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DNA methylome of exposure to particulate matter at three time points in early life

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Methods

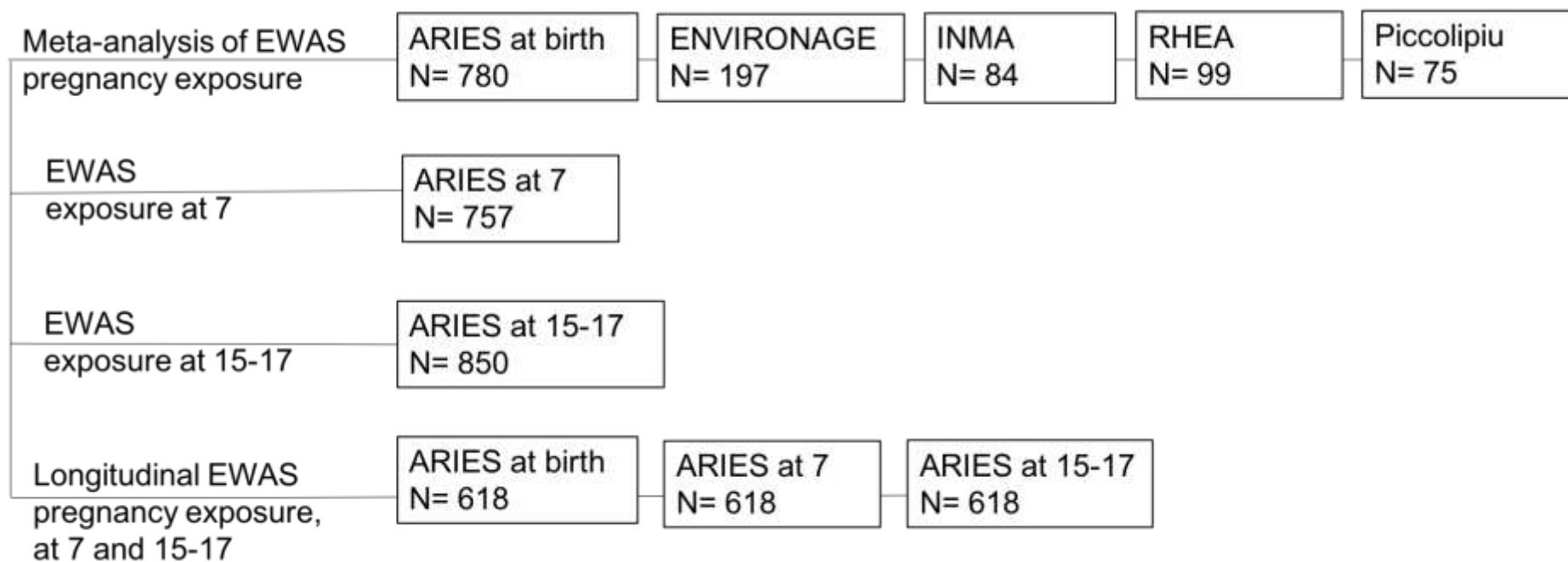
1. Description of methods

The ALSPAC Law and Ethics Committee and the local Research Ethics Committees gave ethical approval for the study. All participants gave written informed consent. Details and data dictionaries of the study can be found online [<http://www.bris.ac.uk/alspac/researchers/data-access/data-dictionary/>]. Blood samples were collected from mothers and their children during several clinical visits. In the framework of the Accessible Resource for Integrated Epigenomics Studies (ARIES) project [<http://www.ariesepigenomics.org.uk/>] DNA methylation data was collected. Mother-offspring pairs (n=1,018) were selected based on the availability of DNA samples of the mother (prenatal and when the child(ren) were at age 17 years) and the children (at birth, at age 7 and at age 15-17 years). The selection did not include information on phenotypic features ²¹.

Within the EXPOsOMICS collaborative European project¹⁵, a subset of four population-based birth cohorts, ENVIRONAGE ¹⁶, INMA ¹⁷, Rhea ^{18, 19} and the Turin centre of the Piccolipiù study ²⁰, was established to conduct DNA methylation analyses. Local hospital ethical committees approved the study in each cohort and written informed consent was collected from participating mothers/parents in all cohorts. The ENVIRONAGE cohort recruited women when they arrived for delivery at the South-East-Limburg Hospital in Genk, Belgium between 2014 and 2015 ¹⁶. INMA cohort centre enrolled women during the pregnancy at public primary health care centres or hospitals in Sabadell, Spain between 2004 and 2006. The Rhea cohort enrolled women during the pregnancy at public primary health care centres or hospitals in Heraklion, Greece between 2007 and 2008. The Turin centre of the Piccolipiù cohort included women giving birth at the main hospital of Turin, Italy, between 2011 and 2013. Cohort inclusion criteria and further protocols can be found in the respective cohort references ¹⁵⁻²⁰. Blood samples were collected from cord vessels, samples were centrifuged and blood tubes were stored at -80 °C. Buffy coat was removed upon DNA extraction (all cohorts) and immediately frozen at -80 °C until analysis. Family lifestyle factors were collected from mothers through questionnaires or interview by trained fieldworkers and medical history for each family was transferred from hospital

records. Samples were selected randomly from each cohort (N= 200 for ENVIRONAGE, N= 99 for Piccolipiù, N= 100 for INMA and N=101 for Rhea) among participants with sufficient sample volume, quality and available covariate data.

Figure S1: Flow chart of the study



EWAS: epigenome-wide analyses study

Figure S2: Violin plot of exposure to PM₁₀ during pregnancy in the 5 participating cohorts

