Supplemental Table 1. *PON1* CpG Sites in Illumina 450K and EPIC arrays

CpG Site Number	Illumina ID	Illumina 450K	Illumina EPIC	Coordinates*	Relation to CpG Island
1	cg22798737	yes	yes	94927713	Open Sea
2	cg01879893	yes	yes	94928192	Open Sea
3	cg09416203	yes	yes	94928249	Open Sea
4	cg22414405		yes	94931749	Open Sea
5	cg01637563		yes	94932920	Open Sea
6	cg05495628		yes	94938373	Open Sea
—	cg05433222**	yes	yes	94948020	Open Sea
7	cg24062571	yes	yes	94950657	North Shelf
8	cg07404485	yes	yes	94953653	North Shore
9	cg05342682	yes	yes	94953680	North Shore
10	cg04155289	yes		94953771	Island
11	cg19678392	yes	yes	94953810	Island
—	cg01497363**		yes	94953947	Island
12	cg21856205	yes		94953878	Island
13	cg17330251	yes	yes	94953956	Island
14	cg01874867	yes	yes	94954059	South Shore
15	cg20119798	yes	yes	94954144	South Shore
16	cg04871131	yes	yes	94954202	South Shore
17	cg23055772	yes	yes	94954438	South Shore
18	cg07809369	yes		94954455	South Shore
—	cg17020263**	yes	yes	94955053	South Shore
19	cg15887283	yes	yes	94955348	South Shore

*hg19

** These CpG sites contained SNPs so their methylation data was not included.

Supplemental Table 2. Urinary dialkyl phosphate (DAP) concentrations (nmol/L) in CHAMACOS mothers averaged over pregnancy

	N	min	max	p25	p50	p75	p90
Maternal mean pregnancy							
Total DAPs	245	11.1	1936.4	61.8	124.6	272.8	495.1
Dimethyl phosphates	245	3.9	1729.0	42.8	90.6	195.2	383.9
Diethyl phosphates	245	1.7	395.0	9.0	20.3	46.0	90.8

Supplemental Table 3. AREase Activity (U/mL) in CHAMACOS mothers and children by *PON1*$_{-108}$ Genotype

	Maternal 26 wk AREase (U/mL)		Child Cord AREase (U/mL)		Child 7 year AREase (U/mL)	
PON1 $_{-108}$ Genotype	Frequency	Mean (SD)	Frequency	Mean (SD)	Frequency	Mean (SD)
CC	36	140.6(33.6)	69	42.8(13.4)	62	137.8(30.4)
CT	63	125.3(28.9)	107	32.0(12.1)	109	121.5(27.6)
TT	33	111.8(32.5)	37	28.1(26.3)	38	103.5(26.3)
All	132	126.1(32.6)	213	34.8(16.8)	209	123.1(30.4)

*Maternal AREase activity is displayed over maternal *PON1*$_{-108}$ genotype. Child cord and 7 year AREase activity is shown over child *PON1*$_{-108}$ genotype.

Supplemental Table 4. Regression models of cord blood *PON1* DNA methylation and cognition in boys

CpG Site Number	Verbal Comprehension n=110 β(95%CI)	p-value	Perceptual Reasoning n=110 β(95%CI)	p-value	Working Memory n=102 β(95%CI)	p-value	Processing Speed n=101 β(95%CI)	p-value	Full-Scale IQ n=101 β(95%CI)	p-value
1	7.67(-6.89,22.24)	0.30	-1.34(-14.80,12.12)	0.84	2.85(-8.96,14.67)	0.63	3.31(-9.72,16.34)	0.61	4.49(-9.06,18.04)	0.51
2	**15.25(2.13,28.37)**	**0.02**	5.04(-7.25,17.32)	0.42	-1.26(-11.48,8.95)	0.81	1.18(-10.69,13.05)	0.84	7.61(-4.59,19.82)	0.22
3	10.49(-2.15,23.14)	0.10	5.92(-5.80,17.65)	0.32	8.40(-1.22,18.02)	0.09	0.61(-10.18,11.41)	0.91	10.02(-1.01,21.05)	0.07
7	8.71(-5.34,22.76)	0.22	-0.53(-13.54,12.48)	0.94	0.54(-11.31,12.40)	0.93	3.35(-9.71,16.41)	0.61	6.96(-6.60,20.52)	0.31
8	-4.17(-12.94,4.60)	0.35	-0.43(-8.53,7.67)	0.92	1.77(-5.04,8.57)	0.61	-2.50(-10.00,5.00)	0.51	-1.02(-8.85,6.81)	0.80
9	-4.97(-13.46,3.52)	0.25	0.75(-7.10,8.61)	0.85	1.34(-5.22,7.89)	0.69	-1.73(-8.96,5.50)	0.64	-0.69(-8.23,6.85)	0.86
10	-4.96(-12.69,2.78)	0.21	0.31(-6.92,7.54)	0.93	0.75(-5.30,6.80)	0.81	-1.31(-7.94,5.31)	0.69	-1.05(-7.90,5.80)	0.76
11	-1.59(-7.00,3.83)	0.56	1.22(-3.83,6.26)	0.63	0.90(-3.38,5.17)	0.68	-1.47(-6.15,3.20)	0.53	0.49(-4.37,5.34)	0.84
12	-8.55(-20.76,3.67)	0.17	1.60(-9.74,12.93)	0.78	2.31(-7.24,11.85)	0.63	-3.57(-14.09,6.94)	0.50	-1.77(-12.75,9.20)	0.75
13	-3.21(-8.22,1.81)	0.21	0.01(-4.64,4.66)	1.00	1.12(-2.75,4.99)	0.57	-1.69(-5.95,2.57)	0.43	-0.87(-5.32,3.58)	0.70
14	-3.12(-8.54,2.31)	0.26	-0.65(-5.66,4.37)	0.80	0.88(-3.32,5.08)	0.68	-2.39(-7.00,2.21)	0.30	-1.24(-6.06,3.58)	0.61
15	-3.07(-10.54,4.39)	0.42	0.04(-6.85,6.92)	0.99	1.26(-4.46,6.99)	0.66	-1.76(-8.08,4.56)	0.58	-0.51(-7.09,6.08)	0.88
16	-3.80(-12.02,4.42)	0.36	0.16(-7.43,7.74)	0.97	2.02(-4.39,8.44)	0.53	-2.02(-9.10,5.06)	0.57	0.13(-7.25,7.51)	0.97
17	-0.64(-16.12,14.84)	0.93	-0.68(-14.91,13.55)	0.92	0.65(-12.55,13.86)	0.92	5.14(-9.39,19.67)	0.48	4.08(-11.14,19.30)	0.60
18	-2.12(-13.52,9.27)	0.71	-2.15(-12.62,8.32)	0.68	-0.11(-9.21,8.99)	0.98	-1.32(-11.35,8.72)	0.80	-0.28(-10.73,10.17)	0.96
19	**11.26(0.02,22.51)**	**0.05**	6.81(-3.64,17.27)	0.20	8.20(-1.12,17.53)	0.08	2.79(-7.66,13.23)	0.60	**11.46(0.82,22.09)**	**0.04**

All models adjusted for maternal education, maternal scores for verbal cognition, cell composition, and batch.

