

Tables of Mediation Model Results

Outcome: predicted child's cognitive ability

Tables A.57.i & ii. Results of mediation model with the predictor congener PCB126, the DNA methylation of the DMR annotated for the gene *RNF19A* as mediator, and the predicted child's cognitive ability as outcome, controlling for confounders.

Table A.57.i. *Regressions*

	Coefficient	SE	95% CI	z	p
Child's cognitive ability ~ PCB126	-0.04	0.44	[-0.75, 1.00]	-0.09	.93
(c)					
Child's cognitive ability ~ Sex	-3.46	0.53	[-4.48, -2.42]	-6.59	< .001
Child's cognitive ability ~ PCB126:Sex	0.58	0.78	[-1.01, 2.03]	0.75	.46
(c:Sex)					
Child's cognitive ability ~ DNAm DMR (<i>RNF19A</i>)	-0.44	0.96	[-2.14, 1.59]	-0.46	.64
(b)					
Child's cognitive ability ~ Birthweight	1.42x10 ⁻⁰³	5.48 x10 ⁻⁰⁴	[0.00, 0.00]	2.59	.01
Child's cognitive ability ~ Mother's BMI before pregnancy	-0.18	0.06	[-0.30, -0.07]	-3.11	.002
Child's cognitive ability ~ CD4T	-2.62	4.70	[-11.77, 6.81]	-0.56	.58
Child's cognitive ability ~ CD8T	-9.38	8.71	[-26.50, 7.68]	-1.08	.28
Child's cognitive ability ~ NK	-6.53	8.80	[-24.25, 10.88]	-0.74	.46
DNAm DMR (<i>RNF19A</i>) ~ PCB126	-0.05	0.03	[-0.11, 0.02]	-1.43	.15
(a)					
DNAm DMR (<i>RNF19A</i>) ~ Sex	0.08	0.05	[-0.01, 0.20]	1.60	.11
DNAm DMR (<i>RNF19A</i>) ~ PCB126:Sex	0.04	0.09	[-0.14, 0.23]	0.46	.65
(a:Sex)					
DNAm DMR (<i>RNF19A</i>) ~ Birthweight	-4.71x10 ⁻⁰⁵	3.67 x10 ⁻⁰⁵	[-0.00, 0.00]	-1.28	.20
DNAm DMR (<i>RNF19A</i>) ~ Mother's BMI before pregnancy	-4.30x10 ⁻⁰³	3.65 x10 ⁻⁰³	[-0.01, 0.00]	-1.18	.24
DNAm DMR (<i>RNF19A</i>) ~ CD4T	1.16	0.45	[0.27, 2.02]	2.59	.01
DNAm DMR (<i>RNF19A</i>) ~ CD8T	2.58	1.12	[0.40, 4.75]	2.31	.02
DNAm DMR (<i>RNF19A</i>) ~ NK	1.71	0.78	[0.22, 3.27]	2.20	.03

Note. Coefficient = *Regressions* beta value, SE = standard error, CI = confidence interval, z = z-statistic, p = p-value, c = c-path, b = b-path, a = a-path.

Table A.57.ii. *Defined model parameters (effects)*

Effect	Coefficient	SE	95% CI	z	p
Indirect (female)	0.02	0.05	[-0.09, 0.13]	0.39	.693
Total (female)	-0.02	0.43	[-0.72, 1.00]	-0.04	.964
Indirect (male)	1.68x10 ⁻⁰³	0.09	[-0.20, 0.16]	0.02	.984
Total (male)	0.54	0.67	[-0.77, 1.88]	0.81	.418
Difference in indirect (male - female)	0.02	0.10	[-0.17, 0.26]	0.18	.854
Difference in indirect (male - female)	-0.56	0.76	[-1.96, 1.01]	-0.74	.460

Note. Coefficient = estimated model parameter, SE = standard error, CI = confidence interval, z = z-statistic, p = p-value.

Tables A.58.i & ii. Results of the mediation model with the predictor congener PCB169, the DNA methylation of the DMP annotated for the gene *CRYBG3* as mediator, and the predicted child's cognitive ability as outcome, controlling for confounders.

Table A.58.i. *Regressions*

	Coefficient	SE	95% CI	z	p
Child's cognitive ability ~ PCB169 (c)	0.07	0.69	[-1.38, 1.32]	0.11	.91
Child's cognitive ability ~ Sex	-3.47	0.50	[-4.46, -2.49]	-6.91	<.001
Child's cognitive ability ~ PCB169:Sex (c:Sex)	0.63	0.83	[-0.92, 2.31]	0.76	.45
Child's cognitive ability ~ DNAm DMP (<i>CRYBG3</i>) (b)	0.71	0.70	[-0.62, 2.15]	1.00	.32
Child's cognitive ability ~ Birthweight	1.41x10 ⁻⁰³	5.14x10 ⁻⁰⁴	[0.00, 0.00]	2.74	.01
Child's cognitive ability ~ Mother's BMI before pregnancy	-0.18	0.06	[-0.30, -0.06]	-2.99	.003
DNAm DMP (<i>CRYBG3</i>) ~ PCB169 (a)	0.13	0.06	[0.02, 0.24]	2.34	.02
DNAm DMP (<i>CRYBG3</i>) ~ Sex	-0.06	0.05	[-0.17, 0.03]	-1.19	.23
DNAm DMP (<i>CRYBG3</i>) ~ PCB169:Sex (a:Sex)	-0.20	0.07	[-0.34, -0.04]	-2.67	.01
DNAm DMP (<i>CRYBG3</i>) ~ Birthweight	5.48x10 ⁻⁰⁵	4.76x10 ⁻⁰⁵	[0.00, 0.00]	1.15	.25
DNAm DMP (<i>CRYBG3</i>) ~ Mother's BMI before pregnancy	1.13x10 ⁻⁰³	5.9x10 ⁻⁰³	[-0.01, 0.01]	0.19	.85

Note. Coefficient = *Regressions* beta value, SE = standard error, CI = confidence interval, z = z-statistic, p = p-value, c = c-path, b = b-path, a = a-path.

Table A.58.ii. *Defined model parameters (effects)*

Effect	Coefficient	SE	95% CI	z	p
Indirect (female)	0.09	0.11	[-0.08, 0.37]	0.83	.408
Total (female)	0.17	0.66	[-1.21, 1.36]	0.25	.800
Indirect (male)	-0.05	0.07	[-0.20, 0.06]	-0.74	.461
Total (male)	0.66	0.45	[-0.27, 1.55]	1.44	.149
Difference in indirect (male - female)	0.14	0.16	[-0.12, 0.50]	0.89	.374
Difference in indirect (male - female)	-0.49	0.79	[-2.08, 0.98]	-0.62	.537

Note. Coefficient = estimated model parameter, SE = standard error, CI = confidence interval, z = z-statistic, p = p-value.

Tables A.59.i & ii. Results of the mediation model with the predictor congener PCDD66, the DNA methylation of the DMR annotated for the gene *EIF2AK4* as mediator, and the predicted child's cognitive ability as outcome, controlling for confounders.

Table A.59.i. *Regressions*

	Coefficient	SE	95% CI	z	p
Child's cognitive ability ~ PCDD66 (c)	-0.09	0.67	[-1.38, 1.23]	-0.13	.90
Child's cognitive ability ~ Sex	-3.40	0.51	[-4.43, -2.43]	-6.61	<.001
Child's cognitive ability ~ PCDD66:Sex (c:Sex)	1.17	0.82	[-0.48, 2.77]	1.43	.15

Child's cognitive ability ~ DNAm DMR (<i>EIF2AK4</i>) (b)	0.92	0.57	[-0.19, 2.07]	1.61	.11
Child's cognitive ability ~ Birthweight	1.39x10 ⁻⁰³	5.10x10 ⁻⁰⁴	[0.00, 0.00]	2.74	.01
Child's cognitive ability ~ Mother's BMI before pregnancy	-0.17	0.06	[-0.28, -0.06]	-	.003
DNAm DMR (<i>EIF2AK4</i>) ~ PCDD66 (a)	-0.13	0.09	[-0.31, 0.05]	-	.15
DNAm DMR (<i>EIF2AK4</i>) ~ Sex	-0.16	0.08	[-0.31, -0.01]	-	.05
DNAm DMR (<i>EIF2AK4</i>) ~ PCDD66:Sex (a:Sex)	-0.03	0.17	[-0.38, 0.31]	-	.88
DNAm DMR (<i>EIF2AK4</i>) ~ Birthweight	5.50x10 ⁻⁰⁶	6.54x10 ⁻⁰⁵	[0.00, 0.00]	0.16	.93
DNAm DMR (<i>EIF2AK4</i>) ~ Mother's BMI before pregnancy	-0.02	7.83x10 ⁻⁰³	[-0.04, 0.00]	-	.01
				2.73	

Note. Coefficient = Regressions beta value, SE = standard error, CI = confidence interval, z = z-statistic, p = p-value, c = c-path, b = b-path, a = a-path.

Table A.59.ii. Defined model parameters (effects)

Effect	Coefficient	SE	95% CI	z	p
Indirect (female)	-0.12	0.12	[-0.41, 0.05]	-0.99	.33
Total (female)	-0.20	0.67	[-1.47, 1.13]	-0.31	.76
Indirect (male)	-0.14	0.17	[-0.54, 0.14]	-0.83	.40
Total (male)	0.94	0.52	[-0.04, 2.01]	1.82	.07
Difference in indirect (male - female)	0.02	0.19	[-0.38, 0.41]	0.13	.89
Difference in indirect (male - female)	-1.15	0.82	[-2.74, 0.48]	-1.39	.16

Note. Coefficient = estimated model parameter, SE = standard error, CI = confidence interval, z = z-statistic, p = p-value.

Tables A.60.i & ii. Results of the mediation model with the predictor congener PCDD67, the DNA methylation of the DMR annotated for the gene *PDE6B* as mediator, and the predicted child's cognitive ability as outcome, controlling for confounders.