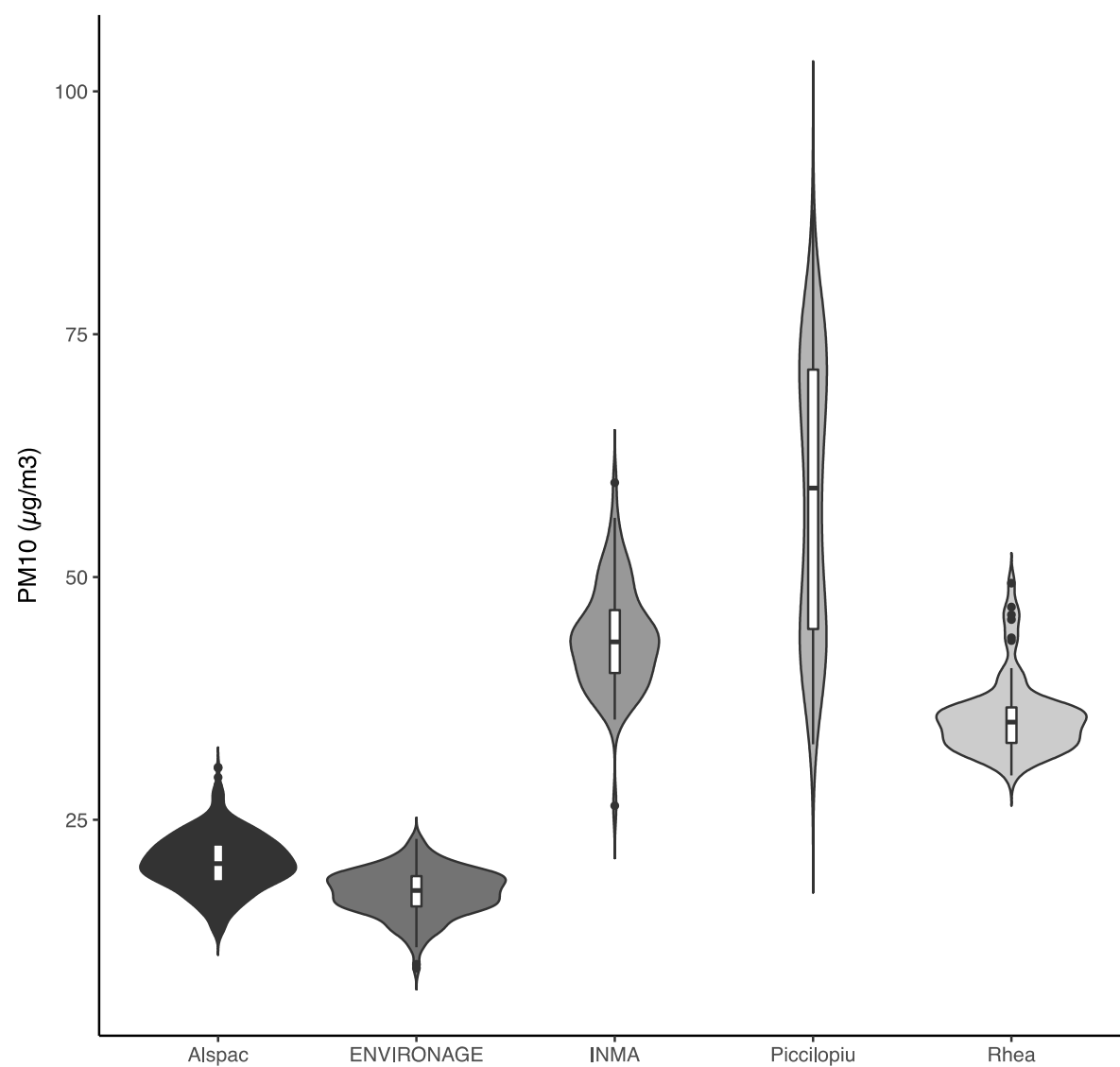
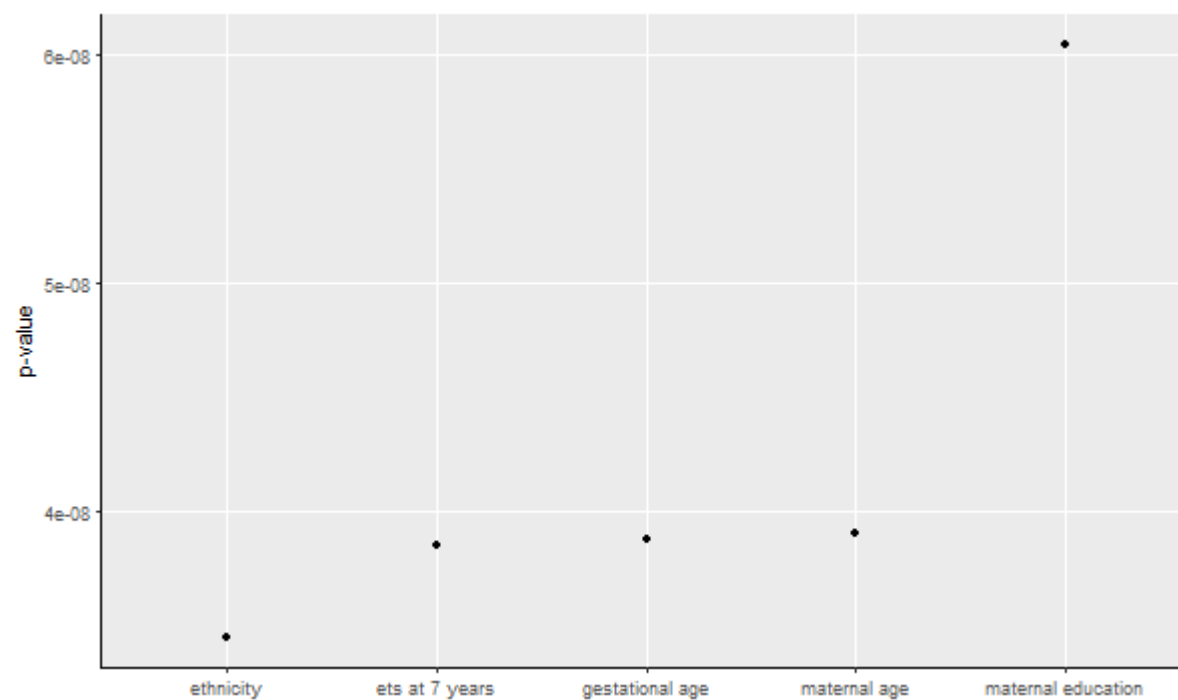
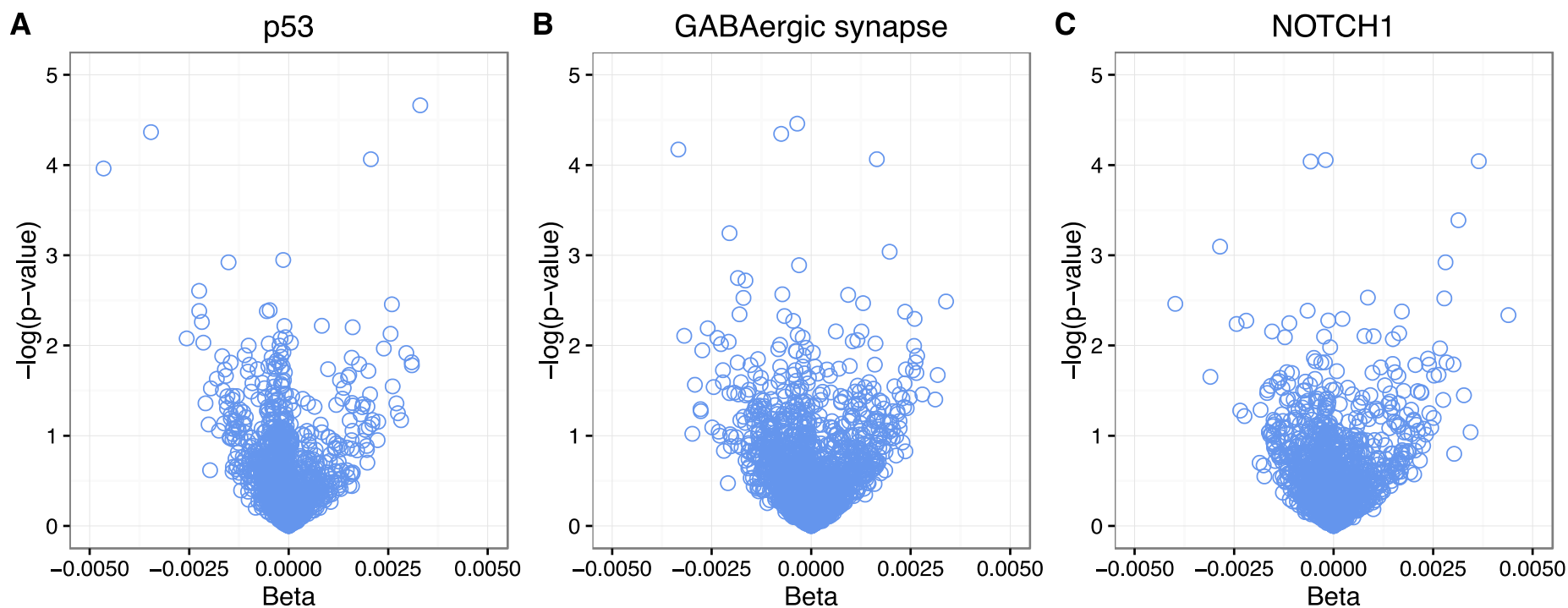


Figure S3: Sensitivity analyses of CpG site cg21785536



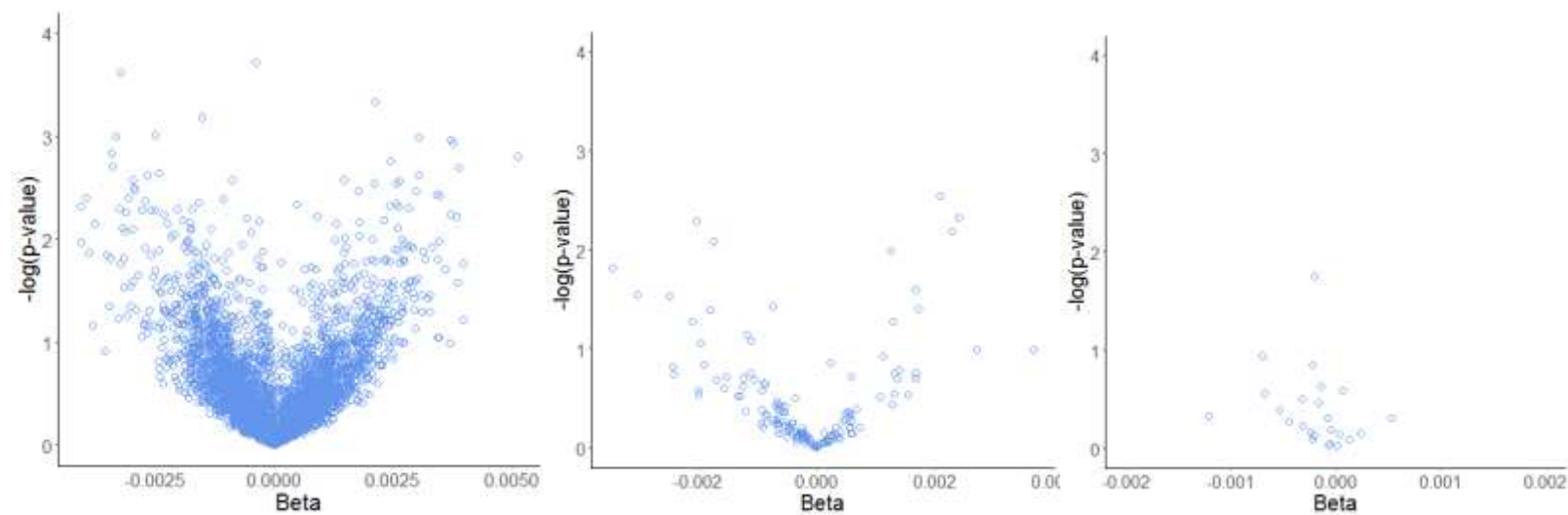
Sensitivity analyses including additionally ethnicity, environmental tobacco smoking, gestational age, maternal age and maternal education level in the main model. The dots represent the adjusted p-value, the original p- value was 3.82-8.

