

Supplementary Information

Generating the simulated variables for TDI, physical activity, TV watching and the composite score

In our analysis of gene x environment interactions for TDI, physical activity, TV watching and the composite score the basic starting equation is as follows:

$$(y|\mathbf{C}, \mathbf{g}, \mathbf{e}) = \mathbf{C} \cdot \mathbf{c} + \boldsymbol{\alpha} \mathbf{g} + \boldsymbol{\beta} \mathbf{e} + \boldsymbol{\varepsilon} \quad (1)$$

where y is BMI, \mathbf{e} is the environmental variable (in this case TDI, TV watching, physical activity or the composite score), \mathbf{g} is the BMI genetic risk score and \mathbf{C} represents important covariates.

Since \mathbf{g} is a genetic risk score for the trait y , α is non-zero but β can be zero. When statistical interaction is tested, the model is changed to

$$(y|\mathbf{C}, \mathbf{g}, \mathbf{e}) = \mathbf{C} \cdot \mathbf{c} + \boldsymbol{\alpha} \mathbf{g} + \boldsymbol{\beta} \mathbf{e} + \boldsymbol{\gamma}(\mathbf{g} * \mathbf{e}) + \boldsymbol{\varepsilon} \quad (2)$$

where $\mathbf{g} * \mathbf{e}$ refers to the element-wise product of two vectors. Let $\boldsymbol{\delta}_e$ denote the concatenated effects for environmental factor \mathbf{e}

$$\boldsymbol{\delta}_e = \begin{pmatrix} \mathbf{c} \\ \boldsymbol{\alpha} \\ \boldsymbol{\beta} \\ \boldsymbol{\gamma} \end{pmatrix}$$

One of the major problems with testing the γ parameter in this model is that if the environmental factor \mathbf{e} is correlated with y and \mathbf{g} the test may yield spurious interaction coefficients but only due to collider bias or biases well-established in secondary trait analysis.

In our simulation analysis rather than running the models above we perform the following:

$$(y|\mathbf{C}, \mathbf{g}, \mathbf{f}) = \mathbf{C} \cdot \mathbf{c} + \alpha \mathbf{g} + \beta \mathbf{f} + \gamma (\mathbf{g} * \mathbf{f}) + \tau \quad (3)$$

where \mathbf{f} relates to y , \mathbf{g} and \mathbf{C} marginally as does e and has the same conditional distribution. In other words we create an artificial environmental variable that behaves marginally exactly as the real environmental variable e .

In practice one can simulate \mathbf{f} easily by regressing e on $[\mathbf{C}, \mathbf{g}, y]$ and add the fitted values to a random permutation of the residuals. This ensures that \mathbf{f} and e have the same conditional expectations and same residual distributions.

Testing for reverse causality

To determine if the BMI genetic variants could influence BMI through primary effects on physical activity or diet related variables we investigated the association of each of the 69 BMI SNPs with physical activity, western diet and TV watching. We then plotted these against the published variant BMI-association to determine if any SNP was more associated with the obesogen than with BMI itself. To test the relationship between BMI and the obesogens we performed instrumental variable analysis (IVW) and a sensitivity analysis known to account for pleiotropy known as Egger Mendelian Randomisation (MR-Egger)¹. The results of these analyses are plotted in supplementary figure 2.

Additional sensitivity analyses

There are (at least) three potential artefacts that can give rise to spurious GxE from stratified genetic analysis:

The first one arises when the ***variance of the outcome variable is dependent on the mean value of the environmental factor***. The simplest configuration that gives rise to this scenario is when the variance of the outcome variable depends on its mean (e.g. log normally, or Poisson distributed) and the environmental factor is correlated with the outcome. This is the case for BMI and most of obesogenic environmental factors. This not only results in heteroscedastic noise, but different outcome variability in the strata. Such artefact can be eliminated by robust linear regression and inverse normal quantile normalization of the outcome variable in each stratum.

Splitting the sample into two groups with different environmental variability can also introduce spurious GxE association. This is typically the case when one stratifies the population using high threshold for the environmental variable. This artificially reduces the environmental variance in one of the groups and hence seemingly increases the observed genetic effect in that stratum. This problem can be reduced by splitting the sample such that the environmental variability is equal in the two groups.

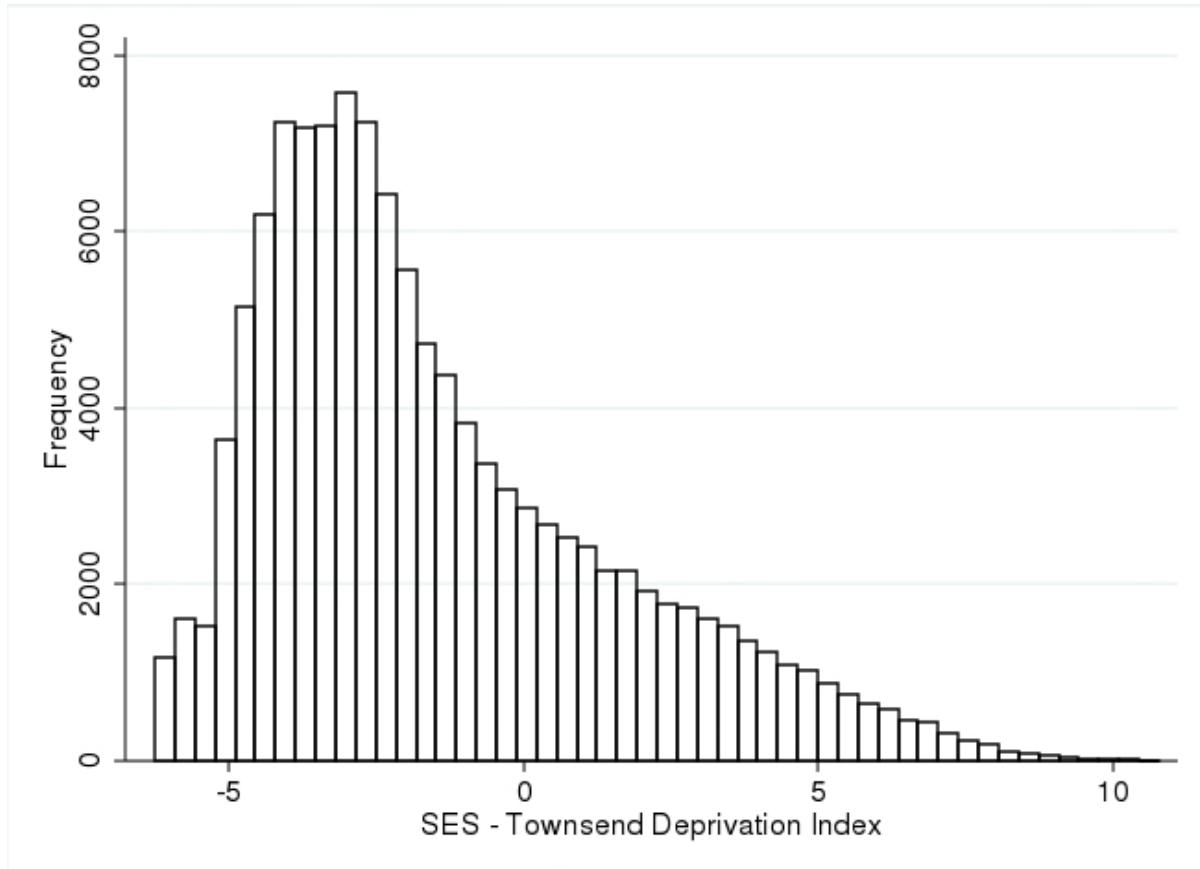
Alternatively, the environmental factor can be kept as a continuous variable and robust interaction model can be applied. In addition to using a continuous variable we also tested BMI genetic risk score – BMI associations when the high risk and low risk groups were defined as 75% people at the highest risk and 25% at low risk. These analyses demonstrated similar results with evidence for larger BMI GRS ~BMI effects in the high risk environment groups (Supplementary Table 10).

The third problem can arise due to index event bias. If the ***genetic variants are shared*** between the outcome and the environmental factor and the ***outcome is causally influencing the environmental factor***. In this case we observe classical index event bias for the estimation of the genetic effect in each stratum. This scenario can be excluded by testing the effect of GRS SNPs on the environmental factor to exclude pleiotropy. There was no correlation between the effect of individual BMI genetic variants on BMI and the effects of the individual BMI genetic variants on TV watching or other measures of the obesogenic environment (Pearson correlation coefficient comparing BMI and TV hour betas of 69 variants = -0.09).

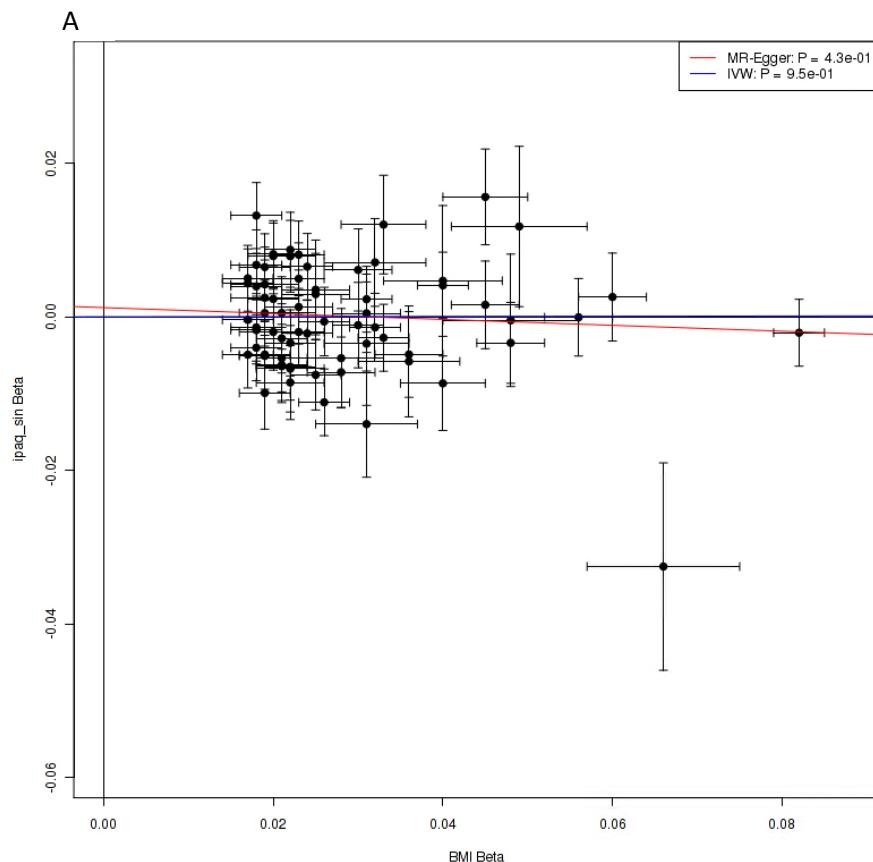
In this study, risk factors in the interaction model - measures of the obesogenic environment – were associated with the outcome – BMI. In theory this problem could have created false positive evidence of interaction but the sensitivity analyses described above suggested this was not the case.

