

Supporting Information to:

**Perspectives and challenges of epigenetic determinants of childhood obesity:
a systematic review**

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Table S1. Search terms combination

Databases	Search Terms	N of articles retrieved
PubMed	(infant[tiab] OR baby[tiab] OR (early life[tiab]) OR toddler*[tiab] OR preschool[tiab] OR schoolchild*[tiab] OR child*[tiab] OR adolescent*[tiab] OR teenage*[tiab] OR juvenil*[tiab] OR pediatric[tiab]) AND (“Pediatric Obesity”[mh] OR obesity[tiab] OR overweight[tiab] OR weight[tiab] OR BMI[tiab] OR (body mass index[tiab]) OR adiposity[tiab] OR (waist-to-hip ratio[tiab]) OR (fat mass[tiab]) OR (waist circumference[tiab]) OR (ponderal index[tiab]) OR (body composition[tiab]) OR (body constitution[tiab]) OR (anthropometry[tiab])) AND (“epigenomics”[mh] OR histon*[tiab] OR methylation[tiab] OR (DNA methylation[tiab]) OR (DNA hydroxymethylation[tiab]) OR (noncoding RNA[tiab]) OR (non-coding RNA[tiab]) OR miRNA[tiab] OR chromatin[tiab]) Filter: Child: birth-18 years, English, Journal Article	359
Scopus	(TITLE-ABS(infant) OR TITLE-ABS(baby) OR TITLE-ABS(early life) OR TITLE-ABS(toddler*) OR TITLE-ABS(preschool) OR TITLE-ABS(schoolchild*) OR TITLE-ABS(child*) OR TITLE-ABS(adolescent*) OR TITLE-ABS(teenage*) OR TITLE-ABS(juvenil*) OR TITLE-ABS(pediatric)) AND (INDEXTERMS(“Pediatric Obesity”) OR TITLE-ABS(obesity) OR TITLE-ABS(overweight) OR TITLE-ABS(weight) OR TITLE-ABS(BMI) OR TITLE-ABS(adiposity) OR TITLE-ABS(waist-to-hip ratio) OR TITLE-ABS(fat mass) OR TITLE-ABS(waist circumference) OR TITLE-ABS (ponderal index) OR TITLE-ABS (body composition) OR TITLE-ABS(body constitution) OR TITLE-ABS (anthropometry)) AND (INDEXTERMS(“epigenomics”) OR TITLE-ABS(histon*) OR TITLE-ABS(methylation) OR TITLE-ABS(DNA methylation) OR TITLE-ABS(DNA hydroxymethylation) OR TITLE-ABS(non-coding RNA) OR TITLE-ABS(noncoding RNA) OR TITLE-ABS(miRNA) OR TITLE-ABS (chromatin)) AND LANGUAGE(english) AND DOCTYPE(ar)	741

N= number

Table S2. Modified Newcastle-Ottawa scale

Study design	Item			Condition to award a star	Unsuccess to award a star
	Domain	N	Description		
Case-control	Selection	1	adequate case assessment	yes, with independent validation *	yes, eg record linkage or based on self-reported no description
		2	representativeness of the cases	consecutive or obviously representative series of cases *	potential for selection biases or not stated
		3	selection of controls	community controls*	hospital controls no description
		4	definition of controls	no history of disease (endpoint) *	no description of source
	Comparability	5	studies controlling the most important factors (age, sex and cell types for DNA methylation analyses)	yes *	no
		6	findings have been validated/replicated	yes *	no
		7	epigenetic measurement	wide studies *	candidate studies
		8	sample size	>=50 *	<50
	Outcome	9	method and statistical analysis	adequate (eg. using adjusted p values) and detailed *	not adequate no description
Longitudinal, cross-sectional, and non-randomized trials	Selection	1	representativeness of the exposed cohort	representative of the average exposure in community *	selection of specific groups no description
		2	selection of non-exposed cohort	drawn from the same community as the exposed cohort *	drawn from a different source
		3	ascertainment of exposure	secure record (eg hospital records) * structured interview*	Self-reported
		4	demonstration that outcome of interest was not present at start of study	yes*	no
	Comparability	5	studies controlling the most important factors (age, sex and cell types for DNA methylation analyses)	yes*	no
		6	findings have been validated/replicated	yes*	no
		7	epigenetic measurement	wide studies *	candidate studies

		8	sample size	>=200 (longitudinal) / >=100 (cross-sectional studies) / >=50 (non-randomized trials) *	<200 (longitudinal) / <100 (cross-sectional studies) / < 50 (non-randomized trials)
	Outcome	9	method and statistical analysis	adequate (eg. using adjusted p values) and detailed *	not adequate no description

N= number

Table S3. Summary table of the studies analysing (a) DNA methylation, (b) non-coding RNAs and (C) histones modification identified in the systematic review.

Nr	Author (year)	Country	Study design	Study population	Anthropometric parameter			Epigenetic markers			Main findings	Confounders	Validation/ Replication	NOS score
					Type	Age	Method	Tissue	Age	Target (method)				
a) Methylation														
1a	Cadiou et al (2020) ¹	UK, France, Spain, Lithuania, Norway and Greece	Cross-sectional	1173 children (mean BMI: 16.9)	BMI	7.9	WHO SD score BMI	Peripheral blood	7.9	Epigenome wide DNA methylation (Illumina array, Infinium HumanMethylation450 BeadChip Array)	Among 1788 CpGs that were associated with SD BMI scores (FDR-adjusted p<0.05) only one (cg02032125) remained significant after adjustment for cell estimates. Restricting the methylome to 2284 CpGs a priori relevant to BMI, 68 CpG were associated with SD BMI.	Maternal pre-pregnancy BMI, maternal education, maternal age, parental country of birth, maternal smoking during pregnancy, cohort, parity, trimester of conception, child age, child sex, ethnicity and estimated blood cells	None	7
2a	Gagné-Ouellet et al (2020a) ²	US	Longitudinal	262 children (mean BMI:16.1)	BMI, skinfold thickness	3	WHO SD score BMI, skinfold thickness sum	Placenta	0	Epigenome wide DNA methylation (Illumina array, Infinium HumanMethylationEpic BeadChip Array)	Lower methylation at cg22436429 and cg22593959 was associated with BMI at 3 years of age (FDR-adjusted p<0.05) and skinfold thickness sum. DMRs at the <i>BMPRI1B</i> , <i>SKAP2</i> , <i>MAGI2</i> and <i>FMN1</i> genes were associated with BMI at 3 years and skinfold thinness sum.	Gestational age at delivery, sex and age of the offspring, estimated blood cells and the first 5 PCs	Replication in a cohort of 187 children identify only cg22593959 methylation levels were similar to the discovery cohort ($\beta = -3.8 \pm 4.1$ vs. -1.18 ± 0.29).	8
3a	Geraghty et al (2020) ³	UK	Longitudinal	63 children (mean BMI centile: 51)	BMI, weight,	6months, 2 and 5 years	BMI centile and continuous weight	Saliva	5	Epigenome wide DNA methylation (Illumina array, Infinium HumanMethylationEpic BeadChip Array)	No measures of weight or adiposity were associated with methylation status at five years of age. Change in weight centiles from birth to five years was associated with PC1 and, in a reduced sample set, weight at six months of age was associated with PC6.	Chip position and child sex	None	6
4a	Henriksson et al (2020) ⁴	Sweden	Case-control	48 infants: 24 infants with the lowest body fatness (range: 0.9–	Fat mass	1 week	Fat mass percentage f	Buccal cells	1 week	Epigenome wide DNA methylation (Illumina array, Infinium	No association was found between body fatness in infants and neonatal buccal cell DNA methylation	None	None	5

Nr	Author (year)	Country	Study design	Study population	Anthropometric parameter			Epigenetic markers			Main findings	Confounders	Validation/ Replication	NOS score
					Type	Age	Method	Tissue	Age	Target (method)				
				9.8% fat mass) and the 24 infants with the highest body fatness (range: 15.1–21.1% fat mass)						HumanMethylation450 BeadChip Array)				
5a	Rastogi et al (2020) ⁵	US	Case-control	120 children: 60 with obesity and asthma and 60 with normal weight and asthma	Obesity	7-11	BMI> 95th percentile for age and sex	Peripheral blood (T cells)	7-11	Epigenome wide DNA methylation (enzyme digestion-based tagging assay, enzyme digestion HELP-tagging assay)	836 CpGs were >10% differentially methylated between children with obesity and asthma and children with normal weight and asthma (p<0.05). Differentially methylated genes in obese children with asthma were enriched in RhoGTPase pathways	Age, sex, and ethnicity, Th-cell subtype proportions	None	8
6a	Vehmeijer et al (2020) ⁶	23 countries (participants were mainly of European ancestry, but there were also cohorts with partly non-European ethnicities)	Longitudinal	4133 children	BMI, obesity	2-5 years (early childhood), 5-10 years (late childhood), and 12-18 years (adolescence)	Age and sex BMI SD, obesity based on BMI> IOTF cut offs	Cord blood and peripheral blood	0-18	Epigenome wide DNA methylation (Illumina array, Infinium HumanMethylation450 BeadChip Array)	cg05937453 (<i>SFRP5</i>), in cord blood was significantly associated with late childhood BMI (Bonferroni p<0.05). Childhood DNA methylation at cg25212453 (<i>SLC43A2</i>) (Bonferroni p<0.05) in addition to other and other 9 CpGs (at FDR adjusted p<0.05) were associated with childhood BMI. DNA methylation in adolescence at cg10040131 (<i>SFXN5</i>) was associated with adolescent BMI (Bonferroni p<0.05). Childhood, DNA methylation at cg06991974 (<i>PRDM16-DT</i>), was associated with obesity in childhood.	Maternal age, maternal educational level, maternal smoking status during pregnancy, maternal pre-pregnancy or early pregnancy BMI and parity, gestational age at birth, batch, and estimated cell type. For childhood analysis birth weight and breastfeeding was added as confounders. For adolescent analysis adolescent age, sex, own smoking status, and puberty status were added as confounders.	None	8
7a	Cao-Lei et al (2019) ⁷	Canada	Case-control	31 adolescents: 5 with obesity and 26 controls	Obesity	13.5	BMI> 97th percentile	Peripheral blood (T cells)	13.5	Epigenome wide DNA methylation (Illumina array, Infinium	43 CpGs were differentially-methylated between children with obesity and controls (FDR-adjusted p<0.05)	None	None	5

Nr	Author (year)	Country	Study design	Study population	Anthropometric parameter			Epigenetic markers			Main findings	Confounders	Validation/ Replication	NOS score
					Type	Age	Method	Tissue	Age	Target (method)				
										HumanMethylation450 BeadChip Array)				
8a	He et al (2019) ⁸	US	Cross-sectional	263 adolescents (mean BMI percentile: 65.4)	BMI	16.7	Continuous CDC percentiles	Peripheral blood	16.7	Epigenome wide DNA methylation (RRBS, Illumina HiSeq. 2500)	No epigenome wide Bonferroni significant site associated with BMI. One CpG on <i>SIM1</i> gene was associated ($\beta=7.2$, $p=4.2E-05$) with BMI among obesity-related genes	Age, race, sex, and batch of assay	None	6
9a	Huang et al (2018) ⁹	US	Cross-sectional	265 children (mean BMI: 17.4)	BMI	~7	CDC SD BMI score	Peripheral blood	~7	Epigenome wide DNA methylation (Illumina array, Infinium HumanMethylation450 BeadChip Array)	SD BMI score in mid-childhood was positively associated with DNA methylation at cg11412418, cg09571082, and cg17298543, and negatively associated with DNA methylation at cg24618739 (FDR $p<0.05$)	Age at blood draw for DNA methylation, cell type proportion, child sex, maternal education and maternal smoking during pregnancy)	None	7
10a	Kaufman et al (2018) ¹⁰	US	Cross-sectional	160 children (mean BMI: 23.1)	BMI	11.5	Continuous BMI	Saliva	11.5	Epigenome wide DNA methylation (Illumina array, Infinium HumanMethylation450 BeadChip Array)	6 CpGs associated with BMI (FDR $p<0.05$)	Age, sex, race, cell type (eg, CD14, CD34, buccal), and the first 3 PCs	cg10264529 on <i>PCK2</i> gene quantified Illumina Infinium Methylation EPIC BeadChip Array was significantly associated with BMI in the replication cohort of 74 children (Bonferroni corrected $p<0.05$)	8
11a	Li et al (2018) ¹¹	China	Case-control	7 children: 3 obese and 4 controls	Obesity	5.3	WHO SD score BMI >2	Peripheral blood	5.3	Epigenome wide DNA methylation (array, Infinium HumanMethylation450 BeadChip Array)	226 CpGs were differentially methylated between obese and controls ($p<0.05$ and beta difference >0.14)	None	Replication in 81 children via bisulfite sequencing PCR showed CpG sites within genes <i>HDAC4</i> , <i>RAX2</i> , <i>APOA5</i> , <i>CES1</i> were differentially	7

Nr	Author (year)	Country	Study design	Study population	Anthropometric parameter			Epigenetic markers			Main findings	Confounders	Validation/ Replication	NOS score
					Type	Age	Method	Tissue	Age	Target (method)				
													methylated between obese and controls	
12a	van Dijk et al (2018) ¹²	Australia	Longitudinal	442 children	BMI (mean BMI SD score: 0.50), body fat (impedance), waist circumference and waist to hip ratio	5	SD BMI scores Continuous body fat, waist circumference and waist to hip ratio	Neonatal bloodspots and peripheral blood	0 and 5	Epigenome wide DNA methylation (Illumina array, Infinium HumanMethylation450 BeadChip Array)	No individual methylation sites at birth or at 5 years were associated with BMI or any other adiposity measure at 5 years using p-value FDR adjusted significant threshold <0.05. BMI at 5 years was associated with DNA methylation in 69 DMRs at birth, 49 DMRs at 5 years with 5 DMRs (including <i>nc886</i> , <i>KCNQ1DN</i> and <i>TNXB</i> regions) in common between the two timepoints	Sex, gestational age and estimated blood cell	Replication found <i>nc886</i> , <i>KCNQ1DN</i> and <i>TNXB</i> DMRs as top differentially methylated in blood from 355 adolescent	9
13a	Samblas et al (2018) ¹³	Spain	Case-control	24 children: 12 with obesity and 12 controls	Obesity	10.7	BMI > 97th Spanish reference percentile	Peripheral blood	10.7	Epigenome wide DNA methylation (Illumina array, Infinium HumanMethylation450 BeadChip Array)	No epigenome wide FDR significant site or DMR was associated with obesity	Age and sex	Among top EWAS results, 3 CpGs of <i>PTPRS</i> and <i>PER3</i> gene quantified by MassArray EpiTyper were negatively correlated with BMI in 91 children (p<0.05)	6
14a	Fradin et al (2017) ¹⁴	France	Case-control	40 children: 20 with obesity and 20 lean controls	Obesity and severe obesity	3-13	WHO SD score BMI > 2.5 (obesity) and 3.5 (severe obesity)	Peripheral blood	3-13	Epigenome wide DNA methylation (Illumina array, Infinium HumanMethylation450 BeadChip Array)	31 and 151 CpGs differentially-methylated between children with obesity and severe obesity, respectively, and controls (FDR-adjusted p<0.05)	Estimated blood cells	None	6
15a	Kresovich et al (2017) ¹⁵	US	Longitudinal	478 children	Skinfold thickness (mean subscapular and triceps skinfold thickness ratio: 0.65) and fat	3.2 (early childhood) and 7.7 (mid childhood)	Skinfold thickness: subscapular and triceps sum and ratio Fat mass continuous and %	Cord blood	0	Epigenome wide DNA methylation (Illumina array, Infinium HumanMethylation450 BeadChip Array)	Subscapular and triceps ratio in early childhood was associated with cord blood methylation at cg11137145 ($\beta = 0.10$, FDRp = 0.02), cg03352173 ($\beta = -0.07$, FDRp = 0.03), cg00885918 ($\beta = -0.15$, FDRp = 0.03), and cg20624923 ($\beta = 0.22$, FDRp = 0.03) and in mid-childhood with cg14974711 ($\beta = 0.19$, FDRp = 0.02). Subscapular and triceps sum in early childhood was associated	Batch, maternal pre-pregnancy BMI, age at enrolment, education, mean folate intake during pregnancy, smoking during pregnancy, and gestational weight gain, and child sex,	None	8

Nr	Author (year)	Country	Study design	Study population	Anthropometric parameter			Epigenetic markers			Main findings	Confounders	Validation/ Replication	NOS score
					Type	Age	Method	Tissue	Age	Target (method)				
					mass (DEXA)						with cord blood methylation at cg09271157 ($\beta = 0.21$, FDRp=0.04), that was nominally significant also in mid-childhood. In DMRs analyses, subscapular and triceps ratio in early childhood was positively associated with methylation at <i>GFPT2</i> region, and in mid-childhood with <i>LOC100049716</i> region methylation. Fat-free mass index in mid-childhood was associated with methylation at <i>LOC102723493</i> region.	race/ethnicity, current age, and cord blood cell composition		
16a	Lillicrop et al (2017) ¹⁶	UK	Longitudinal	21 children	Fat mass (DEXA)	6	Continuous and %	Cord blood	0	Epigenome wide DNA methylation (chromatin immunoprecipitation combined with DNA microarray, Agilent Human Promoter Whole-Genome ChIP-on-chip array)	93 DMRs, including <i>CDKN2A</i> , were associated with % fat mass in the children at 6 years	Validation was adjusted for sex, ethnicity, maternal age, mode of delivery principal component cell type, and batch	Lower <i>CDKN2A</i> methylation at birth measured with pyrosequencing was associated with increasing in the 247 children with triceps skinfold thickness at 1 year, and % fat mass at 4 and 6 years; in 305 children with triceps skinfold thickness at 7 days, and ponderal index at 18 months. In 814 adolescents, lower <i>CDKN2A</i> methylation was cross-sectionally	8

Nr	Author (year)	Country	Study design	Study population	Anthropometric parameter			Epigenetic markers			Main findings	Confounders	Validation/ Replication	NOS score
					Type	Age	Method	Tissue	Age	Target (method)				
													associated with higher BMI at 17 years	
17a	Rzehak et al (2017) ¹⁷	Germany, Belgium, Italy and Spain	Cross-sectional	374 children	BMI, fat mass and fat free mass (impedance)	5.5	BMI: WHO SD scores Fat mass and fat free mass: continuous and index (fat mass and fat free mass / height)	Peripheral blood	5.5	Epigenome wide DNA methylation (Illumina array, Infinium HumanMethylation450 BeadChip Array)	2 differentially methylated probes (located in genes <i>SNED1</i> and <i>KLHL6</i>) were associated with BMI, 5 (located in genes <i>SNED1</i> , <i>WDR51A</i> , <i>CYTH4-ELFN2</i> , <i>CFLAR</i> and <i>PRDM14</i>) with fat mass, 2 (located in genes <i>LOC101929268</i> and <i>MLLT4</i>) with fat free mass, 5 (located in genes <i>SNED1</i> , <i>SOS1</i> , <i>CFLAR</i> , <i>ZNF643</i> and <i>ST6GAL1</i>) with fat mass index and 1 (located in gene <i>CILP2</i>) with fat free mass index	Sex, age, study center, parental education, blood cell types	None	8
18a	Rounge et al (2016) ¹⁸	Finland	Case-control	100 girls: 50 obese and 50 lean controls	Obesity	11	BMI> 90th percentile	Saliva	11	Epigenome wide DNA methylation (targeted bisulfite sequencing, SureSelect Human Methyl-Seq)	No CpG site was genome-wide significant in the EWAS. 7 DMRs and 5 CpG islands differed significantly between the obese and lean girls	Menarcheal status and bisulfite conversion	None	7
19a	Ding et al (2015) ¹⁹	China	Case-control	20 children: 10 obese and 10 lean controls	Obesity	3-6	WHO age- and gender-specific BMI> 85 th percentile	Peripheral blood	3-6	Epigenome wide DNA methylation (methylated DNA immunoprecipitation sequencing, NimbleGen MedIP-chip)	251 promoters and 575 CGIs were demethylated, and 141 promoters and 277 CGIs were hypermethylated in obese children, and their distribution on chromosomes was imbalanced	None	Validation by bisulfite sequencing of 4 genes (<i>FZD7</i> , <i>PRLHR</i> , <i>EXOSC4</i> and <i>EIF6</i>) that were the top differentially methylated in gene ontology analysis confirmed at least one CpG site in each gene was differentially methylated (p<0.05)	6
20a	Eriksson et al (2015) ²⁰	Greece	Case-control	69 children: 24 obese and 23 normal-	Obesity	9-13	BMI> IOTF cut offs	Peripheral blood	9-13	Epigenome wide DNA methylation (Illumina array,	No CpG was differentially methylated in the 2 groups (FDRp<0.05)	Age, sex, Tanner stage and white blood cell	None	7