Figure S4: Volcano plots of gene sets of the P53 signalling pathway and the GABAergic synapse pathway.



Panel a: CpG sites of the p53 pathway (KEGG, 69 genes, 1475 CpG sites); panel b: selection of the GABAergic synapse pathway (KEGG, 88 genes, 2261 CpG sites), panel c: selection of the NOTCH1 pathway (REACTOME, 48, 1623 CpG sites).

Figure S5: Volcano plots of gene sets of maternal smoking and prenatal NO_x exposure.



Panel a: CpG sites associated to maternal smoking (6073 CpG sites); panel b: CpG sites associated to maternal smoking in children (148 CpG sites); panel c: selection of NO_x related CpG sites (25 CpG sites).

Table S1: Pearson correlation between PM₁₀ exposure at birth, at 7 and 15 years of age.

	PM ₁₀ exposure at birth	PM ₁₀ exposure at 7 years	PM ₁₀ exposure at 15 years
PM ₁₀ exposure at birth	1	0.450	0.428
PM ₁₀ exposure at 7 years		1	0.706
PM ₁₀ exposure at 15 years			1

All the pairwise correlations were statistically significant (all p-values < 2.2e-16).

Table S2: Association of the cross-sectional study on DNA methylation and PM₁₀ exposure during childhood (7 years of age) and adolescence (15-17 years of age).

Time point	CpG	CHR	Gene	Localisation on Gene	Localisation on CGI	β	SE	p-value
Childhood	cg00478361	1:26552116	-	-	Island	0.0008	0.0002	1.57e-6
	cg09500738	15:87911464	-	-	-	0.0062	0.0013	3.20e-6
	cg09248660	6:24969848	-	-	-	0.0079	0.0017	5.66e-6
	cg13150306	20:36572111	VSTM2L	Body	North shore	0.0074	0.0017	9.50e-6
	cg16805884	8:131469585	-	-	-	0.0091	0.0020	9.57e-6
	cg20150640	1:23697656	C1orf213	3UTR	South shore	0.0097	0.0023	2.26e-5
	cg13617087	6:31107321	PSORS1C1	Body	-	-0.0033	0.0008	2.49e-5
	cg24120696	8:53853604	-	-	Island	0.0101	0.0024	3.72e-5
	cg19634315	15:71679485	THSD4	Body	-	-0.0008	0.0002	4.30e-5
	cg04349839	4:25789390	SEL1L3	Body	-	-0.0037	0.0009	5.11e-5
	cg01897424	17:64872494	CACNG5	TSS1500	-	-0.0042	0.0010	5.39e-5
	cg09419176	7:157670705	PTPRN2	Body	South shore	0.0105	0.0026	5.79e-5
	cg13403566	15:79357037	RASGRF1	Body	-	-0.0051	0.0013	1.00e-4
	cg13303203	17:4125596	ANKFY1	Body	South shore	0.0009	0.0002	1.02e-4
	cg20264068	1:207842927	CRIL	Body	Island	-0.0042	0.0011	1.04e-4
Adolescence	cg25317460	2:119608121	-	-	South Shore	0.0051	0.0011	5.19e-6
	cg22814740	1:78442554	FUBP1	Body	North Shore	-0.0061	0.0014	8.60e-6
	cg08491437	1:78442533	FUBP1	Body	North Shore	-0.0075	0.0017	9.54e-6
	cg27264249	3:2141686	CNTN4	TSS1500	Island	0.0023	0.0005	1.37e-5
	cg26386273	14:104623477	KIF26A	Body	North Shore	-0.0108	0.0025	1.53e-5
	cg22201153	19:42817302	TMEM145	TSS200	North Shore	0.0012	0.0003	1.94e-5
	cg05802386	1:43422920	SLC2A1	Body	North Shore	-0.0061	0.0014	2.13e-5
	cg16185386	13:29077350	-	-	-	-0.0048	0.0011	2.35e-5
	cg03112877	20:2637429	NOP56	Body	South Shelf	-0.0053	0.0013	2.50e-5
	cg08847919	11:68854196	TPCN2	Body	South Shelf	-0.0091	0.0021	2.54e-5
	cg07174453	16:27476281	GTF3C1	Body	-	-0.0060	0.0014	2.72e-5
	cg08149078	3:128369362	RPN1	Body	Island	-0.0001	0.0000	3.17e-5
	cg25751453	19:8959693	MUC16	Body	-	-0.0014	0.0003	3.31e-5
	cg19266671	10:126712482	CTBP2	Body	South Shore	-0.0085	0.0020	3.31e-5
	cg03077077	4:122685352	TMEM155	5UTR	North Shore	-0.0051	0.0012	3.56e-5

Top 15 CpG sites based on p-values from the epigenome-wide association study of exposure to PM₁₀ at 7 and 15-17 years of age. N at 7 years of age = 757, N at 15-17 years of age = 850, β represents the difference in methylation for every unit ($\mu\text{g}/\text{m}^3$) increase of PM₁₀. . Adjusted p-values (correction for multiple testing) were equal to 0.99 for all the CpGs in childhood and 1 for all the CpGs in adolescence and thus are not shown in the table. TSS = transcription start site, UTR = untranslated region.

Column headers: Gene=UCSC annotated gene; CHR=chromosome and Chromosomal position; localisation on Gene=UCSC gene region feature category; Localisation on CGI= UCSC relation to CpG islands; β = regression coefficient; SE=standard error for regression coefficient. Models were adjusted for technical variables, sex of the child, maternal smoking during pregnancy and estimated blood cell composition.

Table S3: List of 100 strongest association of the epigenome-wide association study in children of 7 years old and PM₁₀ exposure during pregnancy and corrected for the corresponding year of sampling.