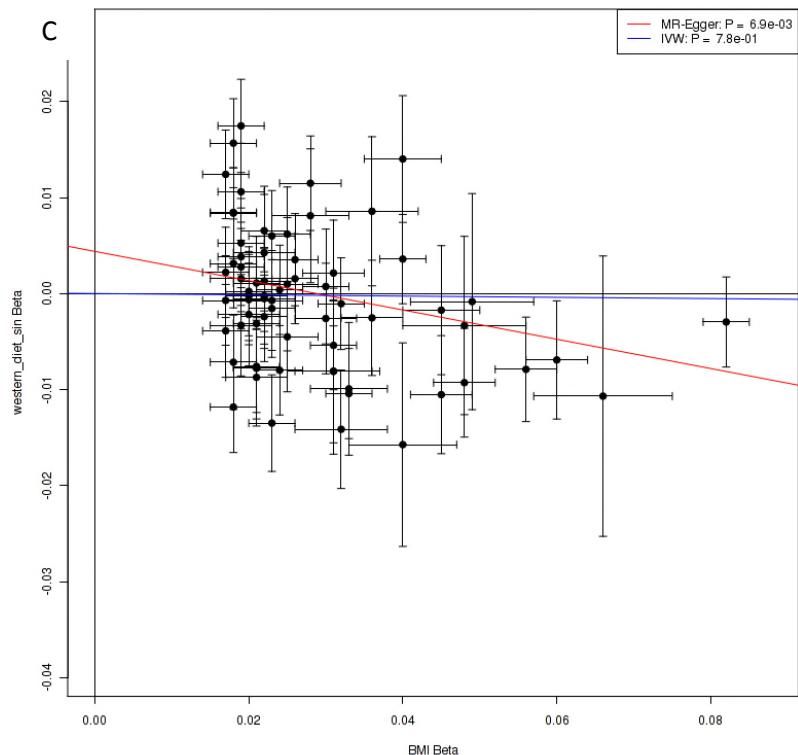
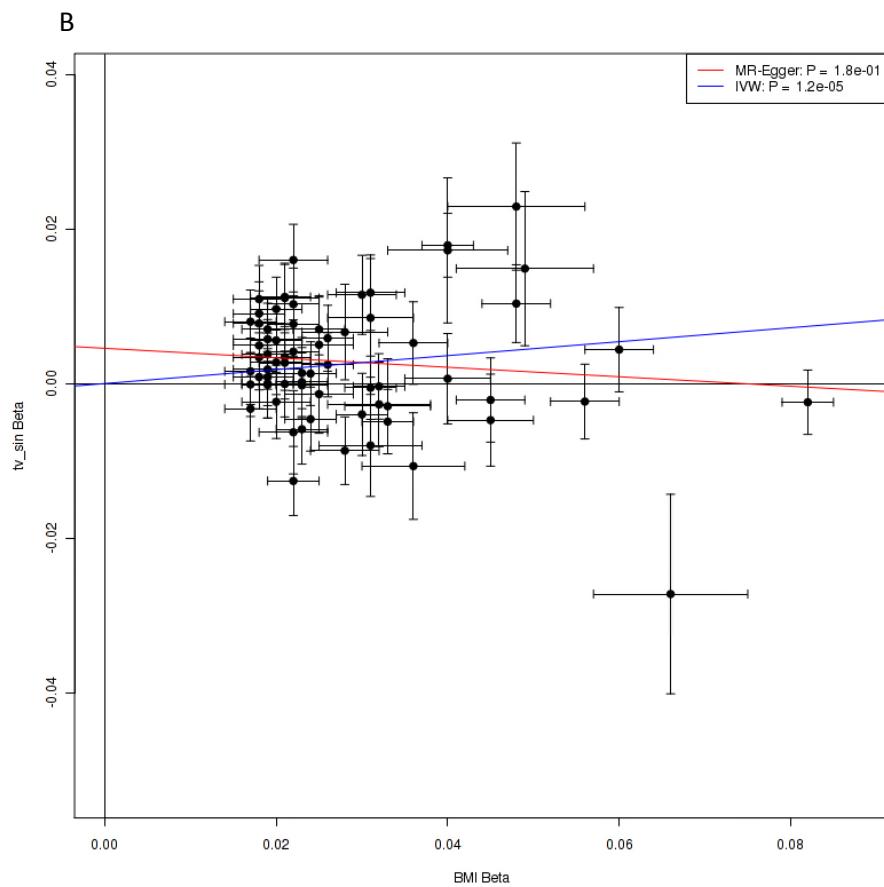
Supplementary figures

Supplementary Figure 1: Histogram showing the distribution of the Townsend Deprivation Index for the 119,733 individuals in the UK Biobank

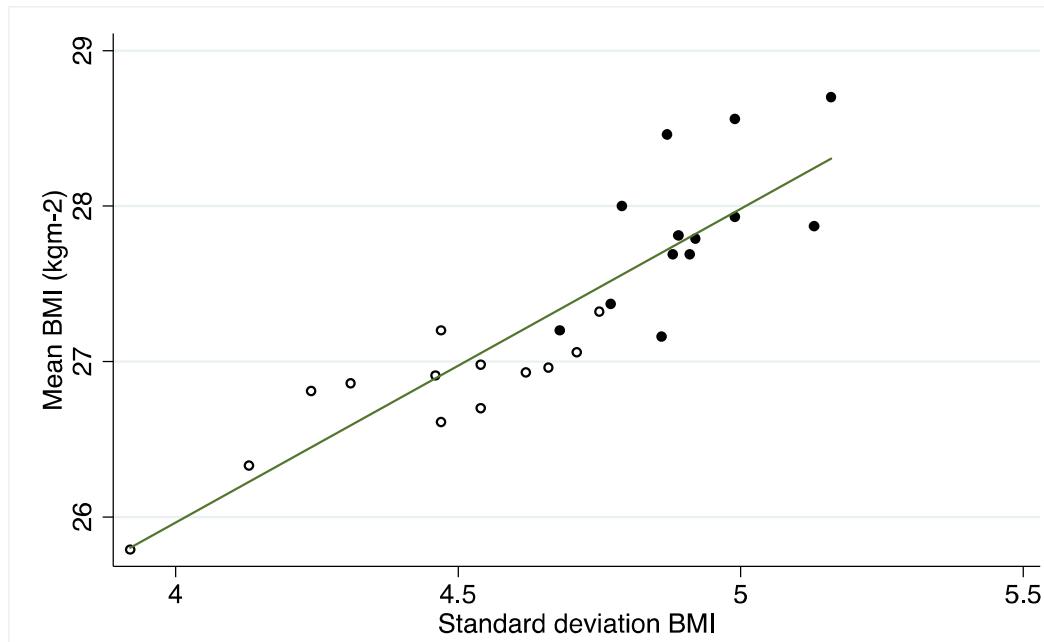


Supplementary figure 2: The 69 BMI SNPs and their association with BMI in the primary GWAS² plotted against their association with A) Physical activity determined by the International Physical Activity Questionnaire, B) TV watching and C) Western diet. The blue lines represent the standard instrumental variable association and the red lines represent a method of sensitivity analysis (Egger Mendelian Randomisation¹)