Nr	Author (year)	Country	Study design	Study population	Anthropometric parameter			Epigenetic markers			Main findings	Confounders	Validation/ Replication	NOS score
					Type	Age	Method	Tissue	Age	Target (method)				
				weight preadolescent girls as well as 11 obese and 11 normal-weight preadolescent boys						Infinium HumanMethylation27 Bead-Chip array)				
21a	Huang et al (2015) ²¹	Australia	Case-control	108 adolescents: 54 boys with severe obesity and 54 controls	Severe obesity	~12	Age- and sex-adjusted BMI > 2.5 SD scores with 2 additional comorbidities or >3 SD scores	Peripheral blood	~12	Epigenome wide DNA methylation (Illumina array, Infinium HumanMethylation450 BeadChip Array)	129 differentially methylated CpG loci were associated with 80 unique genes that had a greater than 10% difference in methylation ($p < 0.05$) between obese and controls	Cell types and sex (in the validation study)	CpG loci within <i>FYN</i> , <i>PIWIL4</i> , and <i>TAOK3</i> quantified by pyrosequencing were differentially methylated between 78 obesity cases and 71 controls ($p < 0.05$)	7
22a	Quilter et al (2014) ²²	UK	Longitudinal	80 infants: 40 with catch-up growth and 40 controls	Catch-up growth	1	>0.67 weight SD increase from birth to 1 year	Cord blood	0	Epigenome wide DNA methylation (Illumina array, Infinium HumanMethylation27 Bead-Chip array)	Among the 24 and 5 CpGs that were found differentially methylated respectively in the males and female with catch-up compared to controls, only the one (cg27398547) located on <i>C14orf39</i> gene was common in analyses of both sexes ($FDRp < 0.05$)	None	None	6
23a	Rastogi et al (2013) ²³	US	Case-control	24 children: 8 with obesity and asthma, 8 normal weight non-asthmatic and 8 healthy controls	Obesity	~9	BMI > 95th percentile for age and sex	Peripheral blood (PBMCs)	~9	Epigenome wide DNA methylation (enzyme digestion-based tagging assay, enzyme digestion HELP-tagging assay)	7119 loci were differentially methylated in obese asthmatics compared to normal-weight asthmatics, 6773 were differentially methylated when compared to healthy controls. Differentially methylated genes in obese children with asthma were enriched in Cell to cell signaling and T lymphocyte differentiation pathways	None	None	6
24a	Kochmanski et al (2019) ²⁴	US	Longitudinal	132 children (obesity %: 7.5 at 1-2 y, 10 at 3-5y and 13.5 at 10-12y)	Obesity and overweight	1-2, 3-5 and 10-12	Obesity: weight for length SD score (for 1-2y) and BMI SD score (for 3-5 and 10-14y) >95 Overweight: weight for length	Neonatal bloodspots	0	<i>LINE-1</i> , <i>IGF2</i> , <i>H19</i> , <i>LEP</i> , <i>PPARA</i> , <i>ESR1</i> , and <i>SREBF1</i> DNA methylation (pyrosequencing)	Neonatal bloodspot <i>LINE-1</i> methylation was negatively associated with obesity at 3-5 y (log odds = -0.40, $p = 0.04$). <i>PPARA</i> methylation at 3-5 y showed a significant positive association with BMI z-score cross-sectionally ($\beta = 0.210$, $p = 0.01$)	None	None	5

Nr	Author (year)	Country	Study design	Study population	Anthropometric parameter			Epigenetic markers			Main findings	Confounders	Validation/Replication	NOS score
					Type	Age	Method	Tissue	Age	Target (method)				
							SD score (for 1-2y) and BMI SD score (for 3-5 and 10-14y) >85 & <95							
25a	Dunstan et al (2017) ²⁵	US	Cross-sectional	431 adolescents (obesity %:18)	Obesity and overweight, BMI, weight and body fat (impedance)	12.8	Obesity: SD BMI score > 95th percentile Overweight: SD BMI score > 85th and < 95th percentile SD BMI and weight scores and body fat percentage	Saliva	12.8	<i>LINE-1</i> , <i>ICAM-1</i> , <i>CRH_01</i> , <i>CRH</i> , and <i>LEP</i> DNA methylation (pyrosequencing)	Obesity, BMI, weight and body fat were negatively associated with <i>LEP</i> methylation in boys	Age and parental BMI	None	5
26a	Perng et al (2013) ²⁶	Colombia	Longitudinal	553 children	BMI, waist circumference and subscapular-to-triceps skinfold thickness ratio at baseline and after 30 months	Baseline: 8.8 and follow-up: 8.8 + 30 months	WHO SD BMI-for-age score, waist circumference SD score, and subscapular-to-triceps skinfold thickness ratio SD score	Peripheral blood	8.8	<i>LINE-1</i> DNA methylation (pyrosequencing)	No significant association was detected in girls. In boys, <i>LINE-1</i> DNA methylation was inversely associated with change in SD waist circumference score (p trend=0.02). Boys in the lowest quartile of <i>LINE-1</i> methylation experienced annual gains in BMI-for-age SD score and skinfold thickness ratio SD score that were 0.06 SD/year (p=0.04) and 0.07 SD/year (p=0.03), respectively, higher than those in the upper three quartiles	Baseline age and socioeconomic status	None	6
27a	Prats-Puig et al (2020a) ²⁷	Spain	Longitudinal	32 children (mean BMI=16.2)	BMI, weight, waist, hip circumference, visceral (ultrasound) and fat mass (impedance)	6	Age- and sex-adjusted SD BMI scores	Placenta	0	DNA methylation at <i>C19MC</i> imprinting control region (pyrosequencing)	Mean methylation levels at placental <i>C19MC</i> imprinting control region was lower in children with higher weight, waist, hip circumference and fat mass after correction for multiple testing (all p ≤ 0.01)	Maternal pre-gestational and gestational weight, maternal height, gestational age, birth weight or length, and child's sex and age	None	4
28a	Pauwels et al (2019) ²⁸	Belgium	Cross-sectional	101 infants	Overweight or obesity	1	Weight for length and BMI for age >1SD scores (using the Belgian reference)	Buccal cells	1	<i>DNMT1</i> , <i>RXRA</i> , <i>LEP</i> and <i>IGF2</i> DNA methylation (pyrosequencing)	No significant association between DNA methylation and overweight or obesity compared to control group	None	None	6

Nr	Author (year)	Country	Study design	Study population	Anthropometric parameter			Epigenetic markers			Main findings	Confounders	Validation/Replication	NOS score
					Type	Age	Method	Tissue	Age	Target (method)				
29a	Gonzalez-Nahm et al (2018) ²⁹	US	Longitudinal	314 children (mean BMI 16.4 at 3 y)	BMI and weight	1 and 3	CDC SD BMI score and weight for length scores	Cord blood	0	DNA methylation at 9 DMRs (<i>MEG3</i> , <i>MEG3-IG</i> , <i>IGF2</i> , <i>H19</i> , <i>PLAGL1</i> , <i>MEST</i> , <i>NNAT</i> , <i>PEG3</i> , and <i>PEG10</i>) (pyrosequencing)	In boys, high <i>PEG10</i> DMR methylation was associated with higher weight at 1 year and BMI at 3 years. In girls, both low and high methylation at the <i>PLAGL1</i> DMR, and at the <i>MEST</i> DMR were associated with low weight at 1 year, and low methylation at the <i>NNAT</i> DMR was associated with higher BMI at age 3	Maternal race, maternal education, maternal pre-pregnancy BMI, maternal smoking, maternal age, gestational age, and paternal race	None	6
30a	Junge et al (2018) ³⁰	Germany	Longitudinal	408 children (mean SD BMI score: -0.16 at 1y and 0.05 at 6y)	BMI	1 and 6	SD BMI scores	Cord blood	0	<i>MEST</i> DNA methylation (Sequenom's MassARRAY)	Cord blood <i>MEST</i> promoter methylation had a direct effect on BMI at one year (direct effect = -4.22, p<0.05), while its effects on BMI at 6 years was mediated by the BMI at year 1 (indirect effect = -0.18, p<0.05)	Gender of the child, smoking during pregnancy, parental school education, solid food introduction, week of gestation at delivery, number of household members, and early delivery	None	6
31a	Ács et al (2017) ³¹	Hungary	Cross-sectional	80 children with obesity (mean BMI: 16.3)	BMI	~12	SD BMI score	Peripheral blood	~12	<i>CYP27B1</i> , <i>VDR</i> , <i>IGF2</i> and <i>POMC</i> DNA methylation (pyrosequencing)	Significant positive correlations between SD BMI score and <i>CYP27B1</i> hypermethylation ($r = 0.24$, $p = 0.03$) and a significant negative correlation between <i>IGF2</i> hypomethylation and SD BMI score ($r = -0.30$, $p < 0.01$) were found	None	None	4
32a	Thakali et al (2017) ³²	US	Longitudinal	78 infants (mean fat mass: 12.7)	Fat mass (plethysmography)	2 weeks	Percentage	Cord blood	0	DNA methylation of 10 metabolite-related and imprinted genes (Bisulfite Amplicon Sequencing)	Infant fat mass at 2 weeks of age was associated with increased cord blood methylation of <i>RAPTOR</i> gene ($p=0.03$)	Maternal gestational weight gain, gestation length, infant birth weight, and sex	None	5
33a	Bowman et al (2019) ³³	Mexico	Longitudinal	250 children (mean SD BMI score<1)	BMI, skinfold thickness, waist circumference	8-14 and 9-17	WHO SD BMI scores; continuous sum of subscapular and triceps skinfold thickness, continuous waist circumference	Peripheral blood	8-14	DNA methylation at 4 CpG sites for <i>H19</i> and 5 CpG sites for <i>HSD11B2</i> (pyrosequencing)	Methylation at <i>H19</i> CpG sites 1 and 4 were positively associated with skinfold thickness using repeated measures in females ($p < 0.05$)	Sex, age, and maternal education, with study visit as a repeated measure	None	6
34a	Do et al (2019) ³⁴	US	Longitudinal	317 children (mean BMI: 16.6)	BMI	3.7	Continuous	Cord blood	0	DNA methylation at <i>DLK1/MEG3</i> and <i>IGF2/H19</i> DMR (pyrosequencing)	<i>IGF2</i> DMR methylation was negatively correlated with BMI ($p<0.05$)	None	None	6

Nr	Author (year)	Country	Study design	Study population	Anthropometric parameter			Epigenetic markers			Main findings	Confounders	Validation/Replication	NOS score
					Type	Age	Method	Tissue	Age	Target (method)				
35a	Bouwland-Both et al (2013) ³⁵	Netherlands	Longitudinal	540 infants (mean weight: 6.2Kg at 3m and 7.7kg at 6m)	Weight gain	3 and 6 months	Difference in age- and sex adjusted SD weight scores between 3/6 months and birth	Cord blood	0	<i>IGF2</i> DMR, <i>H19</i> and <i>MTHFR</i> DNA methylation (Sequenom's MassARRAY)	A weight gain in the first three months after birth was associated with lower <i>IGF2</i> DMR DNA methylation ($\beta=20.53$, $p<0.05$).	Maternal age, education, parity, BMI, folic acid supplement use, smoking and the occurrence of preeclampsia, and child gender	None	6
36a	Deodati et al (2013) ³⁶	Italy	Cross-sectional	85 children (mean SD BMI score ~2)	BMI and fat mass (DEXA)	~12	SD BMI score, fat mass continuous and %	Peripheral blood	~12	<i>IGF2</i> DNA methylation (Methyl-Profiler DNA Methylation qPCR Assay)	No significant correlation was found between <i>IGF2</i> methylation and all the outcomes measured	Age, pubertal stage and BMI	None	4
37a	Hernández-Valero et al (2013) ³⁷	Mexico	Case-control	90 children: 40 lean and 50 overweight or obese	Overweight or obesity	5-11	Sex and age adjusted BMI >85th percentile	Peripheral blood	5-11	<i>H19</i> DNA methylation (Sanger sequencing)	No significant association was found in <i>H19</i> methylation between the two groups	Maternal BMI, residence, and sex	None	5
38a	Perkins et al (2012) ³⁸	US	Longitudinal	204 infants: 172 overweight or obese and 26 not	Overweight or obesity	~1	Weight for age >85th percentile	Cord blood	0	DNA methylation at 3 CpGs at the <i>IGF2</i> DMR and 4 CpGs at the <i>H19</i> DMR (pyrosequencing)	Mean methylation at the <i>H19</i> DMR was higher in children that at 1 year were overweight and obese compared to controls. No differences were found in <i>IGF2</i> DMR methylation	Maternal pre-pregnancy BMI, prenatal morbidity, mode of delivery, race/ethnicity, education, cigarette smoking, birth weight, sex, and caloric intake	None	6
39a	Huang et al (2012) ³⁹	Australia	Cross-sectional	315 adolescents	BMI, weight, waist circumference, skinfold and fat thicknesses	17	Sex-specific SDs cores	Peripheral blood	17	<i>IGF2</i> and <i>H19</i> and DNA methylation (Sequenom's MassARRAY)	A positive association was seen between principal component 1 of <i>IGF2</i> and <i>H19</i> DNA methylation and three measures of skin-fold thicknesses (subscapular, suprailiac, triceps and abdominal) and subcutaneous fat thickness at age 17 (all $p<0.05$).	None	None	6
40a	Prats-Puig et al (2017) ⁴⁰	Spain	Longitudinal	91 children (mean weight increase during the 1 year of life: ~6.5 Kg)	Weight gain and ponderal index	0-1	Continuous weight and % ponderal index	Placenta	0	DNA methylation at the <i>DLK1-DIO3</i> domain (pyrosequencing)	<i>MEG3</i> promoter differentially methylated region methylation correlated negatively with weight increase during the first postnatal year ($\beta = -0.41$, $p<0.01$)	Gestational age, birthweight, gender, maternal age, maternal BMI, and parity	None	5
41a	Shiau et al (2020) ⁴¹	China	Cross-sectional	1145 children (mean BMI: 15.9)	BMI, weight, waist circumference, body	~5.9	Weight-for-age, BMI for age WHO SD-scores Continuous waist circumference,	Peripheral blood	5.9	Epigenetic age acceleration using Horvath and Hannum method (based on DNA methylation	Increased offspring DNA methylation age acceleration by both the Horvath and Hannum methods was associated with increased offspring weight-for-age SD-score,	Age, sex, and prepregnancy BMI, estimated cell-type proportion and 16	None	6

Nr	Author (year)	Country	Study design	Study population	Anthropometric parameter			Epigenetic markers			Main findings	Confounders	Validation/Replication	NOS score
					Type	Age	Method	Tissue	Age	Target (method)				
					fat percentage, subscapular skinfold		body fat percentage, subscapular skinfold			measured via the Infinium HumanMethylationEPIC BeadChip Array)	BMI-for-age SD-score, waist circumference, body fat percentage, subscapular skinfold (all $p < 0.05$)	PCs as technical control		
42a	Bright et al (2019) ⁴²	UK	Longitudinal	785 children	Weight gain	7, 9, 10, 11, 13, 15, and 18	Weight trajectories from 0 to 10 y were modelled using fractional polynomials	Cord blood	0	Epigenetic age acceleration using Bohlin method (based on DNA methylation measured via the Infinium HumanMethylation450K BeadChip Array)	Gestational age acceleration was associated with higher weight after birth, up to 9 months. From 9 months onwards, these differences continued to attenuate and eventually reversed, resulting in approximately 0.6 kg lower weight at age 10 years per week greater gestational age acceleration	Maternal pre-pregnancy BMI, maternal age, maternal education, and maternal smoking during pregnancy	None	6
43a	Huang et al (2019) ⁴³	Australia	Cross-sectional	995 adolescents (mean BMI:24.2)	BMI	17	Continuous log transformed	Peripheral blood	17	Intrinsic epigenetic age acceleration using Horvath method and extrinsic epigenetic age acceleration Hannum method (based on DNA methylation measured via the Infinium HumanMethylation450K BeadChip Array)	BMI was associated with increased extrinsic epigenetic age acceleration at 17 years ($\beta = 0.024$, $FDRp < 0.05$),	Sex, cell-type composition	None	6
44a	Binder et al (2018) ⁴⁴	Chile	Longitudinal	94 girls	BMI	Multiple timepoints during childhood	Continuous WHO SD BMI scores	Peripheral blood at ~ 10 and ~11 y	~ 10 and ~11	Epigenetic age acceleration using Horvath method (based on DNA methylation measured via the Infinium HumanMethylation450K BeadChip Array)	Changes in SD BMI scores over childhood were not associated with peri-pubertal epigenetic age acceleration (averaged over the two timepoints)	Child age, cell-type composition, maternal pre-pregnancy BMI, maternal height, maternal education, as an indicator of socioeconomic status, and birth weight	None	6
45a	Simpkin et al (2017) ⁴⁵	UK	Longitudinal	914 children (mean weight: 26.2 Kg at 7 y and 66.9kg at 17y)	Weight, BMI, and fat mass (DEXA)	7 and 17	Continuous	Cord blood (birth) and peripheral blood (7 years)	0 and 7	Epigenetic age acceleration using Horvath method (based on DNA methylation measured via the Infinium HumanMethylation4	Children with higher age acceleration at birth had faster growth in weight (0.25%/year faster growth per year of age acceleration, $p=0.02$) and BMI (0.03 kg/m ² /year faster growth per year of age acceleration, $p=0.03$) during childhood and adolescence. A 1-year higher AA at birth was associated	Estimated cell counts, sex, birth weight, gestational age, parity, delivery method, maternal age, maternal smoking, maternal alcohol and education	None	7

