

Supplementary Table 1. Analysis information

NEWBORN META-ANALYSIS																		
Cohort	Cohort name in full	Cohort Reference (PMID)	Ascertainment criteria	Country	Ancestry	N individuals	N (%) females	Mean (SD) maternal Hb (g/L)	N (%) maternal Hb < 110 g/L	Mean (SD) gestational week at Hb measurement	Mean (SD) maternal age	Mean (SD) gestational week at birth	Mean (SD) age of the child at methylation sample (years)	N (%) of participants where parity = 0	N (%) of those who stopped smoking in early pregnancy	No (%) of sustained smokers during pregnancy	Maternal education	More explantation for maternal education
ALSPAC	Avon Longitudinal Study of Parents and Children	PMID: 22507743; PMID: 22507742	Birth Cohort	United Kingdom	British (mostly European)	688	360 (52.3)	124.5 (9.0)	31 (4.5)	9.69 (2.44)	29.63 (4.29)	39.61 (1.46)	0	329 (47.81)	4.07	8.87	20.93	No. (%) mothers with University degree (as opposed to none)
EDEN	Étude des Déterminants pré et post natals du développement de la santé de l'Enfant 2003-2006	PMID: 26283636	Birth Cohort	France	European	123	51 (41.5)	119.3 (10.5)	21 (17.1)	27.22 (1.09)	30.79 (5.02)	39.37 (1.53)	0	34 (27.6)	10 (8.13%)	26 (21.14%)	1) Low education (1-4) N=36; 2) Middle education (5-7) N=23; 3) Higher education (8-9) N=64;	1= no education/did not complete college (age 14); 2= completed college (age 14); 3-4= completed preprofessional courses (age 16); 5= completed baccalauréat professionnel (age 18); 6= completed baccalauréat technologique (age 17); 7=completed baccalauréat général (age 17); 8= completed license/bachelor's degree; 9= education beyond bachelor's degree
Generation R	Generation R Study	PMID: 28070760	Birth Cohort	The Netherlands	Dutch (European)	1205	596 (49.5)	124.6 (8.7)	59 (4.9)	14.86 (3.72)	31.71 (4.17)	40.16 (1.49)	0	732 (60.7)	120 (10.0%)	166 (13.8%)	Low education N = 415 (34.4%) High education N = 790 (65.6%)	Low = no education finished, primary finished, secondary finished High = higher education finished
PREDO	Prediction and Prevention of Preeclampsia and Intrauterine Growth Restriction Study	PMID: 27639277	Birth Cohort	Finland	Finnish (European)	709	338 (47.7)	121.0 (12.7)	135 (19.0)	30.30 (7.60)	33.5 (5.61)	39.80 (1.57)	0	218 (30.7)	21 (3%)	5 (0.7%)	1) Primary Education N=32; 2) Secondary Education N=280; 3) Lower Tertiary Education N=168; 4) Upper Tertiary Education, N=229	
INMA	Infancia y Medio Ambiente	PMID: 21471022	Birth Cohort	Spain	European	363	178 (49.0)	115.1 (9.9)	106 (29.2)	32.17 (4.31)	30.3 (4.06)	39.81 (1.34)	0	210 (57.8)	55 (15.15)	49 (13.50)	Low (primary or less) Medium (secondary) High (university)	
PROGRESS	Programming Research in Obesity, Growth Environment and Social Stress Study	PMID: 24916609; PMID: 23750643	Birth Cohort	Mexico	Mexican	395	180 (45.6)	128.2 (9.3)	95 (24.1)	31.60 (1.01)	28.17 (5.43)	38.47 (1.52)	0	147 (37.2)	nonsmoking environment n=315, smoking environment n=80	mothers who smoked during pregnancy were excluded (n=6)	Less than high school education N=160, High school education N=137, More than high school education N=98	