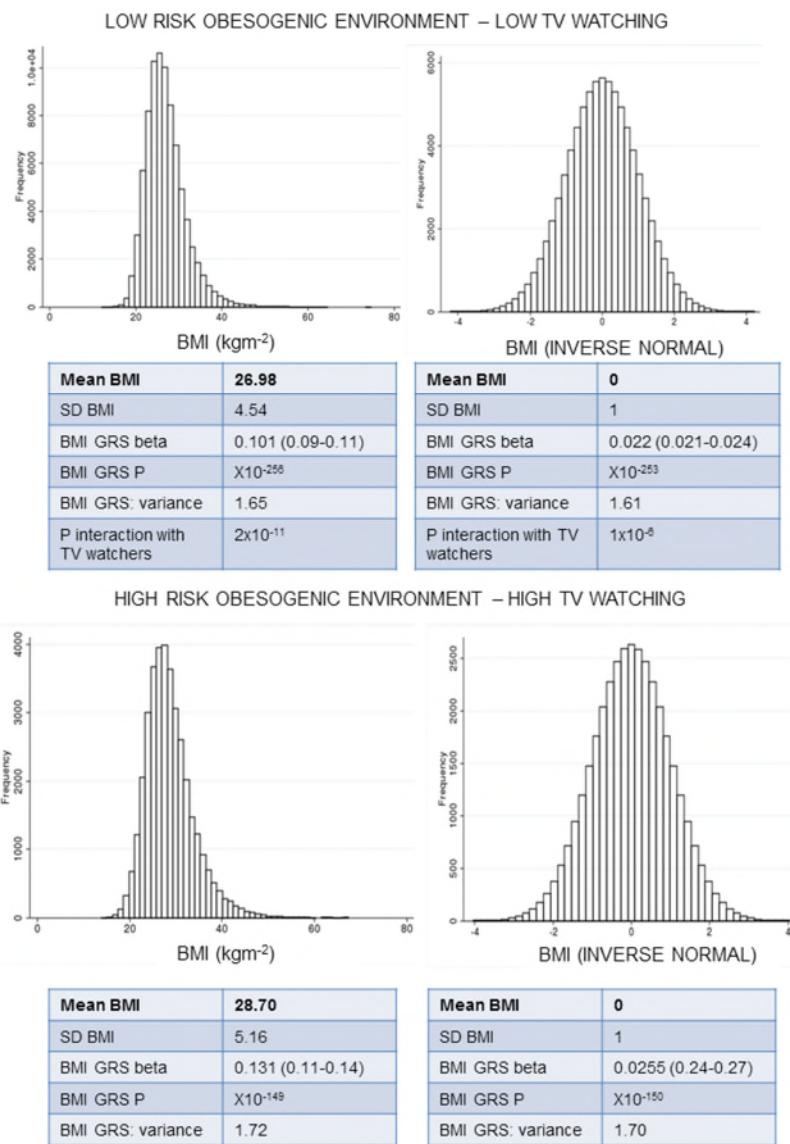




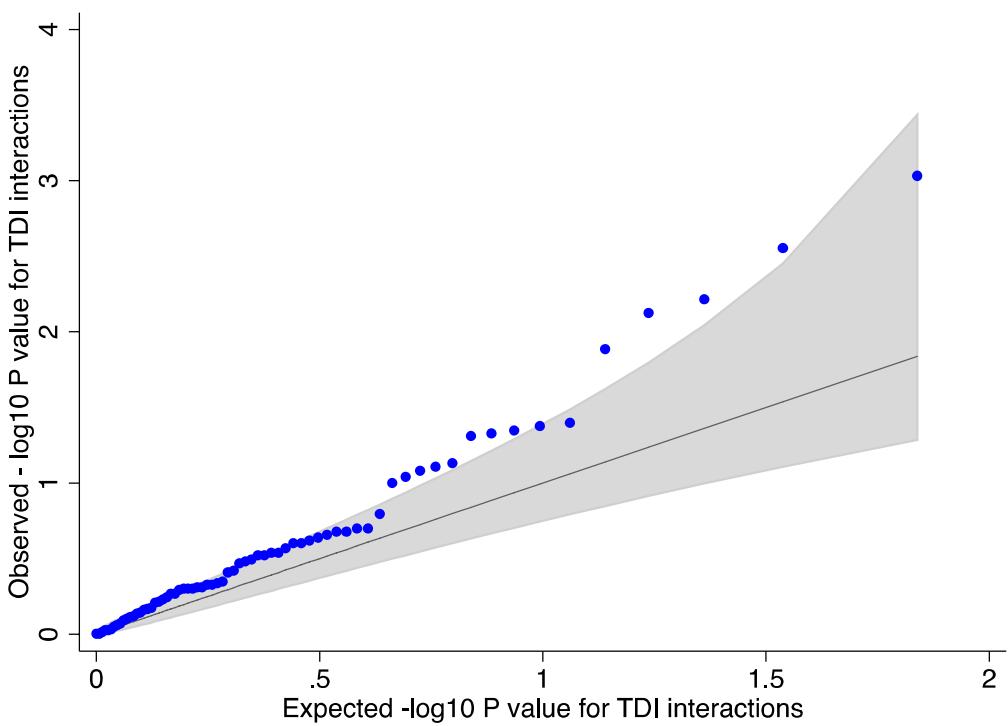
Supplementary figure 3: Scatter graph representing the relationship between mean BMI and the standard deviation of BMI for the 12 dichotomised obesogenic variables and the negative control sun protection use. Empty circles represent the low risk obesogenic variables and the solid circles represent the high risk obesogenic variables. The line of best fit indicates reasonable correlation ($r^2=0.78$).



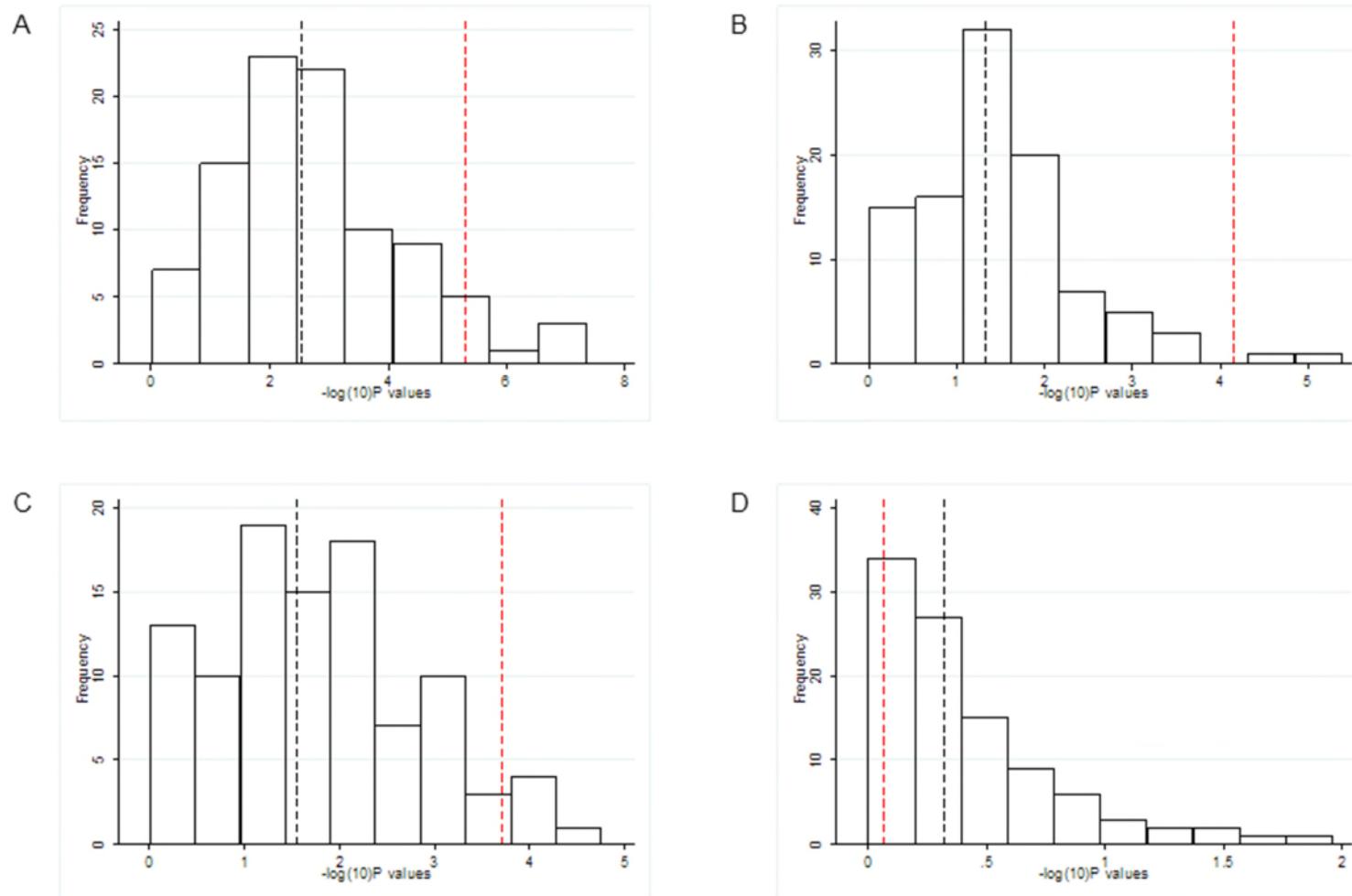
Supplementary Figure 4: Histograms representing the distribution of BMI in high TV watching and low TV watching groups. BMI represents raw BMI but effect sizes and p values are based on BMI adjusted for age, sex, ancestry principal components, assessment centre location and genotyping chip. BMI (INVERSE NORMAL) transforms the BMI residual variable to the inverse normal scale with a mean of zero and standard deviation of 1.



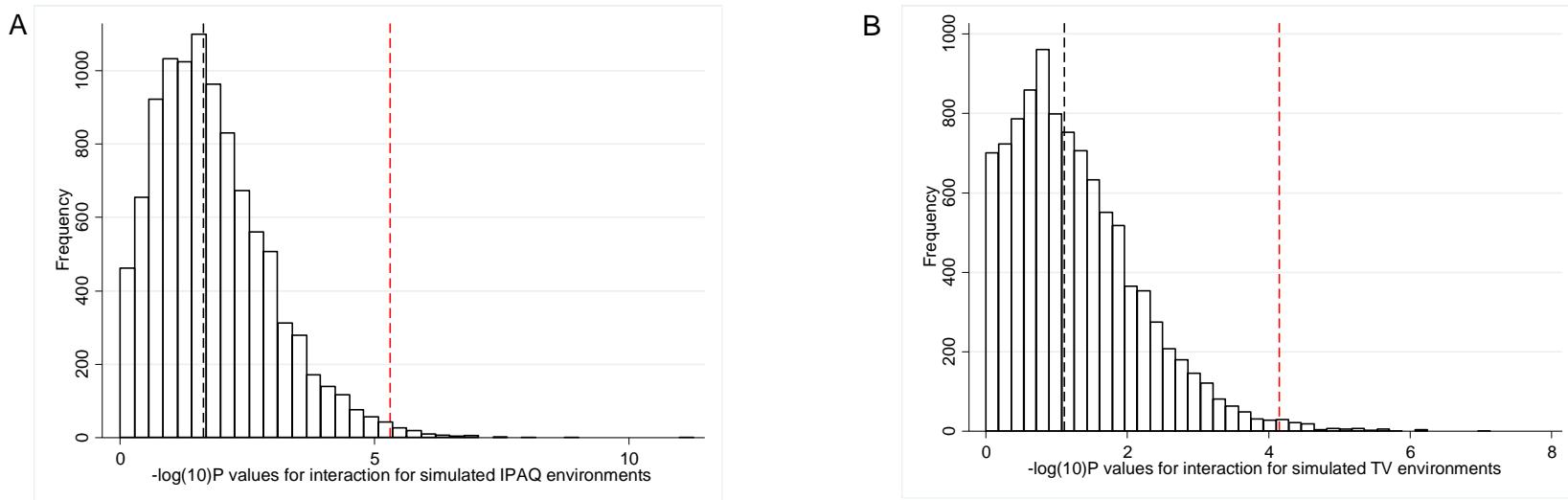
Supplementary Figure 5: QQ plot showing the observed TDI-BMI genetic interaction p-values from the 69 SNPs against the expected p-values

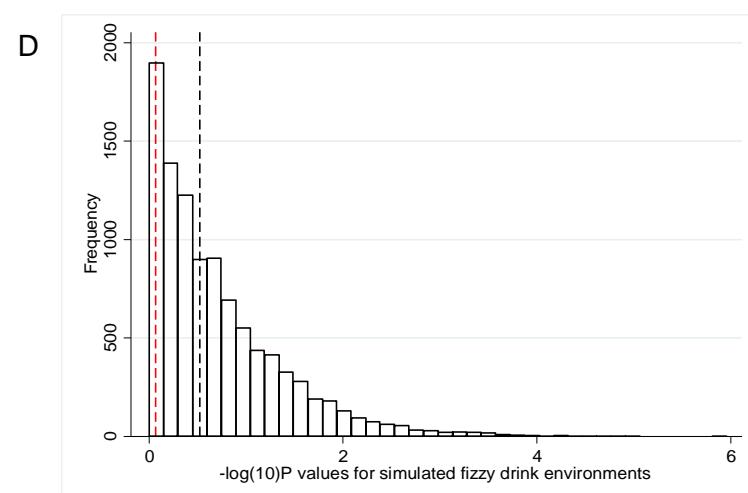
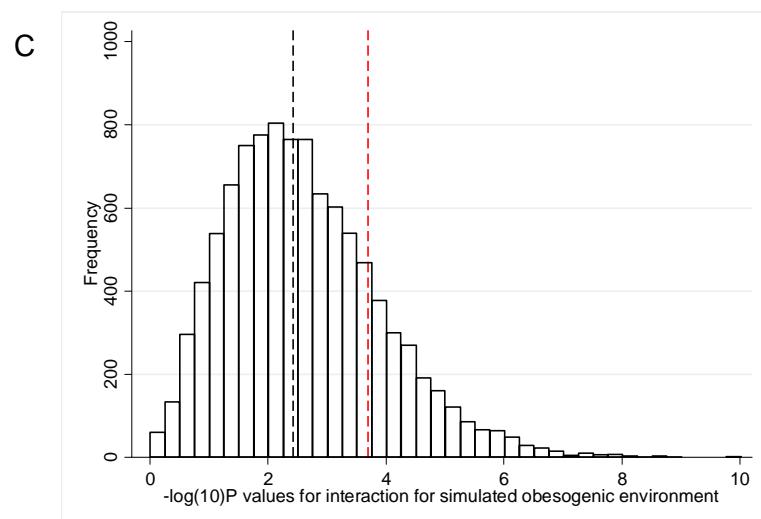


Supplementary Figure 6: Histograms of the $-\log_{10}P$ values from the interaction analyses for the 100 groups generated by meta-heuristic sampling for A) Physical activity, B) TV watching, C) the composite score and D) fizzy drinks. The black dashed line represents the median p-value in the 100 random iterations and the red dashed line represents the interaction p-value obtained in the real data.