Nr	Author (year)	Country	Study design	Study population	Anthropometric parameter			Epigenetic markers			Main findings	Confounders	Validation/Replication	NOS score
					Type	Age	Method	Tissue	Age	Target (method)				
										50K BeadChip Array)	with 1321-g higher fat mass on average across childhood ($p < 0.05$), age acceleration at 7 years was not associated with any outcome measured			
46a	Anguita-Ruiz et al (2020) ⁴⁶	Spain	Cross-sectional	53 girls	BMI	Baseline: 3.5-12.6 Follow-up: 9.7-17.2	SD score BMI (using Spanish reference)	Peripheral blood	Baseline: 3.5-12.6 Follow-up: 9.7-17.2	<i>S100A4</i> DNA methylation at 14 candidate CpGs (selected from the Infinium HumanMethylationEPIC BeadChip Array)	No FDR significant site with SD BMI scores cross-sectionally	Estimated blood cells	None	5
47a	Breton et al (2020) ⁴⁷	Canada	Longitudinal	276 children (mean BMI:16.2)	BMI	3	SD score BMI	Placenta	0	<i>NEGR1</i> DNA methylation (selected from the Infinium HumanMethylationEPIC BeadChip Array)	Placental methylation at cg23166710 ($\beta = 0.12$, $p = 0.04$) and cg26153364 ($\beta = -0.16$, $p = 0.009$) predicted BMI SD score at 3 years	Placenta heterogeneity and gestational age at birth	None	6
48a	Chang et al (2020) ⁴⁸	China	Cross-sectional	152 children who were exposed to plasticizer contamination incidents (mean BMI:17.4)	BMI, weight, waist and hip circumference, and body fat percentage (impedance)	9.9	Continuous weight and SD score weight, BMI, waist and hip circumference, and body fat percentage (BIA)	Peripheral blood	9.9	<i>POLG</i> DNA methylation (PCR, PyroMark PCR Kit)	The odds of hypermethylation at the 2nd CpG site in exon 2 of <i>POLG</i> gene increased among boys ($N=90$) with: -BMI, OR(CI)=1.66 (0.15-3.16), -waist circumference, OR(CI)= 4.49 (0.52-8.47), -hip circumference, OR(CI)= 4.81 (1.04-8.57), -body fat percentage, OR(CI)=5.48 (0.96-10.01)	Age, family income	None	5
49a	Choi et al (2020) ⁴⁹	Korea	Longitudinal	59 children (mean BMI: ~16 at 2, 4, 6 y and 17 at 8 y)	BMI and weight	2, 4, 6, and 8	SD BMI and weight scores (using Korean national growth chart)	Peripheral blood	2 and 6	DNA methylation at 594 obesity-related CpGs (selected from the Infinium HumanMethylation450K, at 2 y, and EPIC, at 6 y, BeadChip Array)	One SD in methylation levels at cg19196862 (<i>IGF2R</i> gene) at age 2 increased BMI at age 2 significantly by 0.37 ($p=0.020$). With one SD increase of methylation at the same CpG at age 2 years, the linear mixed model analysis revealed that BMI during ages 2-8 years significantly increased by 0.49 ($p=0.02$) in girls only	Mother's age at pregnancy, mother's and father's BMI when a child first visited at age 2, maternal smoking status, mother's educational level, preterm birth, underweight at birth, breastfeeding duration, and child's caloric intake, and cell type fraction	None	6

Nr	Author (year)	Country	Study design	Study population	Anthropometric parameter			Epigenetic markers			Main findings	Confounders	Validation/Replication	NOS score
					Type	Age	Method	Tissue	Age	Target (method)				
50a	Diaz et al (2020) ⁵⁰	Spain	Longitudinal	51 infants (mean SD BMI in 30 AGA children: 1.3; mean SD BMI in 21 SGA children:-0.1)	BMI, weight, total fat	1 and 2 years	SD score BMI and weight	Peripheral blood	1	Methylation 10 genes related to SGA (bisulfite pyrosequencing)	Methylation status of <i>NKX6.1</i> and <i>GPR120</i> were independent predictors of total fat at age 12 months and 24 months, respectively. <i>SLC2A8</i> methylation independently explained 42% of the 0-24 month changes in BMI SD score variability.	None	None	5
51a	Gagné-Ouellet et al (2020b) ⁵¹	Canada	Longitudinal	262 children (mean BMI: 16.1)	BMI, subscapular and triceps skinfold	3	WHO SD BMI scores and ratio of subscapular over triceps skinfold thickness	Placenta	0	<i>LEP</i> DNA methylation (selected from the Infinium HumanMethylationEPIC BeadChip Array)	cg05136031 methylation was associated with BMI z-scores ($\beta = -2.69$, $p = 0.05$) and cg15758240 methylation was associated with subscapular-triceps ratio ($\beta = -0.581$, $p = 0.05$) at 3 years of age	Maternal age and BMI at the 1st trimester of pregnancy, gestational age at delivery, sex of the child, and age at follow-up and placenta heterogeneity	None	6
52a	Gallardo-Escribano et al (2020) ⁵²	Spain	Intervention trial	131 children with obesity (mean BMI:24.7) who followed a dietary and lifestyle intervention for 1 year	BMI, waist circumference, body fat	4-9	Continuous BMI, , waist circumference, and body fat	Peripheral blood	Baseline: 4-9, follow-up: after 4 months and 1 year	Methylation 6 candidate genes (bisulfite pyrosequencing)	At baseline, the methylation of the <i>LPL</i> gene correlated negatively with abdominal visceral fat ($r = -0.24$, $p = 0.03$), the methylation at the <i>SCD</i> gene methylation correlated positively with total fat ($r = 0.32$, $p = 0.01$) and the methylation of <i>LEP</i> gene correlated negatively with BMI ($p = 0.02$). After 4months of intervention, the methylation of <i>LPL</i> gene correlated negatively to BMI ($r = -0.22$, $p = 0.04$), waist circumference ($r = -0.23$, $p = 0.03$), and abdominal viscera fat ($r = -0.23$, $p = 0.04$). The methylation level of the <i>LXR</i> gene correlated positively with BMI ($r = 0.48$, $p = 0.001$), WC ($r = 0.38$, $p = 0.01$), abdominal visceral fat mass ($r = 0.41$, $p = 0.01$), abdominal total mass ($r = 0.39$, $p = 0.01$). After 12m of intervention, the methylation of the <i>LPL</i> gene correlated negatively with abdominal visceral fat ($r = -0.24$, $p = 0.04$).	None	None	6
53a	Jakubek-Kipa et al (2020) ⁵³	Poland	Cross-sectional	50 children with obesity	Obesity	7.6	BMI > 95 percentile	Peripheral blood	7.6	<i>LEPR</i> DNA methylation (Combined	Restriction analysis did not bind the cutting sites in any sample	None	None	2

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					Type	Age	Method	Tissue	Age	Target (method)				
										Bisulphite Restriction Analysis)				
54a	Justice et al (2020) ⁵⁴	Australia	Cross-sectional	820 adolescents (mean MI ~23)	Waist circumference	17	Waist circumference (WC) adjusted for BMI (WHRadjBMI), WC-to-hip ratio (WHRadjBMI), and WC-to-height ratio (WCHTadjBMI)	Peripheral blood	17	Methylation at CpG sites associated with adult adiposity (selected from the Infinium HumanMethylation450K BeadChip Array)	cg00994936 in <i>DAZAP1</i> gene was associated with WHRadjBMI, and cg19693031 downstream of <i>TXNIP</i> , was associated with WCadjBMI and WHRadjBMI.	Genetic ancestry, BMI, sex, age, household income, current smoking status, current alcohol consumption, physical activity, batch and estimated cell type	None	6
55a	Loid et al (2020) ⁵⁵	Finland	Cross-sectional	88 children with severe obesity	Severe obesity	13.8	Height adjusted weight >60% before 10 years of age according to the Finnish growth standards	Peripheral blood	13.8	GNAS DNA methylation (MS-MLPA, kit ME031 GNAS)	Analysis of GNAS methylation by MS-MPLA did not identify any epigenetic alterations at the GNAS locus	None	None	2
56a	Mansell et al (2020a) ⁵⁶	Australia	Longitudinal	1074 children (mean BMI 15.6)	BMI, weight, and body fat percentage (DEXA)	4	Continuous BMI and body fat, and British growth chart SD weight score	Cord blood and peripheral blood	Baseline: 0 follow-up: 1	LEP DNA methylation (MS, Sequenom EpiTYPER mass-spectrometry platform)	cg19594666 methylation in blood at 1 year of age is negatively associated with BMI at 4 years of age ($\beta=-0.13$, $p=0.02$). Average cord LEP methylation is correlated with lower BMI ($r=-0.21$, $p=0.02$) and fat mass ($r=-0.25$, $p=0.03$) at 4 years in females	Sex, age at the 1- or 4-year time point, assay batch, cell types, genetic background, bisulphite conversion batch and duration of breastfeeding	None	7
57a	Mansell et al (2020b) ⁵⁷	Australia	Longitudinal	1074 children (mean BMI 15.6)	BMI, weight	4	Continuous BMI and weight	Cord blood and peripheral blood	Baseline: 0 follow-up: 1	HIF3A DNA methylation (MS, Sequenom EpiTYPER mass-spectrometry platform)	No correlation between BMI or weight at 4 years and cord blood or 1 years HIF3A methylation was found in the full population. In sex specific analysis, Cord blood HIF3A DNA methylation was correlated with BMI in males only ($p=0.05$)	Sex, age at the 1 or 4-year time point, assay batch	None	7
58a	Prats-Puig et al (2020b) ⁵⁸	Spain	Longitudinal	12 children (mean SD BMI score=-0.39 in gestational obese group and 0.10 in controls)	BMI and fat mass (impedence)	6	Age- and sex-adjusted SD BMI scores, percentage of fat mass	Cord blood	0	DNA methylation levels at 38 CpG belonging to skeletal muscle specific genes (selected from the Infinium HumanMethylationEPIC BeadChip Array)	BMI was positively associated with <i>TTN1</i> , <i>CXCL13_1</i> and, <i>PAX3</i> (all from $r = 0.65$ to $r = 0.58$ and $p = 0.02$ to $p = 0.04$) and negatively associated with <i>OBSCN_2</i> , <i>BDNF_2</i> , and <i>MYOF</i> (all from $r = -0.66$ to $r = -0.61$ and $p = 0.02$ to $p = 0.03$). Fat mass percentage was associated positively with <i>CXCL2</i> ($r = 0.72$, $p = 0.01$) and negatively with <i>TNNT3</i> ($r = -0.64$; $p = 0.04$), and <i>IL13</i> ($r = -0.64$; $p = 0.04$)	None	None	5
59a	Reed et al (2020) ⁵⁹	UK	Longitudinal	823 children at birth, 906	BMI	7 and 15	Continuous BMI	Cord blood (at birth) and	Baseline: 0	DNA methylation score based on 135	DNA methylation score was associated with BMI in childhood	Sex, age, estimated blood	None	7

Nr	Author (year)	Country	Study design	Study population	Anthropometric parameter			Epigenetic markers			Main findings	Confounders	Validation/ Replication	NOS score
					Type	Age	Method	Tissue	Age	Target (method)				
				during childhood (mean BMI: 16.2 at 7y), 770 during adolescence (mean BMI: 22.6 at 15 y)				peripheral blood (at age 7 and 15)	follow-up: 7 and 15	candidate CpGs (selected from the Infinium HumanMethylation450K BeadChip Array)	(1% variance explained, $p = 2.23 \times 10^{-4}$) and adolescence (3% variance explained, $p = 3.91 \times 10^{-11}$). BMI in childhood was predicting adolescent DNA methylation ($p = 1.52 \times 10^{-6}$ even when adjusting for childhood methylation score). No evidence that methylation score in childhood could be predictive of BMI in adolescence when adjusting for childhood BMI ($p = 0.20$). Cross-lagged models identified the path between childhood methylation and adolescent BMI could be dropped. Mendelian randomisation found little evidence of causal relationship of DNA methylation on BMI	cells, education and smoking		
60a	Rushing et al (2020) ⁶⁰	US	Longitudinal	75 Hispanic children: 28 with obesity (37%) and 47 controls (63%)	Obesity	7.3	CDC BMI >95th percentile	Saliva	4.37	DNA methylation at 17 CpG sites (selected from the Infinium HumanMethylation450K BeadChip Array)	Methylation of cg01307483 (<i>NRF1</i>) at baseline was positively associated with onset of obesity after 3 years ($p=0.04$)	Child age, child baseline SD BMI score, child gender, and parent baseline BMI	None	5
61a	Clark et al (2019) ⁶¹	US	Longitudinal	426 children (mean BMI: 17.1 at 1 y, 16.2 at 2 y, and 17.8 at 10y)	BMI	1,2 and 10	Age- and sex-adjusted SD score BMI	Placenta	0	252 CpGs corresponding to metastable epialleles (selected from array, Infinium HumanMethylationEPIC Beadchip Array)	After adjusting for multiple comparisons, no statistically significant association was found between methylation and changes in BMI SD overall. Methylation at cg11324748 (<i>ANKRD20A11P</i> gene) and cg13012494 (<i>SPATC1L</i> gene) was associated with change in BMI between age 1 and 2 (FDRp <0.05). Sex-stratified analyses revealed a significant association with change in BMI SD overall, after adjusting for multiple comparisons within female placentas for one probe (cg00702231) annotated to the imprinted gene <i>PLAG1</i> Like Zinc Finger 1	Maternal pre-pregnancy BMI (z-score), maternal race, infant sex, insurance status, multiple gestations, and smoking while pregnant	None	6
62a	Han et al (2019) ⁶²	UK	Longitudinal	325 children	BMI	10	Continuous	Peripheral blood	10 and 18	10,212 CpGs (selected from array, Infinium HumanMethylation450 and MethylationEPIC Beadchip Arrays)	BMI at age 10 years was associated with cg08770870 (<i>RPH3AL</i> gene) and cg19663246 (<i>PDE1C</i> gene) methylation changes between 10 and 18 years (FDRp <0.05) and the associations were different between genders	Sex, time, cell type and batch	Replication in 939 children did not show an association between BMI at 5-7 years	8

Nr	Author (year)	Country	Study design	Study population	Anthropometric parameter			Epigenetic markers			Main findings	Confounders	Validation/Replication	NOS score
					Type	Age	Method	Tissue	Age	Target (method)				
													and DNA changes between 7 and 15 years	
63a	Lee (2019a) ⁶³	Korea	Case-control	638 adolescents: 252 with severe obesity and 386 lean	Severe obesity, BMI and waist to hip ratio	~14	Severe obesity: BMI ≥ 35 kg/m ²	Peripheral blood	~14	DNA methylation at 3 CpGs of <i>LRP1B</i> gene (pyrosequencing)	CpGs were hypermethylated in obese cases by 0.76% in cg141441481, 0.34% in cg01852095, and 0.97% in cg141441470 ($p < 0.05$). BMI and waist to hip ratio were significantly associated with all the three CpGs ($p < 0.05$).	Sex and age	None	5
64a	Lee (2019b) ⁶⁴	Korea	Case-control	692 adolescents: 305 with severe obesity and 387 lean	Severe obesity, BMI and waist to hip ratio	~14	Severe obesity: BMI ≥ 35 kg/m ²	Peripheral blood	~14	DNA methylation at 2 CpGs of <i>PTPRN2</i> gene (pyrosequencing)	cg158269415 was hypermethylated in obese cases by 2.93% and its methylation was associated with BMI and waist to hip ratio ($p < 0.05$).	Sex and age	None	5
65a	Lillicrop et al (2019) ⁶⁵	UK	Longitudinal	680 children (mean fat mass: 4.1 at 4y and 6.8 at 6y)	Fat mass (DEXA) and triceps skinfold thickness	Fat mass: 4 and 6 years Triceps skinfold thickness: 6 months, 1, 2, 3 and 6–7 years	Continuous and %	Cord blood	0	DNA methylation 5 CpG sites within the <i>SLC6A4</i> DMR (pyrosequencing)	CpG5 was negatively associated with total fat mass at 4 and 6 years, % fat mass at 6 years, and triceps skinfold thickness at 6 months, 1, 2, 3 and 6 years	Sex and age, batch	In 1200 children of 17 years, the negative association between CpG5 and adiposity measurements (BMI, waist circumference, subcutaneous fat and triceps skinfold thickness) was cross-sectionally confirmed	7
66a	Martin et al (2019) ⁶⁶	UK	Longitudinal	238 children (mean SD BMI score: 0.34)	BMI	4-5	SD BMI score	Cord blood	0	<i>TAPBP</i> DNA methylation (selected from the Infinium HumanMethylation450K BeadChip Array)	In female offspring, two <i>TAPBP</i> CpG sites were associated with SD BMI score (cg23922433: $\beta = 1.58$; cg17621507: $\beta = -1.18$, $FDR p < 0.05$ in both cases)	Maternal age at delivery, race/ethnicity, maternal pre-pregnancy obesity, and smoking status during pregnancy	None	6
67a	Noor et al (2019) ⁶⁷	US	Longitudinal	429 children	BMI	3	CDC SD BMI score	Cord blood	0	DNA methylation at 9 CpGs associated with paternal BMI	cg01029450 methylation (at <i>ARFGAP3</i> gene) was associated	Maternal age, gestational weight	None	6

Nr	Author (year)	Country	Study design	Study population	Anthropometric parameter			Epigenetic markers			Main findings	Confounders	Validation/Replication	NOS score
					Type	Age	Method	Tissue	Age	Target (method)				
										(selected from the Infinium HumanMethylation450K BeadChip Array)	with higher SD BMI at 3 years ($\beta = 0.18$; $p = 0.01$)	gain, household income, maternal education, maternal alcohol use, marital status, infant's sex, race/ethnicity, gestational age at delivery, mode of delivery, birth weight, batch effects, and estimated nucleated cell		
68a	Sherwood et al (2019) ⁶⁸	UK	Longitudinal	297 children: 211 with normal BMI trajectory, 41 with delayed overweight, 33 with early transient overweight and 12 with early persistent obesity	BMI trajectories	1, 4, 10, and 18	Normal, delayed overweight, early transient overweight and early persistent obesity, categories were based on BMI trajectories using WHO (1y) and IOTF BMI (4,10 and 18 y) cut-offs	Peripheral blood	10	DNA methylation at 4 CpGs of the <i>LEP</i> gene associated with breastfeeding (selected from array, and MethylationEPIC Beadchip Arrays)	cg2338105 methylation was positively associated with the early transient overweight trajectory ($p = 0.03$) and cg05091920 methylation was negatively with the early persistent obesity trajectory in children with exclusive breastfeeding ($p = 0.03$)	Child sex, birth weight, gestational age, serum leptin (ng/mL at either 10 or 18 years), BMI (at either 10 or 18 years), maternal socioeconomic status (defined using maternal socioeconomic cluster information: high, low, low-low, low-mid, and mid, using household income, number of rooms, and maternal education), maternal smoking at birth., cell type, parity and maternal age	None	6
69a	Tian et al (2019) ⁶⁹	US	Cross-sectional	236 children (mean SD BMI score: 0.40)	BMI, skinfold thickness and waist-to-hip circumference ratios	7.9	BMI z-score based on the U.S. national data, log2-transformed skinfold thickness (sum of triceps and subscapular) and waist-to-hip	Peripheral blood	7.9	<i>LEP</i> DNA methylation (selected from array, Infinium HumanMethylation450 and MethylationEPIC Beadchip Arrays)	<i>LEP</i> methylation level in blood was associated with lower SD BMI score ($\beta = -3.11$, $p = 0.02$), skinfold thickness ($\beta = -1.92$, $p = 0.01$) and waist-hip ratio ($\beta = -0.18$, $P = 0.07$)	Maternal education level, child sex, race/ethnicity, and age at methylation test	None	5