Table A.60.i. Regressions

	Coefficient	SE	95% CI	z	p
Child's cognitive ability ~ PCDD67 (c)	-0.27	0.79	[-1.88, 1.14]	-	.73
Child's cognitive ability ~ Sex	-3.58	0.50	[-4.60, -2.61]	-	<
Child's cognitive ability ~ PCDD67:Sex (c:Sex)	0.62	0.94	[-1.14, 2.54]	0.34	.51
Child's cognitive ability ~ DNAm DMR (<i>PDE6B</i>) (b)	-0.87	0.69	[-2.22, 0.47]	7.13	.001
Child's cognitive ability ~ Birthweight	1.50x10 ⁻⁰³	5.00x10 ⁻⁰⁴	[0.00, 0.00]	0.66	.20
Child's cognitive ability ~ Mother's BMI before pregnancy	-0.19	0.06	[-0.31, -0.08]	1.27	.20
Child's cognitive ability ~ NK	-5.14	8.96	[-21.94, 12.91]	3.00	.003
DNAm DMR (<i>PDE6B</i>) ~ PCDD67 (a)	0.03	0.09	[-0.15, 0.21]	-	.002
DNAm DMR (<i>PDE6B</i>) ~ Sex	0.01	0.06	[-0.11, 0.13]	3.13	.002
DNAm DMR (<i>PDE6B</i>) ~ PCDD67:Sex (a:Sex)	-0.03	0.11	[-0.26, 0.18]	-	.57
				0.57	.75
				0.32	.81
				-	.76
				0.31	

DNAm DMR (<i>PDE6B</i>) ~ Birthweight	5.94x10 ⁻⁰⁵	6.08x10 ⁻⁰⁵	[-0.00, 0.00]	0.98	.33
DNAm DMR (<i>PDE6B</i>) ~ Mother's BMI before pregnancy	-5.31x10 ⁻⁰³	6.79x10 ⁻⁰³	[-0.02, 0.01]	-	.43
DNAm DMR (<i>PDE6B</i>) ~ NK	2.53	0.92	[0.77, 4.41]	2.75	.01

Note. Coefficient = *Regressions* beta value, *SE* = standard error, CI = confidence interval, *z* = *z*-statistic, *p* = *p*-value, c = c-path, b = b-path, a = a-path.

Table A.60.ii. *Defined model parameters (effects)*

Effect	Coefficient	<i>SE</i>	95% CI	<i>z</i>	<i>p</i>
Indirect (female)	-0.03	0.10	[-0.27, 0.15]	-0.25	.80
Total (female)	-0.29	0.81	[-1.92, 1.19]	-0.37	.72
Indirect (male)	4.51x10 ⁻⁰³	0.08	[-0.16, 0.17]	0.06	.95
Total (male)	0.36	0.49	[-0.66, 1.32]	0.73	.47
Difference in indirect (male - female)	-0.03	0.13	[-0.32, 0.21]	-0.24	.81
Difference in indirect (male - female)	-0.65	0.95	[-2.57, 1.17]	-0.69	.49

Note. Coefficient = estimated model parameter, *SE* = standard error, CI = confidence interval, *z* = *z*-statistic, *p* = *p*-value.

Tables A.61.i & ii. Results of the mediation model with the predictor congener PCDD70, the DNA methylation of the DMP annotated for the gene *H2BC5* as mediator, and the predicted child's cognitive ability as outcome, controlling for confounders.

Table A.61.i. *Regressions*

	Coefficient	<i>SE</i>	95% CI	<i>z</i>	<i>p</i>
Child's cognitive ability ~ PCDD70 (c)	-0.55	0.65	[-1.87, 0.72]	-	.40
Child's cognitive ability ~ Sex	-3.45	0.51	[-4.47, -2.48]	-	<
Child's cognitive ability ~ PCDD70:Sex (c:Sex)	1.82	0.88	[0.07, 3.53]	2.07	.04
Child's cognitive ability ~ DNAm DMP (<i>H2BC5</i>) (b)	0.11	0.40	[-0.48, 1.14]	0.27	.80
Child's cognitive ability ~ Gestational length	0.46	0.19	[0.06, 0.80]	2.40	.02
Child's cognitive ability ~ Mother's BMI before pregnancy	-0.15	0.05	[-0.25, -0.05]	-	.01
DNAm DMP (<i>H2BC5</i>) ~ PCDD70 (a)	0.16	0.11	[-0.05, 0.38]	1.43	.15
DNAm DMP (<i>H2BC5</i>) ~ Sex	3.41x10 ⁻⁰³	0.10	[-0.19, 0.18]	0.04	.97
DNAm DMP (<i>H2BC5</i>) ~ PCDD70:Sex (a:Sex)	0.19	0.32	[-0.31, 0.89]	0.59	.56
DNAm DMP (<i>H2BC5</i>) ~ Gestational length	0.10	0.03	[0.04, 0.17]	2.85	.01
DNAm DMP (<i>H2BC5</i>) ~ Mother's BMI before pregnancy	0.01	7.94x10 ⁻⁰³	[0.00, 0.03]	1.62	.11

Note. Coefficient = *Regressions* beta value, *SE* = standard error, CI = confidence interval, *z* = *z*-statistic, *p* = *p*-value, c = c-path, b = b-path, a = a-path.

Table A.61.ii. *Defined model parameters (effects)*

Effect	Coefficient	<i>SE</i>	95% CI	<i>z</i>	<i>p</i>
Indirect (female)	0.02	0.07	[-0.10, 0.21]	0.22	.82
Total (female)	-0.54	0.66	[-1.85, 0.76]	-0.81	.42
Indirect (male)	0.04	0.12	[-0.20, 0.31]	0.31	.76
Total (male)	1.31	0.54	[0.14, 2.25]	2.45	.01
Difference in indirect (male - female)	-0.02	0.11	[-0.25, 0.23]	-0.18	.86
Difference in indirect (male - female)	-1.84	0.86	[-3.48, -0.10]	-2.15	.03

Note. Coefficient = estimated model parameter, *SE* = standard error, *CI* = confidence interval, *z* = *z*-statistic, *p* = *p*-value.

Tables A.62.i & ii. Results of the mediation model with the predictor congener PCDD75, the DNA methylation of the DMP annotated for the gene *LNFG* as mediator, and the predicted child's cognitive ability as outcome, controlling for confounders.

Table A.62.i. *Regressions*

	Coefficient	<i>SE</i>	95% CI	<i>z</i>	<i>p</i>
Child's cognitive ability ~ PCDD75 (c)	-0.38	0.69	[-1.80, 0.88]	-	.58
Child's cognitive ability ~ Sex	-3.57	0.49	[-4.59, -2.64]	-	<
Child's cognitive ability ~ PCDD75:Sex (c:Sex)	0.98	0.86	[-0.62, 2.76]	1.14	.26
Child's cognitive ability ~ DNAm DMP (<i>LNFG</i>) (b)	0.48	0.45	[-0.52, 1.46]	1.07	.29
Child's cognitive ability ~ Birthweight	1.47x10 ⁻⁰³	5.30x10 ⁻⁰⁴	[0.00, 0.00]	2.77	.01
Child's cognitive ability ~ Mother's BMI before pregnancy	-0.19	0.06	[-0.31, -0.07]	-	.002
DNAm DMP (<i>LNFG</i>) ~ PCDD75 (a)	6.29x10 ⁻⁰³	0.08	[-0.17, 0.14]	0.08	.94
DNAm DMP (<i>LNFG</i>) ~ Sex	0.05	0.10	[-0.13, 0.26]	0.49	.62
DNAm DMP (<i>LNFG</i>) ~ PCDD75:Sex (a:Sex)	0.21	0.21	[-0.12, 0.68]	1.02	.31
DNAm DMP (<i>LNFG</i>) ~ Birthweight	4.76x10 ⁻⁰⁵	8.11x10 ⁻⁰⁵	[0.00, 0.00]	0.59	.56
DNAm DMP (<i>LNFG</i>) ~ Mother's BMI before pregnancy	9.77x10 ⁻⁰⁴	6.75x10 ⁻⁰³	[-0.01, 0.02]	0.14	.89

Note. Coefficient = *Regressions* beta value, *SE* = standard error, *CI* = confidence interval, *z* = *z*-statistic, *p* = *p*-value, c = c-path, b = b-path, a = a-path.

Table A.62.ii. *Defined model parameters (effects)*

Effect	Coefficient	<i>SE</i>	95% CI	<i>z</i>	<i>p</i>
Indirect (female)	3.01x10 ⁻⁰³	0.05	[-0.10, 0.10]	0.06	.95
Total (female)	-0.38	0.68	[-1.78, 0.86]	-0.55	.58
Indirect (male)	0.10	0.11	[-0.15, 0.30]	0.93	.36
Total (male)	0.70	0.50	[-0.31, 1.69]	1.39	.17
Difference in indirect (male - female)	-0.10	0.12	[-0.33, 0.17]	-0.83	.41
Difference in indirect (male - female)	-1.08	0.84	[-2.79, 0.48]	-1.29	.20

Note. Coefficient = estimated model parameter, *SE* = standard error, *CI* = confidence interval, *z* = *z*-statistic, *p* = *p*-value.

Tables A.63.i & ii. Results of the mediation model with the predictor congener PCDF130, the DNA methylation of the hubCpG of the salmon module as mediator, and the predicted child's cognitive ability as outcome, controlling for confounders.

Table A.63.i. *Regressions*

	Coefficient	<i>SE</i>	95% CI	<i>z</i>	<i>p</i>
Child's cognitive ability ~ PCDF130 (c)	0.03	0.49	[-0.92, 1.05]	0.07	.95
Child's cognitive ability ~ Sex	-3.47	0.51	[-4.50, -2.48]	-	<
Child's cognitive ability ~ PCDF130:Sex (c:Sex)	0.86	0.80	[-0.70, 2.44]	1.07	.28

Child's cognitive ability ~ hubCpG (salmon module) (b)	-0.18	0.81	[-1.75, 1.38]	-	.82
Child's cognitive ability ~ Birthweight	1.30x10 ⁻⁰³	5.30x10 ⁻⁰⁴	[0.00, 0.00]	2.46	.01
Child's cognitive ability ~ Mother's BMI before pregnancy	-0.19	0.06	[-0.30, -0.07]	-	.001
Child's cognitive ability ~ age_m	0.04	0.06	[-0.08, 0.15]	0.71	.48
Child's cognitive ability ~ B-cells	-6.09	7.21	[-19.96, 8.58]	-	.40
Child's cognitive ability ~ EPIC array plate	-0.84	0.59	[-1.96, 0.36]	-	.16
hubCpG (salmon module) ~ PCDF130 (a)	0.03	0.05	[-0.08, 0.13]	0.48	.63
hubCpG (salmon module) ~ Sex	0.15	0.05	[0.06, 0.24]	3.19	.001
hubCpG (salmon module) ~ PCDF130:Sex (a:Sex)	-0.06	0.08	[-0.21, 0.10]	-	.48
hubCpG (salmon module) ~ Birthweight	-5.32x10 ⁻⁰⁵	4.19x10 ⁻⁰⁵	[-0.00, 0.00]	-	.21
hubCpG (salmon module) ~ Mother's BMI before pregnancy	1.76x10 ⁻⁰³	5.54x10 ⁻⁰³	[-0.01, 0.01]	0.32	.75
hubCpG (salmon module) ~ age_m	0.01	5.16x10 ⁻⁰³	[0.00, 0.02]	2.04	.04
hubCpG (salmon module) ~ B-cells	-3.48	0.72	[-4.71, -1.86]	-	<
hubCpG (salmon module) ~ EPIC array plate	0.24	0.04	[0.16, 0.33]	5.60	<
					.001

Note. Coefficient = *Regressions* beta value, *SE* = standard error, *CI* = confidence interval, *z* = *z*-statistic, *p* = *p*-value, *c* = *c*-path, *b* = *b*-path, *a* = *a*-path.