Crude p-values <0.05 are bolded.

None of the associations remained significant after controlling for FDR.

*Methylation in cord blood samples were assessed by 450K BeadChip. CpG sites 4, 5, and 6 are not shown because they were not assessed by 450K.

Supplemental Table 5. Regression models of cord blood *PON1* DNA methylation and cognition in girls

CpG Site Number	Verbal Comprehension n=120 β(95%CI)	p-value	Perceptual Reasoning n=122 β(95%CI)	p-value	Working Memory n=111 β(95%CI)	p-value	Processing Speed n=113 β(95%CI)	p-value	Full-Scale IQ n=110 β(95%CI)	p-value
1	5.66(-7.38,18.70)	0.39	4.02(-6.54,14.57)	0.45	8.44(-1.56,18.44)	0.10	-0.04(-7.97,7.88)	0.99	6.73(-3.85,17.31)	0.21
2	-7.30(-19.40,4.80)	0.23	-4.03(-13.86,5.80)	0.42	-8.46(-17.73,0.80)	0.07	-3.96(-11.25,3.33)	0.28	-7.26(-17.02,2.50)	0.14
3	-3.94(-16.85,8.98)	0.55	0.76(-9.64,11.16)	0.89	0.23(-9.72,10.17)	0.96	-1.52(-9.28,6.24)	0.70	-2.67(-13.18,7.85)	0.62
7	7.11(-7.86,22.09)	0.35	3.21(-8.90,15.32)	0.60	-1.12(-12.74,10.50)	0.85	-4.30(-13.39,4.78)	0.35	3.09(-9.24,15.41)	0.62
8	-5.16(-13.90,3.58)	0.24	-3.16(-10.32,4.01)	0.38	-3.01(-9.77,3.75)	0.38	-0.99(-6.17,4.18)	0.70	-4.63(-11.63,2.36)	0.19
9	-2.74(-10.64,5.16)	0.49	-1.18(-7.58,5.22)	0.72	-1.97(-8.19,4.24)	0.53	-0.50(-5.14,4.13)	0.83	-2.49(-8.94,3.97)	0.45
10	-4.92(-11.91,2.08)	0.17	-4.22(-9.93,1.50)	0.15	**-5.85(-11.20,-0.49)**	**0.03**	-0.68(-5.05,3.69)	0.76	**-5.56(-11.12,-0.01)**	**0.05**
11	-2.17(-7.44,3.10)	0.42	-3.11(-7.35,1.12)	0.15	-2.08(-6.15,2.00)	0.31	-0.17(-3.27,2.94)	0.91	-3.15(-7.37,1.08)	0.14
12	-3.71(-15.48,8.05)	0.53	-6.19(-15.65,3.27)	0.20	-4.48(-13.69,4.74)	0.34	-1.96(-8.97,5.06)	0.58	-7.38(-16.93,2.18)	0.13
13	-1.06(-5.89,3.77)	0.67	-1.77(-5.67,2.13)	0.37	-1.93(-5.67,1.82)	0.31	-0.02(-2.85,2.81)	0.99	-2.02(-5.91,1.88)	0.31
14	-1.71(-6.63,3.21)	0.49	-2.08(-6.06,1.89)	0.30	-2.40(-6.19,1.39)	0.21	0.53(-2.50,3.56)	0.73	-2.35(-6.28,1.58)	0.24
15	-2.30(-9.33,4.74)	0.52	-0.59(-6.33,5.14)	0.84	-1.16(-6.64,4.31)	0.67	-1.13(-5.41,3.16)	0.60	-2.15(-7.81,3.50)	0.45
16	-4.83(-12.56,2.90)	0.22	-3.81(-10.07,2.46)	0.23	-2.97(-9.00,3.07)	0.33	2.62(-2.14,7.38)	0.28	-3.78(-10.01,2.45)	0.23
17	**-15.68(-31.00,-0.36)**	**0.04**	-0.21(-12.84,12.43)	0.97	-5.57(-17.76,6.62)	0.37	-7.66(-17.04,1.73)	0.11	-10.37(-23.00,2.26)	0.11
18	-7.22(-19.38,4.93)	0.24	-2.86(-12.74,7.01)	0.57	-2.54(-11.94,6.85)	0.59	-0.79(-8.36,6.79)	0.84	-4.65(-14.31,5.02)	0.34
19	8.33(-3.44,20.10)	0.16	0.32(-9.20,9.84)	0.95	6.75(-2.41,15.91)	0.15	2.72(-4.36,9.80)	0.45	5.90(-3.68,15.48)	0.22

All models adjusted for maternal education, maternal scores for verbal cognition, cell composition, and batch.

Crude p-values <0.05 are bolded.

None of the associations remained significant after controlling for FDR.

*Methylation in cord blood samples were assessed by 450K BeadChip. CpG sites 4, 5, and 6 are not shown because they were not assessed by 450K.

Supplemental Table 6. Regression models of cord blood PON1 methylation and cognition with adjustment for *PON1*$_{-108}$ genotype