CpG	CHR	Gene	Localisation on Gene	Localisation on CGI	Pregnancy exposure to PM ₁₀			exposure to PM ₁₀ in in childhood		
					β	SE	p-value	β	SE	p-value
cg10774480	11:68191716	LRP5	Body	North shore	-0.0005	0.0001	1.38e-6	0.0004	0.0003	1.90e-1
cg14783283	5:535689	-	-	Island	-0.0005	0.0001	3.62e-6	0.0008	0.0003	1.08e-2
cg05565537	12:51773409	GALNT6	Body	-	-0.0012	0.0003	5.33e-6	0.0015	0.0007	3.66e-2
cg03946896	1:44871606	RNF220	5UTR	Island	0.0004	0.0001	6.17e-6	-0.0009	0.0003	1.02e-3
cg07678449	4:171011395	AADAT	TSS1500	Island	-0.0004	0.0001	1.01e-5	0.0006	0.0003	2.14e-2
cg19901801	1:114697032	SYT6	TSS1500	Island	-0.0004	0.0001	1.49e-5	0.0005	0.0002	2.47e-2
cg16661234	17:10541620	MYH3	Body	Island	-0.0005	0.0001	1.49e-5	0.0008	0.0003	2.09e-2
cg14334258	9:110595657	-	-	-	-0.0015	0.0003	1.50e-5	0.0013	0.0010	1.78e-1
cg14131889	17:39913822	JUP	Body	Island	-0.0005	0.0001	1.53e-5	0.0005	0.0003	1.12e-1
cg26364091	22:41633219	CHADL	Body	North shore	-0.0021	0.0005	1.77e-5	0.0018	0.0013	1.60e-1
cg26484631	6:150284518	ULBP1	TSS1500	North shore	-0.0021	0.0005	2.05e-5	0.0038	0.0013	4.41e-3
cg22377963	16:30905861	BCL7C	TSS1500	South shore	-0.0027	0.0006	2.40e-5	0.0082	0.0017	1.80e-6
cg24002010	19:55741862	TMEM86B	TSS1500	-	-0.0006	0.0001	2.59e-5	0.0004	0.0004	2.96e-1
cg03826618	11:117297328	-	-	North shore	-0.0032	0.0008	2.69e-5	0.0059	0.0021	4.51e-3
cg19382157	7:2124566	MAD1L1	Body	-	-0.0039	0.0009	2.84e-5	0.0076	0.0025	3.01e-3
cg22775138	10:135008819	KNDC1	Body	-	-0.0089	0.0021	3.09e-5	0.0104	0.0058	7.34e-2
cg12333160	10:135040091	-	-	Island	0.0049	0.0012	3.28e-5	-0.0068	0.0032	3.34e-2
cg06804210	2:87036948	CD8A	TSS1500	Island	-0.0036	0.0009	3.56e-5	0.0050	0.0023	3.28e-2
cg08844974	10:129796922	PTPRE	5UTR	-	-0.0035	0.0008	3.86e-5	0.0018	0.0023	4.34e-1
cg00606900	22:50175250	BRD1	Body	North shelf	-0.0017	0.0004	4.22e-5	0.0032	0.0011	5.25e-3
cg19225099	12:53243489	KRT78	TSS1500	-	-0.0014	0.0003	4.28e-5	0.0016	0.0009	8.99e-2
cg22093805	4:53588374	-	-	Island	-0.0001	0.0000	4.75e-5	0.0002	0.0001	2.05e-2
cg20699079	2:137199850	-	-	-	-0.0021	0.0005	4.77e-5	0.0029	0.0014	3.72e-2
cg01033005	19:33350931	SLC7A9	Body	Island	-0.0023	0.0006	5.80e-5	0.0038	0.0015	1.25e-2
cg11846598	11:44996168	LOC221122	Body	-	-0.0036	0.0009	5.82e-5	0.0067	0.0024	6.22e-3
cg15417654	3:187959138	LPP	5UTR	-	-0.0021	0.0005	5.94e-5	0.0009	0.0014	5.30e-1
cg21164697	1:6188946	CHD5	Body	Island	-0.0003	0.0001	5.99e-5	0.0003	0.0002	1.31e-1
cg17657322	13:112690816	-	-	North shore	-0.0007	0.0002	6.32e-5	0.0005	0.0005	2.80e-1
cg27201457	17:5984291	WSCD1	Body	-	-0.0002	0.0000	6.77e-5	0.0001	0.0001	3.16e-1
cg09112790	10:127408004	C10orf137	TSS200	Island	0.0002	0.0000	7.02e-5	-0.0003	0.0001	3.69e-3

cg21301258	21:35898717	RCAN1	5UTR	-	-0.0027	0.0007	7.07e-5	0.0061	0.0019	1.23e-3
cg14470729	12:14958487	C12orf69	3UTR	South shelf	0.0069	0.0017	7.16e-5	-0.0075	0.0047	1.10e-1
cg26892308	11:1510724	HCCA2	Body	-	-0.0025	0.0006	7.25e-5	0.0031	0.0017	7.10e-2
cg20912079	15:83736401	BTBD1	TSS1500	South shore	-0.0025	0.0006	7.34e-5	0.0043	0.0017	1.09e-2
cg02617981	4:3449663	HGFAC	Body	Island	-0.0003	0.0001	7.48e-5	0.0007	0.0002	1.74e-3
cg24969902	14:100259020	EML1	TSS1500	North shore	-0.0014	0.0004	7.51e-5	0.0017	0.0010	7.85e-2
cg10375456	19:10380576	ICAM1	TSS1500	Island	0.0004	0.0001	7.77e-5	-0.0004	0.0003	1.32e-1
cg05478824	17:79970135	ASPSCR1	Body	South shelf	-0.0030	0.0008	7.96e-5	0.0043	0.0021	3.77e-2
cg07122006	7:54733223	-	-	South shore	-0.0030	0.0008	8.12e-5	0.0071	0.0021	6.76e-4
cg19699682	3:119349840	-	-	-	0.0036	0.0009	8.20e-5	-0.0028	0.0025	2.71e-1
cg16874252	2:234072769	INPP5D	Body	-	-0.0010	0.0002	8.24e-5	-0.0008	0.0007	2.58e-1
cg19718508	5:176831858	F12	Body	South shore	-0.0024	0.0006	8.62e-5	0.0060	0.0016	2.44e-4
cg05534148	7:1398159	-	-	-	-0.0050	0.0013	8.80e-5	0.0092	0.0034	7.81e-3
cg26357606	6:43230825	TTBK1	Body	Island	-0.0006	0.0001	9.90e-5	0.0004	0.0004	3.15e-1
cg00090197	1:43738732	TMEM125	Body	Island	-0.0016	0.0004	1.04e-4	0.0020	0.0011	6.44e-2
cg17514665	17:1657533	SERPINF2	Body	Island	-0.0004	0.0001	1.09e-4	0.0006	0.0003	4.21e-2
cg23425970	2:129076394	HS6ST1	TSS1500	Island	-0.0028	0.0007	1.11e-4	0.0028	0.0020	1.65e-1
ch.2.1436611R	2:62697620	-	-	-	0.0002	0.0001	1.12e-4	-0.0003	0.0002	7.21e-2
cg06978336	16:88967587	CBFA2T3	Body	South shore	-0.0014	0.0004	1.15e-4	0.0008	0.0010	4.27e-1
cg02202923	10:135040250	-	-	South shore	0.0013	0.0003	1.17e-4	-0.0019	0.0009	4.28e-2
cg13085530	1:117665186	TRIM45	TSS1500	South shore	-0.0026	0.0007	1.17e-4	0.0041	0.0018	2.57e-2
cg27177554	10:16562102	C1QL3	Body	Island	-0.0023	0.0006	1.19e-4	0.0022	0.0017	1.83e-1
cg02812809	19:39361447	RINL	Body	South shore	-0.0030	0.0008	1.24e-4	0.0058	0.0021	5.85e-3
cg00238182	22:43621788	SCUBE1	Body	North shore	-0.0017	0.0004	1.26e-4	0.0033	0.0012	5.85e-3
cg23629166	1:2345368	PEX10	TSS1500	North shore	-0.0033	0.0008	1.27e-4	0.0064	0.0023	5.62e-3
cg06996739	6:25773039	SLC17A4	Body	-	0.0037	0.0010	1.29e-4	-0.0049	0.0027	6.42e-2
cg03790745	11:63679432	RCOR2	Body	Island	-0.0008	0.0002	1.32e-4	0.0008	0.0005	1.44e-1
cg11372818	10:131989849	-	-	South shore	-0.0055	0.0014	1.35e-4	0.0112	0.0039	4.51e-3
cg08165261	19:18977240	UPF1	3UTR	North shore	-0.0019	0.0005	1.36e-4	-0.0001	0.0014	9.57e-1
cg19901994	8:27288146	PTK2B	Body	-	-0.0008	0.0002	1.39e-4	0.0014	0.0006	2.00e-2
cg23257934	1:234858982	-	-	-	-0.0012	0.0003	1.45e-4	0.0022	0.0008	7.62e-3
cg06507221	11:4208449	-	-	Island	0.0002	0.0001	1.47e-4	-0.0003	0.0001	1.91e-2
cg25104511	17:38333503	RAPGEFL1	TSS1500	North shore	-0.0021	0.0006	1.47e-4	0.0049	0.0015	1.24e-3
cg15753916	17:35870705	DUSP14	5UTR	North shelf	-0.0064	0.0017	1.53e-4	0.0112	0.0046	1.46e-2
cg10188131	9:130214136	LRSAM1	TSS1500	Island	0.0002	0.0001	1.53e-4	0.0000	0.0001	8.51e-1
cg14328761	4:188858709	-	-	-	-0.0015	0.0004	1.54e-4	0.0009	0.0011	4.05e-1
cg27460534	17:80046302	FASN	Body	Island	-0.0018	0.0005	1.56e-4	0.0024	0.0013	6.11e-2
cg05633407	17:80654900	RAB40B	Body	North shore	-0.0003	0.0001	1.59e-4	0.0004	0.0002	6.83e-2
cg14342823	17:10584091	SCO1	3UTR	-	-0.0011	0.0003	1.59e-4	0.0015	0.0008	4.72e-2