FinnGeDi	Finnish Gestational Diabetes Study	PMID: 29858213; PMID: 32374401	Birth Cohort, offspring of women with GDM/controls	Finland	Finnish (European)	484	276 (51.4)	123.8 (9.6)	27 (5.6)	36.62 (3.00)	32.03 (5.27)	39.92 (1.31)	0	247 (46.0)	All were non-smokers	All were non-smokers	1) Basic education or less 2) Secondary education 3) Lower-level tertiary education 4) Upper-level tertiary education	

CHILDHOOD META-ANALYSIS																		
Cohort	Cohort name in full	Cohort Reference (PMID)	Ascertainment criteria	Country	Ancestry	N individuals	N (%) females	Mean (SD) maternal Hb (g/L)	N (%) maternal Hb < 110 g/L	Mean (SD) gestational week at Hb measurement	Mean (SD) maternal age	Mean (SD) gestational week at birth	Mean (SD) age of the child at methylation sample (years)	N (%) of participants where parity = 0	N (%) of those who stopped smoking in early pregnancy	No (%) of sustained smokers during pregnancy	Maternal education	More explantation for maternal education
ALSPAC	Avon Longitudinal Study of Parents and Children	PMID: 22507743; PMID: 22507742	Birth Cohort	United Kingdom	British (mostly European)	749	384 (51.3)	124.4 (8.9)	38 (5.1)	9.70 (2.42)	29.64 (4.24)	39.62 (1.47)	7.45 (0.15)	350 (46.73)	3.87	0.35	21.22	No. (%) mothers with University degree (as opposed to none)
EDEN	Étude des Déterminants pré et post natals du développement de la santé de l'Enfant 2003-2006	PMID: 26283636	Birth Cohort	France	European	121	50 (41.3)	119.1 (10.5)	21 (17.4)	27.22 (1.11)	30.77 (5.01)	39.37 (1.54)	5.66 (0.12)	32 (26.45)	10 (8.26%)	26 (21.49%)	1) Low education (1-4) N=35; 2) Middle education (5-7) N=23; 3) Higher education (8-9) N=63;	1= no education/did not complete college (age 14); 2= completed college (age 14); 3-4= completed preprofessional courses (age 16); 5= completed baccalauréat professionnel (age 18); 6= completed baccalauréat technologique (age 17); 7=completed baccalauréat général (age 17); 8= completed license/bachelor's degree; 9= education beyond bachelor's degree
INMA	Infancia y Medio Ambiente	PMID: 21471022	Birth Cohort	Spain	European	185	89 (48.1)	115.0 (10.1)	52 (28.1)	32.60 (3.75)	30.39 (4.28)	39.88 (1.33)	4.38 (0.24)	100 (54.05)	23 (12.43)	20 (10.81)	low (primary or less) medium (secondary) high (university)	
POGO	Postpartum Outcomes in Women with Gestational Diabetes and their Offspring	PMID: 24172698	Birth Cohort, offspring of women with GDM	Germany	Mostly European (N=2 Asian)	71	35 (49.3)	123.8 (11.1)	7 (9.9)	34.67 (4.95)	33.03 (4.84)	38.55 (2.01)	7.61 (3.01)	41 (57.75)	NA (mothers were asked if they smoked during pregnancy, 92.96% answered "No", 7 individuals made no response)	0	1 = none 2 = Hauptschule (secondary school, ranked lower than Realschule and Gymnasium) 3 = Realschule (secondary school, ranked between Hauptschule and Gymnasium) 4 = Gymnasium (secondary school, ranked higher than Hauptschule and Realschule) 5 = Berufsausbildung (completed vocational training) 6 = Studium (university graduation)	score 1-6, indicating the highest graduation of the mother