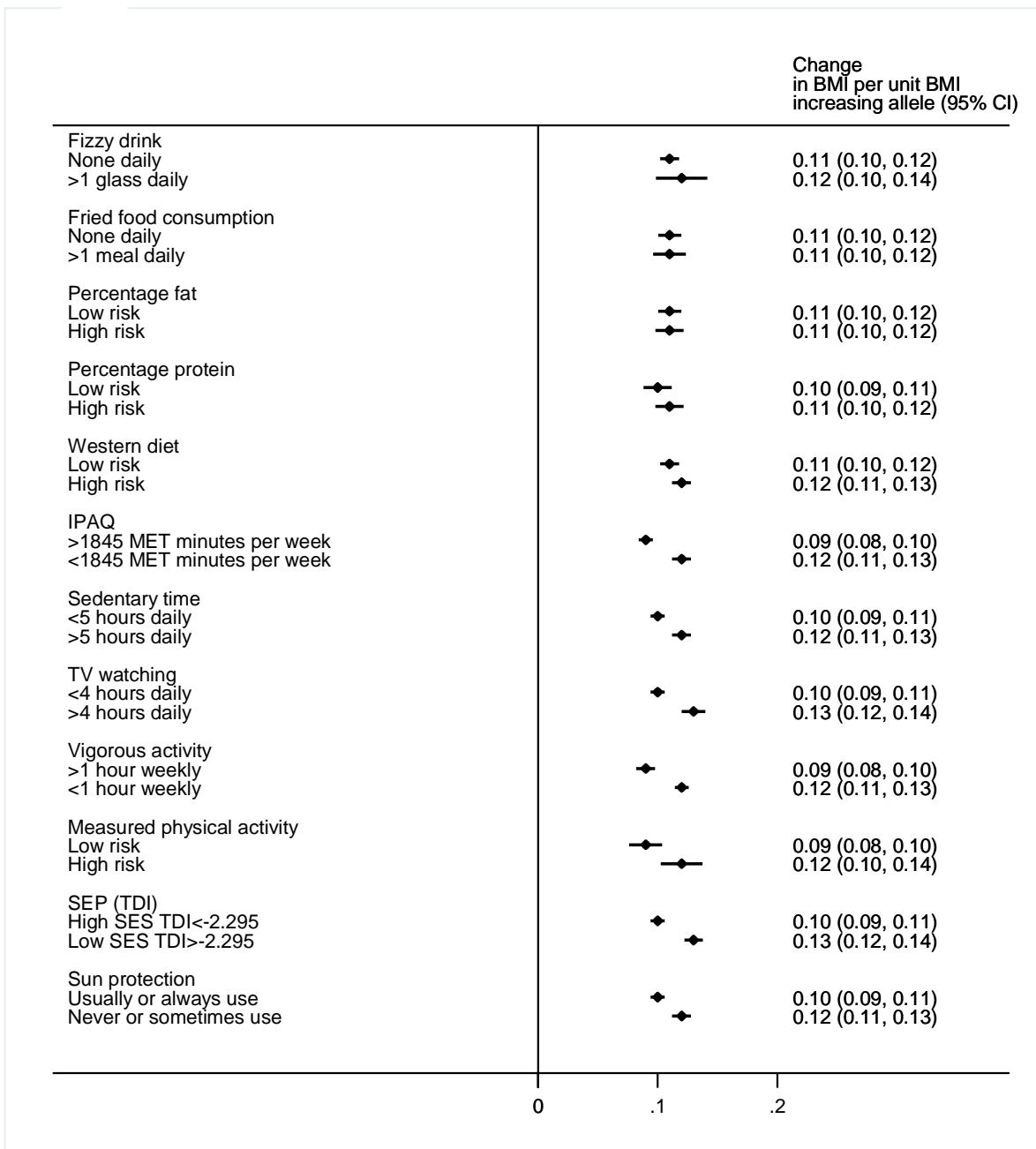


Supplementary figure 7: Histograms representing the interaction p-values for the 10,000 iterations of simulated dummy environments. The simulated environments were forced to have the same correlation with BMI as A) physical activity, B) TV watching, C) the composite score and D) fizzy drinks. The black line on the graphs represents the median interaction p-value in the simulations and the red line on graphs represents the real interaction p value.

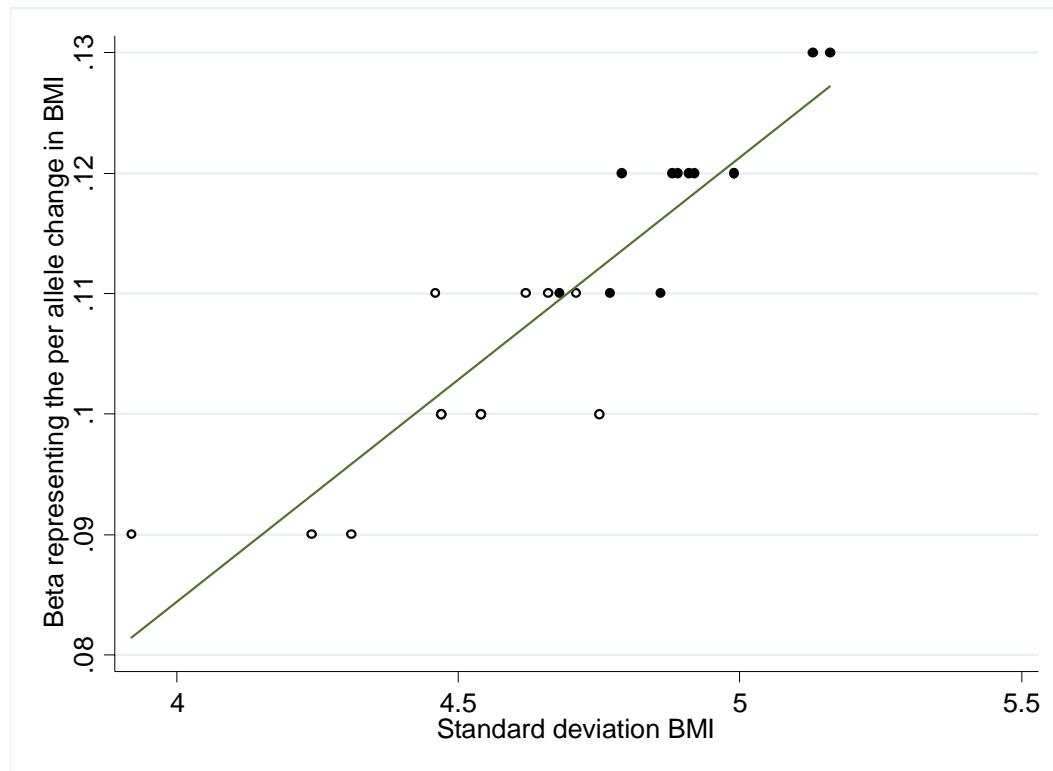




Supplementary figure 8: Forest plot demonstrating the change in BMI on its natural scale (kgm^{-2}), after correcting for age, sex and principle components per allele increase in BMI GRS for the different obesogenic environments.



Supplementary figure 9: Scatter graph representing the relationship between the beta values from the regression analyses for the BMI GRS and BMI and the standard deviation of BMI for the obesogenic variables. Empty circles represent the low risk obesogenic variables and the solid circles represent the high risk obesogenic variables. The line of best fit indicates reasonable correlation ($r^2=0.84$).



Supplementary Tables

Supplementary Table 1: Basic demographics of individuals included in the twelve obesogenic strata

Obesogenic category	Strata	N	Mean age at recruitment (SD)	Male N (%)
Fizzy drink	All	46,368	56.6 (7.8)	21,927 (47.1)
	None daily	39,975	56.8 (7.7)	18,327 (45.9)
	>1 glass daily	6,393	55.6 (8.0)	3,537 (55.3)
Fried food intake	All	46,368	56.6 (7.8)	21,864 (47.2)
	None daily	31,821	56.6 (7.8)	14,485 (45.5)
	>1 meal daily	14,547	56.7 (7.9)	7,379 (50.7)
Percentage fat	All	46,368	56.6 (7.8)	21,864 (47.2)
	Low risk	23,194	56.9 (7.7)	11,080 (47.8)
	High risk	23,174	56.4 (7.9)	10,784 (46.5)
Percentage protein	All	46,368	56.6 (7.8)	21,864 (47.2)
	Low risk	23,188	56.5 (7.8)	12,137 (52.3)
	High risk	23,180	56.7 (7.7)	9,727 (42.0)
Western diet	All	94,040	57.1 (7.9)	44,636 (47.5)
	Low risk	47,027	56.8 (8.0)	19,783 (42.1)
	High risk	47,013	57.3 (7.8)	24,853 (52.9)
IPAQ	All	109,142	56.9 (8.0)	52,328 (47.9)
	>1845 MET minutes per week	54,573	56.9 (8.1)	27,217 (49.9)
	<1845 MET minutes per week	54,569	56.9 (7.9)	25,111 (46.0)
Sedentary time	All	119,688	56.9 (7.9)	56,668 (47.4)
	<5 hours daily	63,343	56.4 (8.0)	25,281 (39.9)
	>5 hours daily	56,345	57.5 (7.8)	31,387 (55.7)
TV watching	All	118,836	56.9 (7.9)	56,362 (47.4)
	<4 hours daily	82,022	56.0 (8.0)	38,866 (47.4)
	>4 hours daily	36,814	59.0 (7.4)	17,496 (47.5)
Minutes vigorous per week	All	109,370	56.9 (8.0)	52,432 (47.9)
	>1 hour weekly	35,242	55.8 (8.2)	18,672 (53.0)
	≤1 hour weekly	74,128	57.4 (7.8)	33,760 (45.5)
Measured physical activity	All	19,268	56.6 (7.7)	8,815 (45.8)
	Low risk	9,632	55.0 (7.7)	4,038 (41.9)
	High risk	9,636	58.2 (7.4)	4,777 (49.6)
Socioeconomic position (TDI)	All	119,733	56.9 (7.9)	56,689 (47.4)
	High SEP TDI≤-2.294	59,872	57.4 (7.8)	
	Low SEP TDI>-2.294	59,861	56.5 (8.1)	
Sun protection use	All	119,068	56.9 (7.9)	56,384 (47.4)
	Usually or always use	68,507	56.6 (7.9)	25,641 (37.4)
	Never or sometimes use	50,561	57.4 (7.9)	30,743 (60.8)

All individuals are of white British descent with BMI and genetic data available (max n=119,688)

Supplementary table 2: Correlations between the ten obesogenic environment variables, Pearson correlation values are presented.