cg27007197	6:44120547	TMEM63B	Body	Island	-0.0015	0.0004	1.63e-4	0.0006	0.0011	5.94e-1
cg19252931	11:33721847	C11orf91	1stExon	Island	-0.0037	0.0010	1.65e-4	0.0027	0.0027	3.16e-1
cg15107724	1:36054124	TFAP2E	Body	-	-0.0026	0.0007	1.67e-4	0.0014	0.0018	4.60e-1
cg07936950	2:172953134	DLX1	3UTR	Island	-0.0007	0.0002	1.67e-4	0.0004	0.0005	4.09e-1
cg07525624	4:77069462	NUP54	1stExon	Island	-0.0003	0.0001	1.73e-4	0.0003	0.0002	1.62e-1
cg03639223	17:7369125	ZBTB4	Body	Island	-0.0043	0.0012	1.73e-4	0.0039	0.0031	2.10e-1
cg00080059	20:61568856	DIDO1	5UTR	Island	0.0004	0.0001	1.76e-4	-0.0004	0.0003	1.04e-1
cg25793425	19:6007842	RFX2	Body	Island	-0.0003	0.0001	1.76e-4	0.0002	0.0002	3.76e-1
cg01614102	12:115134918	-	-	North shore	-0.0007	0.0002	1.78e-4	0.0007	0.0005	2.08e-1
cg21205987	9:102584491	NR4A3	5UTR	Island	0.0002	0.0001	1.79e-4	-0.0003	0.0002	7.67e-2
cg25474442	8:144696604	TSTA3	Body	Island	-0.0003	0.0001	1.79e-4	0.0005	0.0002	4.59e-3
cg08752947	5:148807996	MIR143	TSS1500	-	-0.0009	0.0002	1.85e-4	0.0014	0.0006	2.26e-2
cg17765892	8:97156081	GDF6	3UTR	North shore	-0.0013	0.0004	1.89e-4	0.0017	0.0010	7.64e-2
cg26574777	13:100927476	PCCA	Body	-	-0.0015	0.0004	1.91e-4	0.0009	0.0011	4.05e-1
cg01217984	7:27143235	HOXA2	TSS1500	Island	-0.0033	0.0009	1.98e-4	0.0083	0.0024	6.58e-4
cg05179499	16:83982669	OSGIN1	TSS200	-	0.0115	0.0031	2.00e-4	-0.0216	0.0084	1.06e-2
cg00820056	8:144265337	-	-	North shore	0.0023	0.0006	2.06e-4	-0.0039	0.0016	1.84e-2
cg00650088	1:227169808	CABC1	Body	-	-0.0002	0.0001	2.12e-4	0.0003	0.0002	1.21e-1
cg06406026	10:131989655	-	-	South shore	-0.0053	0.0014	2.17e-4	0.0142	0.0039	2.74e-4
cg15869718	14:100751572	-	-	North shore	-0.0012	0.0003	2.20e-4	0.0025	0.0009	4.54e-3
cg16110940	22:21400158	LOC400891	TSS200	Island	-0.0003	0.0001	2.21e-4	0.0005	0.0002	1.82e-2
cg18548199	3:129281892	PLXND1	Body	-	-0.0003	0.0001	2.21e-4	0.0004	0.0003	1.67e-1
cg19111378	8:39844956	IDO2	Body	-	-0.0010	0.0003	2.22e-4	0.0019	0.0007	1.14e-2
cg13151196	8:67578643	VCPIP1	1stExon	North shore	0.0003	0.0001	2.25e-4	-0.0003	0.0002	2.08e-1
cg12195369	19:55972957	ISOC2	5UTR	Island	0.0002	0.0001	2.29e-4	-0.0003	0.0002	7.96e-2
cg05490233	3:129321847	PLXND1	Body	North shelf	0.0011	0.0003	2.35e-4	-0.0014	0.0008	6.60e-2
cg05316627	6:87861261	-	-	North shore	-0.0033	0.0009	2.43e-4	0.0047	0.0024	5.68e-2
cg02350636	5:1088954	SLC12A7	Body	Island	-0.0008	0.0002	2.45e-4	0.0017	0.0006	5.34e-3
cg10071690	10:666063	DIP2C	Body	North shelf	-0.0032	0.0009	2.47e-4	0.0083	0.0024	4.84e-4
cg11519725	7:69175743	AUTS2	Body	-	0.0051	0.0014	2.48e-4	-0.0074	0.0038	4.83e-2
cg25583264	17:49462727	-	-	-	-0.0022	0.0006	2.54e-4	0.0036	0.0016	2.60e-2

N = 757, β represents the difference in methylation for every unit ($\mu\text{g}/\text{m}^3$) increase of PM_{10} . TSS = transcription start site, UTR = untranslated region.

Column headers: Gene=UCSC annotated gene; CHR=chromosome and Chromosomal position; localisation on Gene=UCSC gene region feature category;

Localisation on CGI= UCSC relation to CpG islands; β = regression coefficient; SE=standard error for regression coefficient. Models were adjusted for technical variables, sex of the child, maternal smoking during pregnancy and estimated blood cell composition.

Table S4: List of 100 strongest association of the epigenome-wide association study in children of 15-17 years old and PM₁₀ exposure during pregnancy and corrected for the corresponding year of sampling.

CpG	CHR	Gene	Localisation on Gene	Localisation on CGI	Pregnancy exposure to PM ₁₀			exposure to PM ₁₀ in adolescence		
					β	SE	p-value	β	SE	p-value
cg24940706	19:1648682	TCF3	Body	South shore	0.0030	0.0006	4.22e-7	-0.0041	0.0014	3.33e-3
cg04648402	4:987561	IDUA	Body	South shore	0.0036	0.0007	8.99e-7	-0.0032	0.0017	5.87e-2
cg00937932	10:35464629	CREM	5UTR	-	0.0025	0.0005	4.41e-6	-0.0036	0.0013	3.96e-3
cg06897442	5:140620284	PCDHB19P	Body	North shore	-0.0071	0.0015	4.61e-6	0.0054	0.0036	1.38e-1
cg03904128	12:129341084	GLT1D1	Body	South shelf	0.0046	0.0010	5.45e-6	-0.0084	0.0024	3.99e-4
cg06163904	17:78964779	CHMP6	TSS1500	North shore	-0.0041	0.0009	6.20e-6	0.0035	0.0021	9.69e-2
cg07270021	8:60627336	-	-	-	0.0020	0.0005	6.63e-6	-0.0032	0.0011	2.79e-3
cg15505103	1:168249943	TBX19	TSS1500	-	0.0021	0.0005	7.34e-6	-0.0017	0.0011	1.25e-1
cg13103190	12:34453300	-	-	-	0.0019	0.0004	1.30e-5	-0.0014	0.0010	1.64e-1
cg01363474	4:6344484	PPP2R2C	Body	-	-0.0059	0.0013	1.35e-5	0.0123	0.0032	1.13e-4
cg03783907	6:26446387	BTN3A3	Body	-	-0.0033	0.0008	1.51e-5	0.0010	0.0018	5.75e-1
cg03574651	4:41992907	SLC30A9	Body	Island	0.0003	0.0001	1.87e-5	-0.0005	0.0001	1.11e-3
cg18150439	2:139537824	NXPH2	TSS200	Island	0.0002	0.0001	1.95e-5	-0.0004	0.0001	1.56e-3
cg14461349	14:76127409	C14orf1	1stExon	Island	0.0004	0.0001	2.25e-5	-0.0006	0.0002	1.06e-2
cg16408843	14:64809251	-	-	South shelf	0.0011	0.0003	2.26e-5	-0.0017	0.0006	7.12e-3
cg17571992	8:23239266	LOXL2	5UTR	-	0.0011	0.0003	2.27e-5	-0.0020	0.0006	1.01e-3
cg04774620	3:78765904	ROBO1	Body	-	0.0045	0.0011	2.34e-5	-0.0057	0.0025	2.01e-2
cg00004818	4:178364146	AGA	TSS1500	South shore	-0.0027	0.0006	2.37e-5	0.0047	0.0015	1.43e-3
cg10933028	12:4479577	FGF23	Body	Island	0.0035	0.0008	2.41e-5	-0.0031	0.0019	1.09e-1
cg23173466	14:65565498	MAX	Body	North shelf	-0.0024	0.0006	2.76e-5	0.0025	0.0014	6.95e-2
cg25575138	19:12761959	MAN2B1	Body	South shelf	0.0013	0.0003	2.86e-5	-0.0022	0.0007	1.69e-3
cg22495460	2:25135724	ADCY3	Body	-	0.0048	0.0011	2.91e-5	-0.0070	0.0027	8.52e-3
cg12617332	12:56849576	MIP	TSS1500	-	0.0014	0.0003	2.95e-5	-0.0029	0.0008	2.85e-4
cg12226430	17:6554869	MED31	5UTR	Island	0.0002	0.0000	3.01e-5	-0.0003	0.0001	3.45e-3
cg13576739	6:33257501	PFDN6	5UTR	South shore	-0.0003	0.0001	3.09e-5	0.0003	0.0002	1.04e-1
cg08445080	2:62084236	-	-	South shelf	0.0017	0.0004	3.46e-5	-0.0019	0.0009	3.58e-2
cg08473330	2:63282883	OTX1	Body	Island	-0.0014	0.0003	3.50e-5	0.0012	0.0008	1.27e-1
cg21509821	12:83079551	TMTC2	TSS1500	North shore	-0.0008	0.0002	3.50e-5	0.0006	0.0005	1.89e-1
cg24795627	11:69634456	FGF3	TSS1500	Island	0.0003	0.0001	3.83e-5	-0.0003	0.0002	9.40e-2
cg21266975	18:2846181	EMILIN2	TSS1500	North shore	-0.0050	0.0012	4.09e-5	0.0062	0.0028	3.06e-2
cg26036648	6:36832884	PPIL1	Body	-	0.0023	0.0006	4.21e-5	-0.0030	0.0013	2.52e-2
cg21498326	21:26735730	-	-	South shore	0.0046	0.0011	4.32e-5	-0.0095	0.0026	2.59e-4