CpG Site Number	Verbal Comprehension n=231		Perceptual Reasoning n=232		Working Memory n=213		Processing Speed n=214		Full-Scale IQ n=211	
	β(95%CI)	p-value	β(95%CI)	p-value	β(95%CI)	p-value	β(95%CI)	p-value	β(95%CI)	p-value
1	3.36(-5.95,12.70)	0.48	1.12(-7.19,9.43)	0.79	4.31(-2.99,11.60)	0.25	-1.40(-8.50,5.71)	0.70	0.25(3.70,209.00)	0.11
2	0.86(-7.76,9.47)	0.85	-0.94(-8.61,6.72)	0.81	-4.52(-11.10,2.09)	0.18	-1.95(-8.50,4.60)	0.56	-1.97(-9.38,5.44)	0.60
3	0.66(-8.07,9.38)	0.88	2.41(-5.35,10.17)	0.54	3.72(-3.02,10.50)	0.28	-1.55(-8.10,5.00)	0.64	1.86(-5.57,9.29)	0.62
7	5.01(-4.87,14.90)	0.32	0.13(-8.68,8.95)	0.98	-1.24(-9.09,6.62)	0.76	-0.01(-7.68,7.67)	1.00	3.15(-5.54,11.80)	0.48
8	-1.12(-8.47,6.23)	0.76	-1.23(-7.80,5.35)	0.71	-2.59(-8.36,3.18)	0.38	-0.65(-6.19,4.88)	0.82	-2.15(-8.48,4.17)	0.50
9	0.03(-6.92,6.97)	0.99	0.69(-5.50,6.88)	0.83	-2.52(-8.04,3.00)	0.37	0.16(-5.04,5.37)	0.95	-0.55(-6.61,5.50)	0.86
10	-2.80(-8.62,3.01)	0.34	-2.61(-7.85,2.63)	0.33	**-5.14(-9.70,-0.57)**	**0.03**	0.32(-4.18,4.83)	0.89	-3.67(-8.68,1.35)	0.15
11	0.66(-4.04,5.36)	0.78	-1.35(-5.56,2.86)	0.53	-2.27(-6.05,1.50)	0.24	-0.13(-3.72,3.47)	0.94	-1.20(-5.34,2.93)	0.57
12	-0.91(-11.10,9.30)	0.86	-2.28(-11.4,6.83)	0.62	-4.73(-13.10,3.63)	0.27	-1.29(-9.25,6.67)	0.75	-4.46(-13.60,4.69)	0.34
13	0.28(-4.00,4.56)	0.90	-0.95(-4.77,2.86)	0.62	-1.77(-5.19,1.66)	0.31	0.12(-3.13,3.36)	0.94	-1.06(-4.82,2.69)	0.58
14	-0.15(-4.53,4.23)	0.95	-1.74(-5.64,2.17)	0.38	-2.41(-5.89,1.06)	0.17	0.39(-3.01,3.80)	0.82	-1.65(-5.46,2.16)	0.39
15	0.86(-5.21,6.93)	0.78	0.49(-4.95,5.94)	0.86	-1.20(-6.01,3.60)	0.62	-0.28(-4.93,4.38)	0.91	-0.26(-5.51,4.99)	0.92
16	-1.77(-7.90,4.36)	0.57	-1.59(-7.06,3.87)	0.57	-1.61(-6.41,3.19)	0.51	1.84(-2.85,6.52)	0.44	-1.06(-6.32,4.19)	0.69
17	-8.90(-19.20,1.40)	0.09	-0.61(-9.86,8.64)	0.90	-3.78(-12.20,4.62)	0.38	-0.39(-8.53,7.74)	0.92	-4.43(-13.60,4.76)	0.34
18	-2.85(-11.30,5.60)	0.51	-2.43(-9.96,5.11)	0.53	-2.66(-9.27,3.94)	0.43	-0.43(-6.96,6.09)	0.90	-2.15(-9.37,5.06)	0.56
19	6.25(-1.53,14.00)	0.12	3.31(-3.62,10.20)	0.35	5.69(-0.45,11.80)	0.07	1.88(-4.09,7.84)	0.54	5.97(-0.76,12.70)	0.08

All models adjusted for maternal education, maternal scores for verbal cognition, cell composition, batch, and *PON1*$_{-108}$ genotype.

Crude p-values <0.05 are bolded.

None of the associations remained significant after controlling for FDR.

*Methylation in cord blood samples were assessed by 450K BeadChip. CpG sites 4, 5, and 6 are not shown because they were not assessed by 450K.