Nr	Author (year)	Country	Study design	Study population	Anthropometric parameter			Epigenetic markers			Main findings	Confounders	Validation/ Replication	NOS score
					Type	Age	Method	Tissue	Age	Target (method)				
70a	Chen et al (2018) ⁷⁰	US	Cross-sectional	219 adolescents (mean BMI: 24.1)	Fat mass (DEXA), and visceral adiposity (MRI)	15–18	Continuous and % circumference ratios	Peripheral blood	15–18	3 candidate CpGs (selected from array, Infinium HumanMethylation450 and MethylationEPIC Beadchip Arrays)	cg07035602 (<i>LPCAT1</i> gene) was significantly associated with visceral adiposity	Age, sex, sexual development, fat free soft tissue mass, energy intake, cell type, and physical activity.	None	6
71a	El Sayed et al (2018) ⁷¹	Egypt	Non-randomized trial	80 children: 30 obese completed 3-month dietary intervention, 30 obese completed 3-month dietary intervention plus folic acid intake, and 20 controls	Obesity	4-17 and after the intervention	BMI >95th percentile	Peripheral blood	4-17 and after the intervention	DNA methylation at <i>LEP</i> and <i>MMP2</i> genes (qMS-PCR)	<i>LEP</i> and <i>MMP2</i> genes promoters' methylation rate was lower in obese children compared to controls and was inversely correlated with weight percentile (all corrected-p < 0.01)	None	None	6
72a	Kwon et al (2018) ⁷²	Korea	Case-control	120 children: 79 normal weight and 41 overweight or obese children	Overweight or obesity	7-9	BMI >85th percentile (using Korean reference)	Peripheral blood	7-9	<i>POMC</i> , <i>MC4R</i> , and <i>HNF4A</i> DNA methylation (pyrosequencing)	<i>POMC</i> , <i>MC4R</i> , and <i>HNF4A</i> methylation levels at CpG sites were significantly different in overweight and obese and normal weight children (p<0.05)	Age	None	6
73a	Tozzi et al (2018) ⁷³	Italy	Longitudinal	38 neonates (with gestational age <34 weeks): 71% with weight EUGR	EUGR (based on weight circumference)	From birth to postmenstrual age 36-42 weeks	>1 SD weight circumference between birth and other measures taken during the hospital stay	Peripheral blood at birth and at discharge	0 and postmenstrual age 36-42 weeks	<i>IC1</i> DNA methylation (MS-MLPA, kit ME030-c3)	Weight circumference EUGR children showed an increased <i>IC1</i> methylation (>5%) from birth to postmenstrual 36-42 weeks (p=0.018 and p=0.0028, respectively)	None	None	4
74a	Wu et al (2018) ⁷⁴	Mexico	Longitudinal	247 children (mean BMI: 15.6)	BMI, waist circumference and body fat	4-6	SD BMI score and continuous waist circumference and body fat	Cord blood	0	<i>TNF-α</i> , <i>IL6</i> and <i>IL8</i> DNA methylation (pyrosequencing)	<i>IL6</i> methylation was associated with BMI SD score, waist circumference and body fat between 4 and 6 years	Maternal pre-pregnancy BMI, parity, socioeconomic status, birth weight, and child total energy intake and percent fat intake of total energy	None	6
75a	Yang et al (2018) ⁷⁵	US	Cross-sectional	258 children	BMI, waist circumference,	10.5	Continuous	Peripheral blood	10.5	DNA methylation at 6 genes related to	<i>SH3PXD2A</i> was significantly (FDR-adjusted P<0.05) associated with multiple adiposity-related outcomes:	Age, sex, race/ethnicity, Tanner stage and	None	5

Nr	Author (year)	Country	Study design	Study population	Anthropometric parameter			Epigenetic markers			Main findings	Confounders	Validation/Replication	NOS score
					Type	Age	Method	Tissue	Age	Target (method)				
					skinfold thickness, visceral (MRI) and subcutaneous adipose tissue					gestational diabetes (pyrosequencing)	BMI, waist circumference, triceps, suprailliac and subscapular skinfold thickness, subcutaneous adipose tissue	pyrosequencing plate.		
76a	Gagné-Ouellet et al (2017) ⁷⁶	Canada	Longitudinal	66 children (mean BMI: 15.1)	BMI, weight, and fat mass (impedance)	5.9	WHO SD BMI, weight, continuous fat mass	Placenta	0	LPL DNA methylation (pyrosequencing)	LPL methylation levels were positively correlated with weight SD-scores ($r = 0.31$, $p = 0.01$) and fat mass ($r = 0.27$, $p = 0.04$)	Gestational age at birth, child sex, maternal age, and pre-pregnancy BMI	None	4
77a	Koh et al (2017) ⁷⁷	Korea	Case-control	671 children: 297 extremely obese and 374 controls	Extreme obesity, BMI, and waist to hip ratio	~13.9	CDC BMI-for-age of > 1.2 times the 95th percentile	Peripheral blood	~13.9	KLF13 DNA methylation (pyrosequencing)	cg07814318 increased by 1.4% in extremely obese children than in control ($p = 2.30 \times 10^{-8}$) and was correlated to BMI and waist to hip ratio	None	Pre-adipocytes (omentum), and islet (pancreas) cells KLF13 DNA methylation measured in 47 donors via Infinium HumanMethylation450 Beadchip Arrays was higher in extremely obese compared to control, while it was similar in adipocytes of cases and controls	7
78a	Lin et al (2017) ⁷⁸	Singapore	Longitudinal	987 children (mean BMI: 15.6)	Weight and BMI	After birth-48 months	WHO SD BMI scores	Cord blood	0	DNA methylation at 8 CpGs at ANK3, CDKN2B, IGDCC4, P4HA3, MIRLET7BHG, CACNA1G, and ZNF423 genes (selected from array, Infinium)	After birth till 48 months weight and BMI were associated with 8 and 6 out of the 8 measured CpGs ($p < 0.05$)	Sex, gestational age, ethnicity, cellular proportions and interactions between ethnicity and cellular proportion	None	7

Nr	Author (year)	Country	Study design	Study population	Anthropometric parameter			Epigenetic markers			Main findings	Confounders	Validation/ Replication	NOS score
					Type	Age	Method	Tissue	Age	Target (method)				
79a	Mansego et al (2017) ⁷⁹	Spain	Case-control	24 children: 12 with obesity and 12 controls	Obesity	10.7	BMI >97th percentile of the Spanish reference	Peripheral blood	10.7	HumanMethylation450 Beadchip Arrays) DNA methylation at 2783 CpGs located in 653 miRNAs coding regions (selected from array, Infinium HumanMethylation450 Beadchip Arrays)	16 CpGs were differentially methylated in obese versus controls (FDRp <0.05)	None	The DNA methylation levels of miR-1203, miR-412 and miR-216a quantified by MassArray EpiTyper was different in obese versus controls (p<0.05)	6
80a	Volberg et al (2017) ⁸⁰	US	Longitudinal	373 children (mean BMI: 20.7)	BMI	9	CDC age- and sex-specific SD BMI scores	Cord blood (birth) and peripheral blood (9 years)	0 and 9	23 <i>PPARγ</i> CpGs (selected from array, Infinium HumanMethylation450 Beadchip Arrays)	Methylation at 9 years at site 1 and site 20 was significantly and inversely associated with 9-year BMI (p<0.05). On the contrary, methylation at birth at either of these sites was not associated with 9-year BMI	Sex and cell type	None	7
81a	Richmond et al (2016) ⁸¹	UK	Longitudinal	974 children	BMI	7 and 17	Continuous	Cord blood (birth) and peripheral blood (7 and 15-17 years)	0 and 7, 15-17	DNA methylation at 3 CpGs of the <i>HIF3A</i> gene (based on DNA methylation measured via the Infinium HumanMethylation450K BeadChip Array)	In cross-sectional analyses, 0.1 increase in the methylation of cg27146050 was associated with a 4.7% (p = 0.01) increase in BMI in adolescence. The association was lost significance in the fully adjusted model. In the longitudinal study, childhood BMI was associated with adolescent cg27146050 methylation the fully adjusted model (p<0.05), suggesting an effect of BMI on methylation rather than the opposite. Mendelian randomization supported methylation at HIF3A did not play a casual role on BMI	Age, sex, batch, , maternal education, social class, maternal smoking, maternal alcohol, birth weight, gestational age and cell types	None	7
82a	Carobin et al (2015) ⁸²	Brasil	Case-control	20 children: 10 with obesity and 10 controls	Obesity	~10-12	BMI>5 th percentile	Peripheral blood	~10-12	<i>SNRPN</i> DNA methylation (PCR)	Methylation levels of the <i>SNRPN</i> did not differ statistically between obese and non-obese children (p>0.05)	None	None	5
83a	Davé et al (2015) ⁸³	US	Cross-sectional	69 children (mean BMI: 20.3)	BMI, obesity and overweight	9	CDC age- and sex-specific SD BMI scores	Peripheral blood	9	DNA methylation of <i>ADIPOR1</i> and <i>PPARG1</i> genes (selected from array, Infinium	No association was found between <i>ADIPOR1</i> and <i>PPARG1</i> methylation and the outcomes measured	None	None	4

Nr	Author (year)	Country	Study design	Study population	Anthropometric parameter			Epigenetic markers			Main findings	Confounders	Validation/Replication	NOS score
					Type	Age	Method	Tissue	Age	Target (method)				
							Overweight and obesity: >85th and >95th percentile			HumanMethylation4 50 Beadchip Arrays)				
84a	Gardner et al (2015) ⁸⁴	US	Case-control	64 children: 32 with obesity and 32 controls	Obesity and fat mass (DEXA)	5-6	BMI for-age percentile > 95 th , fat mass %	Saliva	5-6	DNA methylation at 7 candidate genes (methylation-sensitive restriction enzyme digestion and qRT-PCR)	Lower levels of <i>DNMT3B</i> promoter methylation were associated with higher BMI percentiles in girls (p = 0.05, adjusted-p=0.08)	None	None	5
85a	Pan et al (2015) ⁸⁵	Singapore	Longitudinal	991 children (mean weight: 11.9Kg at 2 y)	Weight	6, 12, 18 and 24 months	Continuous	Cord blood	0	<i>HIF3A</i> DNA methylation (selected from array, Infinium HumanMethylation4 50 Beadchip Arrays)	cg27146050 was associated with weight at 12 months after adjustment for birthweight	Time, child sex, ethnicity, cell type proportions and interactions between ethnicity and proportion	None	7
86a	Shah et al (2015) ⁸⁶	Australia	Cross-sectional	403 adolescents (mean BMI: 20.4)	BMI	14	Age- and gender-specific BMI	Peripheral blood	14	Methylation-profile scores associated with BMI in middle-aged and older adults (selected from array, Infinium HumanMethylation4 50 Beadchip Arrays)	Methylation profiles associated with BMI in middle-aged individuals explained 3.6% of the variation in BMI in adolescents, while methylation profiles associated in older adults did not explain any variation.	None	None	5
87a	Sharp et al (2015) ⁸⁷	UK	Longitudinal	914 children	BMI, waist circumference, fat and lean mass	7 and 15-17	Continuous	Cord blood	0	25 CpG sites associated with maternal obesity/underweight (selected from array, Infinium HumanMethylation4 50 Beadchip Arrays)	CpGs that were hypermethylated in association with maternal obesity or hypomethylated in association with maternal underweight tended to be positively associated with offspring adiposity related outcomes, and sites hypomethylated in association with maternal obesity or hypermethylated in association with maternal underweight tended to be inversely associated with offspring adiposity related outcomes. No association had FDRp<0.05	Batch, sex age, and height	None	6
88a	Simpkin et al (2015) ⁸⁸	UK	Longitudinal	914 children	Weight and fat mass	~17	Continuous	Cord blood	0	224 CpG sites associated with gestational age and 23 with birthweight (selected from array, Infinium HumanMethylation4 50 Beadchip Arrays)	No gestational age-related CpG in cord blood was associated with outcomes at 17 years. Among birthweight related CpGs cg15783941 located at <i>NFIX</i> and genes was associated with fat mass at 17 years (FDRp<0.05)	None	None	6
89a	Wang et al (2015) ⁸⁹	China	Case-control	212 children: 107 with obesity and 105 controls	Severe obesity	7-17	Age- and gender-specific BMI ≥97th percentile	Peripheral blood	7-17	<i>HIF3A</i> DNA methylation (MS, Sequenom's	Methylation levels of <i>HIF3A</i> were higher in obese children than in controls at CpG5	None	None	5

Nr	Author (year)	Country	Study design	Study population	Anthropometric parameter			Epigenetic markers			Main findings	Confounders	Validation/Replication	NOS score
					Type	Age	Method	Tissue	Age	Target (method)				
										MassARRAY system)	(position=46801642) and CpG11 (position=46801699) (p <0.05)			
90a	Wu et al (2015) ⁹⁰	China	Case-control	98 children: 59 with obesity and 39 lean	Obesity	8-18	BMI > 30 kg/m ² and fat mass percentage (FMP) > 40	Peripheral blood	8-18	<i>FAIM2</i> DNA methylation (MS, Sequenom's MassARRAY system)	8 CpG sites were significantly different between the obese and lean (p<0.05)	Age and sex	None	5
91a	Azzi et al (2014) ⁹¹	France	Longitudinal	254 infants (mean BMI: 17.6)	Weight and BMI	1	SD scores	Cord blood	0	<i>ZAC1</i> DNA methylation (allele-specific methylated multiplex real-time quantitative PCR)	<i>ZAC1</i> DMR methylation was correlated positively with weight and BMI at 1 year (respectively, r = 0.14 and 0.15; p = 0.03 and 0.01)	Child's gender, gestational age, and child's age	None	5
92a	Clarke-Harris et al (2014) ⁹²	UK	Longitudinal	40 children	Fat mass (DEXA)	Each year from 9 to 14	Fat mass %	Peripheral blood	5-7	<i>PGC1a</i> DNA methylation (pyrosequencing)	4 CpGs of the <i>PGC1a</i> promoter at 5–7 years were significantly associated with fat mass between 9 and 14 years	Sex, age, pubertal timing, and activity	None	5
93a	García-Cardona et al (2014) ⁹³	Mexico	Case-control	106 adolescents, recruited: 16 with normal weight, 29 overweight, 61 obese	Obesity and BMI	10-16	CDC percentile	Peripheral blood	10-16	<i>LEP</i> and <i>ADIPOQ</i> DNA methylation (methylation-specific PCR)	<i>LEP</i> CpG sites at – 51 and – 31 nt, and <i>ADIPOQ</i> CpG site at – 283 nt were differentially methylated in obese children compare to lean. <i>LEP</i> promoter was negatively associated with BMI (p<0.05)	None	None	5
94a	Su et al (2014) ⁹⁴	US	Case-control	14 adolescents: 7 obese and 7 lean	Obesity	14-18	BMI > 99th percentile	Peripheral blood	14-18	Obesity-related genes DNA methylation (array, Illumina Infinium HumanMethylation27 Bead-Chip array)	CpGs located on <i>LEPR</i> , <i>SNRPN</i> , <i>KREMEN1</i> and <i>LY86</i> genes were differentially methylated between obese and lean groups	None	None	5
95a	Yoo et al (2014) ⁹⁵	Korea	Longitudinal	90 children (mean SD BMI score: - 0.21)	BMI and fat mass (impedance)	7-9	SD BMI scores and fat mass %	Cord blood	0	<i>POMC</i> DNA methylation (pyrosequencing)	There was no significant difference in BMI and fat mass at 7-9 years according to cord blood <i>POMC</i> status	Sex, birth weight, follow-up age, and current <i>POMC</i> methylation	None	4
96a	Moleres et al (2013) ⁹⁶	Spain	Non-randomized trial	107 overweight or obese adolescents undergoing a 10-week intensive lifestyle intervention	BMI, weight, waist circumference and fat mass	12-16 after the intervention	SD BMI scores	Peripheral blood	12-16 and after the intervention	7 candidate CpGs (MS, Sequenom EpiTyper)	CpGs in <i>AQP9</i> , <i>DUSP22</i> , <i>HIPK3</i> , <i>TNNI3</i> and <i>TNNT1</i> genes were significantly associated with changes in body weight, BMI-SD scores, waist circumference and fat mass after the weight loss intervention	None	None	6
97a	Obermann-Borst et al (2013) ⁹⁷	Netherlands	Longitudinal	120 children (men BMI:16.6)	Growth rate and BMI	0-17months	SD BMI scores and continuous growth rate	Peripheral blood	17 months	<i>LEP</i> DNA methylation (MS, Sequenom EpiTyper)	BMI at 17 months was associated with an overall lower <i>LEP</i> methylation (–3.3%/1.3 kg/m ² ; p= 0.04). Postnatal growth rate was not associated with <i>LEP</i> methylation	Bisulfite plate, correlation between individual CpG dinucleotides	None	6

Nr	Author (year)	Country	Study design	Study population	Anthropometric parameter			Epigenetic markers			Main findings	Confounders	Validation/Replication	NOS score
					Type	Age	Method	Tissue	Age	Target (method)				
98a	Kim et al (2012) ⁹⁸	US	Cross-sectional	47 children with obstructive apnoea syndrome and 31 controls	Overweight	~8	CDC SD BMI scores > 1.04	Peripheral blood	~8	<i>FOXP3</i> DNA methylation (pyrosequencing)	No significant differences emerged in <i>FOXP3</i> DNA methylation levels in overweight compared to not overweight children	None	In a subsample of 20 children <i>FOXP3</i> DNA methylation levels measured via pyrosequencing were not associated with SD BMI	5
99a	Groom et al (2012) ⁹⁹	UK	Longitudinal	Cohort 1: 94 children Cohort 2: 161 children	Rapid postnatal growth, BMI, fat mass (DEXA)	Rapid postnatal growth: 8 (cohort 1) and 12 weeks (cohort 2) BMI, fat mass: 11 (cohort 1) and 9 and 15 (cohort 2)	Rapid postnatal growth: difference in age- and sex-adjusted SD score weight between term and 8 (cohort 1) and 12 weeks (cohort 2) > median BMI and fat mass: continuous and SD	Cohort 1: peripheral blood at 11 y Cohort 2: cord blood and peripheral blood at 7 y	Cohort 1: 11 Cohort 2: birth and 7	<i>TACSTD2</i> DNA methylation (qPCR and pyrosequencing)	In cohort 1 <i>TACSTD2</i> DNA methylation at 11 years was higher in children with rapid growth and negatively correlated with fat mass at 11y. In cohort 2 <i>TACSTD2</i> DNA methylation at birth and at 7 years was not associated with rapid growth or fat mass at 7 or 15y	Sex and height	Findings in the two cohorts were inconsistent	7
100a	Relton et al (2012) ¹⁰⁰	UK	Longitudinal	178 children	BMI and fat mass	~9	Continuous	Cord blood	0	24 candidate genes DNA methylation (array, GoldenGate Assay Kit)	Methylation in 4 of the 24 genes studied was associated with at least one index of body composition (BMI, fat mass) at age 9 years, although none of these associations remained after correction for multiple testing	Plate, child sex, age, and height at the measurement	None	5
101a	Godfrey et al (2011) ¹⁰¹	UK	Longitudinal	78 children (mean fat mass: 5.4)	Body fat	9	Continuous	Cord blood	0	78 candidate genes DNA methylation (NimbleGen Systems HG17_min_promoter array), of which 5 were further analysed via Sequenom MassARRAY compact system	Higher methylation at 2 CpGs of the <i>RXRA</i> and <i>eNOS</i> genes was associated with childhood fat mass ($\beta = 17\%$ and 20% respectively, $p < 0.05$)	Child sex, mother's age, adiposity, and smoking	Replication in a cohort of 239 children confirmed association of <i>RXRA</i> cord blood methylation with fat mass at age 6 ($\beta = 6\%$, $p < 0.05$)	6
b) Non-coding RNA														
1b	Lin et al (2020) ¹⁰²	US	Cross-sectional	33 adolescents with obesity	Obesity differentiated in three classes. OB-1: 30 < BMI < 35, OB-2:	10-17	Obesity: BMI > 95th percentile attainment of puberty	Peripheral blood	10-17	179 miRNAs (qPCR, miRCURY LNA universal RT miRNA PCR)	miR-122-5p and miR-885-5p expression was higher in OB-2 compared to OB-3 or OB-1; miR-197-3p, -221-3p, -423-4p, and -125b-5p were lower in the OB-3 compared to the OB-2 group. miR-197-3p expression correlated	None	None	5