cg13527630	4:76862276	NAAA	TSS200	Island	0.0001	0.0000	4.54e-5	-0.0001	0.0001	3.45e-2
cg09504692	2:33169353	LOC100271832	Body	North shelf	0.0046	0.0011	4.59e-5	-0.0082	0.0027	2.22e-3
cg23748965	11:14924450	-	-	North shelf	0.0044	0.0011	5.04e-5	-0.0046	0.0025	6.79e-2
cg07981869	19:34174665	CHST8	5UTR	North shore	-0.0015	0.0004	5.15e-5	0.0006	0.0009	4.62e-1
cg22076203	22:50006993	-	-	North shore	0.0035	0.0009	5.21e-5	-0.0037	0.0020	6.40e-2
cg07052524	19:40009835	SELV	3UTR	South shelf	0.0040	0.0010	5.63e-5	-0.0053	0.0023	2.23e-2
cg17681818	16:70835134	VAC14	TSS200	Island	-0.0007	0.0002	5.64e-5	0.0004	0.0004	2.90e-1
cg11588787	13:28181449	LNK2	5UTR	-	-0.0019	0.0005	5.78e-5	0.0032	0.0011	2.85e-3
cg07188896	10:59546843	-	-	-	-0.0039	0.0010	5.85e-5	0.0034	0.0023	1.34e-1
cg23082393	6:112471108	LAMA4	Body	-	0.0011	0.0003	5.98e-5	-0.0020	0.0006	2.45e-3
cg13723576	9:97403668	FBP1	TSS1500	South shore	0.0010	0.0002	6.13e-5	-0.0006	0.0006	2.82e-1
cg15245598	8:94709667	-	-	North shelf	0.0023	0.0006	6.55e-5	-0.0028	0.0013	3.54e-2
cg19910323	2:47168440	MCFD2	5UTR	Island	0.0001	0.0000	6.65e-5	-0.0002	0.0001	4.88e-3
cg02764722	12:51480175	-	-	South shelf	0.0016	0.0004	6.87e-5	-0.0024	0.0009	7.98e-3
cg25213055	6:680936	EXOC2	5UTR	-	0.0009	0.0002	7.15e-5	-0.0021	0.0006	1.26e-4
cg06455190	13:19451923	-	-	South shelf	0.0013	0.0003	7.35e-5	-0.0009	0.0007	2.22e-1
cg27502457	2:87018585	CD8A	5UTR	South shore	-0.0016	0.0004	7.41e-5	0.0012	0.0009	1.97e-1
cg01396774	2:218299024	DIRC3	Body	-	-0.0024	0.0006	7.62e-5	0.0031	0.0014	2.96e-2
cg09720466	13:75930728	TBC1D4	Body	-	0.0040	0.0010	7.91e-5	-0.0051	0.0023	2.96e-2
cg27589988	1:215147891	-	-	-	0.0027	0.0007	8.04e-5	-0.0032	0.0016	3.96e-2
cg21500895	12:107974296	BTBD11	TSS1500	North shore	0.0010	0.0002	8.08e-5	-0.0016	0.0006	4.74e-3
cg07774177	15:42387287	PLA2G4D	TSS1500	-	0.0017	0.0004	8.51e-5	-0.0025	0.0010	1.33e-2
cg11202785	1:94884090	ABCD3	1stExon	Island	0.0001	0.0000	8.78e-5	-0.0001	0.0001	2.59e-2
cg26538224	22:37591954	-	-	North shelf	0.0012	0.0003	9.08e-5	-0.0023	0.0007	1.33e-3
cg02757236	2:158182140	ERMN	1stExon	-	0.0028	0.0007	9.67e-5	-0.0027	0.0017	9.78e-2
cg06733608	5:10692764	DAP	Body	-	0.0038	0.0010	9.85e-5	-0.0056	0.0023	1.45e-2
cg04963697	16:3570555	CLUAP1	Body	-	0.0015	0.0004	9.89e-5	-0.0028	0.0009	1.49e-3
cg07528216	5:142788776	NR3C1	5UTR	South shelf	0.0028	0.0007	1.01e-4	-0.0035	0.0017	3.72e-2
cg16337574	12:56109265	BLOC1S1	TSS1500	North shore	0.0010	0.0002	1.02e-4	-0.0011	0.0006	4.78e-2
cg16050237	15:25491792	SNORD115-10	TSS1500	-	0.0015	0.0004	1.02e-4	-0.0025	0.0009	6.59e-3
cg01738457	11:86207067	ME3	Body	-	0.0022	0.0006	1.05e-4	-0.0043	0.0013	9.17e-4
cg16480008	10:31288991	ZNF438	5UTR	-	0.0038	0.0010	1.06e-4	-0.0065	0.0023	4.40e-3
cg17591573	6:33156206	COL11A2	Body	North shelf	0.0009	0.0002	1.07e-4	-0.0016	0.0005	2.65e-3
cg21616626	3:49509320	DAG1	5UTR	South shore	0.0023	0.0006	1.09e-4	-0.0037	0.0014	6.50e-3
cg07429047	11:74167536	KCNE3	3UTR	-	0.0026	0.0007	1.10e-4	-0.0055	0.0016	4.58e-4
cg09697644	16:34375039	-	-	-	0.0044	0.0011	1.11e-4	-0.0039	0.0026	1.46e-1
cg17095315	4:2038352	-	-	North shelf	0.0027	0.0007	1.11e-4	-0.0038	0.0016	2.05e-2
cg08713722	1:38942976	-	-	South shore	0.0011	0.0003	1.11e-4	-0.0018	0.0006	5.15e-3
cg07667790	16:72823692	ZFHX3	Body	South shelf	0.0008	0.0002	1.11e-4	-0.0017	0.0005	4.88e-4