		vciq n=67/61		priq n=67/61		wmiq n=64/58		psiq n=64/58		fsiq n=62/58	
CpG Site Number		β(95%CI)	interaction p-value	β(95%CI)	interaction p-value	β(95%CI)	interaction p-value	β(95%CI)	interaction p-value	β(95%CI)	interaction p-value
1	low AREase	3.84(-13.88,21.56)	0.75	8.69(-6.46,23.84)	0.45	9.89(-1.17,20.94)	0.20	8.92(-5.4,23.24)	0.56	11.65(-3.26,26.55)	0.82
	high AREase	-1.65(-17.85,14.54)		-8.7(-26.54,9.15)		-0.13(-15.85,15.59)		-11.51(-25.79,2.77)		-6.84(-22.11,8.43)	
2	low AREase	0.91(-18.08,19.91)	0.53	0.88(-15.53,17.29)	0.21	1.18(-10.62,12.99)	0.54	5.84(-9.09,20.77)	0.64	2.82(-12.88,18.52)	0.83
	high AREase	-9.79(-26.42,6.83)		-1.66(-20.43,17.1)		-12.06(-28.18,4.05)		**-15.64(-30.34,-0.93)**		-10.46(-26.35,5.42)	
3	low AREase	5.68(-12.16,23.52)	0.26	13.37(-1.65,28.38)	0.95	**14.14(3.57,24.7)**	0.20	8.9(-5.46,23.26)	0.23	**14.96(0.37,29.54)**	0.45
	high AREase	-4.84(-20.7,11.01)		-6.2(-23.81,11.41)		5.53(-9.65,20.7)		**-17.97(-31.16,-4.77)**		-7.2(-22.01,7.61)	
7	low AREase	16.28(-4.38,36.95)	0.27	**24.58(7.63,41.54)**	0.89	**13.83(1.13,26.54)**	0.84	11.33(-5.68,28.33)	0.92	**23.67(6.96,40.37)**	0.59
	high AREase	-13.46(-30.92,3.99)		**-21.37(-40.27,-2.48)**		-15.53(-33.21,2.15)		-6.73(-23.72,10.26)		**-17.73(-34.83,-0.62)**	
8	low AREase	-0.99(-14.61,12.63)	0.08	4.97(-6.94,16.87)	0.14	3.09(-5.74,11.92)	0.09	-4.55(-15.65,6.54)	0.30	3.72(-8.17,15.61)	0.06
	high AREase	**-10.28(-19.65,-0.92)**		-4.97(-15.82,5.88)		-4.54(-13.88,4.79)		2.91(-5.87,11.69)		-6.75(-15.77,2.27)	
9	low AREase	0.16(-11.64,11.97)	0.06	5.14(-4.95,15.24)	0.09	4.45(-3.56,12.46)	0.07	-1.62(-11.11,7.87)	0.42	5.31(-5.33,15.95)	**0.04**
	high AREase	**-10.13(-18.78,-1.49)**		-4.04(-14.14,6.07)		-4.36(-13.03,4.31)		2.96(-5.19,11.11)		-6.2(-14.59,2.19)	
10	low AREase	-1.13(-13.02,10.75)	0.11	4.44(-6.44,15.31)	0.16	0.21(-7.87,8.29)	0.09	-1.2(-11.66,9.25)	0.87	3.31(-7.3,13.92)	**0.03**
	high AREase	-6.47(-14.61,1.67)		-5.55(-14.71,3.6)		-6.05(-13.97,1.86)		2.59(-4.96,10.15)		-5.53(-13.32,2.26)	
11	low AREase	0.83(-7.1,8.77)	0.10	1.05(-6.16,8.27)	0.11	2.6(-3.03,8.22)	**0.03**	-1.19(-7.94,5.56)	0.33	3.29(-4.08,10.66)	**0.03**
	high AREase	-3.8(-10.11,2.51)		-1.03(-8.14,6.09)		-1.75(-8,4.49)		3.82(-1.92,9.57)		-1.89(-8.01,4.23)	
12	low AREase	-5.88(-22.84,11.07)	0.27	0.91(-13.81,15.63)	0.13	1.88(-9.62,13.39)	0.09	-4.34(-18.07,9.39)	0.25	0.51(-14.73,15.76)	0.09
	high AREase	-9.77(-23.03,3.5)		-2.11(-17.19,12.98)		-1.77(-15.35,11.81)		7.55(-4.95,20.05)		-4.9(-18.14,8.34)	
13	low AREase	-0.78(-8.07,6.5)	0.14	1.01(-5.28,7.3)	0.28	2.05(-2.97,7.07)	0.09	-0.94(-6.86,4.98)	0.35	1.76(-4.94,8.46)	0.11
	high AREase	-4.26(-10.07,1.55)		-2.49(-9.06,4.08)		-2.41(-8.14,3.31)		3.18(-2.13,8.49)		-2.8(-8.39,2.79)	
14	low AREase	-1.01(-8.65,6.62)	0.12	0.21(-6.48,6.89)	0.24	1.27(-3.94,6.47)	0.10	-0.17(-6.69,6.35)	0.54	1.53(-5.28,8.34)	0.07
	high AREase	-5.11(-10.91,0.7)		-3.41(-10.01,3.19)		-2.93(-8.66,2.8)		2.24(-3.14,7.63)		-3.83(-9.4,1.73)	
15	low AREase	1.75(-8.53,12.02)	0.07	5.01(-3.88,13.9)	0.14	5.22(-1.63,12.07)	**0.04**	-2.85(-11.44,5.74)	0.25	5.03(-4.01,14.08)	0.06
	high AREase	**-7.94(-15.81,-0.07)**		-3.76(-12.82,5.3)		-4.26(-12.04,3.52)		2.51(-4.82,9.84)		-5.32(-12.88,2.24)	
16	low AREase	1.07(-10.07,12.21)	**0.05**	3.4(-6.3,13.1)	0.23	3(-4.39,10.38)	0.07	1.8(-7.58,11.17)	1.00	4.29(-5.42,13.99)	**0.04**
	high AREase	**-12.04(-20.55,-3.53)**		-5.43(-15.55,4.69)		-5.38(-14.09,3.33)		1.68(-6.59,9.95)		-7.6(-15.97,0.78)	
17	low AREase	-5.17(-28.25,17.9)	0.60	6.81(-13.08,26.69)	0.57	8.82(-6.07,23.72)	0.84	1.97(-17.45,21.4)	0.46	7.04(-13.23,27.31)	0.27
	high AREase	**-18.28(-34.16,-2.4)**		**-20.82(-38.43,-3.2)**		-11.87(-28.72,4.98)		-12.03(-27.73,3.66)		**-20.63(-36.32,-4.95)**	
18	low AREase	2.27(-16.38,20.91)	**0.05**	11.68(-4.32,27.67)	0.44	8.95(-2.74,20.63)	0.40	-4.94(-20.57,10.7)	0.25	8.11(-7.36,23.59)	0.18
	high AREase	-8.58(-20.75,3.59)		-7.79(-21.22,5.64)		-3.11(-15.63,9.41)		2.94(-8.77,14.65)		-5.72(-17.72,6.28)	
19	low AREase	6.75(-10.95,24.45)	0.39	**16.22(1.52,30.92)**	0.80	**12.42(1.91,22.93)**	0.27	8.32(-5.61,22.26)	0.54	13.9(-0.32,28.11)	0.60
	high AREase	-1.77(-16.7,13.16)		-8.11(-24.56,8.35)		2.68(-11.91,17.27)		-5.39(-18.95,8.17)		-3.89(-18.16,10.38)	

Supplemental Table 7. Regression of Cord DNA Methylation stratified by maternal AREase activity

All models adjusted for maternal education, maternal scores for verbal cognition, cell composition, and batch.

The β(95%CI) shown are for models stratified by low and high maternal AREase activity while the interaction p-value is based on the interaction term of maternal AREase activity X PON1 DNA methylation at each CpG site.

β(95%CI) with corresponding unadjusted p-values <0.05 and unadjusted interaction p-values<0.05 are bolded.

None of the associations remained significant after controlling for FDR.

Methylation in cord blood samples were assessed by 450K BeadChip. CpG sites 4,5, and 6 are not shown because they were not assessed by 450K.

The N's given are for low and high maternal AREase groups.