Generation R	Generation R Study	PMID: 28070760	Birth Cohort	The Netherlands	Dutch (European)	429	229 (53.4)	124.2 (8.7)	24 (5.6)	14.85 (3.71)	32.23 (4.00)	40.18 (1.56)	6.04 (0.36)	271 (63.2%)	51 (11.9%)	47 (11.0%)	Low education N = 133 (31.0%) High education N = 296 (69.0%)	low = no education finished, primary finished, secondary finished high = higher education finished

ADOLESCENCE META-ANALYSIS																		
Cohort	Cohort name in full	Cohort Reference (PMID)	Ascertainment criteria	Country	Ancestry	N individuals	N (%) females	Mean (SD) maternal Hb (g/L)	N (%) maternal Hb < 110 g/L	Mean (SD) gestational week at Hb measurement	Mean (SD) maternal age	Mean (SD) gestational week at birth	Mean (SD) age of the child at methylation sample (years)	N (%) of participants where parity = 0	N (%) of those who stopped smoking in early pregnancy	No (%) of sustained smokers during pregnancy	Maternal education	More explantation for maternal education
ALSPAC	Avon Longitudinal Study of Parents and Children	PMID: 22507743; PMID: 22507742	Birth Cohort	United Kingdom	British (mostly European)	750	393 (52.4)	124.6 (8.8)	37 (4.9)	9.67 (2.41)	29.63 (4.26)	39.62 (1.47)	17.10 (1.04)	393 (52.40)	3.73	9.33	21.33	No. (%) mothers with University degree (as opposed to none)
Raine Study	Raine Study	PMID: 28064197	Birth Cohort	Australia	Australian (European)	761	375 (49.3)	122.8 (9.0)	48 (6.3)	NA	28.37 (5.84)	39.57 (1.69)	17.10 (0.30)	365 (47.96)	91 (11.96%)	168 (22.07%)	0: None N=368; 1: Trade certificate or apprenticeship N=63; 2: Professional registration (non-degree) N=86; 3: College diploma or degree N=127; 4: University degree N= 80; 5: Other N=37	
NFBC1986	Northern Finland Birth Cohort 1986	PMID: 2976931	Birth Cohort	Finland	Finnish (European)	451	279 (61.9)	131.4 (10.2)	6 (1.3)	10.66 (2.87)	27.91 (5.27)	40.07 (1.27)	16.06 (0.36)	169 (32.31)	14 (2.68)	97 (18.55)	0: Professional N=145(27.7%); 1: Skilled worker N=227(43.4%); 2: Unskilled worker N=131 (25.0%); 3: Farmer N=20 (3.8%)	

Supplementary Table 2. CpG sites with lowest P-values in meta-analysis of associations between maternal haemoglobin during pregnancy and offspring DNA methylation at birth. There are no significant CpG sites after Bonferroni correction (P-value < 6.77E-08). Initial model is adjusted for gestational week at haemoglobin measurement, child sex, DNA methylation batch, selection factor in the case of randomised controlled trial and white blood cell estimates. CpG, cytosine-phosphate-guanine; Chr, chromosome; Regression coefficient, difference in offspring DNA methylation beta value per one SE unit increase in maternal haemoglobin; SE, standard error. Polymorphic CpG sites are indicated with an asterisk after the site name.