	TV watching	IPAQ	Minutes vigorous per week	Measured activity	Western diet	Percentage protein	Fizzy drink	Percentage fat	Fried food consumption	Socioeconomic position (TDI)	Sun protection
Sedentary time	0.64	-0.10	0.03	-0.15	0.12	0.01	0.08	0.03	0.07	0.05	-0.05
TV watching	-	-0.09	0.03	-0.15	0.09	0.04	0.05	0.03	0.06	0.12	-0.02
IPAQ	-	-	0.46	0.17	-0.01	-0.02	-0.01	-0.05	-0.02	NS	0.01
Minutes vigorous per week	-	-	-	0.07	NS	NS	0.01	-0.01	NS	0.04	-0.03
Measured activity	-	-	-	-	-0.07	-0.04	NS	-0.02	-0.02	-0.03	0.03
Western diet	-	-	-	-	-	0.14	0.03	0.05	0.09	-0.04	-0.04
Percentage protein	-	-	-	-	-	-	-0.10	-0.08	-0.12	-0.04	0.08
Fizzy drink	-	-	-	-	-	-	-	NS	0.08	0.03	-0.04
Percentage fat	-	-	-	-	-	-	-	-	0.14	0.03	-0.06
Fried food consumption	-	-	-	-	-	-	-	-	-	0.01	-0.04
Socioeconomic position (TDI)	-	-	-	-	-	-	-	-	-	-	-0.07

NS – association between the two obesogenic measures p>0.05.

Supplementary table 3: Associations between twelve continuous or ordinal obesogenic factors and a range of demographic factors.

Demographic	Regression coefficient (95% CI) representing change in obesogenic factor per unit change in demographic factor	P
Physical Activity Based on IPAQ		
Age	0.00 (-0.00, 0.00)	0.74
Male sex	0.10 (0.08, 0.11)	<1E-15
BMI	-0.04 (-0.04, -0.04)	<1E-15
SEP*	-0.00 (-0.01, 0.00)	0.28
Never smoking	0.00 (-0.01, 0.02)	0.7
Type 2 diabetes (BMI adjusted)	-0.17 (-0.21, -0.13)	4E-17
Sedentary time		
Age	0.005 (0.003, 0.006)	7E-08
Male sex	0.92 (0.90, 0.95)	<1E-15
Body mass index	0.11 (0.10, 0.11)	<1E-15
SEP*	0.04 (0.03, 0.04)	4E-63
Never smoking	-0.67 (-0.71, -0.62)	2E-197
Type 2 diabetes	0.86 (0.79, 0.93)	3E-114
Physical activity	-0.23 (-0.24, -0.22)	<1E-15
TV watching		
Age	0.043 (0.042, 0.045)	<1E-15
Male sex	0.017 (-0.004, 0.037)	0.11
Body mass index	0.076 (0.074, 0.078)	<1E-15
SEP*	0.082 (0.079, 0.086)	<1E-15
Never smoking	-0.77 (-0.81, -0.74)	<1E-15
Type 2 diabetes	0.73 (0.67, 0.78)	<1E-15
Physical activity	-0.13 (-0.14, -0.13)	<1E-15
Vigorous minutes per week		
Age	-1.2 (-1.3, -1.0)	<1E-15
Male sex	33.3 (31.2, 35.3)	<1E-15
Body mass index	-2.3 (-2.5, -2.1)	<1E-15
SEP*	0.29 (-0.06, 0.63)	0.11
Never smoking	6.2 (2.8, 9.6)	0.0004
Type 2 diabetes	-20.8 (-15.0, -26.7)	3E-12
Physical activity	70.7 (69.9, 71.5)	<1E-15
Measured physical activity		
Age	-137001 (-146819, -127183)	<1E-15
Male sex	-454455 (-606000, -302910)	4E-9
Body mass index	-248909 (-265111, -232707)	<1E-15
SEP*	-96115 (-123780, -68450)	1E-11
Never smoking	1590365 (1252624, 1928107)	<1E-15
Type 2 diabetes	-2579057 (-3071767, -2086348)	<1E-15
Physical activity	889837 (819458, 960217)	<1E-15
Western diet		

Age	0.01 (0.01, 0.01)	7E-71
Male sex	0.28 (0.27, 0.29)	<1E-15
Body mass index	0.02 (0.02, 0.03)	1E-301
SEP*	-0.01 (-0.02, -0.01)	5E-33
Never smoking	-0.10 (0.08, 0.12)	3E-19
Type 2 diabetes	0.15 (0.12, 0.19)	5E-18
Physical activity	-0.02 (-0.02, -0.01)	1E-07
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	Fizzy drink**	
Age	-0.02 (-0.03, -0.02)	3E-37
Male sex	0.41 (0.36, 0.46)	5E-52
Body mass index	0.03 (0.03, 0.04)	2E-34
SEP*	0.02 (0.01, 0.03)	5E-04
Never smoking	-0.21 (-0.31, -0.12)	9E-06
Type 2 diabetes	0.05 (-0.11, 0.21)	0.55
Physical activity	-0.04 (-0.06, -0.01)	0.003
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	Fried food**	
Age	0.00 (-0.00, 0.00)	0.28
Male sex	0.25 (0.21, 0.29)	2E-37
Body mass index	0.01 (0.01, 0.01)	4E-07
SEP*	0.00 (-0.01, 0.00)	0.29
Never smoking	0.11 (0.04, 0.18)	2E-03
Type 2 diabetes	0.05 (-0.07, 0.17)	0.41
Physical activity	-0.03 (-0.05, -0.01)	9E-04
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	Percentage fat	
Age	-0.001 (-0.001, -0.001)	1E-15
Male sex	-0.01 (-0.01, -0.00)	1E-04
Body mass index	0.002 (0.001, 0.002)	4E-17
SEP*	0.002 (0.001, 0.002)	8E-08
Never smoking	-0.03 (-0.04, -0.03)	2E-26
Type 2 diabetes	0.04 (0.03, 0.05)	1E-11
Physical activity	-0.01 (-0.01, -0.01)	5E-22
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	Percentage protein	
Age	0.0003 (0.0001, 0.0005)	0.01
Male sex	-0.05 (-0.05, -0.05)	2E-133
Body mass index	0.01 (0.01, 0.01)	5E-118
SEP*	-0.003 (-0.004, -0.002)	7E-14
Never smoking	0.03 (0.03, 0.04)	4E-18
Type 2 diabetes	0.05 (0.04, 0.06)	1E-15
Physical activity	-0.003 (-0.005, -0.001)	0.003
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	Composite Score	
Age	0.018 (0.017, 0.019)	<1E-15
Male sex	0.130 (0.117, 0.143)	<1E-15
Body mass index	0.060 (0.059, 0.061)	<1E-15
SEP*	0.024 (0.022, 0.027)	<1E-15
Never smoking	-0.192 (-0.205, -0.178)	6E-173
Type 2 diabetes	0.506 (0.469, 0.542)	2E-158
Physical activity	-0.448 (-0.453, -0.443)	<1E-15
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	Townsend deprivation index	

Age	-0.024 (-0.026, -0.022)	<1E-15
Male sex	0.071 (0.037, 0.105)	4E-5
Body mass index	0.057 (0.053, 0.060)	<1E-15
Never smoking	-2.00 (-2.05, -1.95)	<1E-15
Type 2 diabetes	0.79 (0.69, 0.88)	<1E-15
Physical activity	-0.008 (-0.024, 0.007)	0.28
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Sun protection use**		
Age	-0.008 (-0.009, -0.006)	<1E-15
Male sex	-0.96 (-0.99, -0.94)	<1E-15
Body mass index	-0.009 (-0.011, -0.007)	8E-15
SEP*	-0.044 (-0.047, -0.040)	<1E-15
Never smoking	0.50 (0.47, 0.54)	<1E-15
Type 2 diabetes	-0.21 (-0.27, -0.15)	5E-12
Physical activity	0.038 (0.029, 0.048)	8E-15

All models adjusted for age and sex

* Socioeconomic position (SEP) is defined by the Townsend deprivation index

** Associations were investigated using ordinal regression due to the distribution of the dependent variable.

Supplementary table 4: Summary of genetic variants previously identified as associated with BMI at genome wide significance