		vciq n=71/153		priq n=72/153		wmiq n=67/138		psiq n=68/138		fsiq n=67/137	
CpG Site Number		β(95%CI)	interaction p-value	β(95%CI)	interaction p-value	β(95%CI)	interaction p-value	β(95%CI)	interaction p-value	β(95%CI)	interaction p-value
1	CC	-5.31(-22.1,11.48)	0.50	-4.23(-20.56,12.1)	0.66	5.45(-7.86,18.77)	0.56	-2.12(-13.17,8.92)	0.68	-2.31(-16.72,12.09)	0.86
	CT/TT	7.42(-3.81,18.66)		4.14(-5.3,13.58)		4.3(-4.7,13.3)		-1.46(-10.9,7.97)		5.39(-4.25,15.03)	
2	CC	-7.4(-24.91,10.1)	0.89	-4.28(-21.33,12.77)	0.70	-8.56(-22.38,5.26)	0.67	-7.58(-18.94,3.78)	0.91	-8.71(-23.6,6.18)	0.97
	CT/TT	3.22(-7.04,13.48)		2.75(-5.8,11.3)		-1.95(-9.84,5.95)		-0.37(-8.88,8.14)		1.26(-7.43,9.95)	
3	CC	-7.28(-21.96,7.39)	0.66	2.67(-11.52,16.85)	0.59	3.1(-8.55,14.74)	0.51	1.12(-8.4,10.64)	0.39	-1.03(-13.59,11.53)	0.77
	CT/TT	6.03(-4.85,16.91)		1.6(-7.55,10.75)		4.25(-4.25,12.75)		-2.03(-11.01,6.94)		4.13(-5.05,13.32)	
7	CC	-0.04(-17.04,16.95)	0.91	-10.1(-26.33,6.12)	0.49	-1.89(-15.65,11.87)	0.54	1.44(-9.86,12.74)	0.40	-3.37(-18.16,11.41)	0.99
	CT/TT	7.16(-5.4,19.72)		5.48(-5.05,16.01)		0.07(-10.04,10.17)		-2.09(-12.77,8.6)		6.64(-4.28,17.56)	
8	CC	-8.45(-23.07,6.17)	0.06	-1.35(-15.56,12.86)	0.43	-6.81(-18.7,5.08)	0.29	-5.9(-15.59,3.79)	0.30	-6.43(-19.26,6.4)	0.12
	CT/TT	-1.12(-8.26,6.02)		0.99(-5.01,7)		1.15(-4.49,6.79)		-0.1(-5.89,5.7)		0.5(-5.53,6.53)	
9	CC	-5.24(-19.8,9.32)	0.06	0.54(-13.4,14.47)	0.40	-6.53(-18.71,5.65)	0.23	-8(-17.71,1.72)	0.13	-4.14(-17.34,9.06)	0.09
	CT/TT	-0.49(-7.1,6.11)		2.09(-3.43,7.61)		1.07(-4.19,6.33)		0.91(-4.41,6.23)		1.35(-4.25,6.95)	
10	CC	-10.99(-22.91,0.93)	**0.03**	-4.46(-16.24,7.33)	0.54	-7.34(-16.99,2.3)	0.45	-5.75(-13.7,2.21)	0.15	-8.84(-19.16,1.49)	0.09
	CT/TT	-1.9(-7.92,4.12)		-0.71(-5.85,4.43)		-1.63(-6.5,3.23)		1.15(-3.91,6.22)		-0.91(-6.04,4.23)	
11	CC	-1.68(-11.3,7.94)	0.26	2.01(-7.3,11.32)	0.94	-2.97(-10.91,4.97)	0.19	-5.66(-12.04,0.72)	0.08	-1.43(-10.01,7.15)	0.25
	CT/TT	-0.78(-5.07,3.52)		-0.6(-4.24,3.04)		0.23(-3.27,3.74)		0.53(-3.02,4.09)		-0.2(-3.91,3.5)	
12	CC	-1.79(-22.34,18.76)	0.57	4.16(-15.7,24.01)	0.92	-3.36(-20.2,13.49)	0.34	-11.83(-25.31,1.66)	0.14	-1.96(-20.1,16.19)	0.50
	CT/TT	-4.24(-14,5.52)		-0.96(-9.14,7.23)		-0.22(-8.26,7.83)		0.34(-7.87,8.55)		-2.7(-11.28,5.87)	
13	CC	-1.86(-11.08,7.37)	0.18	1.54(-7.35,10.44)	0.80	-2.83(-10.5,4.84)	0.20	-4.69(-10.86,1.49)	0.14	-1.52(-9.8,6.77)	0.20
	CT/TT	-0.98(-4.93,2.97)		-0.14(-3.45,3.18)		0.36(-2.82,3.55)		0.42(-2.8,3.65)		-0.2(-3.59,3.19)	
14	CC	-3.66(-12.64,5.31)	0.10	-0.38(-9.1,8.34)	0.61	-4.68(-12.12,2.77)	0.14	-5.01(-11.06,1.04)	0.13	-3.57(-11.64,4.5)	0.12
	CT/TT	-0.71(-4.88,3.46)		-0.42(-3.92,3.08)		0.2(-3.16,3.55)		0.84(-2.66,4.35)		-0.18(-3.73,3.38)	
15	CC	-10.3(-23.53,2.94)	**0.01**	0.29(-12.71,13.28)	0.36	-7.58(-18.71,3.54)	0.14	-6.66(-15.73,2.4)	0.20	-7.18(-19.2,4.84)	**0.03**
	CT/TT	1.02(-4.86,6.89)		2.11(-2.82,7.03)		1.84(-2.81,6.49)		0.19(-4.66,5.04)		1.95(-2.99,6.89)	
16	CC	**-16.83(-29.07,-4.58)**	**1.00E-03**	-6.55(-19.08,5.98)	0.24	-7.95(-18.57,2.68)	0.17	-1.9(-10.84,7.03)	0.39	**-11.74(-22.96,-0.52)**	**0.01**
	CT/TT	0.81(-5.66,7.28)		1.39(-4.04,6.82)		1.96(-3.15,7.07)		1.81(-3.52,7.15)		2.65(-2.76,8.07)	
17	CC	-14.47(-35.3,6.35)	0.53	-10.14(-30.54,10.26)	0.99	-0.94(-17.61,15.73)	0.27	-5.59(-19.27,8.08)	0.68	-11(-28.68,6.68)	0.85
	CT/TT	-5.82(-18.24,6.6)		4.5(-5.91,14.9)		-2.49(-12.8,7.81)		2.39(-8.38,13.15)		1.28(-9.81,12.36)	
18	CC	-14.09(-28.75,0.57)	0.15	**-14.75(-28.95,-0.55)**	0.08	-6.53(-18.5,5.45)	0.52	-6.8(-16.58,2.98)	0.55	**-13.94(-26.35,-1.53)**	0.09
	CT/TT	-1.01(-11.05,9.04)		5.78(-2.59,14.15)		2.63(-5.24,10.5)		1(-7.37,9.36)		4(-4.34,12.33)	
19	CC	7.81(-6.55,22.16)	0.44	3.25(-10.66,17.17)	0.55	5.68(-6.28,17.64)	0.29	0.66(-9.17,10.49)	0.30	6.89(-5.95,19.73)	0.25
	CT/TT	5.47(-4.02,14.96)		3.33(-4.64,11.29)		4.86(-2.69,12.4)		0.57(-7.33,8.47)		4.75(-3.31,12.81)	

Supplemental Table 8. Regression of Cord DNA Methylation stratified by maternal PON1 -108 Genotype (either CC or CT/TT).

All models adjusted for maternal education, maternal scores for verbal cognition, cell composition, and batch.

The β(95%CI) shown are for models stratified by PON1 -108 genotye (grouped by CC or CT/TT) while the interaction p-value is based on the interaction term of PON1 -108 genotypes coded as number of T alleles X PON1 DNA methylation at each CpG site.

β(95%CI) with corresponding unadjusted p-values <0.05 and unadjusted interaction p-values<0.05 are bolded.

None of the associations remained significant after controlling for FDR.

Methylation in cord blood samples were assessed by 450K BeadChip. CpG sites 4,5, and 6 are not shown because they were not assessed by 450K.

The N's given are for maternal PON1 -108 Genotype CC and for CT and TT grouped together.