CpG site	Chr	Gene	Regression coefficient	SE for regression coefficient	P-value	FDR-corrected P-value
cg04181092	3		0.0013	0.0002	1.75E-07	0.097
cg24953596	1	<i>MEGF6</i>	-0.0045	0.0009	2.97E-07	0.097
cg05470963*	5	<i>ARHGAP26</i>	0.0014	0.0003	3.95E-07	0.097
cg15753546*	2		0.0017	0.0003	6.03E-07	0.111
cg21367582	19	<i>CATSPERG</i>	-0.0014	0.0003	1.56E-06	0.172
cg02935826	2		0.0022	0.0005	2.05E-06	0.172
cg10638827	16	<i>MT1M</i>	-0.0046	0.0010	2.29E-06	0.172
cg10250335	8	<i>LOC101927040</i>	0.0058	0.0012	2.31E-06	0.172
cg16815082	7		0.0039	0.0008	2.43E-06	0.172
cg20169893	1	<i>PRDM16</i>	-0.0018	0.0004	2.85E-06	0.172
cg02662362	6	<i>HLA-DPB2</i>	-0.0007	0.0002	3.24E-06	0.172
cg12068257	1	<i>FBLIM1</i>	-0.0031	0.0007	3.38E-06	0.172
cg04342176	4	<i>DCLK2</i>	-0.0007	0.0002	3.48E-06	0.172
cg00736299*	16	<i>MGRN1</i>	0.0026	0.0006	3.60E-06	0.172
cg14500916	18	<i>LOC101927410</i>	0.0009	0.0002	3.93E-06	0.172
cg15570464	6		0.0013	0.0003	3.99E-06	0.172
cg08908586	14	<i>FBLN5</i>	-0.0010	0.0002	4.09E-06	0.172
cg24392197	3	<i>XXYL1-AS2</i>	-0.0033	0.0007	4.19E-06	0.172
cg05946080	2		0.0019	0.0004	4.81E-06	0.185
cg18479141	6	<i>HDAC2</i>	-0.0019	0.0004	5.02E-06	0.185
cg26434370	16	<i>FAM18A</i>	0.0023	0.0005	5.70E-06	0.200
cg23912509	12	<i>MIR135A2</i>	0.0015	0.0003	6.93E-06	0.231
cg06305891	3		0.0024	0.0005	7.21E-06	0.231
cg24231834	1		0.0022	0.0005	7.88E-06	0.234
cg16599974*	15		-0.0016	0.0004	8.25E-06	0.234
cg06928695	17	<i>PITPNM3</i>	-0.0029	0.0006	8.56E-06	0.234
cg23076906	19	<i>ZNF444</i>	-0.0011	0.0002	8.57E-06	0.234
cg16588336	3		0.0016	0.0004	1.01E-05	0.241
cg05277504	17	<i>ASPSCR1</i>	0.0003	0.0001	1.08E-05	0.241
cg13305114	1	<i>VPS13D</i>	0.0008	0.0002	1.08E-05	0.241
cg06522562	2	<i>FAM117B</i>	0.0006	0.0001	1.15E-05	0.241
cg12883014	12	<i>CHST11</i>	0.0031	0.0007	1.16E-05	0.241
cg20757478	6		0.0043	0.0010	1.16E-05	0.241
cg00556627*	2	<i>SPATS2L</i>	0.0023	0.0005	1.21E-05	0.241
cg09126014	15	<i>SCAMP2</i>	0.0021	0.0005	1.23E-05	0.241
cg03927133	15	<i>ITPKA</i>	-0.0008	0.0002	1.28E-05	0.241
cg05924031	16	<i>CACNA1H</i>	0.0024	0.0006	1.29E-05	0.241
cg21056788	13	<i>SPG20</i>	0.0008	0.0002	1.29E-05	0.241
cg17343167	5	<i>N4BP3</i>	-0.0018	0.0004	1.32E-05	0.241
cg08854599	11	<i>NADSYN1</i>	0.0007	0.0002	1.37E-05	0.241

Supplementary Table 3. CpG sites with lowest P-values in meta-analysis of associations between maternal haemoglobin during pregnancy and offspring DNA methylation at childhood. There are no significant CpG sites after Bonferroni correction (P-value < 1.18E-07). Initial model is adjusted for gestational week at haemoglobin measurement, child sex, DNA methylation batch and white blood cell estimates. CpG, cytosine-phosphate-guanine; Chr, chromosome; Regression coefficient, difference in offspring DNA methylation beta value per one SE unit increase in maternal haemoglobin; SE, standard error. Polymorphic CpG sites are indicated with an asterisk after the site name.