Trait	SNP	Locus	Exclude from score	Reason for exclusion	Trait raising allele	Trait lowering allele	Directly genotyped or Imputed	Imputation quality	Beta representing SD change in BMI for each SNP in UK Biobank data	P value
BMI	rs1000940	<i>RABEP1</i>	No	NA	G	A	Imputed	0.99624	0.011 (0.004)	0.016
BMI	rs10132280	<i>STXBP6</i>	No	NA	C	A	Imputed	0.97496	0.020 (0.005)	1x10 ⁻⁵
BMI	rs1016287	<i>FLJ30838</i>	No	NA	T	C	Imputed	0.99411	0.019 (0.004)	2x10 ⁻⁵
BMI	rs10182181	<i>ADCY3</i>	No	NA	G	A	Imputed	0.99521	0.033 (0.004)	1x10 ⁻¹⁵
BMI	rs10733682	<i>LMX1B</i>	No	NA	A	G	Imputed	0.9576	0.019 (0.004)	6x10 ⁻⁶
BMI	rs10938397	<i>GNPDA2</i>	No	NA	G	A	Imputed	1	0.030 (0.004)	6x10 ⁻¹³
BMI	rs10968576	<i>LINGO2</i>	No	NA	G	A	Imputed	1	0.024 (0.004)	7x10 ⁻⁸
BMI	rs11030104	<i>BDNF</i>	Yes	BMI-raising allele also associated with regular smoking (which itself has a causal effect on BMI in opposite direction)	A	G	Imputed	0.99931	NA	NA
BMI	rs11057405	<i>CLIP1</i>	No	NA	G	A	Imputed	1	0.030 (0.007)	5x10 ⁻⁶
BMI	rs11126666	<i>KCNK3</i>	No	NA	A	G	Imputed	0.99485	0.002 (0.005)	0.71
BMI	rs11165643	<i>PTBP2</i>	No	NA	T	C	Imputed	0.99575	0.016 (0.004)	1x10 ⁻⁴
BMI	rs11191560	<i>NT5C2</i>	No	NA	C	T	Imputed	0.99989	0.026 (0.008)	7x10 ⁻⁴
BMI	rs11583200	<i>ELAVL4</i>	No	NA	C	T	Imputed	0.98728	0.019 (0.004)	8x10 ⁻⁶
BMI	rs1167827	<i>HIP1</i>	No	NA	G	A	Imputed	1	0.020 (0.004)	2x10 ⁻⁶
BMI	rs11688816	<i>EHBP1</i>	No	NA	G	A	Imputed	0.98096	0.014 (0.004)	9x10 ⁻⁴
BMI	rs11727676	<i>HHIP</i>	No	NA	T	C	Imputed	1	-0.003 (0.007)	0.66
BMI	rs11847697	<i>PRKD1</i>	No	NA	T	C	Imputed	1	0.014 (0.010)	0.17
BMI	rs12286929	<i>CADM1</i>	No	NA	G	A	Imputed	0.99124	0.010 (0.004)	0.012
BMI	rs12401738	<i>FUBP1</i>	No	NA	A	G	Imputed	0.99528	0.012 (0.004)	0.003
BMI	rs12429545	<i>OLFM4</i>	No	NA	A	G	Imputed	0.97759	0.027 (0.006)	8x10 ⁻⁶
BMI	rs12446632	<i>GPRC5B</i>	No	NA	G	A	Imputed	0.99978	0.028 (0.006)	2x10 ⁻⁶
BMI	rs12566985	<i>FPGT-TNNI3K</i>	No	NA	G	A	Imputed	0.9947	0.011 (0.004)	0.006
BMI	rs12885454	<i>PRKD1</i>	No	NA	C	A	Imputed	0.99569	0.015 (0.004)	5x10 ⁻⁴
BMI	rs12940622	<i>RPTOR</i>	No	NA	G	A	Imputed	0.99796	0.017 (0.004)	6x10 ⁻⁵
BMI	rs13021737	<i>TMEM18</i>	No	NA	G	A	Imputed	0.99072	0.059 (0.005)	9x10 ⁻²⁷

BMI	rs13078960	<i>CADM2</i>	No	NA	G	T	Imputed	0.9915	0.024 (0.005)	3x10 ⁻⁶
BMI	rs13107325	<i>SLC39A8</i>	Yes	Missense Ala/Thr polymorphism located in exon 7 of <i>SLC39A8</i> , which encodes a zinc transporter that also transports cadmium and manganese. It is also associated with BP and HDL levels, and presumably these and the BMI effect are secondary to the metal ion transport variation.	T	C	Imputed	1	NA	NA
BMI	rs13191362	<i>PARK2</i>	No	NA	A	G	Imputed	0.98973	0.026 (0.006)	3x10 ⁻⁵
BMI	rs1516725	<i>ETV5</i>	No	NA	C	T	Imputed	0.99495	0.032 (0.006)	1x10 ⁻⁷
BMI	rs1528435	<i>UBE2E3</i>	No	NA	T	C	Imputed	0.99738	0.014 (0.004)	7x10 ⁻⁴
BMI	rs1558902	<i>FTO</i>	No	NA	A	T	Imputed	0.99914	0.077 (0.004)	2x10 ⁻⁷⁵
BMI	rs16851483	<i>RASA2</i>	No	NA	T	G	Imputed	0.99906	0.028 (0.008)	7x10 ⁻⁴
BMI	rs16951275	<i>MAP2K5</i>	No	NA	T	C	Imputed	0.99819	0.032 (0.005)	4x10 ⁻¹¹
BMI	rs17001654	<i>SCARB2</i>	Yes	SNP not in HWE	G	C	Imputed	0.9483	NA	NA
BMI	rs17024393	<i>GNAT2</i>	No	NA	C	T	Imputed	0.98934	0.074 (0.013)	1x10 ⁻⁸
BMI	rs17094222	<i>HIF1AN</i>	No	NA	C	T	Imputed	0.96874	0.013 (0.005)	0.009
BMI	rs17405819	<i>HNF4G</i>	No	NA	T	C	Imputed	0.99793	0.014 (0.004)	0.001
BMI	rs17724992	<i>PGPEP1</i>	No	NA	A	G	Imputed	0.98342	0.023 (0.005)	1x10 ⁻⁶
BMI	rs1808579	<i>C18orf8</i>	No	NA	C	T	Imputed	0.99797	0.022 (0.004)	2x10 ⁻⁷
BMI	rs1928295	<i>TLR4</i>	No	NA	T	C	Imputed	0.99998	0.010 (0.004)	0.016
BMI	rs2033529	<i>TDRG1</i>	Yes	SNP not available	G	A	NA	NA	NA	NA
BMI	rs2033732	<i>RALYL</i>	No	NA	C	T	Imputed	1	0.002 (0.005)	0.67
BMI	rs205262	<i>C6orf106</i>	No	NA	G	A	Imputed	0.9968	0.028 (0.005)	1x10 ⁻⁹
BMI	rs2075650	<i>TOMM40</i>	Yes	SNP not in HWE	A	G	Imputed	0.9865	NA	NA
BMI	rs2112347	<i>POC5</i>	No	NA	T	G	Imputed	1	0.026 (0.004)	6x10 ⁻¹⁰
BMI	rs2121279	<i>LRP1B</i>	No	NA	T	C	Imputed	0.98723	0.006 (0.006)	0.37
BMI	rs2176598	<i>HSD17B12</i>	No	NA	T	C	Imputed	1	0.023 (0.005)	1x10 ⁻⁶
BMI	rs2207139	<i>TFAP2B</i>	No	NA	G	A	Imputed	0.9989	0.038 (0.005)	2x10 ⁻¹²
BMI	rs2245368	<i>PMS2L11</i>	No	NA	C	T	Imputed	1	0.022 (0.005)	8x10 ⁻⁵
BMI	rs2287019	<i>QPCTL</i>	No	NA	C	T	Imputed	0.97852	0.035 (0.005)	1x10 ⁻¹⁰

BMI	rs2365389	<i>FHIT</i>	No	NA	C	T	Imputed	0.99305	0.029 (0.004)	3x10 ⁻¹²
BMI	rs2650492	<i>SBK1</i>	No	NA	A	G	Imputed	0.98144	0.019 (0.005)	4x10 ⁻⁵
BMI	rs2820292	<i>NAV1</i>	No	NA	C	A	Imputed	1	0.019 (0.004)	4x10 ⁻⁶
BMI	rs29941	<i>KCTD15</i>	No	NA	G	A	Imputed	1	0.018 (0.004)	5x10 ⁻⁵
BMI	rs3101336	<i>NEGR1</i>	No	NA	C	T	Imputed	1	0.027 (0.004)	1x10 ⁻¹⁰
BMI	rs3736485	<i>DMXL2</i>	No	NA	A	G	Imputed	0.98728	0.011 (0.004)	0.006
BMI	rs3810291	<i>ZC3H4</i>	No	NA	A	G	Imputed	1	0.028 (0.004)	2x10 ⁻¹⁰
BMI	rs3817334	<i>MTCH2</i>	No	NA	T	C	Imputed	1	0.031 (0.004)	1x10 ⁻¹³
BMI	rs3849570	<i>GBE1</i>	No	NA	A	C	Imputed	0.99509	0.011 (0.004)	0.008
BMI	rs3888190	<i>ATP2A1</i>	Yes	Associated with lots of other traits and is a big haplotype	A	C	Imputed	0.99808	NA	NA
BMI	rs4256980	<i>TRIM66</i>	No	NA	G	C	Imputed	0.99283	0.021 (0.004)	2x10 ⁻⁶
BMI	rs4740619	<i>C9orf93</i>	No	NA	T	C	Imputed	0.99762	0.017 (0.004)	6x10 ⁻⁵
BMI	rs543874	<i>SEC16B</i>	No	NA	G	A	Imputed	1	0.049 (0.005)	3x10 ⁻²²
BMI	rs6477694	<i>EPB41L4B</i>	No	NA	C	T	Imputed	0.99022	0.008 (0.004)	0.07
BMI	rs6567160	<i>MC4R</i>	No	NA	C	T	Imputed	0.99663	0.054 (0.005)	1x10 ⁻²⁸
BMI	rs657452	<i>AGBL4</i>	No	NA	A	G	Imputed	0.98709	0.014 (0.004)	8x10 ⁻⁴
BMI	rs6804842	<i>RARB</i>	No	NA	G	A	Imputed	0.98778	0.009 (0.004)	0.032
BMI	rs7138803	<i>BCDIN3D</i>	No	NA	A	G	Imputed	1	0.034 (0.004)	1x10 ⁻¹⁵
BMI	rs7141420	<i>NRXN3</i>	No	NA	T	C	Imputed	0.98379	0.019 (0.004)	7x10 ⁻⁶
BMI	rs7243357	<i>GRP</i>	No	NA	T	G	Imputed	0.98998	0.012 (0.005)	0.021
BMI	rs758747	<i>NLRC3</i>	No	NA	T	C	Imputed	0.97187	0.014 (0.005)	0.002
BMI	rs7599312	<i>ERBB4</i>	No	NA	G	A	Imputed	0.97294	0.019 (0.005)	4x10 ⁻⁵
BMI	rs7899106	<i>GRID1</i>	No	NA	G	A	Imputed	0.98612	0.023 (0.009)	0.014
BMI	rs9400239	<i>FOXO3</i>	No	NA	C	T	Imputed	0.99206	0.017 (0.005)	2x10 ⁻⁴
BMI	rs9581854	<i>MTIF3</i>	No	NA	T	C	Imputed	0.98643	0.015 (0.005)	0.006
BMI	rs9925964	<i>KAT8</i>	Yes	SNP not in HWE	A	G	Imputed	1	NA	NA

Supplementary table 5: Association between the various obesogenic measures and the BMI genetic risk score

Obesogenic factor	N	Beta (95%) representing an SD change in obesogenic factor per allele increase in the BMI	P
		weighted allele score	
Sedentary time	119688	0.002 (0.001, 0.003)	0.004
TV watching	118836	0.002 (0.001, 0.003)	1x10 ⁻⁵
IPAQ	109142	-0.0001 (-0.001, 0.001)	0.85
Minutes of vigorous activity	109370	0.001 (0.000, 0.002)	0.044
Total activity	19268	-0.004 (-0.007, -0.001)	0.005
Western diet	94040	-0.001 (-0.002, 0.000)	0.21
Percentage protein	46368	0.005 (0.004, 0.007)	5x10 ⁻¹⁰
Fizzy drink	46368	-0.005 (-0.010, -0.000)	0.04
Percentage fat	46368	0.000 (-0.000, 0.001)	0.16
Fried food consumption	46368	-0.002 (-0.003, -0.001)	0.002
Composite score	86549	0.002 (0.001, 0.003)	0.006
SEP (TDI)	119,733	0.001 (0.000, 0.002)	0.022
Sun protection	119,068	-0.0006 (-0.0016, 0.0004)	0.23

Supplementary Table 6: Differences in BMI by BMI genetic risk score decile (kgm^2) and by allele (inverse normalised scale) for a) Townsend deprivation index split at the median and b) Townsend deprivation index split at the approximate UK average deprivation value. Interaction p-values are calculated using the binary TDI variable for both to enable comparison.