Nr	Author (year)	Country	Study design	Study population	Anthropometric parameter			Epigenetic markers			Main findings	Confounders	Validation/ Replication	NOS score
					Type	Age	Method	Tissue	Age	Target (method)				
					35<BMI<40, and OB-3: BMI>40 Weight and body fat		Continuous weight and body fat percentage				positively with body weight in the OB-3 group ($p < 0.001$) and levels of miR-125b-5p and miR-221-3p were strongly and negatively correlated with percent body fat, but positively associated with muscle mass (only miR-221-3p).			
2b	Mas-Parés et al (2019) ¹⁰³	Spain	Longitudinal	10 infants: 5 SGA-CU and 5 SGA-nonCU	Catch-up growth, weight and waist and hip circumference	1 and 6	Catch-up growth: >0.67 weight SD increase from birth to 1 year Weight and waist and hip circumference: SD scores	Cord blood	0	752 miRNAs (qPCR, miRCURY LNAuniversal RT miRNA PCR human panels I and II Exiqon)	12 miRNAs were differentially expressed between SGA-CU and SGA-nonCU children (miR-128-3p, miR-222-5p, miR-300, miR-374b-3p, miR-501-3p, miR-548c-5p, miR-576-5p, miR-628-5p, miR-770-5p, miR-873-5p, miR-876-3p, and miR-940) (all nominal $p < 0.05$). Among these 12 miRNAs, miR-576-5p showed significant positive associations with weight and catch-up weight at 12 months and weight and waist circumference at 6 years (nominal $p < 0.05$)	Newborn's sex, gestational age, birth weight and height, gestational smoking, parity, maternal BMI, and paternal height	Validation in 64 children confirmed only cord miR-576-5p as positively associated with catch-up growth at 1 year.	8
3b	Iacomino et al (2019) ¹⁰⁴	Belgium, Cyprus, Estonia, Germany, Hungary, Italy, Spain, and Sweden	Case-control	189 children: 159 with obesity and 149 controls	Obesity and BMI	~12	Obesity: IOTF SD score BMI BMI SD scores	Peripheral blood	~12	372 miRNAs (Serum and Plasma 384HC miScript miRNA PCR Arrays)	9 miRNAs were differentially expressed in children with obesity and controls ($p < 0.05$) and 5 (miR-10b-5p, miR-215-5p, miR-501-5p, miR-551a, and miR-874-3p) were correlated with BMI	Validation analysis was adjusted for age, sex, and country of origin	miR-10b-5p, miR-191-3p, miR-215-5p, miR-501-5p, miR-551a, miR-874-3p quantified by RT-qPCR were differentially expressed in children with obesity and controls. miR-874-3p and miR-501-5p in combination better predict obesity (AUC = 0.78)	9
4b	Marzano et al (2019) ¹⁰⁵	Italy	Case-control	16 children: 8 obese and 8 non-obese	Obesity	11.9	Sex- and age-adjusted BMI >95th percentile	Peripheral blood	11.9	Genome wide miRNA expression profile (array, Illumina microRNA sequencing platform)	7 miRNAs (miR-92a-3p, miR-122-5p, miR-423-5p, miR-484, miR-486-3p and miR-532, miR-181b-5p) were differentially expressed in	None	RT-qPCR in 54 children confirmed 2 out of the 7 miRNA	7

Nr	Author (year)	Country	Study design	Study population	Anthropometric parameter			Epigenetic markers			Main findings	Confounders	Validation/ Replication	NOS score
					Type	Age	Method	Tissue	Age	Target (method)				
											children with obesity compared to non-obese (FDRp<0.05)		associations: miR-122-5p and miR-486-3p (p<0.05)	
5b	Liu et al (2018) ¹⁰⁶	China	Case-control	8 children: 4 with obesity and 4 controls	Obesity, BMI, waist circumference and waist to hip ratio	~ 8	Obesity: BMI> 95th Chinese reference percentile SD BMI scores and continuous measurements of waist circumference and waist	Adipose tissue	~ 8	Genome wide long non-coding RNA expression profile (array, KangChen Bio-tech)	1268 long non-coding RNAs > 2-fold change in expression between obese and controls (p<0.05), Co-expression network of long non-coding RNAs and mRNA indicated that 10 lncRNAs were involved in biological processes (immune response, inflammatory response, fatty acid biosynthetic process, low-density lipoprotein particle remodelling, osteoclast differentiation, AMPK signalling pathway)	None	lncRNA RP11-20G13.3, lncRNA GYG2P1 quantified by QRT-PCR in 64 children were correlated with BMI-SDS, waist circumference, and lncRNA GYG2P1 was correlated with waist-hip ratio. In addition lncRNA RP11-20G13.3, LINC00968, AC011891.5, GYG2P1, RP11-529H2.1 and OLMALINC were differentially expressed between obese and controls	6
6b	Carreras-Badosa et al (2017) ¹⁰⁷	Spain	Longitudinal	70 infants (mean weight gain at 1 year: ~6Kg)	Weight gain	1, 4, and 12 months	Continuous	Placenta	0	Genome wide miRNA expression profile (array TaqMan miRNA low-density arrays)	miR-100, miR1285, and miR-487 were independent predictors of weight gain in the first month of life and explained nearly 15% of its variance. miR-100, miR-296, and miR-487 were independent predictors of weight gain at 4 and 12	Gestational age, maternal age, sex of newborn, pregestational BMI, and gestational weight gain	None	8

Nr	Author (year)	Country	Study design	Study population	Anthropometric parameter			Epigenetic markers			Main findings	Confounders	Validation/ Replication	NOS score
					Type	Age	Method	Tissue	Age	Target (method)				
											months of age and explained nearly 20% of its variance			
7b	Cui et al (2018) ¹⁰⁸	China	Case-control	18 children: 9 with obesity and 9 controls	Obesity and BMI	~5	Obesity: WHO SD BMI>3 (if age>60 months), >2 (if age <60 months) SD BMI scores	Peripheral blood	~5	Genome wide miRNA expression profile (array, Illumina microRNA sequencing platform)	94 miRNAs > 2-fold change in expression between obese and controls (p< 0.05)	None	8 miRNAs (miR-222, miR-486, miR-146b, miR-146a, miR-20a, miR-15b and miR-26b, miR-197) quantified by RT-qPCR were differentially expressed in 100 children with obesity and 146 controls (p< 0.05) and were correlated with BMI (p<0.05)	6
8b	Ouyang et al (2017) ¹⁰⁹	China	Case-control	12 children: 6 with obesity and 6 lean	Obesity	3-4	BMI>18.5 and <26 (obese) and >13.5 and <15 (lean)	Peripheral blood (PBMCs)	3-4	800 miRNAs (multiplexed, NanoString nCounter assay)	9 miRNAs (miR-301a-3p, miR-199a-3p/-199b-3p, miR-191-5p, miR-130a-3p, miR-361-5p, miR-126-3p, let-7g-5p, miR-4454) were differentially expressed in obese compared to lean children (p<0.05)	None	None	5
9b	Iacomino et al (2016) ¹¹⁰	Italy	Case-control	20 children: 10 with obesity and 10 controls	Obesity	~10	Obesity: IOTF SD score BMI BMI SD scores	Peripheral blood	~12	372 miRNAs (Serum and Plasma 384HC miScript miRNA PCR Arrays)	8 miRNAs were differentially expressed in children with obesity and controls (p< 0.05, >4-fold change)	Validation analysis was adjusted for age, sex, and country of origin	miR-31-5p, miR-2355-5p, miR-20 quantified by RT-qPCR were differentially expressed in children with obesity and controls (p< 0.05)	7
10b	Masotti et al (2016) ¹¹¹	Italy	Case-control	12 children with obesity: 6 insulin resistant (mean	Subcutaneous abdominal tissue thickness	2.0–5.8	Continuous	Peripheral blood	2.0–5.8	179 miRNAs (qPCR, miRCURY LNA universal RT miRNA PCR)	miRNA-660-5p, miRNA-205-5p and miRNA-95 were negatively correlated with subcutaneous abdominal tissue thickness in the 12 children with obesity	None	None	6

Nr	Author (year)	Country	Study design	Study population	Anthropometric parameter			Epigenetic markers			Main findings	Confounders	Validation/ Replication	NOS score
					Type	Age	Method	Tissue	Age	Target (method)				
				subcutaneous abdominal tissue thickness: 12.7 mm) and 6 controls (mean subcutaneous abdominal tissue thickness: 4.3mm)	(ultrasound)									
11b	Prats-Puig et al (2013) ¹¹²	Spain	Case-control	10 boys: 5 boys with obesity and 5 lean boys	Obesity and BMI	~9	Obesity: SD BMI>2 SD BMI scores	Peripheral blood	~9	Genome wide miRNA expression profile (array, TaqMan miRNA low-density arrays)	193 miRNAs were differentially expressed in children with obesity and lean children (Ct value< 35).	Age and sex	15 miRNAs (miR-486-5p, miR-486-3p, miR-221, miR-28-3p, miR-142-3p, miR-130b, miR-423-5p, miR-532-5p, miR-125b, miR-140-5, miR-16-1, pmiR-328, miR-222, miR-363, miR-122) quantified by RT-qPCR were differentially expressed in 85 lean compared to 40 obese children and 10 miRNAs (miR-486-5p, miR-28-3p, miR-142-3p, miR-130b, miR-532-5p, miR-125b, miR-140-5, miR-16-1, miR-222, miR-122)	8

Nr	Author (year)	Country	Study design	Study population	Anthropometric parameter			Epigenetic markers			Main findings	Confounders	Validation/ Replication	NOS score
					Type	Age	Method	Tissue	Age	Target (method)				
													were significantly associated with normalized BMI changes during 3 year follow-up in 45 children (p< 0.05)	
12b	Cabiati et al (2020) ¹¹³	Italy	Case-control	77 adolescents (25 normal and 52 obese)	Obesity, BMI and fat mass (impedance)	~13	Obesity: BMI> IOTF SD score BMI cut-offs SD BMI scores, fat mass percentage	Peripheral blood	~13	5 miRNAs (miR-33a-3p, miR-223-5p, miR-142-5, miR-199-5p and miR4454) (RT-qPCR)	miR-223-5p and miR-33a-3p resulted significantly (p = 0.05) higher in obese (0.97 ± 0.1; 0.85 ± 0.1, respectively) than in normal adolescents (0.66 ± 0.11; 0.51 ± 0.08, respectively). miR-142-5p, miR-4454 and miR-199-5p correlated positively with fat mass and BMI (all p<0.05)	None	None	6
13b	Duarte et al (2020) ¹¹⁴	Chile	Case-control	44 children (mean BMI: ~18); 24 with type 1 diabetes and 20 without	BMI, waist circumference, and body fat percentage (impedance)	3.2-16.1	Continuous BMI and SD BMI, waist circumference, and body fat percentage	Peripheral blood	3.2-16.1	miRNA 378 (TaqMan PCR)	miRNA 378 expression was not correlated with BMI, waist circumference, and body fat percentage	None	None	5
14b	Al-Rawaf (2019) ¹¹⁵	Saudi Arabia	Case-control	250 adolescents: 100 children with obesity, 100 with overweight and 50 controls	Obesity	12-18	BMI>22 (obese) and >17.4 & <21.45 (overweight)	Peripheral blood	12-18	10 miRNAs (RT-qPCR)	All 10 miRNAs (miR-142-3p, miR-140-5p, miR-222, miR-143, miR-130, miR-532-5p, miR-423-5p, miR-520c-3p, miR-146a, and miR-15a) were differentially expressed in children with obesity and overweight compared to controls	None	None	5
15b	Donghui et al (2019) ¹¹⁶	China	Quasi-randomized controlled before-and-after intervention	67 adolescents: 57 obese completed 6-week diet and exercise intervention (mean BMI pre: 33; post: 30) and 10 normal weight controls (mean BMI	BMI	15.3 and after 6-week intervention	Continuous	Peripheral blood	15.3 and after 6-week intervention	miR-126 (qPCR)	Positive correlation between change in miR-126 and change in BMI following the intervention (r = 0.60, p < 0.01)	None	None	6

Nr	Author (year)	Country	Study design	Study population	Anthropometric parameter			Epigenetic markers			Main findings	Confounders	Validation/Replication	NOS score
					Type	Age	Method	Tissue	Age	Target (method)				
				pre: 23; post: 23)										
16b	Ahmadpour et al (2018) ¹¹⁷	Iran	Case-control	70 children: 35 obese and 35 controls	Obesity	8-16	CDC BMI> 95th percentile for age	Peripheral blood	8-16	miR-34a and miR-149 (RT qPCR)	No difference between the 2 miRNAs in obese and control group was detected	None	None	6
17b	Thompson et al (2017) ¹¹⁸	US	Case-control	30 children: 10 with obesity and NAFLD and 20 controls	Obesity and BMI	8-18	Obesity: BMI> 95th percentile for age BMI continuous	Peripheral blood	8-18	20 miRNAs associated with NAFLD (RT-qPCR, Exiqon Pick-&-Mix miRNA PCR panel)	16 miRNAs (mir15b-5p, mir23a-3p, mir21-5p, mir27b-3p, mir34a-5p, mir103a-5p, mir122-5p, mir155-5p, mir181b-5p, mir223-3p, mir191-5p, mir192-5p, mir199a-5p, mir214-5p, mir222-3p) were differentially expressed (>2fold change and p< 0.05) in children with obesity compared to controls. 5 miRNAs (miR-21, miR-27b, miR-29a, miR-150 and miR-223) were associated with BMI (p< 0.05)	None	None	4
18b	Can et al (2015) ¹¹⁹	Turkey	Case-control	86 adolescents: 45 with obesity and 41 controls	Obesity	~14	BMI> 95th Turkish reference percentile	Peripheral blood	~14	7 miRNAs (RT-qPCR, LNA PCR primary set)	miR-335, miR-143, miR-758, miR-27, miR-378 and miR-370 were differentially expressed in children with obesity and controls (p< 0.05)	None	None	5
19b	Carolan et al (2014) ¹²⁰	Ireland	Case-control	49 children: 29 with obesity and 20 controls	Obesity	6-18	BMI> IOTF SD score BMI cut-offs	Peripheral blood (PBMCs)	6-18	3 miRNAs (qPCR)	miR-33a and miR-33b were differentially expressed (4- and 3-fold changes, respectively and p< 0.05) in children with obesity compared to controls	None	None	4
c) Histone modification														
1c	Scarpato et al (2011) ¹²¹	Italy	Case-control	129 children: 81 overweight/obese and 38 normal weight children	Obesity	11.1	BMI> IOTF SD score BMI cut-offs	Peripheral blood (T cells)	11.1	γ -H2AX (immunofluorescence)	Overweight and obese children had significantly higher levels of H2AX phosphorylation compared to normal weighted children (0.02 vs 0.03 γ -H2AXF per nucleus, p<0.01)	None	None	6

AGA= adequate for gestational age; BIA= bioelectrical impedance analysis; CDC= Centers for Disease Control; EUGR= extra uterine growth restriction; NA= not available information; MR= magnetic resonance; MS= mass spectrometry; MS-MLPA= methylation specific multiplex ligation-dependent probe amplification; lncRNA=long non-coding RNA; NAFLD= non alcoholic fatty liver disease; PBMCs=peripheral blood mononuclear cells; (q)PCR= (quantitative)polymerase chain reaction; RRBS=reduced representation bisulfite sequencing; RT= real time; SGA-CU= small for gestational age without catch-up growth ; SGA-nonCU= SGA without catch-up; WHO= world health organization

Table S4. List of the genes found to be differentially methylated with obesity or anthropometric parameters in infancy and childhood

nr	Author	CpG	Gene	measure
1a	Cadiou et al (2020)	cg02032125		BMI
2a	Gagné-Ouellet et al (2020a)	cg22436429	<i>CPED1, WNT16 FAM3C</i>	BMI
2a	Gagné-Ouellet et al (2020a)	cg22593959	<i>TFAP2E</i>	BMI
2a	Gagné-Ouellet et al (2020a)		<i>BMPR1B</i>	BMI
2a	Gagné-Ouellet et al (2020a)		<i>SKAP2</i>	BMI
2a	Gagné-Ouellet et al (2020a)		<i>MAGI2</i>	BMI
2a	Gagné-Ouellet et al (2020a)		<i>FMN1</i>	BMI
2a	Gagné-Ouellet et al (2020a)	cg22436429	<i>CPED1, WNT16 FAM3C</i>	SS+TR
2a	Gagné-Ouellet et al (2020a)	cg22593959	<i>TFAP2E</i>	SS+TR
2a	Gagné-Ouellet et al (2020a)		<i>BMPR1B</i>	SS+TR
2a	Gagné-Ouellet et al (2020a)		<i>SKAP2</i>	SS+TR
2a	Gagné-Ouellet et al (2020a)		<i>MAGI2</i>	SS+TR
2a	Gagné-Ouellet et al (2020a)		<i>FMN1</i>	SS+TR
6a	Vehmeijer et al (2020)	cg05937453	<i>SFRP5</i>	BMI
6a	Vehmeijer et al (2020)	cg25212453	<i>SLC43A2</i>	BMI
6a	Vehmeijer et al (2020)	cg03500056	<i>ABAT</i>	BMI
6a	Vehmeijer et al (2020)	cg05281708	<i>ZNF35</i>	BMI
6a	Vehmeijer et al (2020)	cg15125798		BMI
6a	Vehmeijer et al (2020)	cg04456029	<i>DTX1</i>	BMI
6a	Vehmeijer et al (2020)	cg03431111	<i>SNORD30</i>	BMI
6a	Vehmeijer et al (2020)	cg26889953	<i>CYFIP1</i>	BMI
6a	Vehmeijer et al (2020)	cg19743522	<i>DTX1</i>	BMI
6a	Vehmeijer et al (2020)	cg25877069		BMI
6a	Vehmeijer et al (2020)	cg13931559	<i>MAP1LC3A</i>	BMI
6a	Vehmeijer et al (2020)	cg10040131	<i>SFXN5</i>	BMI
6a	Vehmeijer et al (2020)	cg06991974	PRDM16-DT	obesity
7a	Cao-Lei et al (2019)	cg00152799	<i>TXNL1</i>	obesity
7a	Cao-Lei et al (2019)	cg00320354	<i>TSPAN5</i>	obesity
7a	Cao-Lei et al (2019)	cg00340052	<i>AGAP1</i>	obesity
7a	Cao-Lei et al (2019)	cg01520956	<i>FAM47E</i>	obesity
7a	Cao-Lei et al (2019)	cg01835922		obesity
7a	Cao-Lei et al (2019)	cg03877767	<i>GREB1</i>	obesity
7a	Cao-Lei et al (2019)	cg05248234	<i>FSCN2</i>	obesity
7a	Cao-Lei et al (2019)	cg05545777		obesity
7a	Cao-Lei et al (2019)	cg05808124		obesity
7a	Cao-Lei et al (2019)	cg05834845	<i>MUC4</i>	obesity
7a	Cao-Lei et al (2019)	cg06052372		obesity
7a	Cao-Lei et al (2019)	cg06508867		obesity

7a	Cao-Lei et al (2019)	cg06549275	ASAP2	obesity
7a	Cao-Lei et al (2019)	cg06916011	EPS8L1	obesity
7a	Cao-Lei et al (2019)	cg07248242	TSPAN9	obesity
7a	Cao-Lei et al (2019)	cg07437923	DNAJA3	obesity
7a	Cao-Lei et al (2019)	cg07618759	COL4A2	obesity
7a	Cao-Lei et al (2019)	cg08282428	RBM46	obesity
7a	Cao-Lei et al (2019)	cg09949906	HLA-DRB1	obesity
7a	Cao-Lei et al (2019)	cg10764750		obesity
7a	Cao-Lei et al (2019)	cg10977910	TTLL7	obesity
7a	Cao-Lei et al (2019)	cg11251367	FMN2	obesity
7a	Cao-Lei et al (2019)	cg11317459		obesity
7a	Cao-Lei et al (2019)	cg14007688	DBH	obesity
7a	Cao-Lei et al (2019)	cg14377951	GSTM5	obesity
7a	Cao-Lei et al (2019)	cg15586842	ANXA8L2	obesity
7a	Cao-Lei et al (2019)	cg16507569	COL11A2	obesity
7a	Cao-Lei et al (2019)	cg19181528		obesity
7a	Cao-Lei et al (2019)	cg19697575		obesity
7a	Cao-Lei et al (2019)	cg20756026	HEXDC	obesity
7a	Cao-Lei et al (2019)	cg21040096	RPH3AL	obesity
7a	Cao-Lei et al (2019)	cg21158163		obesity
7a	Cao-Lei et al (2019)	cg23336892		obesity
7a	Cao-Lei et al (2019)	cg23477460		obesity
7a	Cao-Lei et al (2019)	cg25013753	ARHGAP22	obesity
7a	Cao-Lei et al (2019)	cg25813936	GNE	obesity
7a	Cao-Lei et al (2019)	cg26590106	HLA-DRB1	obesity
7a	Cao-Lei et al (2019)	cg26658743		obesity
7a	Cao-Lei et al (2019)	cg26935333		obesity
7a	Cao-Lei et al (2019)	cg27112983		obesity
7a	Cao-Lei et al (2019)	cg27289463		obesity
7a	Cao-Lei et al (2019)	cg27362989	HLA-DRB5	obesity
7a	Cao-Lei et al (2019)	cg27413643	ANKRD27;RGS9B P	obesity
8a	He et al (2019)	Chr6: 100903612	SIM1	BMI
9a	Huang et al (2018)	cg09571082		BMI
9a	Huang et al (2018)	cg11412418		BMI
9a	Huang et al (2018)	cg17298543	GNAI1	BMI
9a	Huang et al (2018)	cg24618739	PRTFDC1	BMI
10a	Kaufman et al (2018)	cg14855841	CXCL10	BMI
10a	Kaufman et al (2018)	cg01555853	KCNS3	BMI
10a	Kaufman et al (2018)	cg10264529	PCK2	BMI
10a	Kaufman et al (2018)	cg14929207	DHRS13	BMI
10a	Kaufman et al (2018)	cg16110788		BMI
10a	Kaufman et al (2018)	cg26103104		BMI
11a	Li et al (2018)	cg02301920	CES1	obesity

