

Supplementary Material 1: MZ discordant analysis

Twin pairs were analysed to establish the difference between their visceral fat levels. The standard deviation of visceral fat for all participants was determined to be 1382g. Twin pairs that differed in visceral fat levels by more than 1382 (1sd) were considered to be discordant. This identified 48 twin pairs that were discordant with whole blood methylation profiles and 7 twin pairs that were discordant with adipose tissue methylation profiles. Methylation profiles were normalised and a pair wise t-test was then carried out on the methylation levels between the high visceral fat twin and the low visceral fat twin to identify CpG sites that were differentially methylated.

Discordant twin pair results

Despite the small sample size, 10 CpG sites in 9 genes were differentially methylated at FDR <0.05 (Table 1), one of these cg03498175 (*ACSL1*) was identified in the main analysis. This gene also contains SNPs previously associated with Type 2 Diabetes in GWAS. The remaining genes fell into three categories, relating to mental health – that may potentially contribute towards adiposity development, relating to cell proliferation – potentially arising because of adiposity, and relating to cancer.

CpG	P value	Estimate	FDR	Gene	Category
cg16361867	3.92E-08	1.24	0.009	<i>GRIK4</i>	Mental Health
cg16001422	4.09E-08	-1.02	0.009	<i>PLEC1</i>	Cell Proliferation
cg07491702	2.16E-07	-1.00	0.0318	<i>CDAN1</i>	Mental Health
cg10617782	4.11E-07	-1.29	0.0323	<i>Chr7</i>	
cg23654821	4.44E-07	-1.35	0.0323	<i>CSRNP1</i>	Cancer
cg14962774	5.20E-07	-1.40	0.0323	<i>GDAP2;WDR3</i>	Cancer
cg25590444	6.30E-07	1.35	0.0323	<i>Chr1</i>	

cg04576707	6.70E-07		0.0323	<i>MOBKL1A</i>	Cell proliferation/Type 2 diabetes GWAS
		-1.08			
cg03498175	7.77E-07	0.93	0.0323	<i>ACSL1</i>	Type 2 diabetes GWAS
cg05429895	8.03E-07	-1.24	0.0323	<i>TLR4</i>	Mental Health

The results for the 19 VF-DMPs identified from the integrated omics analysis as shown in the table below.

CpG	Gene	Pvalue	Estimate
cg06906087	FASN	0.000101	1.117408
cg20963865	TBC1D14	0.000912	1.105669
cg20592144	FASN	0.00336	1.114668
cg00608661	CHST11	0.001608	-1.2207
cg11950105	FASN	1.76E-05	0.931996
cg24161106	SREBF1	0.000115	0.943561
cg05157970	FASN	0.015564	0.974881
cg04029738	FASN	0.000107	1.236273
cg23875758	SREBF1	3.43E-05	1.30008
cg06259406	FASN	0.000589	1.114668
cg03498175	ACSL1	7.77E-07	0.931996
cg13892570	TAGLN2	0.328359	-0.29274
cg22158723	FASN	0.003174	1.054444
cg23757365	C21orf2	0.000765	0.895501
cg13804838	FASN	0.000304	1.010532
cg03693434	FASN	0.028489	0.737401
cg21834739	BAT2	0.017966	0.970873
cg01599099	PC	0.052299	0.863997

cg06234966	FASN	0.035947	0.661604
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