Trait	Obesogenic category	N	BMI (SD)	BMI difference in 10% lowest genetic risk	BMI difference in 10% highest genetic risk	Per-allele Beta	SE	P association	P interaction*	P Interaction Robust**
Townsend Deprivation Index (natural scale)	High SES TDI \leq -2.294	59,872	27.20 (4.47)			0.022	0.001	$<1\times10^{-15}$	4×10^{-6}	5×10^{-6}
	Low SES TDI $>$ -2.294	59,861	27.87 (5.13)	+0.35 kgm^{-2}	+0.92 kgm^{-2}	0.025	0.001	$<1\times10^{-15}$		
Townsend Deprivation Index (natural scale)	High SES	84,526	27.30 (4.56)			0.022	0.001	$<1\times10^{-15}$	9×10^{-9}	6×10^{-8}
	Low SES	35,357	28.11 (5.37)	+0.42 kgm^{-2}	+1.06 kgm^{-2}	0.027	0.001	$<1\times10^{-15}$		

Supplementary Table 7: BMI genetic risk score association with BMI for different age groups in the UK Biobank. The interaction effect was then investigated for TDI in the three age groups and the P values for normal and robust models are presented.

Age group	N	Beta for BMI GRS against BMI	SE	P	Variance explained (%)	TDI Pinteraction	TDI Pinteraction robust
40-49	25658	0.028	0.001	<1x10 ⁻¹⁵	2	9x10 ⁻⁵	3x10 ⁻⁴
50-59	40131	0.025	0.001	<1x10 ⁻¹⁵	1.7	3x10 ⁻⁵	1x10 ⁻⁴
60-73	53944	0.020	0.0008	<1x10 ⁻¹⁵	1.2	6x10 ⁻⁴	0.001

Supplementary table 8: Individual SNP associations with BMI in high and low Townsend deprivation index groups

SNP	Obesogenic category	Beta	SE	P association	P interaction	P interaction robust
rs1000940	Low SES	0.001	0.006	0.90	0.10	0.13
	High SES	0.020	0.006	0.002		
rs10132280	Low SES	0.020	0.006	0.002	0.30	0.33
	High SES	0.021	0.006	8x10 ⁻⁴		
rs1016287	Low SES	0.007	0.006	0.30	9x10 ⁻⁴	0.002
	High SES	0.031	0.006	1x10 ⁻⁶		
rs10182181	Low SES	0.035	0.006	2x10 ⁻⁹	0.50	0.53
	High SES	0.032	0.006	3x10 ⁻⁸		
rs10733682	Low SES	0.021	0.006	4x10 ⁻⁴	0.99	0.99
	High SES	0.017	0.006	0.004		
rs10938397	Low SES	0.024	0.006	4x10 ⁻⁵	0.013	0.02
	High SES	0.037	0.006	4x10 ⁻¹⁰		
rs10968576	Low SES	0.024	0.006	1x10 ⁻⁴	0.49	0.51
	High SES	0.024	0.006	1x10 ⁻⁴		
rs11057405	Low SES	0.031	0.009	8x10 ⁻⁴	0.61	0.63
	High SES	0.030	0.009	0.001		
rs11126666	Low SES	0.001	0.007	0.93	0.89	0.90
	High SES	0.004	0.007	0.53		
rs11165643	Low SES	0.017	0.006	0.003	0.47	0.49
	High SES	0.014	0.006	0.014		
rs11191560	Low SES	0.037	0.011	6x10 ⁻⁴	0.49	0.71
	High SES	0.019	0.011	0.08		
rs11583200	Low SES	0.020	0.006	0.001	0.54	0.56
	High SES	0.017	0.006	0.005		
rs1167827	Low SES	0.019	0.006	0.001	0.93	0.94
	High SES	0.019	0.006	9x10 ⁻⁴		
rs11688816	Low SES	0.019	0.006	0.001	0.59	0.61
	High SES	0.009	0.006	0.13		
rs11727676	Low SES	0.001	0.010	0.95	0.50	0.52
	High SES	-0.008	0.010	0.41		
rs11847697	Low SES	0.007	0.014	0.61	0.25	0.28
	High SES	0.019	0.014	0.17		
rs12286929	Low SES	0.011	0.006	0.07	0.94	0.95
	High SES	0.010	0.006	0.10		
rs12401738	Low SES	0.008	0.006	0.15	0.46	0.49
	High SES	0.015	0.006	0.011		
rs12429545	Low SES	0.029	0.009	9x10 ⁻⁴	0.27	0.30
	High SES	0.028	0.009	0.001		
rs12446632	Low SES	0.029	0.008	5x10 ⁻⁴	0.45	0.48
	High SES	0.027	0.008	0.001		
rs12566985	Low SES	0.012	0.006	0.044	0.21	0.24
	High SES	0.010	0.006	0.08		
rs12885454	Low SES	0.017	0.006	0.004	0.33	0.35

	High SES	0.014	0.006	0.017		
rs12940622	Low SES	0.021	0.006	3×10^{-4}	0.72	0.74
	High SES	0.013	0.006	0.024		
rs13021737	Low SES	0.049	0.008	1×10^{-10}	0.20	0.23
	High SES	0.067	0.008	6×10^{-18}		
rs13078960	Low SES	0.025	0.007	4×10^{-4}	0.99	0.99
	High SES	0.024	0.007	0.001		
rs13191362	Low SES	0.026	0.009	0.003	0.39	0.43
	High SES	0.023	0.009	0.008		
rs1516725	Low SES	0.034	0.008	5×10^{-5}	0.67	0.69
	High SES	0.029	0.008	7×10^{-4}		
rs1528435	Low SES	0.014	0.006	0.023	0.29	0.32
	High SES	0.014	0.006	0.015		
rs1558902	Low SES	0.072	0.006	5×10^{-34}	0.006	0.010
	High SES	0.081	0.006	3×10^{-43}		
rs16851483	Low SES	0.010	0.012	0.38	0.22	0.26
	High SES	0.045	0.012	1×10^{-4}		
rs16951275	Low SES	0.036	0.007	1×10^{-7}	0.23	0.26
	High SES	0.028	0.007	6×10^{-5}		
rs17024393	Low SES	0.055	0.018	0.003	0.091	0.11
	High SES	0.091	0.018	6×10^{-7}		
rs17094222	Low SES	0.012	0.007	0.09	0.25	0.29
	High SES	0.014	0.007	0.05		
rs17405819	Low SES	0.013	0.006	0.046	0.47	0.50
	High SES	0.018	0.006	0.05		
rs17724992	Low SES	0.017	0.007	0.011	0.68	0.70
	High SES	0.027	0.007	5×10^{-5}		
rs1808579	Low SES	0.019	0.006	9×10^{-4}	0.21	0.24
	High SES	0.023	0.006	9×10^{-5}		
rs1928295	Low SES	0.001	0.006	0.83	0.24	0.27
	High SES	0.018	0.006	0.002		
rs2033732	Low SES	0.011	0.007	0.11	0.07	0.09
	High SES	-0.006	0.007	0.33		
rs205262	Low SES	0.031	0.007	3×10^{-6}	0.76	0.77
	High SES	0.025	0.007	1×10^{-4}		
rs2112347	Low SES	0.029	0.006	2×10^{-6}	0.54	0.57
	High SES	0.024	0.006	7×10^{-5}		
rs2121279	Low SES	0.009	0.009	0.33	0.50	0.53
	High SES	0.004	0.009	0.67		
rs2176598	Low SES	0.016	0.007	0.018	0.30	0.33
	High SES	0.028	0.007	2×10^{-5}		
rs2207139	Low SES	0.037	0.008	2×10^{-6}	0.38	0.41
	High SES	0.042	0.008	5×10^{-8}		
rs2245368	Low SES	0.028	0.008	3×10^{-4}	0.57	0.60
	High SES	0.016	0.008	0.046		
rs2287019	Low SES	0.028	0.008	2×10^{-4}	0.29	0.32
	High SES	0.041	0.008	5×10^{-8}		
rs2365389	Low SES	0.035	0.006	2×10^{-9}	0.94	0.95