11a	Li et al (2018)	cg05995465	<i>HDAC4</i>	obesity
11a	Li et al (2018)	cg12556569	<i>APOA5</i>	obesity
11a	Li et al (2018)	cg27288829	<i>RAX2</i>	obesity
12a	van Dijk et al (2018)	region	<i>KCNQ1DN</i>	BMI
12a	van Dijk et al (2018)	region	<i>nc886</i>	BMI
12a	van Dijk et al (2018)	region	<i>TNXB</i>	BMI
14a	Fradin et al (2017)	cg00103778		obesity
14a	Fradin et al (2017)	cg00204501	<i>TJP1</i>	severe obesity
14a	Fradin et al (2017)	cg00256512	<i>COLEC11</i>	severe obesity
14a	Fradin et al (2017)	cg00468146	<i>ID4</i>	severe obesity
14a	Fradin et al (2017)	cg00481644	<i>LOC254559</i>	severe obesity
14a	Fradin et al (2017)	cg00562180		obesity
14a	Fradin et al (2017)	cg00642749	<i>SEMA5A</i>	severe obesity
14a	Fradin et al (2017)	cg00699945	<i>NKX6-2</i>	severe obesity
14a	Fradin et al (2017)	cg00745170	<i>TEKT5</i>	severe obesity
14a	Fradin et al (2017)	cg00810836	<i>DNM1L</i>	severe obesity
14a	Fradin et al (2017)	cg00912939	<i>PRKRIP1</i>	severe obesity
14a	Fradin et al (2017)	cg01145903		severe obesity
14a	Fradin et al (2017)	cg01370575	<i>CLK3</i>	severe obesity
14a	Fradin et al (2017)	cg01436254	<i>CD86</i>	severe obesity
14a	Fradin et al (2017)	cg01612292	<i>FAM83H</i>	severe obesity
14a	Fradin et al (2017)	cg01826211	<i>ATP2A1</i>	severe obesity
14a	Fradin et al (2017)	cg01883662	<i>TM4SF19</i>	severe obesity
14a	Fradin et al (2017)	cg01971089	<i>SH3GL1</i>	severe obesity
14a	Fradin et al (2017)	cg02008175	<i>NDUFB4</i>	severe obesity
14a	Fradin et al (2017)	cg02139338	<i>STK32C</i>	severe obesity
14a	Fradin et al (2017)	cg02332525	<i>GRM7</i>	severe obesity
14a	Fradin et al (2017)	cg02399233	<i>NADSYN1</i>	obesity
14a	Fradin et al (2017)	cg02477354	<i>SHFM1</i>	severe obesity
14a	Fradin et al (2017)	cg02553520	<i>ATP6V1C2</i>	severe obesity
14a	Fradin et al (2017)	cg02585091		severe obesity
14a	Fradin et al (2017)	cg02644867	<i>C19orf23</i>	severe obesity
14a	Fradin et al (2017)	cg02674870		severe obesity
14a	Fradin et al (2017)	cg02825171	<i>DACT2</i>	severe obesity
14a	Fradin et al (2017)	cg02825977	<i>CYP26C1</i>	severe obesity
14a	Fradin et al (2017)	cg03495195	<i>COL2A1</i>	severe obesity
14a	Fradin et al (2017)	cg03607644		obesity
14a	Fradin et al (2017)	cg04052934		obesity
14a	Fradin et al (2017)	cg04286337	<i>TNXB</i>	severe obesity
14a	Fradin et al (2017)	cg04361015	<i>CUX1</i>	severe obesity
14a	Fradin et al (2017)	cg04483469	<i>EPHB4</i>	severe obesity
14a	Fradin et al (2017)	cg04617936		severe obesity
14a	Fradin et al (2017)	cg04655995	<i>ATP2C2</i>	severe obesity

14a	Fradin et al (2017)	cg04749646	<i>MARCH03</i>	severe obesity
14a	Fradin et al (2017)	cg04974899	<i>ENTPD6</i>	severe obesity
14a	Fradin et al (2017)	cg05129568	<i>FLOT1</i>	severe obesity
14a	Fradin et al (2017)	cg05209584	<i>FBN2</i>	severe obesity
14a	Fradin et al (2017)	cg05338930	<i>MGAT5B</i>	severe obesity
14a	Fradin et al (2017)	cg05370555	<i>C14orf166B</i>	severe obesity
14a	Fradin et al (2017)	cg05503968	<i>FAM59A</i>	severe obesity
14a	Fradin et al (2017)	cg05663573	<i>SLC7A14</i>	severe obesity
14a	Fradin et al (2017)	cg05896042	<i>RAB3D</i>	severe obesity
14a	Fradin et al (2017)	cg06022832	<i>NCOA1</i>	severe obesity
14a	Fradin et al (2017)	cg06076277		severe obesity
14a	Fradin et al (2017)	cg06491244	<i>WNT3</i>	severe obesity
14a	Fradin et al (2017)	cg06560169		severe obesity
14a	Fradin et al (2017)	cg06593910	<i>CYBA</i>	severe obesity
14a	Fradin et al (2017)	cg06686058	<i>ADM</i>	severe obesity
14a	Fradin et al (2017)	cg06686058	<i>ADM</i>	obesity
14a	Fradin et al (2017)	cg06769708	<i>DLGAP4</i>	severe obesity
14a	Fradin et al (2017)	cg06769708	<i>DLGAP4</i>	obesity
14a	Fradin et al (2017)	cg06797156		severe obesity
14a	Fradin et al (2017)	cg06822090	<i>RADIL</i>	severe obesity
14a	Fradin et al (2017)	cg06915343	<i>HDAC4</i>	severe obesity
14a	Fradin et al (2017)	cg06918474	<i>MARCH03</i>	obesity
14a	Fradin et al (2017)	cg06954761	<i>ITPR3</i>	severe obesity
14a	Fradin et al (2017)	cg06960457	<i>GMDS</i>	severe obesity
14a	Fradin et al (2017)	cg07060864		severe obesity
14a	Fradin et al (2017)	cg07060864		obesity
14a	Fradin et al (2017)	cg07065008	<i>SAMM50</i>	severe obesity
14a	Fradin et al (2017)	cg07269557	<i>MCF2L2</i>	severe obesity
14a	Fradin et al (2017)	cg07364162	<i>PRDM16</i>	severe obesity
14a	Fradin et al (2017)	cg07423363	<i>SLC16A1</i>	severe obesity
14a	Fradin et al (2017)	cg07533824	<i>CACNA1A</i>	severe obesity
14a	Fradin et al (2017)	cg07607077	<i>C7orf20</i>	severe obesity
14a	Fradin et al (2017)	cg07607077	<i>C7orf20</i>	obesity
14a	Fradin et al (2017)	cg07944420	<i>ACSF3</i>	severe obesity
14a	Fradin et al (2017)	cg07962934	<i>FAM83H</i>	severe obesity
14a	Fradin et al (2017)	cg08025415	<i>TLE2</i>	obesity
14a	Fradin et al (2017)	cg08169949	<i>RPA2</i>	severe obesity
14a	Fradin et al (2017)	cg08468401		obesity
14a	Fradin et al (2017)	cg08478709		severe obesity
14a	Fradin et al (2017)	cg08515072		obesity
14a	Fradin et al (2017)	cg08892370	<i>MGC12982</i>	severe obesity
14a	Fradin et al (2017)	cg09075268	<i>CACNA1H</i>	severe obesity
14a	Fradin et al (2017)	cg09471611		severe obesity

14a	Fradin et al (2017)	cg09559189	<i>EBF2</i>	severe obesity
14a	Fradin et al (2017)	cg09694782		severe obesity
14a	Fradin et al (2017)	cg10200202	<i>RGS10</i>	severe obesity
14a	Fradin et al (2017)	cg10269548	<i>RASL11B</i>	severe obesity
14a	Fradin et al (2017)	cg10519460		severe obesity
14a	Fradin et al (2017)	cg11324650		obesity
14a	Fradin et al (2017)	cg11337289	<i>DZIP1</i>	severe obesity
14a	Fradin et al (2017)	cg11496093	<i>GMPS</i>	severe obesity
14a	Fradin et al (2017)	cg11562028	<i>FAT2</i>	severe obesity
14a	Fradin et al (2017)	cg11671115		severe obesity
14a	Fradin et al (2017)	cg11969213	<i>LOC100133991; FMNL1</i>	severe obesity
14a	Fradin et al (2017)	cg12093371		severe obesity
14a	Fradin et al (2017)	cg12093371		obesity
14a	Fradin et al (2017)	cg12656475	<i>STEAP2</i>	severe obesity
14a	Fradin et al (2017)	cg12808596	<i>ZP1</i>	severe obesity
14a	Fradin et al (2017)	cg13195955	<i>NEU1</i>	severe obesity
14a	Fradin et al (2017)	cg13740815	<i>SHANK1</i>	severe obesity
14a	Fradin et al (2017)	cg13844049		severe obesity
14a	Fradin et al (2017)	cg13844049		obesity
14a	Fradin et al (2017)	cg13867039	<i>PRDM16</i>	severe obesity
14a	Fradin et al (2017)	cg14294240	<i>VLDLR</i>	severe obesity
14a	Fradin et al (2017)	cg14314029		severe obesity
14a	Fradin et al (2017)	cg14712531		severe obesity
14a	Fradin et al (2017)	cg14720024		severe obesity
14a	Fradin et al (2017)	cg14720024		obesity
14a	Fradin et al (2017)	cg14779951	<i>C3orf25</i>	severe obesity
14a	Fradin et al (2017)	cg15450098	<i>HLX</i>	severe obesity
14a	Fradin et al (2017)	cg15555970	<i>TGIF1</i>	severe obesity
14a	Fradin et al (2017)	cg15584221	<i>HHAT</i>	severe obesity
14a	Fradin et al (2017)	cg15676040	<i>RUSC1</i>	severe obesity
14a	Fradin et al (2017)	cg15882999	<i>P4HB</i>	severe obesity
14a	Fradin et al (2017)	cg15991546	<i>DPYD</i>	severe obesity
14a	Fradin et al (2017)	cg15991546	<i>DPYD</i>	obesity
14a	Fradin et al (2017)	cg16081228	<i>ACVR2A</i>	severe obesity
14a	Fradin et al (2017)	cg16111073	<i>DNAH10</i>	severe obesity
14a	Fradin et al (2017)	cg16209860	<i>ARFRP1; ZGPAT</i>	severe obesity
14a	Fradin et al (2017)	cg16331674		obesity
14a	Fradin et al (2017)	cg16334849		severe obesity
14a	Fradin et al (2017)	cg16334849		obesity
14a	Fradin et al (2017)	cg16427670	<i>ARHGEF7</i>	obesity
14a	Fradin et al (2017)	cg16451431	<i>NXPH4</i>	severe obesity
14a	Fradin et al (2017)	cg16668042	<i>HSPA4</i>	severe obesity
14a	Fradin et al (2017)	cg16705578		obesity

14a	Fradin et al (2017)	cg16906712	<i>HIST1H2BG;HIST1H2AE</i>	obesity
14a	Fradin et al (2017)	cg16946840	<i>MED12L</i>	severe obesity
14a	Fradin et al (2017)	cg17023648	<i>ASAP3</i>	severe obesity
14a	Fradin et al (2017)	cg17112828	<i>LRRN2</i>	severe obesity
14a	Fradin et al (2017)	cg17128312	<i>FBXW9</i>	obesity
14a	Fradin et al (2017)	cg17594047		severe obesity
14a	Fradin et al (2017)	cg17946714	<i>DOPEY2</i>	severe obesity
14a	Fradin et al (2017)	cg18008451	<i>COL1A1</i>	severe obesity
14a	Fradin et al (2017)	cg18192252	<i>STL</i>	severe obesity
14a	Fradin et al (2017)	cg18347642	<i>KCNIP4</i>	severe obesity
14a	Fradin et al (2017)	cg18548288	<i>ZNF766</i>	severe obesity
14a	Fradin et al (2017)	cg18592294	<i>THOP1</i>	severe obesity
14a	Fradin et al (2017)	cg19058414	<i>COX6B1</i>	severe obesity
14a	Fradin et al (2017)	cg19393008	<i>KRT82</i>	severe obesity
14a	Fradin et al (2017)	cg19596755	<i>CPT1A</i>	severe obesity
14a	Fradin et al (2017)	cg19733463	<i>NMUR1</i>	severe obesity
14a	Fradin et al (2017)	cg19835478	<i>COL6A1</i>	severe obesity
14a	Fradin et al (2017)	cg19835478	<i>COL6A1</i>	obesity
14a	Fradin et al (2017)	cg19868691	<i>WNT10A</i>	severe obesity
14a	Fradin et al (2017)	cg20172500	<i>GRM7</i>	severe obesity
14a	Fradin et al (2017)	cg21000165	<i>HNRNPA1L2</i>	severe obesity
14a	Fradin et al (2017)	cg21014159	<i>DSCAML1</i>	severe obesity
14a	Fradin et al (2017)	cg21090033	<i>TM4SF19</i>	severe obesity
14a	Fradin et al (2017)	cg21213617	<i>LHX6</i>	severe obesity
14a	Fradin et al (2017)	cg21773820		severe obesity
14a	Fradin et al (2017)	cg21869027	<i>MIR365-2</i>	severe obesity
14a	Fradin et al (2017)	cg21940756	<i>GRK4</i>	severe obesity
14a	Fradin et al (2017)	cg22218447		severe obesity
14a	Fradin et al (2017)	cg22318948	<i>LENG8</i>	severe obesity
14a	Fradin et al (2017)	cg22496559	<i>TM4SF19</i>	severe obesity
14a	Fradin et al (2017)	cg22588640	<i>KCNIP3</i>	severe obesity
14a	Fradin et al (2017)	cg22951128	<i>DIP2C</i>	severe obesity
14a	Fradin et al (2017)	cg23043119	<i>STARD4</i>	severe obesity
14a	Fradin et al (2017)	cg23043119	<i>STARD4</i>	obesity
14a	Fradin et al (2017)	cg23314826		severe obesity
14a	Fradin et al (2017)	cg23314826		obesity
14a	Fradin et al (2017)	cg23470598	<i>KLC1</i>	severe obesity
14a	Fradin et al (2017)	cg23606023	<i>CBFA2T3</i>	severe obesity
14a	Fradin et al (2017)	cg24317742		obesity
14a	Fradin et al (2017)	cg24379332	<i>S1PR5</i>	severe obesity
14a	Fradin et al (2017)	cg24604214	<i>PRKCZ</i>	severe obesity
14a	Fradin et al (2017)	cg24635736	<i>PSTK</i>	severe obesity
14a	Fradin et al (2017)	cg24858417	<i>MAD1L1</i>	severe obesity

14a	Fradin et al (2017)	cg25124966	<i>TMEM45B</i>	severe obesity
14a	Fradin et al (2017)	cg25326491		severe obesity
14a	Fradin et al (2017)	cg25655069	<i>SPR</i>	severe obesity
14a	Fradin et al (2017)	cg25739882	<i>HAR1B; HAR1A</i>	severe obesity
14a	Fradin et al (2017)	cg25955817	<i>TAX1BP3</i>	severe obesity
14a	Fradin et al (2017)	cg26138821	<i>CHORDC1</i>	obesity
14a	Fradin et al (2017)	cg26645655		obesity
14a	Fradin et al (2017)	cg26823535		severe obesity
14a	Fradin et al (2017)	cg26834418	<i>CHORDC1</i>	severe obesity
14a	Fradin et al (2017)	cg26834418	<i>CHORDC1</i>	obesity
14a	Fradin et al (2017)	cg26856316	<i>GPR149</i>	severe obesity
14a	Fradin et al (2017)	cg27187555	<i>PRDM16</i>	severe obesity
14a	Fradin et al (2017)	cg27274322	<i>KIAA1530</i>	severe obesity
14a	Fradin et al (2017)	cg27328245		severe obesity
14a	Fradin et al (2017)	cg27590049	<i>LMX1A</i>	severe obesity
14a	Fradin et al (2017)	cg27665181	<i>MTSS1L</i>	severe obesity
15a	Kresovich et al (2017)	cg00885918	<i>MYLK2</i>	SS:TR
15a	Kresovich et al (2017)	cg03352173	<i>SLC9A10</i>	SS:TR
15a	Kresovich et al (2017)	cg09271157	<i>PPAPDC1A</i>	SS+TR
15a	Kresovich et al (2017)	cg11137145	<i>KPRP</i>	SS:TR
15a	Kresovich et al (2017)	cg14974711	<i>MMP25</i>	SS:TR
15a	Kresovich et al (2017)	cg20624923	<i>PRLHR</i>	SS:TR
15a	Kresovich et al (2017)	region	<i>GFPT2</i>	SS:TR
15a	Kresovich et al (2017)	region	<i>LOC100049716</i>	SS:TR
15a	Kresovich et al (2017)	region	<i>LOC102723493</i>	fat free mass
16a	Lillicrop et al (2017)	region	<i>CDKN2A</i>	BMI
17a	Rzehak et al (2017)	cg00384539	<i>PRDM14</i>	fat mass
17a	Rzehak et al (2017)	cg01706498	<i>KLHL6</i>	BMI
17a	Rzehak et al (2017)	cg04010122	<i>SOS1</i>	fat mass index
17a	Rzehak et al (2017)	cg08074767	<i>(MLLT4)</i>	fat free mass
17a	Rzehak et al (2017)	cg08692210	<i>WDR51A</i>	fat mass
17a	Rzehak et al (2017)	cg13850887	<i>SNED1</i>	BMI
17a	Rzehak et al (2017)	cg13850887	<i>SNED1</i>	fat mass index
17a	Rzehak et al (2017)	cg13850887	<i>SNED1</i>	fat mass index
17a	Rzehak et al (2017)	cg14518658	<i>(CYTH4-ELFN2)</i>	fat mass
17a	Rzehak et al (2017)	cg15026574	<i>ST6GAL1</i>	fat mass index
17a	Rzehak et al (2017)	cg17935297	<i>CILP2</i>	fat free mass index
17a	Rzehak et al (2017)	cg24332767	<i>C3orf70</i>	fat free mass
17a	Rzehak et al (2017)	cg26401512	<i>ZNF643</i>	fat mass index
17a	Rzehak et al (2017)	cg26627956	<i>CFLAR</i>	fat mass
17a	Rzehak et al (2017)	cg26627956	<i>CFLAR</i>	fat mass index
17a	Rzehak et al (2017)	cg27038634	<i>(LOC101929268)</i>	fat free mass
18a	Rounge et al (2016)	region	<i>CpGi:73</i>	obesity