cg04311821	2:242612900	ATG4B	3UTR	North shelf	0.0027	0.0007	1.14e-4	-0.0022	0.0016	1.73e-1
cg18118399	3:136471562	STAG1	TSS1500	Island	0.0001	0.0000	1.15e-4	-0.0002	0.0001	1.04e-2
cg02615468	3:58563618	FAM107A	TSS200	-	0.0030	0.0008	1.15e-4	-0.0069	0.0018	1.72e-4
cg13604445	9:116342046	RGS3	Body	-	-0.0006	0.0002	1.16e-4	0.0010	0.0004	1.01e-2
cg15633096	12:124270340	DNAH10	Body	North shore	0.0031	0.0008	1.16e-4	-0.0050	0.0019	7.37e-3
cg12333160	10:135040091	-	-	Island	0.0044	0.0011	1.23e-4	-0.0072	0.0027	7.31e-3
cg26816312	1:20446845	PLA2G2D	TSS1500	-	0.0023	0.0006	1.23e-4	-0.0050	0.0014	2.88e-4
cg20894727	3:13521120	HDAC11	TSS1500	Island	0.0002	0.0001	1.24e-4	-0.0002	0.0001	1.32e-1
cg17819963	10:135191943	PAOX	TSS1500	Island	0.0002	0.0001	1.25e-4	-0.0002	0.0002	1.33e-1
cg12511310	11:11629778	GALNTL4	Body	-	0.0012	0.0003	1.27e-4	-0.0023	0.0008	2.61e-3
cg07861790	13:112761844	-	-	South shore	-0.0037	0.0010	1.29e-4	0.0056	0.0023	1.39e-2
cg08913922	11:79149704	ODZ4	5UTR	Island	-0.0021	0.0005	1.30e-4	0.0033	0.0013	1.01e-2
cg14474003	11:117389755	DSCAML1	Body	South shore	0.0016	0.0004	1.30e-4	-0.0034	0.0010	6.06e-4
cg02242239	2:46150090	PRKCE	Body	-	0.0048	0.0012	1.34e-4	-0.0082	0.0029	4.97e-3
cg19861606	22:25573408	KIAA1671	Body	North shore	0.0013	0.0003	1.36e-4	-0.0027	0.0008	6.40e-4
cg04639421	6:32411897	HLA-DRA	3UTR	-	0.0023	0.0006	1.36e-4	-0.0037	0.0014	9.77e-3
cg24852319	6:113278378	-	-	-	0.0038	0.0010	1.36e-4	-0.0064	0.0023	5.04e-3
cg07179816	8:49647907	EFCAB1	TSS200	Island	0.0003	0.0001	1.37e-4	-0.0002	0.0002	2.90e-1
cg11220397	12:49524893	TUBA1B	Body	Island	0.0002	0.0001	1.39e-4	-0.0001	0.0001	5.40e-1
cg03750606	1:217262978	ESRRG	TSS200	North shore	-0.0008	0.0002	1.42e-4	0.0006	0.0005	2.11e-1
cg20821800	13:54422912	-	-	-	0.0039	0.0010	1.43e-4	-0.0048	0.0024	4.26e-2
cg26787863	1:204286467	PLEKHA6	5UTR	-	0.0018	0.0005	1.46e-4	-0.0027	0.0011	1.13e-2
cg15705203	1:46089693	CCDC17	5UTR	South shore	0.0023	0.0006	1.46e-4	-0.0041	0.0014	3.66e-3
cg18632154	3:73105046	PPP4R2	Body	-	0.0038	0.0010	1.49e-4	-0.0036	0.0023	1.22e-1
cg15331693	6:151373267	MTHFD1L	Body	-	0.0013	0.0003	1.50e-4	-0.0021	0.0008	7.49e-3
cg01840268	6:26402776	BTN3A1	5UTR	-	-0.0005	0.0001	1.51e-4	0.0009	0.0003	5.02e-3
cg00841090	17:2651101	-	-	North shore	0.0025	0.0007	1.52e-4	-0.0031	0.0015	4.58e-2
cg01874084	12:56320851	WIBG	Body	Island	0.0001	0.0000	1.55e-4	-0.0002	0.0001	4.68e-3
cg07576376	15:86299708	-	-	North shelf	-0.0026	0.0007	1.56e-4	0.0035	0.0016	2.89e-2

N = 850, β represents the difference in methylation for every unit ($\mu\text{g}/\text{m}^3$) increase of PM_{10} . TSS = transcription start site, UTR = untranslated region. Column headers: Gene=UCSC annotated gene; CHR=chromosome and Chromosomal position; localisation on Gene=UCSC gene region feature category; Localisation on CGI= UCSC relation to CpG islands; β = regression coefficient; SE=standard error for regression coefficient. Models were adjusted for technical variables, sex of the child, maternal smoking during pregnancy and estimated blood cell composition.

Table S5: 100 strongest association of the longitudinal study on DNA methylation and PM₁₀ exposure during pregnancy, childhood (7 years of age) and adolescence (15-17 years of age).

CpG	Gene	CHR:MAPINFO	Localisation on CGI	Localisation on gene	β	SE	p-value	q-value
cg21785536	C3orf64	3:69063328	South shore	TSS1500	-0.0012	0.0002	3.82e-8	0.0164
cg09417683	MYO3A	10:26222250	North shore	TSS1500	0.0049	0.0010	1.02e-6	0.2199
cg22126437	-	18:45932281	North shelf	-	-0.0023	0.0005	3.35e-6	0.4708
cg10123224	RNPC3	1:104068567	Island	TSS200	-0.0008	0.0002	4.38e-6	0.4708
cg03942471	SGSM1	22:25205117	South shelf	Body	0.0031	0.0007	8.76e-6	0.5419
cg17329422	LYRM2	6:90344688	North shelf	Body	0.0017	0.0004	1.27e-5	0.5419
ch.11.2451667R	BCL9L	11:118775282	-	Body	-0.0005	0.0001	1.29e-5	0.5419
cg04093349	SMAD6	15:66998947	South shelf	Body	-0.0003	0.0001	1.33e-5	0.5419
cg13594174	-	18:24237640	South shore	-	-0.0026	0.0006	1.47e-5	0.5419
cg05342240	-	16:9246537	-	-	-0.0023	0.0005	1.49e-5	0.5419
cg19322065	-	1:37701025	-	-	0.0063	0.0015	1.66e-5	0.5419
cg00048743	PCDHGA4	5:140782367	South shelf	Body	-0.0030	0.0007	1.94e-5	0.5419
cg20519483	LOC285830	6:29704545	-	Body	0.0033	0.0008	2.15e-5	0.5419
cg06539449	CCND1	11:69461008	North shore	Body	0.0033	0.0008	2.17e-5	0.5419
cg04612949	-	2:3609017	South shelf	-	0.0048	0.0011	2.21e-5	0.5419
cg14827056	EIF2C2	8:141550539	-	Body	-0.0034	0.0008	2.24e-5	0.5419
cg05854695	TRPC3	4:122854336	South shore	Body	0.0051	0.0012	2.26e-5	0.5419
cg27454789	LGI1	10:95516788	-	TSS1500	-0.0015	0.0004	2.39e-5	0.5419
cg01758993	SLC35C2	20:44993436	South shore	TSS1500	-0.0022	0.0005	2.39e-5	0.5419
cg20251837	Mar-04	2:217220696	-	Body	0.0052	0.0012	2.74e-5	0.5867
cg00047683	PKD1L3	16:72034122	-	TSS1500	0.0012	0.0003	2.90e-5	0.5867
cg06362776	RRAS2	11:14379620	North shore	Body	-0.0011	0.0003	3.16e-5	0.5867
cg09135866	ZNF611	19:53238498	Island	TSS200	-0.0010	0.0003	3.30e-5	0.5867
cg06872185	-	1:151831144	-	-	-0.0031	0.0007	3.37e-5	0.5867
cg13626544	GABARAP	17:7146054	Island	TSS1500	-0.0004	0.0001	3.47e-5	0.5867
cg18120808	NAF1	4:164088659	South shore	TSS1500	0.0034	0.0008	3.63e-5	0.5867
cg09276072	TSNAXIP1	16:67858885	-	Body	-0.0021	0.0005	3.68e-5	0.5867
cg07723902	-	12:42987806	South shelf	-	0.0015	0.0004	4.03e-5	0.5893
cg15837383	KCNG4	16:84256190	Island	Body	-0.0030	0.0007	4.25e-5	0.5893
cg22697239	CD82	11:44626708	-	Body	-0.0035	0.0008	4.31e-5	0.5893
cg25545336	FARSB	2:223520958	South shore	TSS200	-0.0011	0.0003	4.36e-5	0.5893
cg23221504	GAD1	2:171673110	Island	TSS200	-0.0008	0.0002	4.51e-5	0.5893
cg26234550	CAPN1	11:64952354	South shore	Body	0.0014	0.0004	4.73e-5	0.5893
cg08296665	-	13:113000032	South shore	-	0.0027	0.0007	4.75e-5	0.5893
cg19528830	MCF2L	13:113685296	South shore	Body	0.0025	0.0006	4.79e-5	0.5893
cg16018921	PALLD	4:169616009	-	Body	0.0033	0.0008	5.65e-5	0.6016