Table A.63.ii. *Defined model parameters (effects)*

Effect	Coefficient	<i>SE</i>	95% <i>CI</i>	<i>z</i>	<i>p</i>
Indirect (female)	-4.63x10 ⁻⁰³	0.05	[-0.12, 0.10]	-0.09	0.926
Total (female)	0.03	0.49	[-0.93, 1.04]	0.06	0.953
Indirect (male)	5.36x10 ⁻⁰³	0.05	[-0.10, 0.14]	0.10	.92
Total (male)	0.90	0.69	[-0.44, 2.30]	1.30	.20
Difference in indirect (male - female)	-9.99x10 ⁻⁰³	0.08	[-0.20, 0.15]	-0.12	.90
Difference in indirect (male - female)	-0.87	0.80	[-2.47, 0.69]	-1.08	.28

Note. Coefficient = estimated model parameter, *SE* = standard error, *CI* = confidence interval, *z* = *z*-statistic, *p* = *p*-value.

Tables A.64.i & ii. Results of the mediation model with the predictor congener PCDF130, the DNA methylation of the hubCpG of the brown module as mediator, and the predicted child's cognitive ability as outcome, controlling for confounders.

Table A.64.i. *Regressions*

	Coefficient	<i>SE</i>	95% <i>CI</i>	<i>z</i>	<i>p</i>
Child's cognitive ability ~ PCDF130 (c)	0.09	0.51	[-0.91, 1.07]	0.18	.86
Child's cognitive ability ~ Sex	-3.44	0.52	[-4.47, -2.44]	-6.67	<
Child's cognitive ability ~ PCDF130:Sex (c:Sex)	0.88	0.83	[-0.73, 2.56]	1.06	.29
Child's cognitive ability ~ hubCpG (brown module) (b)	-0.35	0.67	[-1.66, 0.93]	-0.52	.61
Child's cognitive ability ~ Birthweight	1.28x10 ⁻⁰³	5.10x10 ⁻⁰⁴	[0.00, 0.00]	2.51	.01

Child's cognitive ability ~ Mother's BMI before pregnancy	-0.18	0.06	[-0.30, -0.06]	-2.95	.003
Child's cognitive ability ~ CD4T	5.36	8.33	[-10.88, 22.24]	0.64	.52
Child's cognitive ability ~ Monocytes	12.91	8.54	[-2.67, 31.20]	1.51	.13
Child's cognitive ability ~ NK	1.76	11.85	[-21.37, 25.95]	0.15	.88
Child's cognitive ability ~ Granulocytes	7.77	7.50	[-6.53, 23.28]	1.04	.30
Child's cognitive ability ~ B-cells	-4.14	12.55	[-28.08, 21.46]	-0.33	.74
hubCpG (brown module) ~ PCDF130 (a)	0.08	0.08	[-0.07, 0.24]	1.07	.28
hubCpG (brown module) ~ Sex	-0.02	0.07	[-0.15, 0.11]	-0.33	.74
hubCpG (brown module) ~ PCDF130:Sex (a:Sex)	-0.13	0.10	[-0.33, 0.08]	-1.23	.22
hubCpG (brown module) ~ Birthweight	-1.93x10 ⁻⁰⁴	6.53x10 ⁻⁰⁵	[-0.00, -0.00]	-2.95	.003
hubCpG (brown module) ~ Mother's BMI before pregnancy	3.14x10 ⁻⁰⁴	6.98x10 ⁻⁰³	[-0.01, 0.01]	0.04	.96
hubCpG (brown module) ~ CD4T	-5.99	1.64	[-9.60, -3.17]	-3.65	< .001
hubCpG (brown module) ~ Monocytes	-4.76	1.96	[-9.10, -1.33]	-2.43	.02
hubCpG (brown module) ~ NK	-8.57	1.71	[-12.43, -5.77]	-5.02	< .001
hubCpG (brown module) ~ Granulocytes	-7.01	1.56	[-10.61, -4.51]	-4.49	< .001
hubCpG (brown module) ~ B-cells	-15.34	1.23	[-17.94, -13.06]	-12.50	< .001

Note. Coefficient = *Regressions* beta value, *SE* = standard error, *CI* = confidence interval, *z* = *z*-statistic, *p* = *p*-value, *c* = *c*-path, *b* = *b*-path, *a* = *a*-path.

Table A.64.ii. *Defined model parameters (effects)*

Effect	Coefficient	<i>SE</i>	95% <i>CI</i>	<i>z</i>	<i>p</i>
Indirect (female)	-0.03	0.08	[-0.22, 0.12]	-0.36	.72
Total (female)	0.06	0.51	[-0.94, 1.06]	0.12	.90
Indirect (male)	0.02	0.06	[-0.10, 0.17]	0.24	.81
Total (male)	0.99	0.69	[-0.31, 2.39]	1.44	.15
Difference in indirect (male - female)	-0.04	0.12	[-0.32, 0.17]	-0.38	.71
Difference in indirect (male - female)	-0.93	0.83	[-2.58, 0.68]	-1.12	.26

Note. Coefficient = estimated model parameter, *SE* = standard error, *CI* = confidence interval, *z* = *z*-statistic, *p* = *p*-value.

Tables A.65.i & ii. Results of the mediation model with the predictor congener PCDF130, the DNA methylation of the hubCpG of the yellow module as mediator, and the predicted child's cognitive ability as outcome, controlling for confounders.

Table A.65.i. *Regressions*

	Coefficient	<i>SE</i>	95% <i>CI</i>	<i>z</i>	<i>p</i>
Child's cognitive ability ~ PCDF130 (c)	0.02	0.52	[-1.01, 1.02]	0.04	.97
Child's cognitive ability ~ Sex	-3.49	0.51	[-4.51, -2.53]	-6.85	< .001
Child's cognitive ability ~ PCDF130:Sex (c:Sex)	0.97	0.82	[-0.55, 2.61]	1.19	.23

Child's cognitive ability ~ hubCpG (yellow module)	-1.28	0.82	[-2.92, 0.28]	-1.56	.12
(b)					
Child's cognitive ability ~ Birthweight	1.27x10 ⁻⁰³	5.30x10 ⁻⁰⁴	[0.00, 0.00]	2.40	.02
Child's cognitive ability ~ Mother's BMI before pregnancy	-0.19	0.06	[-0.31, -0.07]	-3.11	.002
Child's cognitive ability ~ CD4T	0.05	6.11	[-11.88, 12.34]	8.96x10 ⁻⁰³	.99
Child's cognitive ability ~ Granulocytes	1.86	4.93	[-8.21, 11.48]	0.38	.71
Child's cognitive ability ~ B-cells	-11.75	9.61	[-29.61, 7.94]	-1.22	.22
Child's cognitive ability ~ EPIC array plate	-0.98	0.53	[-1.99, 0.08]	-1.85	.06
hubCpG (yellow module) ~ PCDF130	-0.07	0.07	[-0.21, 0.08]	-0.93	.35
(a)					
hubCpG (yellow module) ~ Sex	-0.03	0.05	[-0.12, 0.07]	-0.55	.58
hubCpG (yellow module) ~ PCDF130:Sex (a:Sex)	0.10	0.09	[-0.07, 0.28]	1.09	.27
hubCpG (yellow module) ~ Birthweight	-4.43x10 ⁻⁰⁵	4.90x10 ⁻⁰⁵	[-0.00, 0.00]	-0.91	.37
hubCpG (yellow module) ~ Mother's BMI before pregnancy	-2.15x10 ⁻⁰³	5.98x10 ⁻⁰³	[-0.02, 0.01]	-0.36	.72
hubCpG (yellow module) ~ CD4T	-1.69	0.69	[-3.13, -0.39]	-2.46	.01
hubCpG (yellow module) ~ Granulocytes	-1.46	0.47	[-2.48, -0.64]	-3.13	.002
hubCpG (yellow module) ~ B-cells	-6.65	0.84	[-8.29, -4.95]	-7.89	<.001
hubCpG (yellow module) ~ EPIC array plate	-0.13	0.04	[-0.22, -0.04]	-2.97	.003

Note. Coefficient = *Regressions* beta value, *SE* = standard error, *CI* = confidence interval, *z* = *z*-statistic, *p* = *p*-value, c = c-path, b = b-path, a = a-path.

Table A.65.ii. *Defined model parameters (effects)*

Effect	Coefficient	<i>SE</i>	95% <i>CI</i>	<i>z</i>	<i>p</i>
Indirect (female)	0.09	0.13	[-0.11, 0.41]	0.68	.50
Total (female)	0.11	0.50	[-0.86, 1.11]	0.21	.83
Indirect (male)	-0.04	0.08	[-0.23, 0.09]	-0.48	.63
Total (male)	0.96	0.69	[-0.31, 2.38]	1.39	.17
Difference in indirect (male - female)	0.13	0.16	[-0.11, 0.53]	0.79	.43
Difference in indirect (male - female)	-0.85	0.82	[-2.47, 0.71]	-1.04	.30

Note. Coefficient = estimated model parameter, *SE* = standard error, *CI* = confidence interval, *z* = *z*-statistic, *p* = *p*-value.

Tables A.66.i & ii. Results of the mediation model with the predictor congener PCDF130, the DNA methylation of the hubCpG of the white module as mediator, and the predicted child's cognitive ability as outcome, controlling for confounders.