Supplemental Table 9. Regression models of 7-year old blood *PON1* DNA methylation and cognition in boys

CpG Site Number	Verbal Comprehension n=86 β(95%CI)	p-value	Perceptual Reasoning n=86 β (95%CI)	p-value	Working Memory n=80 β (95%CI)	p-value	Processing Speed n=80 β (95%CI)	p-value	Full-Scale IQ n=80 β (95%CI)	p-value
1	0.16(-10.55,10.87)	0.98	-6.63(-17.09,3.83)	0.21	0.83(-7.90,9.57)	0.85	2.93(-7.17,13.03)	0.56	-1.64(-11.57,8.30)	0.74
2	1.57(-3.29,6.43)	0.52	-1.77(-6.56,3.01)	0.46	-1.16(-5.19,2.87)	0.57	-0.21(-4.89,4.47)	0.93	-0.77(-5.36,3.82)	0.74
3	1.19(-5.20,7.58)	0.71	1.51(-4.79,7.81)	0.63	3.85(-1.48,9.18)	0.15	2.86(-3.41,9.13)	0.37	2.11(-4.02,8.24)	0.49
4	2.17(-6.68,11.01)	0.63	0.25(-8.48,8.99)	0.95	-3.09(-10.08,3.90)	0.38	-0.05(-8.20,8.09)	0.99	-0.21(-8.21,7.80)	0.96
5	1.74(-2.35,5.82)	0.40	0.39(-3.68,4.45)	0.85	1.93(-1.44,5.30)	0.26	0.06(-3.86,3.98)	0.98	0.91(-2.95,4.77)	0.64
6	**5.46(0.50,10.42)**	**0.03**	4.66(-0.27,9.59)	0.06	3.48(-0.51,7.48)	0.09	3.11(-1.56,7.78)	0.19	**5.11(0.63,9.59)**	**0.03**
7	1.97(-7.11,11.05)	0.67	2.28(-6.68,11.23)	0.61	-0.61(-7.95,6.73)	0.87	0.28(-8.07,8.63)	0.95	0.92(-7.44,9.27)	0.83
8	-0.17(-6.96,6.62)	0.96	0.70(-6.00,7.40)	0.84	-2.39(-7.76,2.98)	0.38	-4.37(-10.55,1.80)	0.16	-1.91(-8.05,4.22)	0.54
9	-3.97(-10.91,2.97)	0.26	0.38(-6.69,7.45)	0.91	-2.57(-8.23,3.09)	0.37	-3.59(-10.13,2.95)	0.28	-3.41(-9.82,2.99)	0.29
11	-0.32(-5.50,4.85)	0.90	0.99(-4.12,6.09)	0.70	-1.55(-5.64,2.53)	0.45	-3.73(-8.40,0.93)	0.11	-1.21(-5.86,3.45)	0.61
13	0.29(-3.39,3.98)	0.87	0.82(-2.81,4.46)	0.65	-1.18(-4.08,1.73)	0.42	-2.30(-5.63,1.04)	0.17	-0.59(-3.91,2.73)	0.72
14	-0.12(-3.93,3.69)	0.95	0.40(-3.35,4.16)	0.83	-1.35(-4.36,1.65)	0.37	-2.26(-5.72,1.20)	0.20	-0.92(-4.36,2.51)	0.59
15	-0.56(-5.64,4.52)	0.83	0.29(-4.73,5.30)	0.91	-1.41(-5.43,2.61)	0.49	-2.46(-7.10,2.18)	0.29	-1.31(-5.89,3.27)	0.57
16	0.18(-3.43,3.79)	0.92	0.56(-3.01,4.12)	0.76	-1.60(-4.45,1.24)	0.26	-2.15(-5.43,1.13)	0.20	-0.79(-4.05,2.47)	0.63
17	-3.17(-13.23,6.88)	0.53	**-10.52(-20.17,-0.87)**	**0.03**	-3.03(-11.40,5.33)	0.47	-3.67(-13.35,6.02)	0.45	-7.14(-16.54,2.26)	0.13
19	-5.20(-12.38,1.99)	0.15	0.46(-6.73,7.65)	0.90	-0.48(-6.58,5.62)	0.88	1.37(-5.69,8.43)	0.70	-1.78(-8.71,5.14)	0.61

All models adjusted for maternal education, maternal scores for verbal cognition, cell composition, and batch.

Crude p-values <0.05 are bolded.

None of the associations remained significant after controlling for FDR.

*Methylation in 7-year old blood samples were assessed by EPIC BeadChip. CpG sites 10 and 18 are not shown because they were not assessed by EPIC.

Supplemental Table 10. Regression models of 7-year old blood *PON1* DNA methylation and cognition in girls

CpG Site Number	Verbal Comprehension n=103		Perceptual Reasoning n=103		Working Memory n=95		Processing Speed n=95		Full-Scale IQ n=94	
	β (95%CI)	p-value	β (95%CI)	p-value	β (95%CI)	p-value	β (95%CI)	p-value	β (95%CI)	p-value
1	8.60(-2.17,19.37)	0.12	8.35(-1.11,17.80)	0.08	3.07(-5.56,11.69)	0.48	**8.05(0.94,15.16)**	**0.03**	7.94(-1.31,17.18)	0.09
2	-2.81(-7.49,1.86)	0.24	-1.05(-5.18,3.07)	0.61	-0.89(-4.57,2.80)	0.63	-1.25(-4.33,1.83)	0.42	-2.41(-6.33,1.52)	0.23
3	3.21(-2.39,8.81)	0.26	-0.44(-5.42,4.54)	0.86	0.36(-4.28,4.99)	0.88	1.91(-1.87,5.68)	0.32	1.38(-3.56,6.32)	0.58
4	3.09(-6.22,12.41)	0.51	3.58(-4.63,11.79)	0.39	1.31(-6.03,8.65)	0.72	-1.30(-7.47,4.87)	0.68	1.95(-5.92,9.81)	0.62
5	-1.15(-4.81,2.51)	0.53	-1.10(-4.30,2.09)	0.49	-2.31(-5.19,0.57)	0.11	0.32(-2.07,2.72)	0.79	-1.60(-4.65,1.45)	0.30
6	-0.40(-5.19,4.40)	0.87	-3.01(-7.20,1.18)	0.16	-1.11(-4.95,2.74)	0.57	0.31(-2.88,3.50)	0.85	-1.72(-5.79,2.36)	0.40
7	4.39(-4.18,12.96)	0.31	0.88(-6.71,8.47)	0.82	-0.46(-7.39,6.46)	0.89	0.85(-4.81,6.51)	0.76	2.03(-5.30,9.35)	0.58
8	-0.18(-5.83,5.47)	0.95	-2.73(-7.69,2.23)	0.28	-0.34(-4.81,4.14)	0.88	-0.27(-3.94,3.40)	0.88	-1.02(-5.74,3.71)	0.67
9	0.55(-5.50,6.60)	0.86	-2.74(-8.05,2.57)	0.31	-0.80(-5.66,4.05)	0.74	-0.72(-4.71,3.27)	0.72	-1.30(-6.43,3.83)	0.62
11	-1.24(-5.93,3.44)	0.60	-2.55(-6.66,1.56)	0.22	-1.74(-5.47,1.99)	0.36	-0.67(-3.75,2.42)	0.67	-1.87(-5.82,2.08)	0.35
13	-1.51(-5.04,2.01)	0.40	-1.02(-4.16,2.11)	0.52	-0.59(-3.47,2.28)	0.68	-0.70(-3.04,1.64)	0.55	-1.23(-4.26,1.80)	0.42
14	-0.67(-4.06,2.72)	0.70	-2.04(-5.01,0.93)	0.18	-0.72(-3.43,1.99)	0.60	-0.50(-2.72,1.73)	0.66	-1.24(-4.10,1.62)	0.39
15	-0.59(-4.94,3.76)	0.79	-1.68(-5.48,2.12)	0.38	-0.71(-4.23,2.81)	0.69	-0.47(-3.35,2.42)	0.75	-1.12(-4.84,2.60)	0.55
16	-0.26(-3.30,2.77)	0.86	-1.41(-4.07,1.25)	0.30	-0.72(-3.22,1.78)	0.57	-0.33(-2.38,1.72)	0.75	-0.87(-3.52,1.77)	0.51
17	1.34(-6.97,9.66)	0.75	1.10(-6.23,8.43)	0.77	-1.94(-8.38,4.51)	0.55	-1.47(-6.82,3.88)	0.59	0.07(-6.83,6.97)	0.98
19	-3.45(-10.10,3.20)	0.31	-2.32(-8.18,3.55)	0.43	-0.97(-6.27,4.34)	0.72	-1.07(-5.35,3.21)	0.62	-3.49(-9.07,2.10)	0.22