cg01413501	-	4:132643925	North shore	-	-0.0024	0.0006	5.81e-5	0.6016
cg14798020	SNORD116-11	15:25320167	-	TSS1500	0.0041	0.0010	6.02e-5	0.6016
cg27243405	NHSL1	6:138859576	-	Body	-0.0014	0.0003	6.03e-5	0.6016
cg21663181	-	18:5889750	North shore	-	0.0015	0.0004	6.08e-5	0.6016
cg12200478	SLC39A2	14:21466565	-	TSS1500	-0.0019	0.0005	6.27e-5	0.6016
cg13418710	SLC6A1	3:11059050	Island	Body	-0.0033	0.0008	6.72e-5	0.6016
cg00762659	TPRKB	2:73964772	South shore	TSS1500	-0.0006	0.0001	6.81e-5	0.6016
cg03466007	PHLPP2	16:71716385	-	Body	0.0030	0.0008	7.32e-5	0.6016
cg11765913	EVI5L	19:7926080	North shore	Body	-0.0030	0.0008	7.36e-5	0.6016
cg06650379	LOC100130872-SPON2	4:1185915	North shelf	Body	-0.0015	0.0004	7.50e-5	0.6016
cg27425314	DHDDS	1:26797619	North shore	3UTR	-0.0028	0.0007	7.80e-5	0.6016
cg12896146	MTNR1A	4:187477065	South shore	TSS1500	0.0036	0.0009	7.85e-5	0.6016
cg05861708	C6orf176	6:166400871	North shore	Body	-0.0020	0.0005	7.89e-5	0.6016
cg10898776	-	7:92100819	-	-	0.0042	0.0011	8.02e-5	0.6016
cg12827946	LRIG1	3:66513559	-	Body	0.0027	0.0007	8.11e-5	0.6016
cg21418534	-	13:112800020	-	-	-0.0024	0.0006	8.19e-5	0.6016
cg20585428	-	6:169274032	-	-	0.0047	0.0012	8.21e-5	0.6016
cg06900938	GNB2L1	5:180671419	North shore	TSS1500	-0.0006	0.0001	8.21e-5	0.6016
cg18488266	-	4:3752338	South shelf	-	-0.0029	0.0007	8.39e-5	0.6016
cg09141856	-	16:5498227	-	-	0.0041	0.0010	8.43e-5	0.6016
cg24914474	NUDT9P1	10:92913238	North shore	TSS1500	-0.0038	0.0010	8.45e-5	0.6016
cg20837354	CACNA1C	12:2398146	-	Body	0.0017	0.0004	8.60e-5	0.6016
cg02605178	TP53I3	2:24308831	South shore	TSS1500	0.0021	0.0005	8.62e-5	0.6016
cg13804457	NARG2	15:60771615	South shore	TSS1500	-0.0006	0.0001	8.67e-5	0.6016
cg23970856	RPS27A	2:55459633	-	5UTR	-0.0002	0.0001	8.79e-5	0.6016
cg03930153	TBL1XR1	3:176868896	-	5UTR	0.0036	0.0009	9.05e-5	0.6016
cg18053505	KAT2B	3:20081161	North shore	TSS1500	-0.0006	0.0001	9.11e-5	0.6016
cg20268208	PRKAR1B	7:618210	South shore	Body	0.0018	0.0005	9.23e-5	0.6016
cg23102632	ZFP64	20:50723227	South shore	Body	0.0035	0.0009	9.34e-5	0.6016
cg15062795	ETV6	12:11802217	Island	TSS1500	-0.0001	0.0000	9.36e-5	0.6016
cg25602049	VAR52	6:30881920	Island	TSS200	-0.0001	0.0000	9.37e-5	0.6016
cg16641903	-	10:23164775	-	-	0.0018	0.0005	9.77e-5	0.6130
cg10363202	USP20	9:132636787	Island	Body	-0.0041	0.0011	9.90e-5	0.6130
cg08806622	PHF12	17:27279525	Island	TSS1500	-0.0014	0.0004	1.00e-4	0.6130
cg18125208	MRPL55	1:228297275	Island	TSS1500	-0.0010	0.0003	1.04e-4	0.6130
cg01056945	RHOQ	2:46769064	North shore	TSS1500	-0.0006	0.0002	1.05e-4	0.6130
cg09691317	KIAA1530	4:1379690	-	Body	-0.0021	0.0005	1.05e-4	0.6130
cg14742187	ADD3	10:111842681	-	5UTR	0.0042	0.0011	1.05e-4	0.6130
cg01199327	CD82	11:44626750	-	Body	-0.0047	0.0012	1.09e-4	0.6162
cg09044219	CCDC77	12:510474	North shore	TSS1500	-0.0005	0.0001	1.10e-4	0.6162
cg14569380	-	9:137036533	-	-	0.0017	0.0004	1.14e-4	0.6162
cg06275028	WDR90	16:707601	North shelf	Body	-0.0028	0.0007	1.14e-4	0.6162
cg22275872	TOLLIP	11:1316436	Island	Body	0.0041	0.0011	1.15e-4	0.6162

cg14689456	DYSF	2:71754492	-	Body	0.0033	0.0009	1.15e-4	0.6162
cg16211438	GRAMD1C	3:113560972	South shelf	Body	0.0030	0.0008	1.16e-4	0.6162
cg15910994	NCAPH	2:97001734	Island	Body	-0.0002	0.0000	1.20e-4	0.6162
cg16365842	C6orf122	6:170191057	South shore	Body	0.0049	0.0013	1.22e-4	0.6162
cg01026256	VWA5B2	3:183959088	Island	Body	-0.0041	0.0011	1.25e-4	0.6162
cg04134305	C7orf13	7:156433520	Island	TSS200	-0.0005	0.0001	1.26e-4	0.6162
cg26906217	-	11:17251956	South shore	-	-0.0025	0.0006	1.27e-4	0.6162
cg14726769	JMJD1C	10:65224694	North shore	Body	-0.0031	0.0008	1.29e-4	0.6162
cg15182221	GTF2F1	19:6391004	North shore	Body	-0.0015	0.0004	1.31e-4	0.6162
cg00922281	JPH3	16:87715775	South shore	Body	-0.0022	0.0006	1.31e-4	0.6162
cg05421550	UBXN6	19:4446485	Island	Body	-0.0040	0.0011	1.34e-4	0.6162
cg00527382	CALCOCO1	12:54121607	-	TSS1500	-0.0012	0.0003	1.34e-4	0.6162
cg16332060	C11orf60	11:118436807	-	TSS200	-0.0003	0.0001	1.36e-4	0.6162
cg11601375	KRT6B	12:52846073	-	TSS200	0.0065	0.0017	1.36e-4	0.6162
cg17376041	SPTBN1	2:54856335	Island	Body	-0.0023	0.0006	1.37e-4	0.6162
cg03209395	-	7:1295653	-	-	-0.0033	0.0009	1.39e-4	0.6162
cg24455158	-	7:157314073	-	-	-0.0022	0.0006	1.41e-4	0.6162
cg12449837	TUG1	22:31364356	North shore	TSS1500	0.0025	0.0007	1.41e-4	0.6162
cg00827176	NPM2	8:21885702	South shelf	Body	-0.0023	0.0006	1.44e-4	0.6162
cg26840462	PKNOX2	11:125220543	-	5UTR	-0.0014	0.0004	1.45e-4	0.6162
cg06689961	CDKN1B	12:12870959	Island	1stExon	-0.0003	0.0001	1.47e-4	0.6162

N = 618, β represents the difference in methylation for every unit ($\mu\text{g}/\text{m}^3$) increase of PM_{10} . TSS = transcription start site, UTR = untranslated region. Column headers: Gene=UCSC annotated gene; CHR=chromosome and Chromosomal position; localisation on Gene=UCSC gene region feature category; Localisation on CGI= UCSC relation to CpG islands; β = regression coefficient; SE=standard error for regression coefficient. Models were adjusted for technical variables, sex of the child, maternal smoking during pregnancy and estimated blood cell composition.