CpG site	Chr	Gene	Regression coefficient	SE for regression coefficient	P-value	FDR-corrected P-value
cg02313554	10		0.0150	0.0031	1.84E-06	0.268
cg19519626	19	<i>NPHS1</i>	0.0052	0.0011	2.12E-06	0.268
cg10406759*	17		-0.0024	0.0005	2.45E-06	0.268
cg23028721	1	<i>OR2M3</i>	-0.0067	0.0014	3.25E-06	0.268
cg06245037	11	<i>ALX4</i>	0.0012	0.0003	4.36E-06	0.268
cg12048341	1	<i>NAV1</i>	0.0051	0.0011	4.92E-06	0.268
cg07121693*	10		0.0046	0.0010	5.96E-06	0.268
cg07184465*	5	<i>SPZ1</i>	0.0028	0.0006	7.16E-06	0.268
cg07222908	15	<i>SLC28A2</i>	-0.0051	0.0011	7.41E-06	0.268
cg22372355	1		0.0040	0.0009	8.26E-06	0.268
cg07880478	5		0.0053	0.0012	8.28E-06	0.268
cg21972567	5	<i>EBF1</i>	0.0038	0.0009	8.30E-06	0.268
cg10697882*	13	<i>MYO16</i>	0.0072	0.0016	8.81E-06	0.268
cg06634732*	1		-0.0019	0.0004	9.57E-06	0.268
cg11423998	10	<i>DIP2C</i>	-0.0023	0.0005	9.70E-06	0.268
cg01615827*	10	<i>LOC100188947</i>	0.0029	0.0007	1.01E-05	0.268
cg24233194*	10		0.0034	0.0008	1.19E-05	0.278
cg24790471	12	<i>NTN4</i>	0.0019	0.0004	1.23E-05	0.278
cg10721030*	1		0.0028	0.0006	1.30E-05	0.278
cg01290934	6		0.0010	0.0002	1.31E-05	0.278
cg02660870	12		0.0028	0.0007	1.58E-05	0.292
cg26163885	10		0.0018	0.0004	1.59E-05	0.292
cg02489219	2	<i>C2orf66</i>	0.0025	0.0006	1.68E-05	0.292
cg04337854	6	<i>BVES</i>	-0.0027	0.0006	1.79E-05	0.292
cg02137691	4	<i>FGFR3</i>	-0.0026	0.0006	1.84E-05	0.292
cg14112997*	22	<i>IL17RA</i>	-0.0411	0.0096	1.84E-05	0.292
cg25545739	18	<i>FAM69C</i>	0.0016	0.0004	1.86E-05	0.292
cg13906045*	3	<i>CHCHD4, TMEM43</i>	0.0002	0.0001	2.12E-05	0.315
cg02486096	19		0.0037	0.0009	2.22E-05	0.315
cg25202877	6	<i>EHMT2</i>	0.0021	0.0005	2.22E-05	0.315
cg06295856	11	<i>CALCA</i>	-0.0035	0.0008	2.40E-05	0.328
cg19747195	12		0.0032	0.0008	2.47E-05	0.328
cg22165175*	1	<i>KCNA2</i>	-0.0030	0.0007	2.67E-05	0.343
cg04611161	16		0.0037	0.0009	2.74E-05	0.343
cg13054119	1	<i>RSPO1</i>	-0.0021	0.0005	3.05E-05	0.346
cg04577809	17	<i>RHBDF2</i>	0.0021	0.0005	3.16E-05	0.346
cg27268110	10	<i>C10orf58</i>	0.0033	0.0008	3.30E-05	0.346
cg03329539	2		-0.0048	0.0012	3.36E-05	0.346
cg09027493	6	<i>TCP11</i>	-0.0036	0.0009	3.49E-05	0.346
cg08447200	22	<i>PANX2</i>	-0.0039	0.0010	3.50E-05	0.346

Supplementary Table 4. CpG sites with lowest P-values in meta-analysis of associations between maternal haemoglobin during pregnancy and offspring DNA methylation at childhood. There are no significant CpG sites after Bonferroni correction (P-value < 1.18E-07). Fully adjusted model is adjusted for gestational week at maternal haemoglobin measurement, maternal parity, maternal education, maternal smoking, child sex, gestational age at birth, child age at time of DNA methylation measurement, DNA methylation batch and white blood cells estimates. CpG, cytosine-phosphate-guanine; Chr, chromosome; Regression coefficient, difference in offspring DNA methylation beta value per one SE unit increase in maternal haemoglobin; SE, standard error. Polymorphic CpG sites are indicated with an asterisk after the site name.