All models adjusted for maternal education, maternal scores for verbal cognition, cell composition, and batch.

Crude p-values <0.05 are bolded.

None of the associations remained significant after controlling for FDR.

*Methylation in 7-year old blood samples were assessed by EPIC BeadChip. CpG sites 10 and 18 are not shown because they were not assessed by EPIC.

Supplemental Table 11. Regression models of 7-year old PON1 methylation and WISC-IV IQ at age 7 years with adjustment for *PON1*$_{-108}$ genotype

CpG Site Number	Verbal Comprehension n=178 β (95%CI)	p-value	Perceptual Reasoning n=177 β (95%CI)	p-value	Working Memory n=165 β (95%CI)	p-value	Processing Speed n=165 β (95%CI)	p-value	Full-Scale IQ n=164 β (95%CI)	p-value
1	6.84(-0.99,14.70)	0.09	2.68(-4.52,9.87)	0.46	1.74(-4.38,7.85)	0.58	**6.57(0.45,12.70)**	**0.04**	4.46(-2.41,11.30)	0.20
2	-1.27(-4.80,2.26)	0.48	-1.31(-4.52,1.91)	0.42	-1.95(-4.66,0.76)	0.16	-0.95(-3.70,1.80)	0.50	-2.06(-5.10,0.98)	0.18
3	3.16(-1.17,7.50)	0.15	0.46(-3.52,4.44)	0.82	1.27(-2.22,4.75)	0.47	1.79(-1.69,5.26)	0.31	1.49(-2.39,5.36)	0.45
4	2.72(-3.87,9.30)	0.42	1.71(-4.32,7.75)	0.58	-1.45(-6.46,3.56)	0.57	-0.97(-6.04,4.10)	0.71	0.25(-5.34,5.84)	0.93
5	0.16(-2.57,2.89)	0.91	-0.66(-3.16,1.84)	0.60	-0.91(-3.04,1.22)	0.40	0.37(-1.74,2.48)	0.73	-0.72(-3.07,1.63)	0.55
6	2.09(-1.40,5.58)	0.24	-0.01(-3.21,3.20)	1.00	1.00(-1.70,3.69)	0.47	1.70(-0.99,4.38)	0.21	1.19(-1.81,4.18)	0.44
7	3.20(-3.11,9.50)	0.93	1.78(-4.00,7.55)	0.29	-1.03(-5.95,3.88)	0.24	0.19(-4.63,5.01)	0.64	1.51(-3.95,6.98)	0.21
8	5.05(-1.81,11.90)	0.32	-4.08(-10.40,2.21)	0.54	-1.14(-6.43,4.16)	0.68	-0.25(-5.57,5.07)	0.94	-0.41(-6.36,5.54)	0.59
9	2.14(-5.06,9.34)	0.15	-4.43(-11.00,2.18)	0.20	-2.13(-7.70,3.45)	0.67	-0.46(-6.06,5.13)	0.93	-2.52(-8.74,3.71)	0.89
11	1.80(-3.93,7.52)	0.56	-4.25(-9.46,0.95)	0.19	-2.28(-6.62,2.06)	0.45	-1.28(-5.63,3.06)	0.87	-1.90(-6.75,2.94)	0.43
13	1.57(-2.68,5.83)	0.54	-2.01(-5.91,1.88)	0.11	-0.97(-4.26,2.31)	0.30	-0.79(-4.05,2.46)	0.56	-0.70(-4.35,2.95)	0.44
14	2.05(-2.06,6.17)	0.47	-3.51(-7.24,0.23)	0.31	-1.40(-4.55,1.75)	0.56	-0.56(-3.69,2.57)	0.63	-1.19(-4.70,2.32)	0.71
15	2.55(-2.85,7.96)	0.33	-3.22(-8.12,1.69)	0.07	-1.42(-5.56,2.72)	0.38	0.27(-3.89,4.42)	0.73	-0.87(-5.51,3.77)	0.50
16	2.38(-1.27,6.04)	0.35	-1.75(-5.10,1.61)	0.20	-1.44(-4.27,1.40)	0.50	-0.15(-3.00,2.69)	0.90	-0.34(-3.51,2.84)	0.71
17	1.04(-5.48,7.56)	0.20	-2.62(-8.58,3.34)	0.31	-3.53(-8.52,1.47)	0.32	-2.27(-7.29,2.75)	0.92	-2.07(-7.67,3.53)	0.84
19	-4.61(-9.72,0.50)	0.75	-1.28(-5.99,3.43)	0.39	-0.26(-4.25,3.73)	0.17	0.11(-3.84,4.06)	0.37	-2.92(-7.33,1.49)	0.47

All models adjusted for maternal education, maternal scores for verbal cognition, cell composition, batch, and *PON1*$_{-108}$ genotype.

Crude p-values <0.05 are bolded.

None of the associations remained significant after controlling for FDR.