Table A.66.i. *Regressions*

	Coefficient	<i>SE</i>	95% <i>CI</i>	<i>z</i>	<i>p</i>
Child's cognitive ability ~ PCDF130	0.04	0.50	[-0.96, 1.00]	0.09	.93
(c)					
Child's cognitive ability ~ Sex	-3.59	0.49	[-4.58, -2.66]	-7.29	<.001

Child's cognitive ability ~ PCDF130:Sex (c:Sex)	1.09	0.81	[-0.41, 2.75]	1.35	.18
Child's cognitive ability ~ hubCpG (white module) (b)	1.80	0.72	[0.39, 3.26]	2.49	.01
Child's cognitive ability ~ Birthweight	1.28x10 ⁻⁰³	5.24x10 ⁻⁰⁴	[0.00, 0.00]	2.45	.01
Child's cognitive ability ~ Mother's BMI before pregnancy	-0.19	0.06	[-0.31, -0.08]	-3.32	<.001
Child's cognitive ability ~ CD4T	-3.77	5.00	[-13.06, 6.58]	-0.76	.45
Child's cognitive ability ~ B-cells	-14.97	8.43	[-30.74, 2.40]	-1.78	.08
Child's cognitive ability ~ EPIC array plate	-0.99	0.52	[-1.98, 0.06]	-1.91	.06
hubCpG (white module) ~ PCDF130 (a)	0.03	0.07	[-0.11, 0.16]	0.45	.65
hubCpG (white module) ~ Sex	0.05	0.05	[-0.04, 0.15]	1.13	.26
hubCpG (white module) ~ PCDF130:Sex (a:Sex)	-0.11	0.09	[-0.28, 0.06]	-1.24	.21
hubCpG (white module) ~ Birthweight	2.21x10 ⁻⁰⁶	4.70x10 ⁻⁰⁵	[-0.00, 0.00]	0.05	.96
hubCpG (white module) ~ Mother's BMI before pregnancy	3.85x10 ⁻⁰³	5.34x10 ⁻⁰³	[-0.01, 0.02]	0.72	.47
hubCpG (white module) ~ CD4T	1.48	0.48	[0.52, 2.41]	3.10	.002
hubCpG (white module) ~ B-cells	5.73	0.78	[4.07, 7.14]	7.35	<.001
hubCpG (white module) ~ EPIC array plate	0.11	0.04	[0.03, 0.20]	2.47	.01

Note. Coefficient = *Regressions* beta value, *SE* = standard error, *CI* = confidence interval, *z* = *z*-statistic, *p* = *p*-value, *c* = *c*-path, *b* = *b*-path, *a* = *a*-path.

Table A.66.ii. *Defined model parameters (effects)*

Effect	Coefficient	<i>SE</i>	95% <i>CI</i>	<i>z</i>	<i>p</i>
Indirect (female)	0.05	0.14	[-0.18, 0.39]	0.39	.70
Total (female)	0.10	0.50	[-0.88, 1.07]	0.20	.84
Indirect (male)	-0.14	0.12	[-0.42, 0.03]	-1.20	.23
Total (male)	1.00	0.68	[-0.26, 2.41]	1.47	.14
Difference in indirect (male - female)	0.19	0.20	[-0.10, 0.69]	0.96	.34
Difference in indirect (male - female)	-0.90	0.80	[-2.52, 0.64]	-1.12	.26

Note. Coefficient = estimated model parameter, *SE* = standard error, *CI* = confidence interval, *z* = *z*-statistic, *p* = *p*-value.

Tables A.67.i & ii. Results of the mediation model with the predictor congener PCDF130, the EigenCpG of the lightcyan1 module as mediator, and the predicted child's cognitive ability as outcome, controlling for confounders.

Table A.67.i. *Regressions*

	Coefficient	<i>SE</i>	95% <i>CI</i>	<i>z</i>	<i>p</i>
Child's cognitive ability ~ PCDF130 (c)	-0.04	0.53	[-1.09, 1.00]	-0.07	.94
Child's cognitive ability ~ Sex	-3.43	0.50	[-4.45, -2.49]	-6.88	<.001
Child's cognitive ability ~ PCDF130:Sex (c:Sex)	1.07	0.82	[-0.49, 2.74]	1.31	.19
Child's cognitive ability ~ hubCpG (lightcyan1 module) (b)	-1.59	1.31	[-4.10, 0.98]	-1.22	.22

Child's cognitive ability ~ Birthweight	1.36x10 ⁻⁰³	5.45x10 ⁻⁰⁴	[0.00, 0.00]	2.50	.01
Child's cognitive ability ~ Mother's BMI before pregnancy	-0.19	0.06	[-0.30, -0.08]	-3.25	.001
Child's cognitive ability ~ CD4T	3.07	6.19	[-8.63, 15.84]	0.50	.62
Child's cognitive ability ~ B-cells	6.59	11.96	[-16.12, 31.33]	0.55	.58
hubCpG (lightcyan1 module) ~ PCDF130 (a)	-0.08	0.03	[-0.14, -0.02]	-2.41	.02
hubCpG (lightcyan1 module) ~ Sex	0.07	0.03	[0.01, 0.13]	2.30	.02
hubCpG (lightcyan1 module) ~ PCDF130:Sex (a:Sex)	0.02	0.05	[-0.09, 0.12]	0.43	.67
hubCpG (lightcyan1 module) ~ Birthweight	2.87x10 ⁻⁰⁵	2.37x10 ⁻⁰⁵	[-0.00, 0.00]	1.21	.23
hubCpG (lightcyan1 module) ~ Mother's BMI before pregnancy	-2.64x10 ⁻⁰⁴	3.25x10 ⁻⁰³	[-0.01, 0.01]	-0.08	.94
hubCpG (lightcyan1 module) ~ CD4T	3.16	0.32	[2.54, 3.81]	9.83	<.001
hubCpG (lightcyan1 module) ~ B-cells	6.72	0.48	[5.70, 7.59]	14.04	<.001

Note. Coefficient = Regressions beta value, SE = standard error, CI = confidence interval, z = z-statistic, p = p-value, c = c-path, b = b-path, a = a-path.

Table A.67.ii. *Defined model parameters (effects)*

Effect	Coefficient	SE	95% CI	z	p
Indirect (female)	0.12	0.13	[-0.07, 0.43]	0.96	.34
Total (female)	0.08	0.52	[-0.92, 1.08]	0.16	.87
Indirect (male)	0.08	0.11	[-0.08, 0.34]	0.80	.43
Total (male)	1.12	0.68	[-0.17, 2.50]	1.66	.010
Difference in indirect (male - female)	0.04	0.11	[-0.15, 0.33]	0.32	.75
Difference in indirect (male - female)	-1.04	0.83	[-2.71, 0.56]	-1.25	.21

Note. Coefficient = estimated model parameter, SE = standard error, CI = confidence interval, z = z-statistic, p = p-value.

Tables A.68.i & ii. Results of the mediation model with the predictor congener PCDF130, the DNA methylation of the hubCpG of the red module as mediator, and the predicted child's cognitive ability as outcome, controlling for confounders.

Table A.68.i. *Regressions*

	Coefficient	SE	95% CI	z	p
Child's cognitive ability ~ PCDF130 (c)	0.13	0.51	[-0.87, 1.14]	0.25	.80
Child's cognitive ability ~ Sex	-3.61	0.49	[-4.58, -2.67]	-7.40	<.001
Child's cognitive ability ~ PCDF130:Sex (c:Sex)	0.84	0.80	[-0.66, 2.48]	1.05	.29
Child's cognitive ability ~ hubCpG (red module) (b)	0.91	0.49	[-0.08, 1.86]	1.87	.06
Child's cognitive ability ~ Birthweight	1.29x10 ⁻⁰³	5.31x10 ⁻⁰⁴	[0.00, 0.00]	2.42	.02
Child's cognitive ability ~ Mother's BMI before pregnancy	-0.19	0.06	[-0.30, -0.08]	-3.37	<.001
Child's cognitive ability ~ EPIC array plate	-1.07	0.53	[-2.08, 0.02]	-2.01	.04

hubCpG (red module) ~ PCDF130 (a)	-0.01	0.10	[-0.22, 0.19]	-	.92
hubCpG (red module) ~ Sex	0.12	0.08	[-0.05, 0.27]	1.48	.14
hubCpG (red module) ~ PCDF130:Sex (a:Sex)	0.02	0.13	[-0.25, 0.27]	0.13	.90
hubCpG (red module) ~ Birthweight	5.92x10 ⁻⁰⁶	7.36x10 ⁻⁰⁵	[0.00, 0.00]	0.08	.94
hubCpG (red module) ~ Mother's BMI before pregnancy	6.50x10 ⁻⁰³	9.71x10 ⁻⁰³	[-0.01, 0.03]	0.67	.50
hubCpG (red module) ~ EPIC array plate	0.28	0.08	[0.14, 0.43]	3.74	< .001

Note. Coefficient = *Regressions* beta value, *SE* = standard error, CI = confidence interval, *z* = *z*-statistic, *p* = *p*-value, c = c-path, b = b-path, a = a-path.

Table A.68.ii. *Defined model parameters (effects)*

Effect	Coefficient	SE	95% CI	<i>z</i>	<i>p</i>
Indirect (female)	-0.01	0.10	[-0.21, 0.23]	-0.10	.92
Total (female)	0.12	0.50	[-0.86, 1.11]	0.24	.81
Indirect (male)	5.57x10 ⁻⁰³	0.09	[-0.18, 0.18]	0.07	.95
Total (male)	0.98	0.67	[-0.26, 2.37]	1.46	.15
Difference in indirect (male - female)	-0.02	0.13	[-0.28, 0.29]	-0.12	.91
Difference in indirect (male - female)	-0.86	0.80	[-2.48, 0.69]	-1.07	.29

Note. Coefficient = estimated model parameter, *SE* = standard error, CI = confidence interval, *z* = *z*-statistic, *p* = *p*-value.

Tables A.69.i & ii. Results of the mediation model with the predictor congener PCDF130, the EigenCpG of the brown module as mediator, and the predicted child's cognitive ability as outcome, controlling for confounders in the female subsample.

Table A.69.i. *Regressions*

	Coefficient	SE	95% CI	<i>z</i>	<i>p</i>
Child's cognitive ability ~ PCDF130 (c)	0.20	0.52	[-0.76, 1.27]	0.39	.70
Child's cognitive ability ~ EigenCpG (brown module) (b)	5.75	5.70	[-7.27, 14.03]	1.01	.31
Child's cognitive ability ~ Mother's BMI before pregnancy	-0.16	0.08	[-0.33, 0.00]	-	.07
Child's cognitive ability ~ B-cells	3.04	11.18	[-18.45, 25.55]	1.84	.79
Child's cognitive ability ~ EPIC array plate	-1.49	0.92	[-3.05, 0.49]	-	.11
EigenCpG (brown module) ~ PCDF130 (a)	4.87x10 ⁻⁰³	0.02	[-0.03, 0.04]	1.62	.80
EigenCpG (brown module) ~ Mother's BMI before pregnancy	-1.91x10 ⁻⁰³	1.85x10 ⁻⁰³	[-0.01, 0.00]	0.25	.30
EigenCpG (brown module) ~ B-cells	-1.25	0.56	[-2.42, -0.22]	-	.03
EigenCpG (brown module) ~ EPIC array plate	0.08	0.03	[0.02, 0.13]	2.23	.01

Note. Coefficient = *Regressions* beta value, *SE* = standard error, CI = confidence interval, *z* = *z*-statistic, *p* = *p*-value, c = c-path, b = b-path, a = a-path.