CpG site	Chr	Gene	Regression coefficient	SE for regression coefficient	P-value	FDR-corrected P-value
cg19747195	12		0.0037	0.0007	2.92E-07	0.124
cg02313554	10		0.0158	0.0032	8.18E-07	0.134
cg19519626	19	<i>NPHS1</i>	0.0054	0.0011	9.43E-07	0.134
cg10406759*	17		-0.0025	0.0005	1.54E-06	0.164
cg01615827*	10	<i>LOC100188947</i>	0.0030	0.0006	3.94E-06	0.240
cg07121693*	10		0.0047	0.0010	4.09E-06	0.240
cg07222908	15	<i>SLC28A2</i>	-0.0053	0.0012	4.16E-06	0.240
cg13402624	9	<i>VAV2</i>	-0.0018	0.0004	4.81E-06	0.240
cg18126802	1	<i>DNM3</i>	0.0018	0.0004	6.10E-06	0.240
cg08508724	6	<i>TRIM10</i>	-0.0024	0.0005	6.64E-06	0.240
cg27268110	10	<i>C10orf58</i>	0.0035	0.0008	6.70E-06	0.240
cg06245037	11	<i>ALX4</i>	0.0012	0.0003	7.02E-06	0.240
cg07184465*	5	<i>SPZ1</i>	0.0029	0.0006	7.35E-06	0.240
cg22372355	1		0.0041	0.0009	8.79E-06	0.267
cg07880478	5		0.0053	0.0012	1.14E-05	0.312
cg26163885	10		0.0019	0.0004	1.26E-05	0.312
cg11423998	10	<i>DIP2C</i>	-0.0024	0.0006	1.33E-05	0.312
cg00646492	10	<i>GSTO1</i>	-0.0018	0.0004	1.35E-05	0.312
cg06634732*	1		-0.0019	0.0004	1.42E-05	0.312
cg13834112	15		-0.0040	0.0009	1.58E-05	0.312
cg23028721	1	<i>OR2M3</i>	-0.0064	0.0015	1.62E-05	0.312
cg01290934	6		0.0010	0.0002	1.70E-05	0.312
cg16225947	15	<i>TJP1</i>	0.0028	0.0006	1.84E-05	0.312
cg12048341	1	<i>NAV1</i>	0.0052	0.0012	1.85E-05	0.312
cg24233194*	10		0.0033	0.0008	1.89E-05	0.312
cg11105319	15		0.0016	0.0004	2.08E-05	0.312
cg27186323	7		-0.0054	0.0013	2.08E-05	0.312
cg09027493	6	<i>TCP11</i>	-0.0036	0.0008	2.09E-05	0.312
cg02486096	19		0.0037	0.0009	2.28E-05	0.312
cg12502403	11	<i>MARK2</i>	0.0009	0.0002	2.32E-05	0.312
cg10721030*	1		0.0027	0.0006	2.35E-05	0.312
cg02137691	4	<i>FGFR3</i>	-0.0026	0.0006	2.36E-05	0.312
cg04337854	6	<i>BVES</i>	-0.0027	0.0006	2.42E-05	0.312
cg24790471	12	<i>NTN4</i>	0.0019	0.0005	2.73E-05	0.327
cg12296751	7	<i>CAV1</i>	0.0011	0.0003	2.74E-05	0.327
cg14112997*	22	<i>IL17RA</i>	-0.0405	0.0097	2.78E-05	0.327
cg00691125	1	<i>SLC19A2</i>	0.0002	0.0001	2.85E-05	0.327
cg22914987	12		0.0024	0.0006	3.02E-05	0.336
cg05649708	10		0.0041	0.0010	3.09E-05	0.336
cg17993442	11	<i>ZBTB44</i>	0.0052	0.0013	3.23E-05	0.341

Supplementary Table 5. CpG sites with lowest P-values in meta-analysis of associations between maternal haemoglobin during pregnancy and offspring DNA methylation at adolescence. There are no significant CpG sites after Bonferroni correction (P-value < 1.19E-07). Initial model is adjusted for child sex, DNA methylation batch and white blood cell estimates. CpG, cytosine-phosphate-guanine; Chr, chromosome; Regression coefficient, difference in offspring DNA methylation beta value per one SE unit increase in maternal haemoglobin; SE, standard error. Polymorphic CpG sites are indicated with an asterisk after the site name.

