

Supplementary materials and results:

Predictive epigenetic biomarkers of successful weight-loss intervention in pre-pubertal children with obesity

Supplementary Table S2. Top 10 GO terms targeted by the 214 prioritised CpGs. In the first column is the GO term ID; then the ontology - "BP" for biological process, "CC" for cellular component and "MF" for molecular function - and its description. In the fourth column is the number of genes for each GO term (N); then the number of differentially methylated genes (DE), *P*-value for over-representation of the GO term (*P*.DE); and in the last column is the False discovery rate (FDR).

ID	Ontology	Term	N	DE	<i>P</i> .DE	FDR
GO:0045345	BP	Positive regulation of MHC class I biosynthetic process	6	2	<0.001	1
GO:0045341	BP	MHC class I biosynthetic process	8	2	<0.001	1
GO:0045343	BP	Regulation of MHC class I biosynthetic process	8	2	<0.001	1
GO:1905331	BP	Negative regulation of morphogenesis of an epithelium	8	2	<0.001	1
GO:0060272	BP	Embryonic skeletal joint morphogenesis	11	2	<0.001	1
GO:0006686	BP	Sphingomyelin biosynthetic process	11	2	<0.001	1
GO:0001715	BP	Ectodermal cell fate specification	1	1	<0.001	1
GO:0042665	BP	Regulation of ectodermal cell fate specification	1	1	<0.001	1
GO:0042666	BP	Negative regulation of ectodermal cell fate specification	1	1	<0.001	1
GO:0045751	BP	Negative regulation of Toll signaling pathway	1	1	<0.001	1

Supplementary Table S3. Top 10 KEGG pathways targeted by the 214 prioritised CpGs. In the first column are the KEGG pathways IDs; then its description; the number of genes in for each KEGG pathway (N); then the number of differentially methylated genes (DE), *P*-value for over-representation of the KEGG pathways (*P*.DE); and in the last column is the False discovery rate (FDR).

ID	Description	N	DE	<i>P</i> .DE	FDR
hsa04714	Thermogenesis	220	5	<0.001	1
hsa04136	Autophagy - other	32	2	<0.001	1
hsa04940	Type I diabetes mellitus	41	2	<0.001	1
hsa04934	Cushing syndrome	155	4	<0.001	1
hsa00600	Sphingolipid metabolism	54	2	<0.001	1
hsa04071	Sphingolipid signaling pathway	120	3	<0.001	1
hsa05217	Basal cell carcinoma	63	2	<0.001	1
hsa00310	Lysine degradation	63	2	<0.001	1
hsa04213	Longevity regulating pathway	61	2	<0.001	1
hsa04360	Axon guidance	181	4	<0.001	1