Table A.69.ii. *Defined model parameters (effects)*

Effect	Coefficient	SE	95% CI	<i>z</i>	<i>p</i>
Indirect	0.03	0.15	[-0.40, 0.23]	0.19	.85
Total	0.23	0.51	[-0.77, 1.24]	0.45	.66

Note. Coefficient = estimated model parameter, *SE* = standard error, *CI* = confidence interval, *z* = *z*-statistic, *p* = *p*-value.

Tables A.70.i & ii. Results of the mediation model with the predictor congener PCDF130, the EigenCpG of the lightcyan1 module as mediator, and the predicted child's cognitive ability as outcome, controlling for confounders in the female subsample.

Table A.70.i. *Regressions*

	Coefficient	<i>SE</i>	95% CI	<i>z</i>	<i>p</i>
Child's cognitive ability ~ PCDF130 (c)	0.06	0.53	[-0.99, 1.09]	0.11	.91
Child's cognitive ability ~ EigenCpG (lightcyan1 module) (b)	-4.11	5.82	[-14.12, 8.04]	-0.71	.48
Child's cognitive ability ~ CD4T	-1.88	7.40	[-16.92, 12.50]	-0.25	.80
EigenCpG (lightcyan1 module) ~ PCDF130 (a)	1.63x10 ⁻⁰³	0.02	[-0.03, 0.04]	0.09	.92
EigenCpG (lightcyan1 module) ~ CD4T	1.05	0.28	[0.50, 1.60]	3.78	< .001

Note. Coefficient = *Regressions* beta value, *SE* = standard error, *CI* = confidence interval, *z* = *z*-statistic, *p* = *p*-value, c = c-path, b = b-path, a = a-path.

Table A.70.ii. *Defined model parameters (effects)*

Effect	Coefficient	<i>SE</i>	95% CI	<i>z</i>	<i>p</i>
indirect	-6.70x10 ⁻⁰³	0.13	[-0.39, 0.14]	-0.05	.96
Total	0.05	0.54	[-1.06, 1.07]	0.10	.92

Note. Coefficient = estimated model parameter, *SE* = standard error, *CI* = confidence interval, *z* = *z*-statistic, *p* = *p*-value.

Tables A.71.i & ii. Results of the mediation model with the predictor congener PCDF130, the EigenCpG of the red module as mediator, and the predicted child's cognitive ability as outcome, controlling for confounders in the female subsample.

Table A.71.i. *Regressions*

	Coefficient	<i>SE</i>	95% CI	<i>z</i>	<i>p</i>
Child's cognitive ability ~ PCDF130 (c)	0.17	0.54	[-0.91, 1.20]	0.31	.75
Child's cognitive ability ~ EigenCpG (red module) (b)	4.90	2.99	[-0.51, 11.43]	1.64	.10
Child's cognitive ability ~ Mother's BMI before pregnancy	-0.17	0.08	[-0.34, -0.02]	-2.04	.04
Child's cognitive ability ~ EPIC array plate	-1.52	0.76	[-2.98, -0.04]	-2.00	.05
EigenCpG (red module) ~ PCDF130 (a)	0.01	0.02	[-0.03, 0.06]	0.61	.54
EigenCpG (red module) ~ Mother's BMI before pregnancy	1.14x10 ⁻⁰³	3.06x10 ⁻⁰³	[0.00, 0.01]	0.37	.71
EigenCpG (red module) ~ EPIC array plate	0.09	0.02	[0.05, 0.13]	4.02	< .001

Note. Coefficient = *Regressions* beta value, *SE* = standard error, *CI* = confidence interval, *z* = *z*-statistic, *p* = *p*-value, c = c-path, b = b-path, a = a-path.

Table A.71.ii. *Defined model parameters (effects)*

Effect	Coefficient	<i>SE</i>	95% CI	<i>z</i>	<i>p</i>
indirect	0.07	0.15	[-0.14, 0.47]	0.43	.66
Total	0.24	0.52	[-0.75, 1.26]	0.46	.65

Note. Coefficient = estimated model parameter, *SE* = standard error, *CI* = confidence interval, *z* = *z*-statistic, *p* = *p*-value.

Tables A.72.i & ii. Results of the mediation model with the predictor congener PCDF130, the EigenCpG of the salmon module as mediator, and the predicted child's cognitive ability as outcome, controlling for confounders in the female subsample.

Table A.72.i. *Regressions*

	Coefficient	SE	95% CI	z	p
Child's cognitive ability ~ PCDF130 (c)	0.07	0.56	[-0.98, 1.21]	0.12	.90
Child's cognitive ability ~ EigenCpG (salmon module) (b)	7.27	5.13	[-3.49, 16.39]	1.42	.16
Child's cognitive ability ~ Mother's BMI before pregnancy	-0.17	0.09	[-0.35, 0.02]	-2.01	.05
Child's cognitive ability ~ EPIC array plate	-2.04	1.07	[-3.95, 0.22]	-1.90	.06
EigenCpG (salmon module) ~ PCDF130 (a)	0.02	0.02	[-0.02, 0.06]	1.17	.24
EigenCpG (salmon module) ~ Mother's BMI before pregnancy	1.04x10 ⁻⁰³	2.41x10 ⁻⁰³	[0.00, 0.01]	0.43	.67
EigenCpG (salmon module) ~ EPIC array plate	0.13	0.02	[0.09, 0.17]	6.03	< .001

Note. Coefficient = *Regressions* beta value, SE = standard error, CI = confidence interval, z = z-statistic, p = p-value, c = c-path, b = b-path, a = a-path.

Table A.72.ii. *Defined model parameters (effects)*

Effect	Coefficient	SE	95% CI	z	p
indirect	0.17	0.19	[-0.23, 0.54]	0.91	.36
Total	0.24	0.52	[-0.75, 1.27]	0.46	.65

Note. Coefficient = estimated model parameter, SE = standard error, CI = confidence interval, z = z-statistic, p = p-value.

Tables A.73.i & ii. Results of the mediation model with the predictor congener PCDF130, the EigenCpG of the white module as mediator, and the predicted child's cognitive ability as outcome, controlling for confounders in the female subsample.

Table A.73.i. *Regressions*

	Coefficient	SE	95% CI	z	p
Child's cognitive ability ~ PCDF130 (c)	0.07	0.50	[-0.90, 1.05]	0.15	.88
Child's cognitive ability ~ EigenCpG (white module) (b)	0.11	3.52	[-6.88, 6.90]	0.03	.97
Child's cognitive ability ~ Gestational length	0.68	0.37	[-0.17, 1.26]	1.84	.07
Child's cognitive ability ~ B-cells	-3.00	8.40	[-20.35, 12.92]	-0.36	.72
EigenCpG (white module) ~ PCDF130 (a)	-0.02	0.02	[-0.07, 0.02]	-0.93	.35
EigenCpG (white module) ~ Gestational length	0.03	8.89x10 ⁻⁰³	[0.01, 0.04]	3.05	.002
EigenCpG (white module) ~ B-cells	-0.95	0.31	[-1.60, -0.39]	-3.09	.002

Note. Coefficient = *Regressions* beta value, SE = standard error, CI = confidence interval, z = z-statistic, p = p-value, c = c-path, b = b-path, a = a-path.

Table A.73.ii. *Defined model parameters (effects)*

Effect	Coefficient	SE	95% CI	z	p
indirect	-2.43x10 ⁻⁰³	0.11	[-0.20, 0.27]	-0.02	0.982
Total	0.07	0.49	[-0.86, 1.04]	0.14	0.886

Note. Coefficient = estimated model parameter, SE = standard error, CI = confidence interval, z = z-statistic, p = p-value.

Tables A.74.i & ii. Results of the mediation model with the predictor congener PCDF130, the EigenCpG of the yellow module as mediator, and the predicted child's cognitive ability as outcome, controlling for confounders in the female subsample.

Table A.74.i. *Regressions*

	Coefficient	SE	95% CI	z	p
Child's cognitive ability ~ PCDF130 (c)	0.13	0.50	[-0.86, 1.12]	0.27	.80
Child's cognitive ability ~ EigenCpG (yellow module) (b)	1.40	4.74	[-7.66, 10.43]	0.30	.77
Child's cognitive ability ~ B-cells EigenCpG (yellow module) ~ PCDF130 (a)	-2.00	9.91	[-21.51, 17.63]	-0.20	.84
EigenCpG (yellow module) ~ B-cells	-0.02	0.02	[-0.06, 0.02]	-0.83	.40
EigenCpG (yellow module) ~ B-cells	-1.13	0.47	[-2.11, -0.28]	-2.41	.02

Note. Coefficient = *Regressions* beta value, SE = standard error, CI = confidence interval, z = z-statistic, p = p-value, c = c-path, b = b-path, a = a-path.

Table A.74.ii. *Defined model parameters (effects)* of the mediation model with the predictor congener PCDF130, the EigenCpG of the yellow module as mediator as mediator, and the predicted child's cognitive ability as outcome, controlling for confounders in the female subsample.

Effect	Coefficient	SE	95% CI	z	p
indirect	-0.03	0.16	[-0.45, 0.23]	-0.17	.87
Total	0.11	0.52	[-0.95, 1.10]	0.21	.84

Note. Coefficient = estimated model parameter, SE = standard error, CI = confidence interval, z = z-statistic, p = p-value.

Tables. A.75.i & ii. Results of the mediation model with the predictor congener PCB126, the mean DNA methylation of the CpGs in the promoter region of AR, and the predicted child's cognitive ability as outcome, controlling for confounders for the female and male subsample separately.

Table A.75.i. *Regressions*

	Coefficient	SE	95% CI	z	p
Child's cognitive ability ~ PCB126 (c [female])	-0.12	0.46	[-0.85, 0.99]	-0.27	.79
Child's cognitive ability ~ DNAm AR (b [female])	1.22	1.72	[-4.89, 1.67]	0.71	.48
Child's cognitive ability ~ Mother's education level	0.36	0.33	[-0.33, 0.97]	1.07	.28
DNAm AR ~ PCB126 (a [female])	-0.15	0.15	[-0.52, 0.03]	-0.99	.32
DNAm AR ~ Mother's education level	0.06	0.06	[-0.02, 0.22]	1.07	.29
Child's cognitive ability ~ PCB126 (c [male])	0.41	0.63	[-0.80, 1.67]	0.65	.52
Child's cognitive ability ~ DNAm AR (b [male])	-0.54	0.48	[-0.96, 0.52]	-1.11	.27
Child's cognitive ability ~ Mother's education level	0.68	0.30	[0.10, 1.29]	2.24	.03
DNAm AR ~ PCB126 (a [male])	-7.99x10 ⁻⁰³	0.11	[-0.25, 0.17]	-0.07	.94
DNAm AR ~ Mother's education level	-0.05	0.06	[-0.18, 0.05]	-0.92	.36

Note. Coefficient = *Regressions* beta value, SE = standard error, CI = confidence interval, z = z-statistic, p = p-value, c = c-path, b = b-path, a = a-path.

