nut	servings/d	0.5±0.6	0.4±0.6	0.3±0.4	0.3±0.4
Whole grain	servings/d	1.2±1.0	1.1±1.1	0.9±1.0	0.8±0.9
Legume	servings/d	0.5±0.4	0.4±0.4	0.3±0.3	0.3±0.3
Fish	servings/d	0.4±0.3	0.3±0.3	0.3±0.2	0.3±0.2
Red meat	servings/d	0.8±0.6	0.8±0.5	0.8±0.6	0.8±0.6
MUFA/SAT ratio		1.1±0.2	1.1±0.2	1.0±0.2	1.0±0.2
Alcohol	g/d	10±14	11±15	10±12	11±14
		Follow-up			
MDS		10±4	12±4	13±4	16±4
Vegetable	servings/d	2.3±1.9	2.7±1.7	2.9±1.9	3.4±2.1
Fruit	servings/d	1.6±1.2	1.9±1.4	1.9±1.3	2.3±1.5
Nut	servings/d	0.5±0.7	0.6±0.8	0.7±0.8	0.9±0.9
Whole grain	servings/d	0.9±1.1	1.0±0.9	1.2±1.1	1.4±1.1
Legume	servings/d	0.3±0.4	0.4±0.4	0.4±0.3	0.5±0.5
Fish	servings/d	0.2±0.2	0.3±0.3	0.3±0.3	0.4±0.3
Red meat	servings/d	0.9±0.6	0.8±0.6	0.8±0.5	0.7±0.6
MUFA/SAT ratio		1.1±0.3	1.2±0.3	1.2±0.3	1.3±0.3
Alcohol	g/d	10±15	12±16	11±14	11±14

Values are mean and standard deviation.
MUFA/SFA ratio=ratio of monounsaturated fatty acids to saturated fatty acids.
MDS=Mediterranean-style Dietary Score.

Table S6. Associations between change in AHEI and change in ectopic fat depots.

	Quartile ΔAHEI						
	Q1	Q2	Q3	Q4	Per SD Increase in		Sex-interaction of ΔAHEI
Median ΔAHEI	-6	2	9	18	ΔAHEI	P-value	P-interaction
Change in VAT volume, cm^3							
Model 1	699 (632, 766)	630 (565, 695)	665 (600, 730)	573 (506, 640)	-47 (-81, -13)	0.007	0.01
Model 2	699 (632, 766)	633 (567, 698)	667 (602, 732)	571 (504, 638)	-45 (-79, -11)	0.01	0.01
Change in SAT volume, cm^3							
Model 1	572 (500, 644)	529 (459, 599)	544 (474, 613)	421 (350, 492)	-59 (-96, -21)	0.002	0.15
Model 2	568 (496, 640)	535 (465, 605)	543 (473, 612)	420 (349, 492)	-58 (-95, -20)	0.003	0.16
Change in VSR							
Model 1	0.11 (0.09, 0.13)	0.10 (0.08, 0.12)	0.09 (0.08, 0.11)	0.09 (0.07, 0.11)	-0.01 (-0.02, 0.00)	0.03	0.05
Model 2	0.11 (0.09, 0.13)	0.10 (0.08, 0.11)	0.09 (0.08, 0.11)	0.09 (0.07, 0.11)	-0.01 (-0.02, 0.00)	0.06	0.02
Change in PAT volume, cm^3							
Model 1	0.6 (-1.5, 3.0)	-2.2 (-4.2, -0.1)	-2.3 (-4.4, -0.3)	-5.8 (-7.9, -3.7)	-2.3 (-3.4, -1.2)	<0.001	0.85
Model 2	0.6 (-1.5, 2.7)	-2.1 (-4.2, 0)	-2.3 (-4.4, -0.2)	-5.8 (-7.9, -3.7)	-2.3 (-3.4, -1.1)	<0.001	0.81

Values are adjusted mean (95%CI)

Model 1 adjusted for sex, age, baseline adipose tissue (e.g., baseline VAT for ΔVAT or baseline VSR for ΔVSR), baseline AHEI, baseline energy intake, baseline physical activity, and baseline smoking status; Model 2 adjusted for model 1 covariates plus baseline BMI, change in energy intake, physical activity, and smoking status. In model 2, we also adjusted for baseline SAT in analysis for ΔVAT and baseline VAT in analysis for ΔSAT.