CpG site	Chr	Gene	Regression coefficient	SE for regression coefficient	P-value	FDR-corrected P-value
cg24480012*	12	<i>FAM19A2</i>	-0.0020	0.0004	2.47E-06	0.664
cg24058386	1	<i>C1orf61</i>	-0.0048	0.0010	3.77E-06	0.664
cg09215588*	12		0.0012	0.0003	7.60E-06	0.664
cg10553748	17	<i>CHRNE, C17orf107</i>	-0.0064	0.0014	7.73E-06	0.664
cg10095352	15	<i>RAB11A</i>	0.0009	0.0002	9.74E-06	0.664
cg18388270	1		-0.0117	0.0027	1.16E-05	0.664
cg14371590*	12	<i>SLC26A10</i>	-0.0032	0.0007	1.45E-05	0.664
cg13609939*	10	<i>OAT</i>	0.0010	0.0002	1.58E-05	0.664
cg03592833	3	<i>ATP13A3</i>	0.0008	0.0002	1.75E-05	0.664
cg08645879*	1		0.0011	0.0003	1.79E-05	0.664
cg06558800	5		0.0010	0.0002	1.94E-05	0.664
cg19531351	18		0.0017	0.0004	1.98E-05	0.664
cg09458618	7		0.0015	0.0004	2.28E-05	0.664
cg27176262	6	<i>TAP2</i>	0.0016	0.0004	2.50E-05	0.664
cg12156838	5	<i>HSD17B4</i>	0.0010	0.0002	2.53E-05	0.664
cg18121829	12	<i>CRY1</i>	0.0015	0.0004	2.64E-05	0.664
cg02034222	2	<i>DQX1</i>	0.0012	0.0003	2.70E-05	0.664
cg15946310	5	<i>TTC1</i>	-0.0005	0.0001	2.94E-05	0.683
cg16931969	4	<i>ANK2</i>	-0.0082	0.0020	3.19E-05	0.701
cg08008233*	18	<i>TCEB3C, KATNAL2</i>	0.0029	0.0007	3.46E-05	0.703
cg14961391	2	<i>ORC4L</i>	0.0020	0.0005	3.53E-05	0.703
cg24406898	7	<i>COL1A2</i>	-0.0075	0.0018	3.99E-05	0.757
cg23520075*	19	<i>MYADM</i>	0.0005	0.0001	4.63E-05	0.764
cg14529146	17	<i>FKBP10, SC65</i>	0.0006	0.0002	4.68E-05	0.764
cg15515095	1	<i>HS2ST1</i>	0.0015	0.0004	4.74E-05	0.764
cg11155432	5	<i>CDH9</i>	0.0048	0.0012	5.04E-05	0.764
cg09854317	12	<i>CDK2AP1</i>	-0.0015	0.0004	5.90E-05	0.764
cg14724318	6	<i>CSNK2B</i>	0.0010	0.0002	5.92E-05	0.764
cg09495303	17	<i>CHRNE, C17orf107</i>	-0.0077	0.0019	5.96E-05	0.764
cg03185775	19	<i>INSR</i>	0.0009	0.0002	5.96E-05	0.764
cg15010603	7	<i>SNX13</i>	0.0019	0.0005	6.04E-05	0.764
cg05970916	10	<i>LOC100188947</i>	0.0009	0.0002	6.15E-05	0.764
cg00848033	3	<i>TTC14</i>	0.0035	0.0009	6.82E-05	0.764
cg17037491	6	<i>LRRC16A</i>	-0.0018	0.0005	6.99E-05	0.764
cg26791384	16	<i>SYCE1L</i>	-0.0018	0.0005	7.06E-05	0.764
cg15473186	3	<i>CACNA1D</i>	-0.0028	0.0007	7.16E-05	0.764
cg07570142	6	<i>MOXD1</i>	-0.0013	0.0003	7.35E-05	0.764
cg04667158	7	<i>ACN9</i>	0.0009	0.0002	7.59E-05	0.764
cg25742761*	4	<i>GAB1</i>	0.0018	0.0005	7.59E-05	0.764
cg24547184	6		-0.0030	0.0008	8.20E-05	0.764

Supplementary Table 6. CpG sites with lowest P-values in meta-analysis of associations between maternal haemoglobin during pregnancy and offspring DNA methylation at adolescence. There are no significant CpG sites after Bonferroni correction (P-value < 1.19E-07). Fully adjusted model is adjusted for maternal parity, maternal education, maternal smoking, child sex, gestational age at birth, child age at time of DNA methylation measurement, DNA methylation batch and white blood cells estimates. CpG, cytosine-phosphate-guanine; Chr, chromosome; Regression coefficient, difference in offspring DNA methylation beta value per one SE unit increase in maternal haemoglobin; SE, standard error. Polymorphic CpG sites are indicated with an asterisk after the site name.