Table A.75.ii. *Defined model parameters (effects)*

Effect	Coefficient	SE	95% CI	z	p
Indirect (female)	-0.18	0.23	[-0.75, 0.15]	-0.78	.44
Total (female)	-0.31	0.50	[-1.17, 0.83]	-0.61	.54
Indirect (male)	4.28x10 ⁻⁰³	0.07	[-0.08, 0.19]	0.06	.95
Total (male)	0.41	0.63	[-0.78, 1.68]	0.66	.51
Difference in indirect (male - female)	-0.19	0.24	[-0.79, 0.15]	-0.76	.45
Difference in indirect (male - female)	-0.72	0.80	[-2.26, 0.92]	-0.90	.37

Note. Coefficient = estimated model parameter, SE = standard error, CI = confidence interval, z = z-statistic, p = p-value.

Tables A.76.i & ii. Results of the mediation model with the predictor congener PCB169, the mean DNA methylation of the CpGs in the promoter region of *AR*, and the predicted child's cognitive ability as outcome, controlling for confounders for the female and male subsample separately.

Table A.76.i. *Regressions*

	Coefficient	SE	95% CI	z	p
Child's cognitive ability ~ PCB169 (c [female])	0.70	0.54	[-0.44, 1.66]	1.31	.19
Child's cognitive ability ~ DNAm <i>AR</i> (b [female])	1.37	1.75	[-4.86, 1.83]	0.78	.43
Child's cognitive ability ~ Mother's education level	0.15	0.30	[-0.44, 0.74]	0.51	.61
DNAm <i>AR</i> ~ PCB169 (a [female])	-0.21	0.14	[-0.53, 0.01]	-1.50	.13
DNAm <i>AR</i> ~ Mother's education level	0.08	0.06	[-0.01, 0.21]	1.31	.19
Child's cognitive ability ~ PCB169 (c [male])	0.54	0.57	[-0.63, 1.60]	0.94	.35
Child's cognitive ability ~ DNAm <i>AR</i> (b [male])	-0.57	0.45	[-0.93, 0.39]	-1.26	.21
Child's cognitive ability ~ Mother's education level	0.64	0.34	[0.00, 1.31]	1.91	.06
DNAm <i>AR</i> ~ PCB169 (a [male])	0.09	0.19	[-0.31, 0.45]	0.49	.62
DNAm <i>AR</i> ~ Mother's education level	-0.08	0.06	[-0.21, 0.03]	-1.25	.21

Note. Coefficient = *Regressions* beta value, SE = standard error, CI = confidence interval, z = z-statistic, p = p-value, c = c-path, b = b-path, a = a-path.

Table A.76.ii. *Defined model parameters (effects)*

Effect	Coefficient	SE	95% CI	z	p
Indirect (female)	-0.29	0.25	[-0.85, 0.13]	-1.16	.25
Total (female)	0.41	0.58	[-0.82, 1.45]	0.71	.48
Indirect (male)	-0.05	0.12	[-0.26, 0.23]	-0.45	.65
Total (male)	0.48	0.58	[-0.66, 1.59]	0.84	.40
Difference in indirect (male - female)	-0.24	0.28	[-0.87, 0.21]	-0.86	.39
Difference in indirect (male - female)	-0.07	0.82	[-1.71, 1.47]	-0.09	.93

Note. Coefficient = estimated model parameter, SE = standard error, CI = confidence interval, z = z-statistic, p = p-value.

Tables A.77.i & ii. Results of the mediation model with the predictor congener PCB77, the mean DNA methylation of the CpGs in the promoter region of *AR*, and the predicted child's cognitive ability as outcome, controlling for confounders for the female and male subsample separately.

Table A.77.i. *Regressions*

	Coefficient	SE	95% CI	z	p
Child's cognitive ability ~ PCB77 (c [female])	1.18	0.89	[-0.40, 3.07]	1.32	.19
Child's cognitive ability ~ DNAm <i>AR</i> (b [female])	1.23	1.64	[-4.60, 1.64]	0.75	.45
Child's cognitive ability ~ Mother's education level	0.30	0.30	[-0.33, 0.87]	1.00	.32
DNAm <i>AR</i> ~ PCB77 (a [female])	0.01	0.10	[-0.17, 0.24]	0.11	.91
DNAm <i>AR</i> ~ Mother's education level	0.03	0.03	[-0.02, 0.10]	0.86	.39
Child's cognitive ability ~ PCB77 (c [male])	-1.05	0.76	[-2.50, 0.57]	-1.39	.17
Child's cognitive ability ~ DNAm <i>AR</i> (b [male])	-0.46	0.51	[-0.95, 0.65]	-0.90	.37
Child's cognitive ability ~ Mother's education level	0.76	0.28	[0.21, 1.32]	2.68	.01
DNAm <i>AR</i> ~ PCB77 (a [male])	0.32	0.32	[-0.14, 1.09]	0.99	.32
DNAm <i>AR</i> ~ Mother's education level	-0.06	0.07	[-0.21, 0.07]	-0.79	.43

Note. Coefficient = *Regressions* beta value, SE = standard error, CI = confidence interval, z = z-statistic, p = p-value, c = c-path, b = b-path, a = a-path.

Table A.77.ii. *Defined model parameters (effects)*

Effect	Coefficient	SE	95% CI	z	p
Indirect (female)	0.01	0.15	[-0.21, 0.40]	0.09	.93
Total (female)	1.19	0.90	[-0.37, 3.13]	1.32	.19
Indirect (male)	-0.15	0.19	[-0.57, 0.18]	-0.78	.43
Total (male)	-1.20	0.72	[-2.54, 0.35]	-1.67	.10
Difference in indirect (male - female)	0.16	0.24	[-0.24, 0.71]	0.68	.50

Difference in indirect (male - female)	2.39	1.15	[0.19, 4.78]	2.07	.04
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Note. Coefficient = estimated model parameter, *SE* = standard error, *CI* = confidence interval, *z* = *z*-statistic, *p* = *p*-value.

Tables A.78.i & ii. Results of the mediation model with the predictor congener PCB81, the mean DNA methylation of the CpGs in the promoter region of *AR*, and the predicted child's cognitive ability as outcome, controlling for confounders for the female and male subsample separately.

Table A.78.i. *Regressions*

	Coefficient	<i>SE</i>	95% CI	<i>z</i>	<i>p</i>
Child's cognitive ability ~ PCB81 (c [female])	-0.08	0.39	[-0.82, 0.72]	-0.21	.84
Child's cognitive ability ~ DNAm <i>AR</i> (b [female])	1.23	1.72	[-4.89, 1.66]	0.71	.48
Child's cognitive ability ~ Mother's education level	0.34	0.32	[-0.34, 0.93]	1.04	.30
DNAm <i>AR</i> ~ PCB81 (a [female])	-0.04	0.04	[-0.13, 0.04]	-0.96	.34
DNAm <i>AR</i> ~ Mother's education level	0.03	0.03	[-0.02, 0.11]	1.06	.29
Child's cognitive ability ~ PCB81 (c [male])	-1.03	0.53	[-1.96, 0.14]	-1.94	.05
Child's cognitive ability ~ DNAm <i>AR</i> (b [male])	-0.48	0.48	[-0.96, 0.64]	-0.99	.32
Child's cognitive ability ~ Mother's education level	0.87	0.27	[0.35, 1.42]	3.21	.001
DNAm <i>AR</i> ~ PCB81 (a [male])	0.11	0.12	[-0.10, 0.39]	0.94	.35
DNAm <i>AR</i> ~ Mother's education level	-0.07	0.07	[-0.22, 0.05]	-1.01	.31

Note. Coefficient = *Regressions* beta value, *SE* = standard error, *CI* = confidence interval, *z* = *z*-statistic, *p* = *p*-value, c = c-path, b = b-path, a = a-path.

Table A.78.ii. *Defined model parameters (effects)*

Effect	Coefficient	<i>SE</i>	95% CI	<i>z</i>	<i>p</i>
Indirect (female)	-0.05	0.08	[-0.17, 0.18]	-0.60	.55
Total (female)	-0.13	0.39	[-0.84, 0.69]	-0.33	.74
Indirect (male)	-0.05	0.07	[-0.20, 0.09]	-0.77	.44
Total (male)	-1.08	0.52	[-1.99, 0.09]	-2.07	.04
Difference in indirect (male - female)	6.89x10 ⁻⁰³	0.11	[-0.18, 0.26]	0.06	.95
Difference in indirect (male - female)	0.95	0.65	[-0.41, 2.14]	1.47	.14

Note. Coefficient = estimated model parameter, *SE* = standard error, *CI* = confidence interval, *z* = *z*-statistic, *p* = *p*-value.

Tables A.79.i & ii. Results of the mediation model with the predictor congener PCDD48, the mean DNA methylation of the CpGs in the promoter region of *AR*, and the predicted child's cognitive ability as outcome, controlling for confounders for the female and male subsample separately.

Table A.79.i. *Regressions*

	Coefficient	<i>SE</i>	95% CI	<i>z</i>	<i>p</i>
Child's cognitive ability ~ PCDD48 (c [female])	-0.53	0.52	[-1.59, 0.45]	-1.01	.31
Child's cognitive ability ~ DNAm <i>AR</i> (b [female])	1.15	1.65	[-4.80, 1.63]	0.70	.49
Child's cognitive ability ~ Mother's education level	0.39	0.30	[-0.20, 0.98]	1.32	.19
DNAm <i>AR</i> ~ PCDD48 (a [female])	-0.14	0.10	[-0.37, 0.01]	-1.42	.16
DNAm <i>AR</i> ~ Mother's education level	0.04	0.04	[-0.02, 0.14]	1.10	.27
Child's cognitive ability ~ PCDD48 (c [male])	0.05	0.44	[-0.84, 0.89]	0.11	.92
Child's cognitive ability ~ DNAm <i>AR</i> (b [male])	-0.54	0.51	[-0.96, 0.58]	-1.07	.29
Child's cognitive ability ~ Mother's education level	0.75	0.30	[0.18, 1.36]	2.51	.01
DNAm <i>AR</i> ~ PCDD48 (a [male])	0.12	0.10	[-0.06, 0.34]	1.20	.23
DNAm <i>AR</i> ~ Mother's education level	-0.08	0.07	[-0.23, 0.05]	-1.06	.29

Note. Coefficient = *Regressions* beta value, *SE* = standard error, *CI* = confidence interval, *z* = *z*-statistic, *p* = *p*-value, c = c-path, b = b-path, a = a-path.