BMI=Body Mass Index; VAT=Visceral Adipose Tissue; SAT=Subcutaneous Adipose Tissue; VSR=VAT to SAT Ratio; PAT=Pericardial Adipose Tissue; AHEI=Alternative Healthy Eating Index; SD=Standard Deviation

Table S7. Associations between genetic risk scores for BMI and WHR and baseline and change in corresponding ectopic fat volumes in overall sample.

	Model 1			Model 2		
	Effect	SE	p-value	Effect	SE	p-value
BMI GRS (*per standard deviation increase*)						
Baseline VAT, cm^3	49	21	0.02	56	20	0.01
Change in VAT, cm^3	19	17	0.26	19	17	0.25
Baseline SAT, cm^3	165	33	<0.001	174	32	<0.001
Change in SAT, cm^3	11	18	0.55	12	18	0.51
Baseline VSR	-0.02	0.01	0.02	-0.01	0.01	0.03
Change in VSR	0.007	0.005	0.14	0.007	0.005	0.12
Baseline PAT, cm^3	2	1	0.06	2	1	0.03
Change in PAT, cm^3	0	1	0.68	0	1	0.78
WHR GRS (*per standard deviation increase*)						
Baseline VAT, cm^3	37	21	0.09	55	15	<0.001
Change in VAT, cm^3	-5	17	0.77	-5	17	0.79
Baseline SAT, cm^3	-26	34	0.45	10	18	0.58
Change in SAT, cm^3	-6	19	0.73	-10	19	0.59
Baseline VSR	0.02	0.01	0.002	0.02	0.01	0.002
Change in VSR	0	0.005	0.94	0	0	0.85
Baseline PAT, cm^3	0	1	0.67	1	1	0.20
Change in PAT, cm^3	1	1	0.36	0	1	0.39

For the analyses of association between baseline ectopic fat volumes and GRSs, Model 1 adjusted for sex, age, and smoking status and Model 2 additionally adjusted for other genetic components (e.g., in analysis for baseline VAT using BMI GRS, we adjusted for WHR GRS and VAT GRS) and baseline smoking status, physical activity, energy intake, and MDS. The WHR GRS analyses also adjusted for baseline BMI in Model 2. For the analyses of association between change in ectopic fat depot volumes and GRSs, Model 1 adjusted for sex, age, smoking status, and baseline ectopic fat volume and Model 2 additionally adjusted for other genetic components (e.g., in analysis for ΔVAT using BMI GRS, we adjusted for WHR GRS and VAT GRS), baseline BMI (only in analysis using WHR GRS), and change in smoking status, physical activity, energy intake, and MDS. VAT=Visceral Adipose Tissue; SAT= Abdominal Subcutaneous Adipose Tissue; VSR=VAT to SAT Ratio; PAT=Pericardial Adipose Tissue; GRS=Genetic Risk Score; MDS=Mediterranean-style Diet Score; BMI=Body Mass Index; SE=Standard Error; WHR=Waist to Hip Ratio.

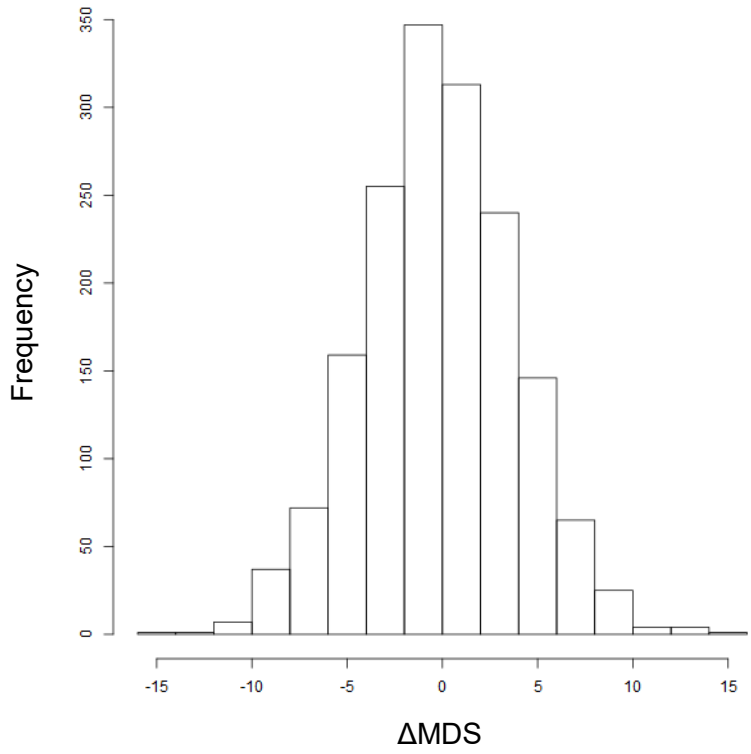

Figure S1. Distribution of ΔMDS (Change in Mediterranean-style diet score).

