Table S1. Details of the measured amplicons and the PCR primers

Gene Name	**Genomic location (NCBI b36.1)**	**Function**	**Primer forward [b]**
(alias)	**CpG sites analyzed [a]**	**Features / (genetic) associations**	**Primer reverse [c]**
IL10	chr1:205012634-205012962	Anti-inflammatory	TGATTGGTTGAATATGAATTTTTGTAT
	CpG 1, 2&3, 4	Promoter, MIR retrotransposon, CpG 4 is an ATF6, XBP1, PPARG binding site / atherosclerosis, schizophrenia	CACCCCCTCATTTTTACTTAAAAA
GNASAS	chr20:56859210-56859503	Imprinting control region GNAS locus	GTAATTTGTGGTATGAGGAAGAGTGA
(*NESPAS*)	CpG 1&2, 3&4, 6, 7, 8&9, 10-12, 13&14, 15, 17-19	promoter / Pseudohypoparathyroidism 1B, QTL blood pressure	TAAATAACCCAACTAAATCCCAACA
INSIGF	chr11:2138912-2139216	Embryonic growth, metabolism	GTTTTGAGGAAGAGGTGTTGA
(*INS*)	CpG 2, 4, 5, 6	Promoter, imprinted / SGA, *IGF2* levels in umbilical cord	ACCTAAAATCCAACCACCCTAA
LEP	chr7:127668290-127668646	Appetite regulation & fat metabolism	GTTTTTGGAGGGATATTAAGGATTT
	CpG 1, 16&17, 19-21, 22, 25, 27	Promoter, CpG 22 is an C/EBP binding site controlling basal gene expression / birth weight, BMI, blood pressure	CTACCAAAAAAAACCAACAAAAAAA
MEG3	chr14:100361166-100361395	Embryonic growth inhibitor	TTTTTTTTAATAGTATTTTGATTTTTG
(*GTL2*)	CpG 2, 3, 4, 5&6, 8&9, 10&11	Promoter, CTCF binding site, part of DLK1-DIO3 imprinting control mechanism	AAATAATCCCCACACACATACC
ABCA1	chr9:106730323-106730642	Cholesterol transport	ATTTTATTGGTGTTTTTGGTTGT
	CpG 1, 3&4, 6-9, 10-13, 15&16, 17&18, 19-21, 22&23, 24, 25	Promoter, CpG 10-13 Arnt & USF1 binding site / atherosclerosis, cholesterol levels	ATCAAAACCTATACTCTCCCTCCTC
IGF2R	chr6:160346346-160346595	Embryonic growth, apoptosis	AGGTAGAAAAAGGTTTTGGAAG
	CpG 4&5, 8-10, 11-13, 20&21	Putatively imprinted human IGF2 DMR2 / birth weight	CAAATCTTAAAAACTAACTAAAAACC
APOC1	chr19:50109726-50110115	Lipid metabolism	GGAGGAGGGAGATTAATATTAATTTGT
	CpG 1, 2, 3, 4, 10, 11	Intron & exons / coronary artery disease	ACCCCAAACCTATAACCACCTT
FTO	chr16:52383225-52383575	Development, nucleic acid demethylation	GTTTGTAATTTTAGTATTTTGGGAGGT
	CpG 8&9, 10&11, 17, 19	Linkage area GWAS / BMI, Diabetes	TTTATTTCCATTTATCCATTCTCAAA
KCNQ1OT1	chr11:2677737-2678040	Imprinting control region 11p15.5	TTTGGTAGGATTTTGTTGAGGAGTTTT
(*KvDMR1*)	CpG 1, 6, 8&9, 10-12, 15, 16,	Minimal repressor, promoter / Diabetes, Beckwith-	CTCACACCCAACCAATACCTCATAC

	17&18, 20, 21, 24, 25, 26&27	Wiedemann syndrome, Silver Russell syndrome	
NR3C1	chr5:142763741-142764104	HPA-axis	GATTTGGTTTTTTTGGGG
(*GR*)	CpG 4, 7&8, 9, 10&11, 14, 15&16, 17-20, 31, 33&34, 42	Exon I7, CpG 7 is part of a NGF1-A binding site / depression	TCCCTTCCCTAAAACCT
TNF	chr6_qbl_hap2:2790712-2791113	Pro-inflammatory	GGGTATTTTTGATGTTTGTGTGTT
	CpG 1-3, 5, 9, 10, 11	Promoter / Graves' disease, asthma	CAATACTCATAATATCCTTTCCAAAAAA
GRB10	chr7:50818080-50818483	IIS inhibitor	GGAATTTTAGGATTAAATTTATGTGA
	CpG 7, 8, 17, 22&23, 24, 25	Promoter, CpG island / diabetes type 2, birth size	AACTTCCAAAAAAAACCTCTCC
CRH	chr8:67253246-67253686	Stress response/ HPA-axis	TGGTTGTTGTTTTTTTGGTAGG
(*CRP, CRF*)	CpG 1, 2, 9, 10	Promoter, CpG 2 and 10 are TFBS / length of pregnancy, HPA axis	AATTTCTCCACTCCAAAACCTAAA
GNAS(A/B)	chr20:56896823-56897145	Growth/Lypolytic processes	ATGATTTAATTAAGGTTTTAGGAAAGG
	CpG 1, 3&4, 7, 8, 9&10, 12, 13-15, 16-19	Promoter / blood pressure QTL	TAAAAATACAAAACCTCCCCTACTC

[a] CpG sites measured in each amplicon. Counting starts from the part of the amplicon that has the identical sequence of the forward primer. Multiple CpG sites that are named together between brackets were not individually resolved by fragmentation in the mass spectrometer and thus measured simultaneously.

[b] Forward primer that will amplify the bisulfite converted genomic DNA. For the Epityper methodology a 10mer spacer tag is added at the 5' primer end with the following sequence: 5'-AGGAAGAGAG+primer

[c] Reverse primer that will amplify the bisulfite converted genomic DNA. For the Epityper methodology a T7 promoter is added to the 5' primer end with the following sequence: 5'-CAGTAATACGACTCACTATAGGGAGAAGGCT+primer

Abbreviations: MIR = type of retrotransposon, QTL = quantative trait locus, SGA = small for gestational age, BMI = body mass index, TFBS = transcription factor binding sites, HPA = hypothalamus-Pituitary axis, IIS = insulin signaling, NGF1-A = a transcription factor reported by Weaver *et al*. to influence NR3C1 expression (*Nat. Neurosci*. 2004), GWAS = genome wide association study