	High SES	0.024	0.006	4x10 ⁻⁵		
rs2650492	Low SES	0.020	0.006	0.002	0.97	0.97
	High SES	0.019	0.006	0.004		
rs2820292	Low SES	0.021	0.006	4x10 ⁻⁴	0.73	0.75
	High SES	0.019	0.006	0.001		
rs29941	Low SES	0.007	0.006	0.22	0.049	0.06
	High SES	0.026	0.006	2x10 ⁻⁵		
rs3101336	Low SES	0.023	0.006	1x10 ⁻⁴	0.045	0.06
	High SES	0.031	0.006	1x10 ⁻⁷		
rs3736485	Low SES	0.014	0.006	0.014	0.08	0.10
	High SES	0.008	0.006	0.18		
rs3810291	Low SES	0.026	0.006	3x10 ⁻⁵	0.047	0.06
	High SES	0.029	0.006	2x10 ⁻⁶		
rs3817334	Low SES	0.027	0.006	3x10 ⁻⁶	0.040	0.06
	High SES	0.034	0.006	8x10 ⁻⁹		
rs3849570	Low SES	0.004	0.006	0.50	0.32	0.35
	High SES	0.016	0.006	0.009		
rs4256980	Low SES	0.017	0.006	0.006	0.20	0.23
	High SES	0.024	0.006	6x10 ⁻⁵		
rs4740619	Low SES	0.016	0.006	0.007	0.81	0.82
	High SES	0.016	0.006	0.007		
rs543874	Low SES	0.040	0.007	2x10 ⁻⁸	0.008	0.013
	High SES	0.056	0.007	4x10 ⁻¹⁵		
rs6477694	Low SES	0.000	0.006	0.99	0.042	0.06
	High SES	0.014	0.006	0.023		
rs6567160	Low SES	0.046	0.007	2x10 ⁻¹¹	0.003	0.005
	High SES	0.060	0.007	1x10 ⁻¹⁸		
rs657452	Low SES	0.017	0.006	0.005	0.79	0.80
	High SES	0.012	0.006	0.048		
rs6804842	Low SES	0.008	0.006	0.16	0.77	0.78
	High SES	0.010	0.006	0.08		
rs7138803	Low SES	0.037	0.006	5x10 ⁻¹⁰	0.85	0.86
	High SES	0.030	0.006	4x10 ⁻⁷		
rs7141420	Low SES	0.023	0.006	9x10 ⁻⁵	0.34	0.37
	High SES	0.014	0.006	0.019		
rs7243357	Low SES	0.023	0.008	0.002	0.16	0.19
	High SES	0.004	0.008	0.59		
rs758747	Low SES	0.007	0.007	0.27	0.62	0.64
	High SES	0.021	0.007	0.001		
rs7599312	Low SES	0.015	0.007	0.025	0.49	0.52
	High SES	0.024	0.007	3x10 ⁻⁴		
rs7899106	Low SES	0.033	0.013	0.014	0.87	0.88
	High SES	0.015	0.013	0.27		
rs9400239	Low SES	0.015	0.006	0.020	0.51	0.53
	High SES	0.019	0.006	0.003		
rs9581854	Low SES	0.012	0.007	0.10	0.08	0.10
	High SES	0.016	0.008	0.029		

Supplementary table 9: Differences in BMI by allele (inverse normalised scale) for TDI in the CoLaus Study, occupational status in the 1958 Birth Cohort and the UK Biobank and educational years in the UK Biobank

Study	Obesogenic category	N	BMI (SD)	Per-allele Beta	SE	P association	P interaction*	P Interaction Robust**
CoLaus	High SES based on TDI	2,623	25.53 (4.33)	0.030	0.004	6×10^{-15}	0.35	0.34
	Low SES based on TDI	2,614	26.18 (4.78)	0.022	0.004	1×10^{-8}		
UK Biobank	High job class	38,942	27.15 (4.57)	0.025	0.001	$<1 \times 10^{-15}$	0.78	0.79
	Low job class	37,374	27.68 (4.89)	0.024	0.001	$<1 \times 10^{-15}$		
1958 Birth Cohort	High job class	2,873	27.17 (4.55)	0.026	0.003	2×10^{-14}	0.62	0.62
	Low job class	3,298	27.55 (5.10)	0.024	0.003	1×10^{-12}		
UK Biobank	High educational years (19-20)	55,203	27.15 (4.67)	0.024	0.001	$<1 \times 10^{-15}$	0.76	0.76
	Low educational years (<=15)	63,572	27.86 (4.93)	0.023	0.001	$<1 \times 10^{-15}$		

BMI adjusted for age, sex, ancestral principal components and assessment centre location. Models additionally adjusted for genotyping platform

* Interaction p-value

** Interaction p-value accounting for heteroscedasticity using robust standard errors

Supplementary table 10: Change in BMI (single inverse normal scale) per allele increase in the BMI GRS when the obesogenic environments were dichotomised at approximately 25% low risk, 75% high risk.

Trait	Obesogenic category	N	Beta	SE	P association	P interaction*
Percentage fat	Low risk	11592	0.024	0.002	<1x10 ⁻¹⁵	0.93
	High risk	34776	0.023	0.001	<1x10 ⁻¹⁵	
Percentage protein	Low risk	11591	0.022	0.002	<1x10 ⁻¹⁵	0.68
	High risk	34777	0.023	0.001	<1x10 ⁻¹⁵	
Western diet	Low risk	23510	0.021	0.001	<1x10 ⁻¹⁵	0.029
	High risk	70530	0.025	0.001	<1x10 ⁻¹⁵	
IPAQ	Low risk	27298	0.022	0.001	<1x10 ⁻¹⁵	0.08
	High risk	81844	0.023	0.001	<1x10 ⁻¹⁵	
Sedentary time	Low risk	30520	0.023	0.001	<1x10 ⁻¹⁵	0.40
	High risk	89168	0.024	0.001	<1x10 ⁻¹⁵	
TV	Low risk	53537	0.022	0.001	<1x10 ⁻¹⁵	0.007
	High risk	65299	0.025	0.001	<1x10 ⁻¹⁵	
Vigorous activity	Low risk	21676	0.021	0.001	<1x10 ⁻¹⁵	0.003
	High risk	87511	0.024	0.001	<1x10 ⁻¹⁵	
TDI	Low risk	29,946	0.022	0.001	<1x10 ⁻¹⁵	4x10⁻⁴
	High risk	89,787	0.024	0.001	<1x10 ⁻¹⁵	

* Interaction P-value calculated using the BMI GRS * dichotomous variable. Presented p-values were calculated with robust standard errors

Supplementary table 11: Change in BMI per allele increase in the BMI genetic risk score in individuals adjusted for smoking status (never, former and current) and the other obesogens that demonstrated significant interactions.

Trait	Obesogenic category	N	Beta (SE)	P association	P interaction robust (P interaction robust*)
IPAQ	>1845 MET minutes per week	53,822	0.022 (0.001)	<1x10 ⁻¹⁵	2x10 ⁻⁵
	≤1845 MET minutes per week	53,768	0.025 (0.001)	<1x10 ⁻¹⁵	(0.014)
TV watching	<4 hours daily	80,837	0.022 (0.001)	<1x10 ⁻¹⁵	0.026
	≥4 hours daily	36,243	0.026 (0.001)	<1x10 ⁻¹⁵	(0.94)
Composite score*	Low risk	42,738	0.022 (0.001)	<1x10 ⁻¹⁵	1x10 ⁻⁴
	High risk	42,666	0.025 (0.001)	<1x10 ⁻¹⁵	(0.51)
TDI	High SEP TDI≤-2.294	59,872	0.022 (0.001)	<1x10 ⁻¹⁵	4x10 ⁻⁷
	Low SEP TDI>-2.294	59,861	0.025 (0.001)	<1x10 ⁻¹⁵	(3x10 ⁻⁶)
Sun protection use	Usually or always use	68,507	0.022 (0.001)	<1x10 ⁻¹⁵	8x10 ⁻⁴
	Never or sometimes use	50,561	0.025 (0.001)	<1x10 ⁻¹⁵	(0.005)

BMI adjusted for age, sex, ancestral principal components and assessment centre location. Models additionally adjusted for genotyping platform, smoking status and the obesogens demonstrating significant interaction with BMI genetics (e.g. for TDI it is adjusted for IPAQ, TV watching and the composite score).

*P-value for interaction including adjustment for interaction terms for the other obesogens and smoking status.

Supplementary table 12: Change in BMI (natural scale kg/m²) per allele increase in the BMI genetic risk score

Trait	Obesogenic category	N	Beta	SE	P association	P interaction	P Interaction Robust*
Fizzy drink	None daily	39975	0.11	0.004	<1x10 ⁻¹⁵	0.28	0.34
	≥1 glass daily	6393	0.12	0.011	<1x10 ⁻¹⁵		
Fried food consumption	None daily	31821	0.11	0.005	<1x10 ⁻¹⁵	0.63	0.65
	≥1 meal daily	14547	0.11	0.007	<1x10 ⁻¹⁵		
Percentage fat^	Low risk	23194	0.11	0.005	<1x10 ⁻¹⁵	0.33	0.36
	High risk	23174	0.11	0.006	<1x10 ⁻¹⁵		
Percentage protein^	Low risk	23188	0.10	0.006	<1x10 ⁻¹⁵	0.50	0.55
	High risk	23180	0.11	0.006	<1x10 ⁻¹⁵		
Western diet^	Low risk	47027	0.11	0.004	<1x10 ⁻¹⁵	0.006	0.008
	High risk	47013	0.12	0.004	<1x10 ⁻¹⁵		
IPAQ	>1845 MET minutes per week	54573	0.09	0.003	<1x10 ⁻¹⁵	5x10⁻¹³	9x10⁻¹¹
	≤1845 MET minutes per week	54569	0.12	0.004	<1x10 ⁻¹⁵		
Sedentary time	<5 hours daily	63343	0.10	0.003	<1x10 ⁻¹⁵	2x10⁻⁶	2x10⁻⁵
	≥5 hours daily	56345	0.12	0.004	<1x10 ⁻¹⁵		
TV watching	<4 hours daily	82022	0.10	0.003	<1x10 ⁻¹⁵	3x10⁻¹²	8x10⁻¹⁰
	≥4 hours daily	36814	0.13	0.005	<1x10 ⁻¹⁵		
Vigorous activity	>1 hour weekly	35183	0.09	0.004	<1x10 ⁻¹⁵	0.13	0.20
	≤1 hour weekly	74004	0.12	0.003	<1x10 ⁻¹⁵		
Measured physical activity*	Low risk	9,632	0.09	0.007	<1x10 ⁻¹⁵	6x10⁻⁶	0.049
	High risk	9,636	0.12	0.009	<1x10 ⁻¹⁵		
Townsend Derivation Index	High SES TDI≤-2.295	59,872	0.10	0.003	<1x10 ⁻¹⁵	5x10⁻¹⁷	7x10⁻¹⁴
	Low SES TDI>-2.295	59,861	0.13	0.004	<1x10 ⁻¹⁵		
Sun protection use	Usually or always use	68,507	0.10	0.003	<1x10 ⁻¹⁵	2x10⁻⁴	4x10⁻⁴
	Never or sometimes use	50,561	0.12	0.004	<1x10 ⁻¹⁵		

Residuals were taken of BMI adjusted for age, sex, ancestry principal components and centre location. The models were further adjusted for genotyping platform at runtime.

*P-value for interaction term using robust standard errors in the regression model.

^ Data were split on the basis of an arbitrary median value

References

- 1 Bowden, J., Davey Smith, G. & Burgess, S. Mendelian randomization with invalid instruments: effect estimation and bias detection through Egger regression. *International journal of epidemiology* **44**, 512-525, doi:10.1093/ije/dyv080 (2015).
- 2 Locke, A. E. *et al.* Genetic studies of body mass index yield new insights for obesity biology. *Nature* **518**, 197-206, doi:10.1038/nature14177 (2015).