Table A.79.ii. *Defined model parameters (effects)*

Effect	Coefficient	<i>SE</i>	95% CI	<i>z</i>	<i>p</i>
Indirect (female)	-0.16	0.15	[-0.51, 0.12]	-1.02	0.307

Total (female)	-0.68	0.52	[-1.77, 0.28]	-1.31	0.192
Indirect (male)	-0.07	0.07	[-0.20, 0.06]	-1.01	0.314
Total (male)	-0.02	0.44	[-0.88, 0.83]	-0.04	0.966
Difference in indirect (male - female)	-0.09	0.17	[-0.47, 0.21]	-0.55	0.585
Difference in indirect (male - female)	-0.66	0.68	[-2.05, 0.63]	-0.97	0.330

Note. Coefficient = estimated model parameter, *SE* = standard error, CI = confidence interval, *z* = *z*-statistic, *p* = *p*-value.

Tables A.80.i & ii. Results of the mediation model with the predictor congener PCDD54, the mean DNA methylation of the CpGs in the promoter region of *AR*, and the predicted child's cognitive ability as outcome, controlling for confounders for the female and male subsample separately.

Table A.80.i. *Regressions*

	Coefficient	<i>SE</i>	95% CI	<i>z</i>	<i>p</i>
Child's cognitive ability ~ PCDD54 (c [female])	-0.04	0.72	[-1.49, 1.34]	-0.05	.96
Child's cognitive ability ~ DNAm <i>AR</i> (b [female])	1.23	1.70	[-4.87, 1.70]	0.72	.47
Child's cognitive ability ~ Mother's education level	0.33	0.31	[-0.31, 0.90]	1.07	.29
DNAm <i>AR</i> ~ PCDD54 (a [female])	-0.29	0.19	[-0.73, -0.01]	-1.54	.12
DNAm <i>AR</i> ~ Mother's education level	0.06	0.05	[-0.01, 0.18]	1.29	.20
Child's cognitive ability ~ PCDD54 (c [male])	0.63	0.58	[-0.61, 1.71]	1.08	.28
Child's cognitive ability ~ DNAm <i>AR</i> (b [male])	-0.55	0.46	[-0.95, 0.42]	-1.21	.22
Child's cognitive ability ~ Mother's education level	0.66	0.31	[0.06, 1.29]	2.13	.03
DNAm <i>AR</i> ~ PCDD54 (a [male])	0.08	0.15	[-0.24, 0.37]	0.51	.61
DNAm <i>AR</i> ~ Mother's education level	-0.07	0.06	[-0.20, 0.05]	-1.08	.28

Note. Coefficient = *Regressions* beta value, *SE* = standard error, CI = confidence interval, *z* = *z*-statistic, *p* = *p*-value, c = c-path, b = b-path, a = a-path.

Table A.80.ii. *Defined model parameters (effects)*

Effect	Coefficient	<i>SE</i>	95% CI	<i>z</i>	<i>p</i>
Indirect (female)	-0.36	0.34	[-1.08, 0.29]	-1.07	.28
Total (female)	-0.40	0.76	[-1.95, 1.04]	-0.53	.60
Indirect (male)	-0.04	0.09	[-0.21, 0.19]	-0.46	.64
Total (male)	0.58	0.58	[-0.62, 1.68]	1.00	.32
Difference in indirect (male - female)	-0.32	0.35	[-1.08, 0.33]	-0.91	.36
Difference in indirect (male - female)	-0.98	0.96	[-2.90, 0.93]	-1.02	.31

Note. Coefficient = estimated model parameter, *SE* = standard error, CI = confidence interval, *z* = *z*-statistic, *p* = *p*-value.

Tables A.81.i & ii. Results of the mediation model with the predictor congener PCDD66, the mean DNA methylation of the CpGs in the promoter region of *AR*, and the predicted child's cognitive ability as outcome, controlling for confounders for the female and male subsample separately.

Table A.81.i. *Regressions*

	Coefficient	<i>SE</i>	95% CI	<i>z</i>	<i>p</i>
Child's cognitive ability ~ PCDD66 (c [female])	0.12	0.69	[-1.30, 1.41]	0.17	.86
Child's cognitive ability ~ DNAm <i>AR</i> (b [female])	1.26	1.73	[-4.93, 1.71]	0.73	.47
Child's cognitive ability ~ Mother's education level	0.30	0.30	[-0.30, 0.88]	0.99	.32
DNAm <i>AR</i> ~ PCDD66 (a [female])	-0.31	0.19	[-0.74, -0.01]	-1.61	.11
DNAm <i>AR</i> ~ Mother's education level	0.08	0.06	[-0.01, 0.21]	1.36	.18
Child's cognitive ability ~ PCDD66 (c [male])	0.83	0.60	[-0.35, 2.02]	1.39	.16
Child's cognitive ability ~ DNAm <i>AR</i> (b [male])	-0.56	0.46	[-0.99, 0.45]	-1.20	.23
Child's cognitive ability ~ Mother's education level	0.58	0.32	[-0.03, 1.25]	1.80	.07
DNAm <i>AR</i> ~ PCDD66 (a [male])	0.06	0.18	[-0.35, 0.39]	0.31	.76
DNAm <i>AR</i> ~ Mother's education level	-0.07	0.07	[-0.22, 0.06]	-0.94	.35

Note. Coefficient = *Regressions* beta value, *SE* = standard error, CI = confidence interval, *z* = *z*-statistic, *p* = *p*-value, c = c-path, b = b-path, a = a-path.

Table A.81.ii. *Defined model parameters (effects)*

Effect	Coefficient	SE	95% CI	z	p
Indirect (female)	-0.38	0.35	[-1.09, 0.34]	-1.11	.27
Total (female)	-0.27	0.73	[-1.76, 1.11]	-0.37	.71
Indirect (male)	-0.03	0.11	[-0.25, 0.20]	-0.29	.77
Total (male)	0.80	0.60	[-0.37, 2.01]	1.33	.18
Difference in indirect (male - female)	-0.35	0.36	[-1.09, 0.39]	-0.97	.33
Difference in indirect (male - female)	-1.06	0.94	[-2.97, 0.75]	-1.13	.26

Note. Coefficient = estimated model parameter, SE = standard error, CI = confidence interval, z = z-statistic, p = p-value.

Tables A.82.i & ii. Results of the mediation model with the predictor congener PCDD67, the mean DNA methylation of the CpGs in the promoter region of AR, and the predicted child's cognitive ability as outcome, controlling for confounders for the female and male subsample separately.

Table A.82.i. *Regressions*

	Coefficient	SE	95% CI	z	p
Child's cognitive ability ~ PCDD67 (c [female])	0.24	0.74	[-1.35, 1.56]	0.33	.74
Child's cognitive ability ~ DNAm AR (b [female])	1.28	1.69	[-4.71, 1.77]	0.76	.45
Child's cognitive ability ~ Mother's education level	0.29	0.30	[-0.33, 0.87]	0.94	.35
DNAm AR ~ PCDD67 (a [female])	-0.29	0.19	[-0.73, 0.01]	-1.52	.13
DNAm AR ~ Mother's education level	0.07	0.05	[-0.01, 0.19]	1.31	.19
Child's cognitive ability ~ PCDD67 (c [male])	0.13	0.58	[-0.97, 1.30]	0.23	.82
Child's cognitive ability ~ DNAm AR (b [male])	-0.54	0.47	[-0.97, 0.58]	-1.15	.25
Child's cognitive ability ~ Mother's education level	0.74	0.31	[0.13, 1.36]	2.36	.02
DNAm AR ~ PCDD67 (a [male])	0.10	0.15	[-0.22, 0.38]	0.63	.53
DNAm AR ~ Mother's education level	-0.08	0.07	[-0.22, 0.05]	-1.10	.27

Note. Coefficient = *Regressions* beta value, SE = standard error, CI = confidence interval, z = z-statistic, p = p-value, c = c-path, b = b-path, a = a-path.

Table A.82.ii. *Defined model parameters (effects)*

Effect	Coefficient	SE	95% CI	z	p
Indirect (female)	-0.37	0.33	[-1.13, 0.20]	-1.12	.26
Total (female)	-0.13	0.78	[-1.80, 1.28]	-0.17	.86
Indirect (male)	-0.05	0.09	[-0.21, 0.16]	-0.57	.57
Total (male)	0.08	0.57	[-1.00, 1.29]	0.14	.89
Difference in indirect (male - female)	-0.32	0.35	[-1.11, 0.26]	-0.93	.35
Difference in indirect (male - female)	-0.21	0.96	[-2.24, 1.51]	-0.22	.82

Note. Coefficient = estimated model parameter, SE = standard error, CI = confidence interval, z = z-statistic, p = p-value.

Tables A.83.i & ii. Results of the mediation model with the predictor congener PCDD70, the mean DNA methylation of the CpGs in the promoter region of AR, and the predicted child's cognitive ability as outcome, controlling for confounders for the female and male subsample separately.

Table A.83.i. *Regressions*

	Coefficient	SE	95% CI	z	p
Child's cognitive ability ~ PCDD70 (c [female])	-0.39	0.65	[-1.69, 0.87]	-0.60	.55
Child's cognitive ability ~ DNAm AR (b [female])	1.18	1.71	[-4.87, 1.65]	0.69	.49
Child's cognitive ability ~ Mother's education level	0.36	0.30	[-0.24, 0.91]	1.22	.22
DNAm AR ~ PCDD70 (a [female])	-0.25	0.18	[-0.65, 0.02]	-1.44	.15
DNAm AR ~ Mother's education level	0.05	0.04	[-0.02, 0.15]	1.21	.23
Child's cognitive ability ~ PCDD70 (c [male])	0.99	0.68	[-0.37, 2.26]	1.47	.14
Child's cognitive ability ~ DNAm AR (b [male])	-0.57	0.44	[-0.97, 0.41]	-1.29	.20
Child's cognitive ability ~ Mother's education level	0.62	0.31	[0.02, 1.24]	2.00	.05

DNAm AR ~ PCDD70 (a [male])	0.10	0.15	[-0.19, 0.39]	0.70	.48
DNAm AR ~ Mother's education level	-0.07	0.07	[-0.22, 0.05]	-1.05	.29

Note. Coefficient = *Regressions* beta value, *SE* = standard error, *CI* = confidence interval, *z* = *z*-statistic, *p* = *p*-value, *c* = *c*-path, *b* = *b*-path, *a* = *a*-path.