18a	Rounge et al (2016)	region	<i>CpGi:76/MPL</i>	obesity
18a	Rounge et al (2016)	region	<i>IP6K1</i>	obesity
18a	Rounge et al (2016)	region	<i>KCNMB4, intron 5609/ABLM2 6512</i>	obesity
18a	Rounge et al (2016)	region	<i>LDHAL6B, MYO1E, MIR2116</i>	obesity
18a	Rounge et al (2016)	region	<i>NXN, gc16094767, rs62070219, rs62070218</i>	obesity
18a	Rounge et al (2016)	region	<i>TRPV5</i>	obesity
19a	Ding et al (2015)	region	<i>EIF6</i>	obesity
19a	Ding et al (2015)	region	<i>PRLHR</i>	obesity
19a	Ding et al (2015)	region	<i>EXOSC4</i>	obesity
19a	Ding et al (2015)	region	<i>FZD7</i>	obesity
21a	Huang et al (2015)	cg16436762	<i>PIWIL4</i>	obesity
21a	Huang et al (2015)	cg17627898	<i>TAOK3</i>	obesity
21a	Huang et al (2015)	cg26846943	<i>FYN</i>	obesity
21a	Huang et al (2015)	Chr6: 112165053	<i>FYN</i>	obesity
21a	Huang et al (2015)	Chr6: 112165057	<i>FYN</i>	obesity
22a	Quilter et al (2014)	cg27398547	<i>C14orf39</i>	infant weight gain
24a	Kochmanski et al (2019)	region	<i>PPARA</i>	obesity
24a	Kochmanski et al (2019)	region	<i>LINE-1</i>	obesity
25a	Dunstan et al (2017)	region	<i>LEP</i>	BMI
25a	Dunstan et al (2017)	region	<i>LEP</i>	weight
25a	Dunstan et al (2017)	region	<i>LEP</i>	obesity
25a	Dunstan et al (2017)	region	<i>LEP</i>	body fat
26a	Perng et al (2013)	region	<i>LINE-1</i>	BMI
26a	Perng et al (2013)	region	<i>LINE-1</i>	waist circumference
26a	Perng et al (2013)	region	<i>LINE-1</i>	SS:TR
27a	Prats-Puig et al (2020a)	region	<i>C19MC</i>	weight
27a	Prats-Puig et al (2020a)	region	<i>C19MC</i>	waist circumference
27a	Prats-Puig et al (2020a)	region	<i>C19MC</i>	hip circumference
27a	Prats-Puig et al (2020a)	region	<i>C19MC</i>	fat mass
29a	Gonzalez-Nahm et al (2018)	region	<i>PLAGL1</i>	infant weight
29a	Gonzalez-Nahm et al (2018)	region	<i>PEG10</i>	obesity
29a	Gonzalez-Nahm et al (2018)	region	<i>NNAT</i>	BMI
29a	Gonzalez-Nahm et al (2018)	region	<i>MEST</i>	infant weight
29a	Gonzalez-Nahm et al (2018)	region	<i>PEG10</i>	weight
30a	Junge et al (2018)	region	<i>MEST</i>	infant BMI
30a	Junge et al (2018)	region	<i>MEST</i>	BMI
31a	Ács et al (2017)	region	<i>IGF2</i>	BMI
31a	Ács et al (2017)	region	<i>CYP27B1</i>	BMI
32a	Thakali et al (2017)	region	<i>RAPTOR</i>	infant fat mass
33a	Bowman et al (2019)	region	<i>H19</i>	SS+TR

34a	Do et al (2019)	region	<i>IGF2</i>	BMI
35a	Bouwland-Both et al (2013)	region	<i>IGF2</i>	infant weight gain
38a	Perkins et al (2012)	region	<i>H19</i>	infant obesity
39a	Huang et al (2012)	region	<i>IGF2/H19</i>	skinfold thickness
39a	Huang et al (2012)	region	<i>IGF2/H19</i>	SAT
40a	Prats-Puig et al (2017)	region	<i>MEG3</i>	infant weight gain
47a	Breton et al (2020)	cg23166710	<i>NEGR1</i>	BMI
47a	Breton et al (2020)	cg26153364	<i>NEGR1</i>	BMI
48a	Chang et al (2020)	2 CpGs	<i>POLG</i>	BMI
48a	Chang et al (2020)	2 CpGs	<i>POLG</i>	waist circumference
48a	Chang et al (2020)	2 CpGs	<i>POLG</i>	body fat
48a	Chang et al (2020)	2 CpGs	<i>POLG</i>	hip circumference
49a	Choi et al (2020)	cg19196862	<i>IGF2R</i>	BMI
49a	Choi et al (2020)	cg19196862	<i>IGF2R</i>	infant BMI
50a	Diaz et al (2020)	region	<i>NKX6.1</i>	infant total fat
50a	Diaz et al (2020)	region	<i>GPR120</i>	infant total fat
50a	Diaz et al (2020)	region	<i>SLC2A8</i>	BMI
51a	Gagné-Ouellet et al (2020b)	cg05136031	<i>LEP</i>	BMI
51a	Gagné-Ouellet et al (2020b)	cg15758240	<i>LEP</i>	SS:TR
52a	Gallardo-Escribano et al (2020)	region	<i>LPL</i>	visceral fat
52a	Gallardo-Escribano et al (2020)	region	<i>LPL</i>	BMI
52a	Gallardo-Escribano et al (2020)	region	<i>LPL</i>	waist circumference
52a	Gallardo-Escribano et al (2020)	region	<i>SCD</i>	total fat
52a	Gallardo-Escribano et al (2020)	region	<i>LEP</i>	BMI
52a	Gallardo-Escribano et al (2020)	region	<i>LXR</i>	BMI
52a	Gallardo-Escribano et al (2020)	region	<i>LXR</i>	waist circumference
52a	Gallardo-Escribano et al (2020)	region	<i>LXR</i>	visceral fat
52a	Gallardo-Escribano et al (2020)	region	<i>LXR</i>	abdominal total mass
54a	Justice et al (2020)	cg00994936	<i>DAZAP1</i>	waist
54a	Justice et al (2020)	cg19693031	<i>TXNIP</i>	waist
56a	Mansell et al (2020a)	cg19594666	<i>LEP</i>	BMI
57a	Mansell et al (2020b)	region	<i>HIF3A</i>	BMI
58a	Prats-Puig et al (2020b)	<i>TTN_1</i>	<i>TTN</i>	BMI
58a	Prats-Puig et al (2020b)	<i>PAX3</i>	<i>PAX3</i>	BMI
58a	Prats-Puig et al (2020b)	<i>CXCL13_1</i>	<i>CXCL13</i>	BMI
58a	Prats-Puig et al (2020b)	<i>OBSCN_2</i>	<i>OBSCN</i>	BMI
58a	Prats-Puig et al (2020b)	<i>BDNF_2</i>	<i>BDNF</i>	BMI

58a	Prats-Puig et al (2020b)	<i>MYOF</i>	<i>MYOF</i>	BMI
58a	Prats-Puig et al (2020b)	<i>CXCL2</i>	<i>CXCL2</i>	fat mass
58a	Prats-Puig et al (2020b)	<i>TNNT3</i>	<i>TNNT3</i>	fat mass
58a	Prats-Puig et al (2020b)	<i>IL13</i>	<i>IL13</i>	fat mass
60a	Rushing et al (2020)	cg01307483	<i>NRF1</i>	obesity
61a	Clark et al (2019)	cg11324748	<i>ANKRD20A11P</i>	infant BMI gain
61a	Clark et al (2019)	cg13012494	<i>SPATC1L</i>	infant BMI gain
62a	Han et al (2019)	cg08770870	<i>RPH3AL</i>	BMI
62a	Han et al (2019)	cg19663246	<i>PDE1C</i>	BMI
63a	Lee (2019a)	cg01852095	<i>LRP1B</i>	BMI
63a	Lee (2019a)	cg01852095	<i>LRP1B</i>	waist to hip ratio
63a	Lee (2019a)	cg141441470	<i>LRP1B</i>	BMI
63a	Lee (2019a)	cg141441470	<i>LRP1B</i>	waist to hip ratio
63a	Lee (2019a)	cg141441481	<i>LRP1B</i>	BMI
63a	Lee (2019a)	cg141441481	<i>LRP1B</i>	waist to hip ratio
64a	Lee (2019b)	cg158269415	<i>PTPRN2</i>	BMI
64a	Lee (2019b)	cg158269415	<i>PTPRN2</i>	waist to hip ratio
65a	Lillicrop et al (2019)	CpG5	<i>SLC6A4</i>	fat mass
65a	Lillicrop et al (2019)	CpG5	<i>SLC6A4</i>	TR
65a	Lillicrop et al (2019)	CpG5	<i>SLC6A4</i>	infant TR
66a	Martin et al (2019)	cg17621507	<i>TAPBP</i>	BMI
66a	Martin et al (2019)	cg23922433	<i>TAPBP</i>	BMI
67a	Noor et al (2019)	cg01029450	<i>ARFGAP3</i>	BMI
68a	Sherwood et al (2019)	cg05091920	<i>LEP</i>	BMI
68a	Sherwood et al (2019)	cg2338105	<i>LEP</i>	BMI
69a	Tian et al (2019)	region	<i>LEP</i>	BMI
69a	Tian et al (2019)	region	<i>LEP</i>	waist to hip ratio
69a	Tian et al (2019)	region	<i>LEP</i>	SS+TR
70a	Chen et al (2018)	cg07035602	<i>LPCAT1</i>	visceral adiposity
71a	El Sayed et al (2018)	region	<i>MMP2</i>	obesity
71a	El Sayed et al (2018)	region	<i>LEP</i>	obesity
72a	Kwon et al (2018)	region	<i>POMC</i>	obesity
72a	Kwon et al (2018)	region	<i>NHF4A</i>	obesity
72a	Kwon et al (2018)	region	<i>MC4R</i>	obesity
73a	Tozzi et al (2018)	region	<i>IC1</i>	infant weight gain
74a	Wu et al (2018)	region	<i>IL6</i>	BMI
75a	Yang et al (2018)	region	<i>SH3PXD2A</i>	BMI
75a	Yang et al (2018)	region	<i>SH3PXD2A</i>	waist circumference
75a	Yang et al (2018)	region	<i>SH3PXD2A</i>	TR
75a	Yang et al (2018)	region	<i>SH3PXD2A</i>	Suprailiac skinfold thickness
75a	Yang et al (2018)	region	<i>SH3PXD2A</i>	SS
75a	Yang et al (2018)	region	<i>SH3PXD2A</i>	SAT
76a	Gagné-Ouellet et al (2017)	region	<i>LPL</i>	weight

76a	Gagné-Ouellet et al (2017)	region	<i>LPL</i>	fat mass
77a	Koh et al (2017)	cg07814318	<i>KLF13</i>	obesity
77a	Koh et al (2017)	cg07814318	<i>KLF13</i>	BMI
77a	Koh et al (2017)	cg07814318	<i>KLF13</i>	waist to hip ratio
78a	Lin et al (2017)	cg00510507	<i>ANK3</i>	infant weight
78a	Lin et al (2017)	cg00510507	<i>ANK3</i>	infant BMI
78a	Lin et al (2017)	cg02729344	<i>ZNF423</i>	infant weight
78a	Lin et al (2017)	cg02729344	<i>ZNF423</i>	infant BMI
78a	Lin et al (2017)	cg08390209	<i>CDKN2B</i>	infant weight
78a	Lin et al (2017)	cg08390209	<i>CDKN2B</i>	infant BMI
78a	Lin et al (2017)	cg14300531	<i>P4HA3</i>	infant weight
78a	Lin et al (2017)	cg14300531	<i>P4HA3</i>	infant BMI
78a	Lin et al (2017)	cg22383874	<i>CACNA1G</i>	infant weight
78a	Lin et al (2017)	cg22383874	<i>CACNA1G</i>	infant BMI
78a	Lin et al (2017)	cg23671997	<i>IGDCC4</i>	infant weight
78a	Lin et al (2017)	cg23671997	<i>IGDCC4</i>	infant BMI
78a	Lin et al (2017)	cg25487405	<i>MIRLET7BHG</i>	infant weight
78a	Lin et al (2017)	cg25685359	<i>MIRLET7BHG</i>	infant weight
79a	Mansego et al (2017)	cg00944580	<i>miR548D2</i>	obesity
79a	Mansego et al (2017)	cg02206323	<i>miR1180</i>	obesity
79a	Mansego et al (2017)	cg03918703	<i>miR208B</i>	obesity
79a	Mansego et al (2017)	cg04735660	<i>miR488</i>	obesity
79a	Mansego et al (2017)	cg06606539	<i>miR572</i>	obesity
79a	Mansego et al (2017)	cg07059402	<i>miR659</i>	obesity
79a	Mansego et al (2017)	cg08316488	<i>miR2114</i>	obesity
79a	Mansego et al (2017)	cg11210138	<i>miR1203</i>	obesity
79a	Mansego et al (2017)	cg11755251	<i>miR557</i>	obesity
79a	Mansego et al (2017)	cg15554966	<i>miR519E</i>	obesity
79a	Mansego et al (2017)	cg15787712	<i>miR24-2; miR23A; miR27A</i>	obesity
79a	Mansego et al (2017)	cg21230021	<i>miR412; miR410; miR409; miR369; miR541</i>	obesity
79a	Mansego et al (2017)	cg21285564	<i>miR1306</i>	obesity
79a	Mansego et al (2017)	cg24343835	<i>miR216A</i>	obesity
79a	Mansego et al (2017)	cg27069588	<i>miR892A</i>	obesity
79a	Mansego et al (2017)	cg27337176	<i>miR1-1</i>	obesity
80a	Volberg et al (2017)	region	<i>PPARγ</i>	BMI
81a	Richmond et al (2016)	cg27146050	<i>HIF3A</i>	BMI
84a	Gardner et al (2015)	region	<i>DNMT3B</i>	BMI
85a	Pan et al (2015)	cg27146050	<i>HIF3A</i>	infant weight
88a	Simpkin et al (2015)	cg15783941	<i>NFIX</i>	fat mass
89a	Wang et al (2015)	46801642	<i>HIF3A</i>	obesity
89a	Wang et al (2015)	46801699	<i>HIF3A</i>	obesity

90a	Wu et al (2015)	region	<i>FAIM2</i>	obesity
91a	Azzi et al (2014)	DMR	<i>ZAC1</i>	infant BMI
92a	Clarke-Harris et al (2014)	region	<i>PGC1a</i>	fat mass
93a	García-Cardona et al (2014)	region	<i>LEP</i>	obesity
93a	García-Cardona et al (2014)	region	<i>LEP</i>	BMI
93a	García-Cardona et al (2014)	region	<i>ADIPOQ</i>	obesity
94a	Su et al (2014)	cg01791232	<i>KREMEN1</i>	obesity
94a	Su et al (2014)	cg02212836	<i>LY86</i>	obesity
94a	Su et al (2014)	cg21655790	<i>LEPR</i>	obesity
94a	Su et al (2014)	cg26033681	<i>SNRPN</i>	obesity
96a	Moleres et al (2013)	region	<i>TNNT1</i>	weight
96a	Moleres et al (2013)	region	<i>TNNI3</i>	weight
96a	Moleres et al (2013)	region	<i>HIPK3</i>	weight
96a	Moleres et al (2013)	region	<i>DUSP22</i>	weight
96a	Moleres et al (2013)	region	<i>AQP9</i>	weight
96a	Moleres et al (2013)	region	<i>TNNT1</i>	BMI
96a	Moleres et al (2013)	region	<i>TNNI3</i>	BMI
96a	Moleres et al (2013)	region	<i>HIPK3</i>	BMI
96a	Moleres et al (2013)	region	<i>DUSP22</i>	BMI
96a	Moleres et al (2013)	region	<i>AQP9</i>	BMI
96a	Moleres et al (2013)	region	<i>TNNT1</i>	waist circumference
96a	Moleres et al (2013)	region	<i>TNNI3</i>	waist circumference
96a	Moleres et al (2013)	region	<i>HIPK3</i>	waist circumference
96a	Moleres et al (2013)	region	<i>DUSP22</i>	waist circumference
96a	Moleres et al (2013)	region	<i>AQP9</i>	waist circumference
96a	Moleres et al (2013)	region	<i>TNNT1</i>	fat mass
96a	Moleres et al (2013)	region	<i>TNNI3</i>	fat mass
96a	Moleres et al (2013)	region	<i>HIPK3</i>	fat mass
96a	Moleres et al (2013)	region	<i>DUSP22</i>	fat mass
96a	Moleres et al (2013)	region	<i>AQP9</i>	fat mass
97a	Obermann-Borst et al (2013)	region	<i>LEP</i>	infant BMI
99a	Groom et al (2012)	region	<i>TACSTD2</i>	infant weight gain
99a	Groom et al (2012)	region	<i>TACSTD2</i>	fat mass
100a	Relton et al (2012)	CASP10_P2	<i>CASP10</i>	BMI
100a	Relton et al (2012)	CDKN1C_P2	<i>CDKN1C</i>	BMI
100a	Relton et al (2012)	CDKN1C_P2	<i>CDKN1C</i>	Fat mass
100a	Relton et al (2012)	EPHA1_P	<i>EPHA1</i>	BMI
100a	Relton et al (2012)	EPHA1_P	<i>EPHA1</i>	Fat mass
100a	Relton et al (2012)	HLA_DOB3	<i>HLA_DOB3</i>	Fat mass
101a	Godfrey et al (2011)	chr9:136355885+	<i>RXRA</i>	fat mass
101a	Godfrey et al (2011)	region	<i>eNOS</i>	fat mass

SAT= subcutaneous adipose tissue; SS= subscapular skinfold thickness; TR= triceps skinfold thickness

Table S5. List of the non-coding RNAs found to be differentially expressed with obesity or anthropometric parameters in infancy and childhood

Nr	Author	miRNA	Associated anthropometric measure
1b	Lin et al (2020)	miR-122-5p	obesity
1b	Lin et al (2020)	miR-885-5p	obesity
1b	Lin et al (2020)	miR-197-3p	obesity
1b	Lin et al (2020)	miR-221-3p	obesity
1b	Lin et al (2020)	miR-423-4p	obesity
1b	Lin et al (2020)	miR-125b-5p	obesity
1b	Lin et al (2020)	miR-197-3p	weight
1b	Lin et al (2020)	miR-125b-5p	body fat
1b	Lin et al (2020)	miR-221-3p	body fat
2b	Mas-Parés et al (2019)	miR-576	infant weight gain
3b	Iacomino (2019)	miR-10b-5p	obesity
3b	Iacomino (2019)	miR-215-5p	obesity
3b	Iacomino (2019)	miR-501-5p	obesity
3b	Iacomino (2019)	miR551a	obesity
3b	Iacomino (2019)	miR-874-3pr	obesity
3b	Iacomino (2019)	miR-191-3p	obesity
4b	Marzano et al (2019)	miR-484	obesity
4b	Marzano et al (2019)	miR-92a-3p	obesity
4b	Marzano et al (2019)	miR-122-5p	obesity
4b	Marzano et al (2019)	miR-181b-5p	obesity
4b	Marzano et al (2019)	miR-423-5p	obesity
4b	Marzano et al (2019)	miR-486-3p	obesity
4b	Marzano et al (2019)	miR-532	obesity
5b	Liu et al (2018)	lncRNAGYG2P1	obesity
5b	Liu et al (2018)	lncRNARP11-20G13.3	obesity
6b	Carreras-Badosa et al (2017)	miR-100	infant weight gain
6b	Carreras-Badosa et al (2017)	miR-1285	infant weight gain
6b	Carreras-Badosa et al (2017)	miR-296	infant weight gain
6b	Carreras-Badosa et al (2017)	miR-487	infant weight gain
7b	Cui et al (2018)	miR-146a	BMI
7b	Cui et al (2018)	miR-146a	obesity
7b	Cui et al (2018)	miR-146b	BMI
7b	Cui et al (2018)	miR-146b	obesity
7b	Cui et al (2018)	miR-15b	BMI
7b	Cui et al (2018)	miR-15b	obesity
7b	Cui et al (2018)	miR-197	BMI
7b	Cui et al (2018)	miR-197	obesity
7b	Cui et al (2018)	miR-20a	BMI
7b	Cui et al (2018)	miR-20a	obesity