CpG site	Chr	Gene	Regression coefficient	SE for regression coefficient	P-value	FDR-corrected P-value
cg18388270	1		-0.0125	0.0027	3.87E-06	0.556
cg24058386	1	<i>C1orf61</i>	-0.0048	0.0011	5.42E-06	0.556
cg10553748	17	<i>CHRNE, C17orf107</i>	-0.0065	0.0015	7.39E-06	0.556
cg10095352	15	<i>RAB11A</i>	0.0009	0.0002	7.97E-06	0.556
cg24480012*	12	<i>FAM19A2</i>	-0.0019	0.0004	8.63E-06	0.556
cg14961391	2	<i>ORC4L</i>	0.0022	0.0005	9.29E-06	0.556
cg09215588*	12		0.0012	0.0003	9.31E-06	0.556
cg06000530	20	<i>HM13, PSIMCT-1</i>	-0.0025	0.0006	1.39E-05	0.695
cg27176262	6	<i>TAP2</i>	0.0016	0.0004	1.65E-05	0.695
cg16931969	4	<i>ANK2</i>	-0.0085	0.0020	1.70E-05	0.695
cg13609939*	10	<i>OAT</i>	0.0010	0.0002	1.98E-05	0.695
cg02034222	2	<i>DQX1</i>	0.0012	0.0003	2.18E-05	0.695
cg18281525*	20	<i>ADRM1</i>	0.0033	0.0008	2.19E-05	0.695
cg14371590*	12	<i>SLC26A10</i>	-0.0031	0.0007	2.39E-05	0.695
cg24547184*	6		-0.0032	0.0008	2.65E-05	0.695
cg04168479*	2	<i>CACNB4</i>	0.0027	0.0006	3.23E-05	0.695
cg09854317	12	<i>CDK2AP1</i>	-0.0016	0.0004	3.50E-05	0.695
cg18121829	12	<i>CRY1</i>	0.0015	0.0004	3.53E-05	0.695
cg19531351	18		0.0017	0.0004	4.22E-05	0.695
cg12156838	5	<i>HSD17B4</i>	0.0010	0.0002	4.46E-05	0.695
cg06558800	5		0.0010	0.0002	4.52E-05	0.695
cg15946310	5	<i>TTC1</i>	-0.0005	0.0001	4.54E-05	0.695
cg17037491	6	<i>LRRC16A</i>	-0.0019	0.0005	4.83E-05	0.695
cg03592833	3	<i>ATP13A3</i>	0.0007	0.0002	5.12E-05	0.695
cg08948841	4	<i>CTBP1, C4orf42</i>	0.0067	0.0017	5.29E-05	0.695
cg01901434	5	<i>FBN2</i>	0.0028	0.0007	5.58E-05	0.695
cg23520075*	19	<i>MYADM</i>	0.0005	0.0001	5.69E-05	0.695
cg09458618	7		0.0015	0.0004	6.04E-05	0.695
cg05138150	12	<i>RIMBP2</i>	0.0030	0.0008	6.40E-05	0.695
cg08645879*	1		0.0011	0.0003	7.03E-05	0.695
cg14529146	17	<i>FKBP10, SC65</i>	0.0006	0.0002	7.05E-05	0.695
cg07289841	5	<i>SNCAIP</i>	0.0031	0.0008	7.35E-05	0.695
cg21287347	8		0.0016	0.0004	7.39E-05	0.695
cg00539368	18		0.0012	0.0003	7.41E-05	0.695
cg24377495	19		-0.0043	0.0011	7.42E-05	0.695
cg08008233*	18	<i>TCEB3C, KATNAL2</i>	0.0028	0.0007	7.44E-05	0.695
cg02873885	7		-0.0032	0.0008	7.60E-05	0.695
cg04908077	3		0.0013	0.0003	8.26E-05	0.695
cg19995856	14		0.0056	0.0014	8.38E-05	0.695
cg14724318	6	<i>CSNK2B</i>	0.0010	0.0003	8.40E-05	0.695