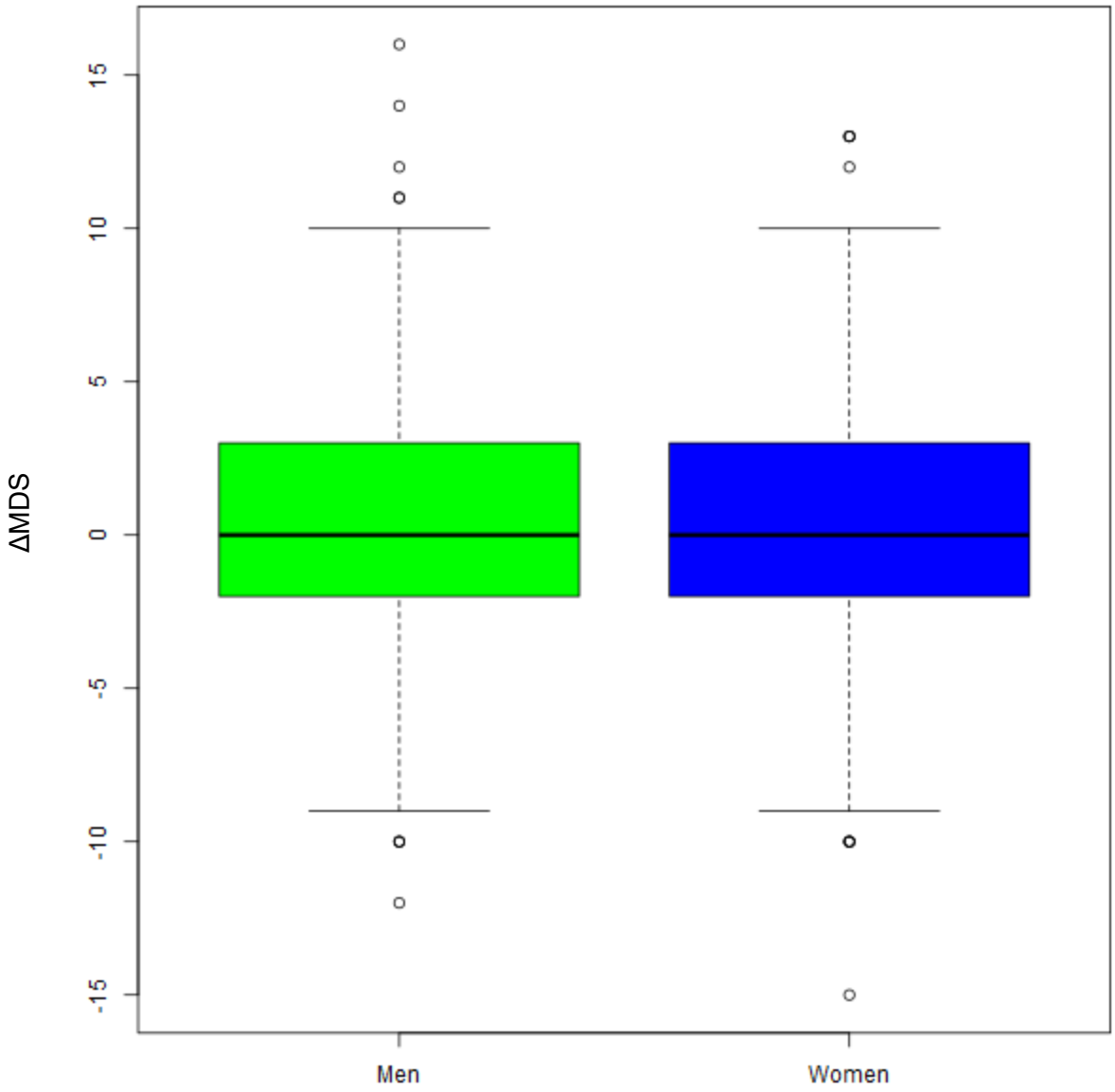

Figure S2. Sex-specific distribution of ΔMDS (Change in Mediterranean-style diet score).