7b	Cui et al (2018)	miR-222	BMI
7b	Cui et al (2018)	miR-222	obesity
7b	Cui et al (2018)	miR-26b	BMI
7b	Cui et al (2018)	miR-26b	obesity
7b	Cui et al (2018)	miR-486	BMI
7b	Cui et al (2018)	miR-486	obesity
8b	Ouyang et al (2017)	let-7g-5p	obesity
8b	Ouyang et al (2017)	miR-301a-3p	obesity
8b	Ouyang et al (2017)	miR-361-5p	obesity
8b	Ouyang et al (2017)	miR-4454	obesity
8b	Ouyang et al (2017)	miR-126-3p	obesity
8b	Ouyang et al (2017)	miR-130a-3p	obesity
8b	Ouyang et al (2017)	miR-191-5p	obesity
8b	Ouyang et al (2017)	miR-199a-3p/-199b-3p	obesity
9b	Iacomino (2016)	miR-31-5p	BMI
9b	Iacomino (2016)	miR-20	BMI
9b	Iacomino (2016)	miR-2355-5p	BMI
10b	Masotti et al (2016)	miR-205	SAT
10b	Masotti et al (2016)	miR-660	SAT
10b	Masotti et al (2016)	miR-95	SAT
11b	Prats-Puig et al (2013)	miR-130b	obesity
11b	Prats-Puig et al (2013)	miR-221	obesity
11b	Prats-Puig et al (2013)	miR-328	obesity
11b	Prats-Puig et al (2013)	miR-363	obesity
11b	Prats-Puig et al (2013)	miR-122	obesity
11b	Prats-Puig et al (2013)	miR-122	BMI
11b	Prats-Puig et al (2013)	miR-125b	obesity
11b	Prats-Puig et al (2013)	miR-125b	BMI
11b	Prats-Puig et al (2013)	miR-130b	BMI
11b	Prats-Puig et al (2013)	miR-140-5p	obesity
11b	Prats-Puig et al (2013)	miR-140-5p	BMI
11b	Prats-Puig et al (2013)	miR-142-3p	obesity
11b	Prats-Puig et al (2013)	miR-142-3p	BMI
11b	Prats-Puig et al (2013)	miR-16-1	obesity
11b	Prats-Puig et al (2013)	miR-16-1	BMI
11b	Prats-Puig et al (2013)	miR-532-5p	obesity
11b	Prats-Puig et al (2013)	miR-222	obesity
11b	Prats-Puig et al (2013)	miR-222	BMI
11b	Prats-Puig et al (2013)	miR-28-3p	obesity
11b	Prats-Puig et al (2013)	miR-28-3p	BMI
11b	Prats-Puig et al (2013)	miR-423-5p	obesity
11b	Prats-Puig et al (2013)	miR-486-3p	obesity
11b	Prats-Puig et al (2013)	miR-486-5p	obesity

11b	Prats-Puig et al (2013)	miR-486-5p	BMI
11b	Prats-Puig et al (2013)	miR-532-5p	BMI
12b	Cabiati et al (2020)	miR-223-5p	obesity
12b	Cabiati et al (2020)	miR-33a-3p	obesity
12b	Cabiati et al (2020)	miR-142-5p	BMI
12b	Cabiati et al (2020)	miR-4454	BMI
12b	Cabiati et al (2020)	miR-199-5p	BMI
12b	Cabiati et al (2020)	miR-142-5p	fat mass
12b	Cabiati et al (2020)	miR-4454	fat mass
12b	Cabiati et al (2020)	miR-199-5p	fat mass
13b	Duarte et al (2014)	miR-378	BMI
14b	Al-Rawaf (2019)	miR-143	obesity
14b	Al-Rawaf (2019)	miR-143	BMI
14b	Al-Rawaf (2019)	miR-130	obesity
14b	Al-Rawaf (2019)	miR-130	BMI
14b	Al-Rawaf (2019)	miR-140-5p	obesity
14b	Al-Rawaf (2019)	miR-140-5p	BMI
14b	Al-Rawaf (2019)	miR-146a	obesity
14b	Al-Rawaf (2019)	miR-146a	BMI
14b	Al-Rawaf (2019)	miR-222	obesity
14b	Al-Rawaf (2019)	miR-222	BMI
14b	Al-Rawaf (2019)	miR-423-5p	obesity
14b	Al-Rawaf (2019)	miR-423-5p	BMI
14b	Al-Rawaf (2019)	miR-520c-3p	obesity
14b	Al-Rawaf (2019)	miR-520c-3p	BMI
14b	Al-Rawaf (2019)	miR-532-5p	obesity
14b	Al-Rawaf (2019)	miR-532-5p	BMI
14b	Al-Rawaf (2019)	miR-15a	obesity
14b	Al-Rawaf (2019)	miR-15a	BMI
14b	Al-Rawaf (2019)	miR-142-3p	obesity
14b	Al-Rawaf (2019)	miR-142-3p	BMI
15b	Donghui et al (2019)	miR-126	BMI
17b	Thompson et al (2017)	miR-103a-5p	obesity
17b	Thompson et al (2017)	miR-122-5p	obesity
17b	Thompson et al (2017)	miR-150	BMI
17b	Thompson et al (2017)	miR-155-5p	obesity
17b	Thompson et al (2017)	miR-15b-5p	obesity
17b	Thompson et al (2017)	miR-181b-5p	obesity
17b	Thompson et al (2017)	miR-191-5p	obesity
17b	Thompson et al (2017)	miR-192-5p	obesity
17b	Thompson et al (2017)	miR-199a-5p	obesity
17b	Thompson et al (2017)	miR-21	BMI
17b	Thompson et al (2017)	miR-214-5p	obesity

17b	Thompson et al (2017)	miR-21-5p	obesity
17b	Thompson et al (2017)	miR-222-3p	obesity
17b	Thompson et al (2017)	miR-223	BMI
17b	Thompson et al (2017)	miR-223-3p	obesity
17b	Thompson et al (2017)	miR-23a-3p	obesity
17b	Thompson et al (2017)	miR-27b	BMI
17b	Thompson et al (2017)	miR-27b-3p	obesity
17b	Thompson et al (2017)	miR-29a	BMI
17b	Thompson et al (2017)	miR-29a-3p	obesity
17b	Thompson et al (2017)	miR-34a-5p	obesity
18b	Can et al (2015)	miR-143	obesity
18b	Can et al (2015)	miR-27	obesity
18b	Can et al (2015)	miR-335	obesity
18b	Can et al (2015)	miR-370	obesity
18b	Can et al (2015)	miR-378	obesity
18b	Can et al (2015)	miR-758	obesity
19b	Carolan et al (2014)	miR-33a	obesity
19b	Carolan et al (2014)	miR-33b	obesity

SAT= subcutaneous adipose tissue

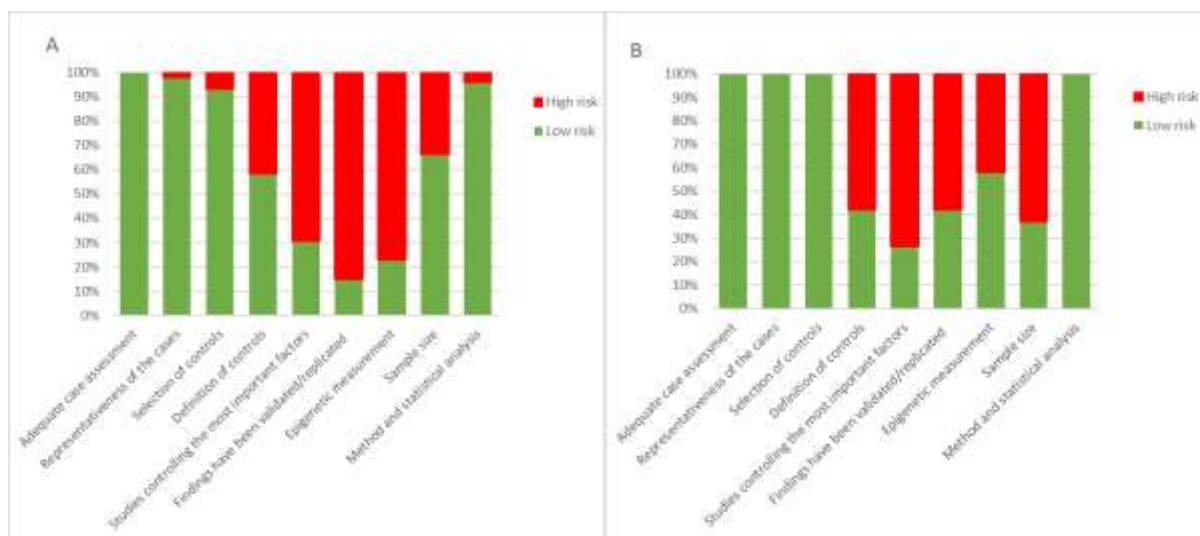
Table S6. Risk of bias in individual studies using the modified Newcastle-Ottawa scale (NOS)

Nr	Author (year)	Item									NOS score
		1	2	3	4	5	6	7	8	9	
Methylation											
1a	Cadiou et al (2020) ¹	*	*	*		*		*	*	*	7
2a	Gagné-Ouellet et al (2020) ²	*	*	*		*	*	*	*	*	8
3a	Geraghty et al (2020) ³	*	*	*	*			*		*	6
4a	Henriksson et al (2020) ⁴	*	*	*				*		*	5
5a	Rastogi et al (2020) ⁵	*	*	*	*	*		*	*	*	8
6a	Vehmeijer et al (2020) ⁶	*	*	*	*	*		*	*	*	8
7a	Cao-Lei et al (2019) ⁷	*	*	*				*		*	5
8a	He et al (2019) ⁸	*	*	*				*	*	*	6
9a	Huang et al (2018) ⁹	*	*	*		*		*	*	*	7
10a	Kaufman et al (2018) ¹⁰	*	*	*		*	*	*	*	*	8
11a	Li et at (2018) ¹¹	*	*	*	*		*	*		*	7
12a	van Dijk et al (2018) ¹²	*	*	*	*	*	*	*	*	*	9
13a	Samblas et al (2018) ¹³	*	*	*			*	*		*	6
14a	Fradin et al (2017) ¹⁴	*	*	*		*		*		*	6
15a	Kresovich et al (2017) ¹⁵	*	*	*	*	*		*	*	*	8
16a	Lillicrop et al (2017) ¹⁶	*	*	*	*	*	*	*		*	8
17a	Rzehak et al (2017) ¹⁷	*	*	*	*	*		*	*	*	8
18a	Rounge et al (2016) ¹⁸	*	*	*	*			*	*	*	7
19a	Ding et al (2015) ¹⁹	*	*	*			*	*		*	6
20a	Eriksson et al (2015) ²⁰	*	*	*		*		*	*	*	7
21a	Huang et al (2015) ²¹	*	*	*			*	*	*	*	7
22a	Quilter et al (2014) ²²	*	*	*	*			*		*	6
23a	Rastogi et al (2013) ²³	*	*	*	*			*		*	6
24a	Kochmanski et al (2019) ²⁴	*	*	*	*					*	5
25a	Dunstan et al (2017) ²⁵	*	*	*					*	*	5
26a	Perng et al (2012) ²⁶	*	*	*	*				*	*	6
27a	Prats-Puig et al (2020) ²⁷	*	*	*						*	4
28a	Pauwels et al (2019) ²⁸	*	*	*	*				*	*	6
29a	Gonzalez-Nahm et al (2018) ²⁹	*	*	*	*				*	*	6
30a	Junge et al (2018) ³⁰	*	*	*	*				*	*	6
31a	Ács et al (2017) ³¹	*	*	*						*	4
32a	Thakali et al (2017) ³²	*	*	*	*					*	5
33a	Bowman et al (2019) ³³	*	*	*	*				*	*	6
34a	Do et al (2019) ³⁴	*	*	*	*				*	*	6
35a	Bouwland-Both et al (2013) ³⁵	*	*	*	*				*	*	6
36a	Deodati et al (2013) ³⁶	*	*	*						*	4
37a	Hernández-Valero et al (2013) ³⁷	*	*	*					*	*	5
38a	Perkins et al (2012) ³⁸	*	*	*	*				*	*	6
39a	Huang et al (2012) ³⁹	*	*	*	*				*	*	6

40a	Prats-Puig et al (2017) ⁴⁰	*	*	*	*					*	5
41a	Shiau et al (2020) ⁴¹	*	*	*		*			*	*	6
42a	Bright et al (2019) ⁴²	*	*	*	*				*	*	6
43a	Huang et al (2019) ⁴³	*	*	*		*			*	*	6
44a	Binder et al (2018) ⁴⁴	*	*	*	*	*				*	6
45a	Simpkin et al (2017) ⁴⁵	*	*	*	*	*			*	*	7
46a	Anguita-Ruiz et al (2020) ⁴⁶	*	*	*	*					*	5
47a	Breton et al (2020) ⁴⁷	*	*	*		*			*	*	6
48a	Chang et al (2020) ⁴⁸	*	*	*					*	*	5
49a	Choi et al (2020) ⁴⁹	*	*	*	*	*				*	6
50a	Diaz et al (2020) ⁵⁰	*	*	*	*					*	5
51a	Gagné-Ouellet et al (2020) ⁵¹	*	*	*		*			*	*	6
52a	Gallardo-Escribano et al (2020) ⁵²	*	*	*	*				*	*	6
53a	Jakubek-Kipa et al (2020) ⁵³	*		*							2
54a	Justice et al (2020) ⁵⁴	*	*	*		*			*	*	6
55a	Loid et al (2020) ⁵⁵	*		*							2
56a	Mansell et al (2020a) ⁵⁶	*	*	*	*	*			*	*	7
57a	Mansell et al (2020b) ⁵⁷	*	*	*					*	*	5
58a	Prats-Puig et al (2020) ⁵⁸	*	*	*	*					*	5
59a	Reed et al (2020) ⁵⁹	*	*	*	*	*			*	*	7
60a	Rushing et al (2020) ⁶⁰	*	*	*	*					*	5
61a	Clark et al (2019) ⁶¹	*	*	*	*				*	*	6
62a	Han et al (2019) ⁶²	*	*	*	*	*	*		*	*	8
63a	Lee (2019) ⁶³	*	*	*					*	*	5
64a	Lee (2019) ⁶⁴	*	*	*					*	*	5
65a	Lillicrop et al (2019) ⁶⁵	*	*	*	*		*		*	*	7
66a	Martin et al (2019) ⁶⁶	*	*	*	*				*	*	6
67a	Noor et al (2019) ⁶⁷	*	*	*	*	*			*	*	6
68a	Sherwood et al (2019) ⁶⁸	*	*	*	*	*			*	*	6
69a	Tian et al (2019) ⁶⁹	*	*	*					*	*	5
70a	Chen et al (2018) ⁷⁰	*	*	*		*			*	*	6
71a	El Sayed et al (2018) ⁷¹	*	*	*	*				*	*	6
72a	Kwon et al (2018) ⁷²	*	*	*	*				*	*	6
73a	Tozzi et al (2018) ⁷³	*	*	*	*						4
74a	Wu et al (2018) ⁷⁴	*	*	*	*				*	*	6
75a	Yang et al (2018) ⁷⁵	*	*	*					*	*	5
76a	Gagné-Ouellet (2017) ⁷⁶	*	*	*						*	4
77a	Koh et al (2017) ⁷⁷	*	*	*	*		*		*	*	7
78a	Lin et al (2017) ⁷⁸	*	*	*	*	*			*	*	7
79a	Mansego et al (2017) ⁷⁹	*	*	*	*		*			*	6
80a	Volberg et al (2017) ⁸⁰	*	*	*	*	*			*	*	7
81a	Richmond et al (2016) ⁸¹	*	*	*	*	*			*	*	7
82a	Carobin et al (2015) ⁸²	*	*	*	*					*	5
83a	Davé et al (2015) ⁸³	*	*	*						*	4
84a	Gardner et al (2015) ⁸⁴	*	*	*					*	*	5

85a	Pan et al (2015) ⁸⁵	*	*	*	*	*			*	*	7
86a	Shah et al (2015) ⁸⁶	*	*	*					*	*	5
87a	Sharp et al (2015) ⁸⁷	*	*	*	*				*	*	6
88a	Simpkin et al (2015) ⁸⁸	*	*	*	*				*	*	6
89a	Wang et al (2015) ⁸⁹	*	*	*	*				*		5
90a	Wu et al (2015) ⁹⁰	*	*	*					*	*	5
91a	Azzi et al (2014) ⁹¹	*	*	*					*	*	5
92a	Clarke-Harris et al (2014) ⁹²	*	*	*		*				*	5
93a	García-Cardona et al (2014) ⁹³	*	*	*					*	*	5
94a	Su et al (2014) ⁹⁴	*	*	*	*					*	5
95a	Yoo et al (2014) ⁹⁵	*	*	*						*	4
96a	Moleres et al (2013) ⁹⁶	*	*	*	*				*	*	6
97a	Obermann-Borst et al (2013) ⁹⁷	*	*	*	*				*	*	6
98a	Kim et al (2012) ⁹⁸	*	*	*			*			*	5
99a	Groom et al (2012) ⁹⁹	*	*	*	*		*		*	*	7
100a	Relton et al (2012) ¹⁰⁰	*	*	*	*					*	5
101a	Godfrey et al (2011) ¹⁰¹	*	*	*			*		*	*	6
Non-coding RNA											
1b	Lin et al (2020) ¹⁰²	*	*	*				*		*	5
2b	Mas-Parés et al (2019) ¹⁰³	*	*	*	*	*	*	*		*	8
3b	Iacomino et al (2019) ¹⁰⁴	*	*	*	*	*	*	*	*	*	9
4b	Marzano et al (2019) ¹⁰⁵	*	*	*	*		*	*		*	7
5b	Liu et al (2018) ¹⁰⁶	*	*	*			*	*		*	6
6b	Carreras-Badosa et al (2017) ¹⁰⁷	*	*	*	*	*	*	*		*	8
7b	Cui et al (2018) ¹⁰⁸	*	*	*			*	*		*	6
8b	Ouyang et al (2017) ¹⁰⁹	*	*	*				*		*	5
9b	Iacomino et al (2016) ¹¹⁰	*	*	*		*	*	*		*	7
10b	Masotti et al (2016) ¹¹¹	*	*	*	*			*		*	6
11b	Prats-Puig et al (2013) ¹¹²	*	*	*		*	*	*	*	*	8
12b	Cabiati et al (2020) ¹¹³	*	*	*	*				*	*	6
13b	Duarte et al (2020) ¹¹⁴	*	*	*				*		*	5
14b	Al-Rawaf (2019) ¹¹⁵	*	*	*					*	*	5
15b	Donghui et al (2019) ¹¹⁶	*	*	*	*				*	*	6
16b	Ahmadpour et al (2018) ¹¹⁷	*	*	*	*				*	*	6
17b	Thompson et al (2017) ¹¹⁸	*	*	*						*	4
18b	Can et al (2015) ¹¹⁹	*	*	*					*	*	5
19b	Carolan et al (2014) ¹²⁰	*	*	*						*	4
Chromatin regulation											
1c	Scarpato et al (2011) ¹²¹	*	*	*	*				*	*	6

Fig S1. Risk of bias across studies using the modified Newcastle-Ottawa scale



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