*Methylation in 7-year old blood samples were assessed by EPIC BeadChip. CpG sites 10 and 18 are not shown because they were not assessed by EPIC.

Supplemental Table 12. Mediation analysis of OPs, PON1 DNA methylation, and child cognition

	Mediation Model 1: Mean (95%CI)	Mediation Model 2: Mean (95%CI)
Natural Indirect Effect	-0.05(-0.41,0.31)	-0.41(-1.77,2.0E-3)
Controlled Direct Effect	-5.15(-10.07,-0.22)	-2.27(-6.06,1.77)
Total Effect	-5.19(-10.13,-0.26)	-2.68(-6.62,1.25)

Mediation model 1 assessed mediation by cord blood methylation of CpG site 19 of DEP exposure on verbal comprehension IQ at age 7 yr.
Mediation model 2 assessed mediation by 7-year old blood methylation of CpG site 1 of total DAP exposure on processing speed IQ at age 7 yr.
Both models adjusted for maternal education, maternal scores for verbal cognition, cell composition, and batch.

Supplemental Table 13. Regression models of log 10 average pregnancy DAPs with cord blood DNA methylation

CpG Site Number	Total DAPs β(95%CI)	p-value	DMs β (95%CI)	p-value	DEs β (95%CI)	p-value
1	0.00(-0.06,0.06)	0.94	0.02(-0.03,0.07)	0.46	-0.04(-0.10,0.02)	0.18
2	-0.04(-0.11,0.03)	0.22	-0.03(-0.10,0.03)	0.29	-0.02(-0.09,0.05)	0.50
3	-0.05(-0.11,0.02)	0.16	-0.02(-0.08,0.04)	0.51	**-0.08(-0.14,-0.01)**	**0.02**
7	-0.06(-0.11,0.00)	0.06	-0.03(-0.09,0.02)	0.19	**-0.07(-0.12,-0.01)**	**0.03**
8	-0.05(-0.14,0.04)	0.31	-0.04(-0.12,0.04)	0.36	-0.03(-0.12,0.06)	0.54
9	-0.05(-0.15,0.05)	0.31	-0.04(-0.13,0.05)	0.39	-0.03(-0.13,0.06)	0.49
10	-0.04(-0.16,0.07)	0.43	-0.03(-0.13,0.07)	0.55	-0.03(-0.13,0.08)	0.66
11	-0.11(-0.26,0.04)	0.16	-0.12(-0.25,0.02)	0.09	0.01(-0.14,0.15)	0.95
12	-0.04(-0.11,0.02)	0.21	-0.04(-0.10,0.02)	0.17	-0.01(-0.08,0.05)	0.68
13	-0.10(-0.26,0.06)	0.21	-0.10(-0.24,0.04)	0.17	-0.04(-0.19,0.12)	0.67
14	-0.09(-0.25,0.06)	0.24	-0.09(-0.22,0.05)	0.22	-0.04(-0.19,0.11)	0.58
15	-0.05(-0.16,0.06)	0.40	-0.05(-0.14,0.05)	0.38	-0.02(-0.13,0.09)	0.77
16	-0.05(-0.15,0.05)	0.33	-0.04(-0.13,0.05)	0.37	-0.04(-0.15,0.06)	0.39
17	-0.032(-0.09,0.02)	0.26	-0.02(-0.07,0.03)	0.33	-0.02(-0.08,0.03)	0.44
18	-0.02(-0.09,0.06)	0.68	-0.01(-0.07,0.06)	0.85	-0.03(-0.11,0.04)	0.36
19	-0.01(-0.08,0.07)	0.90	0.02(-0.05,0.08)	0.62	-0.06(-0.13,0.01)	0.11

DAPs- dialkyl phosphates DMs-dimethyl phosphates DEs-diethyl phosphates

All models adjusted for cell composition and batch.

*Methylation in cord blood samples were assessed by 450K BeadChip. CpG sites 4,5, and 6 are not shown because they were not assessed by 450K.

Supplemental Table 14. Regression models of log 10 average pregnancy DAPs with 7-year old blood DNA methylation

CpG Site Number	Total DAPs β (95%CI)	p-value	DMs β (95%CI)	p-value	DEs β (95%CI)	p-value
1	-0.11(-0.22,0.01)	0.07	-0.07(-0.18,0.03)	0.18	-0.07(-0.17,0.04)	0.24
2	0.18(-0.08,0.43)	0.18	0.15(-0.08,0.38)	0.19	0.09(-0.15,0.33)	0.48
3	-0.10(-0.31,0.11)	0.36	-0.04(-0.22,0.15)	0.69	-0.14(-0.33,0.06)	0.16
4	-0.02(-0.16,0.11)	0.75	-0.03(-0.15,0.09)	0.59	0.10(-0.02,0.22)	0.10
5	-0.03(-0.36,0.30)	0.86	-0.02(-0.32,0.27)	0.88	0.03(-0.27,0.33)	0.84
6	0.11(-0.14,0.35)	0.39	0.05(-0.17,0.27)	0.66	0.12(-0.10,0.35)	0.28
7	0.03(-0.11,0.18)	0.64	0.04(-0.09,0.17)	0.52	0.01(-0.13,0.14)	0.89
8	0.05(-0.15,0.25)	0.63	0.02(-0.16,0.20)	0.82	0.03(-0.15,0.22)	0.72
9	-0.01(-0.20,0.18)	0.89	-0.04(-0.20,0.13)	0.68	-0.00(-0.18,0.17)	0.96
11	0.07(-0.18,0.32)	0.59	0.04(-0.18,0.26)	0.73	0.01(-0.22,0.24)	0.95
13	0.09(-0.24,0.43)	0.58	0.04(-0.27,0.34)	0.82	0.08(-0.24,0.39)	0.63
14	0.11(-0.23,0.46)	0.51	0.05(-0.25,0.36)	0.74	0.09(-0.23,0.40)	0.59
15	0.05(-0.22,0.31)	0.72	0.02(-0.22,0.25)	0.90	0.02(-0.22,0.26)	0.87
16	0.14(-0.23,0.51)	0.46	0.06(-0.27,0.40)	0.71	0.16(-0.19,0.50)	0.37
17	-0.04(-0.17,0.10)	0.62	-0.05(-0.18,0.07)	0.41	-0.00(-0.13,0.12)	0.95
19	0.04(-0.14,0.21)	0.69	0.11(-0.05,0.27)	0.18	-0.12(-0.28,0.05)	0.16

DAPs- dialkyl phosphates DMs-dimethyl phosphates DEs-diethyl phosphates
All models adjusted for cell composition and batch.
*Methylation in 7-year old blood samples were assessed by EPIC BeadChip. CpG sites 10 and 18 are not shown because they were not assessed by EPIC.