Table A.83.ii. *Defined model parameters (effects)*

Effect	Coefficient	<i>SE</i>	95% <i>CI</i>	<i>z</i>	<i>p</i>
Indirect (female)	-0.30	0.29	[-0.93, 0.22]	-1.04	.30
Total (female)	-0.69	0.67	[-2.03, 0.60]	-1.03	.31
Indirect (male)	-0.06	0.09	[-0.24, 0.14]	-0.63	.53
Total (male)	0.94	0.68	[-0.43, 2.23]	1.38	.17
Difference in indirect (male - female)	-0.24	0.30	[-0.90, 0.29]	-0.79	.43
Difference in indirect (male - female)	-1.62	0.95	[-3.51, 0.25]	-1.70	.09

Note. Coefficient = estimated model parameter, *SE* = standard error, *CI* = confidence interval, *z* = *z*-statistic, *p* = *p*-value.

Tables A.84.i & ii. Results of the mediation model with the predictor congener PCDD73, the mean DNA methylation of the CpGs in the promoter region of *AR*, and the predicted child's cognitive ability as outcome, controlling for confounders for the female and male subsample separately.

Table A.84.i. *Regressions*

	Coefficient	<i>SE</i>	95% <i>CI</i>	<i>z</i>	<i>p</i>
Child's cognitive ability ~ PCDD73 (c [female])	0.03	0.56	[-1.06, 1.15]	0.05	.96
Child's cognitive ability ~ DNAm AR (b [female])	1.24	1.71	[-4.89, 1.68]	0.72	.47
Child's cognitive ability ~ Mother's education level	0.32	0.32	[-0.34, 0.90]	0.99	.32
DNAm AR ~ PCDD73 (a [female])	-0.14	0.12	[-0.42, 0.04]	-1.19	.24
DNAm AR ~ Mother's education level	0.06	0.05	[-0.02, 0.18]	1.17	.24
Child's cognitive ability ~ PCDD73 (c [male])	0.49	0.48	[-0.46, 1.46]	1.02	.31
Child's cognitive ability ~ DNAm AR (b [male])	-0.57	0.46	[-1.04, 0.51]	-1.24	.21
Child's cognitive ability ~ Mother's education level	0.64	0.30	[0.06, 1.24]	2.15	.03
DNAm AR ~ PCDD73 (a [male])	0.11	0.15	[-0.18, 0.41]	0.76	.45
DNAm AR ~ Mother's education level	-0.08	0.08	[-0.27, 0.06]	-0.97	.33

Note. Coefficient = *Regressions* beta value, *SE* = standard error, *CI* = confidence interval, *z* = *z*-statistic, *p* = *p*-value, *c* = *c*-path, *b* = *b*-path, *a* = *a*-path.

Table A.84.ii. *Defined model parameters (effects)*

Effect	Coefficient	<i>SE</i>	95% <i>CI</i>	<i>z</i>	<i>p</i>
Indirect (female)	-0.17	0.19	[-0.61, 0.16]	-0.93	.36
Total (female)	-0.14	0.57	[-1.27, 0.97]	-0.25	.80
Indirect (male)	-0.07	0.11	[-0.32, 0.09]	-0.62	.54
Total (male)	0.43	0.49	[-0.53, 1.41]	0.87	.39
Difference in indirect (male - female)	-0.11	0.21	[-0.57, 0.31]	-0.50	.62
Difference in indirect (male - female)	-0.57	0.75	[-2.07, 0.91]	-0.76	.45

Note. Coefficient = estimated model parameter, *SE* = standard error, *CI* = confidence interval, *z* = *z*-statistic, *p* = *p*-value.

Tables A.85.i & ii. Results of the mediation model with the predictor congener PCDD75, the mean DNA methylation of the CpGs in the promoter region of *AR*, and the predicted child's cognitive ability as outcome, controlling for confounders for the female and male subsample separately.

Table A.85.i. *Regressions*

	Coefficient	<i>SE</i>	95% <i>CI</i>	<i>z</i>	<i>p</i>
Child's cognitive ability ~ PCDD75 (c [female])	-0.08	0.67	[-1.50, 1.16]	-0.12	.91
Child's cognitive ability ~ DNAm AR (b [female])	1.22	1.72	[-4.93, 1.74]	0.71	.48
Child's cognitive ability ~ Mother's education level	0.33	0.31	[-0.30, 0.90]	1.08	.28
DNAm AR ~ PCDD75 (a [female])	-0.30	0.19	[-0.71, 0.02]	-1.58	.12

DNAm AR ~ Mother's education level	0.07	0.05	[-0.01, 0.18]	1.33	.18
Child's cognitive ability ~ PCDD75 (c [male])	0.58	0.53	[-0.42, 1.70]	1.09	.28
Child's cognitive ability ~ DNAm AR (b [male])	-0.58	0.46	[-0.98, 0.42]	-1.27	.21
Child's cognitive ability ~ Mother's education level	0.67	0.29	[0.12, 1.27]	2.29	.02
DNAm AR ~ PCDD75 (a [male])	0.14	0.13	[-0.09, 0.42]	1.08	.28
DNAm AR ~ Mother's education level	-0.08	0.08	[-0.24, 0.06]	-1.02	.31

Note. Coefficient = *Regressions* beta value, *SE* = standard error, *CI* = confidence interval, *z* = *z*-statistic, *p* = *p*-value, c = c-path, b = b-path, a = a-path.

Table A.85.ii. *Defined model parameters (effects)*

Effect	Coefficient	<i>SE</i>	95% <i>CI</i>	<i>z</i>	<i>p</i>
Indirect (female)	-0.36	0.33	[-1.07, 0.30]	-1.08	.28
Total (female)	-0.44	0.70	[-1.92, 0.83]	-0.62	.53
Indirect (male)	-0.08	0.09	[-0.27, 0.07]	-0.90	.37
Total (male)	0.50	0.55	[-0.51, 1.67]	0.91	.36
Difference in indirect (male - female)	-0.28	0.34	[-1.03, 0.39]	-0.82	.41
Difference in indirect (male - female)	-0.94	0.89	[-2.81, 0.69]	-1.06	.29

Note. Coefficient = estimated model parameter, *SE* = standard error, *CI* = confidence interval, *z* = *z*-statistic, *p* = *p*-value.

Tables A.86.i & ii. Results of the mediation model with the predictor congener PCDF114, the mean DNA methylation of the CpGs in the promoter region of *AR*, and the predicted child's cognitive ability as outcome, controlling for confounders for the female and male subsample separately.

Table A.86.i. *Regressions*

	Coefficient	<i>SE</i>	95% <i>CI</i>	<i>z</i>	<i>p</i>
Child's cognitive ability ~ PCDF114 (c [female])	-0.57	0.68	[-1.95, 0.76]	-0.83	.41
Child's cognitive ability ~ DNAm AR (b [female])	1.14	1.68	[-4.90, 1.66]	0.68	.50
Child's cognitive ability ~ Mother's education level	0.42	0.31	[-0.19, 1.01]	1.35	.18
DNAm AR ~ PCDF114 (a [female])	-0.30	0.20	[-0.75, 0.01]	-1.53	.13
DNAm AR ~ Mother's education level	0.08	0.06	[-0.01, 0.21]	1.31	.19
Child's cognitive ability ~ PCDF114 (c [male])	0.63	0.64	[-0.65, 1.89]	0.98	.33
Child's cognitive ability ~ DNAm AR (b [male])	-0.56	0.46	[-0.96, 0.49]	-1.24	.22
Child's cognitive ability ~ Mother's education level	0.65	0.32	[0.03, 1.31]	1.99	.05
DNAm AR ~ PCDF114 (a [male])	0.12	0.20	[-0.28, 0.52]	0.63	.53
DNAm AR ~ Mother's education level	-0.08	0.06	[-0.22, 0.04]	-1.20	.23

Note. Coefficient = *Regressions* beta value, *SE* = standard error, *CI* = confidence interval, *z* = *z*-statistic, *p* = *p*-value, c = c-path, b = b-path, a = a-path.

Table A.86.ii. *Defined model parameters (effects)*

Effect	Coefficient	<i>SE</i>	95% <i>CI</i>	<i>z</i>	<i>p</i>
Indirect (female)	-0.34	0.32	[-1.04, 0.21]	-1.09	.28
Total (female)	-0.91	0.71	[-2.33, 0.47]	-1.29	.20
Indirect (male)	-0.07	0.12	[-0.30, 0.21]	-0.56	.57
Total (male)	0.56	0.65	[-0.69, 1.85]	0.87	.38
Difference in indirect (male - female)	-0.27	0.34	[-1.04, 0.31]	-0.81	.42
Difference in indirect (male - female)	-1.47	0.96	[-3.39, 0.37]	-1.54	.13

Note. Coefficient = estimated model parameter, *SE* = standard error, *CI* = confidence interval, *z* = *z*-statistic, *p* = *p*-value.

Tables A.87.i & ii. Results of the mediation model with the predictor congener PCDF118, the mean DNA methylation of the CpGs in the promoter region of *AR*, and the predicted child's cognitive ability as outcome, controlling for confounders for the female and male subsample separately.

Table A.87.i. *Regressions*

	Coefficient	<i>SE</i>	95% <i>CI</i>	<i>z</i>	<i>p</i>
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Child's cognitive ability ~ PCDF118 (c [female])	-0.56	0.78	[-2.16, 0.93]	-0.72	.47
Child's cognitive ability ~ DNAm AR (b [female])	1.15	1.77	[-5.11, 1.66]	0.65	.51
Child's cognitive ability ~ Mother's education level	0.38	0.30	[-0.22, 0.95]	1.27	.20
DNAm AR ~ PCDF118 (a [female])	-0.37	0.23	[-0.89, -0.02]	-1.61	.11
DNAm AR ~ Mother's education level	0.07	0.05	[-0.01, 0.19]	1.26	.21
Child's cognitive ability ~ PCDF118 (c [male])	1.20	0.63	[-0.08, 2.42]	1.89	.06
Child's cognitive ability ~ DNAm AR (b [male])	-0.57	0.42	[-0.95, 0.31]	-1.36	.18
Child's cognitive ability ~ Mother's education level	0.61	0.30	[0.04, 1.23]	2.01	.05
DNAm AR ~ PCDF118 (a [male])	0.09	0.21	[-0.38, 0.47]	0.41	.69
DNAm AR ~ Mother's education level	-0.07	0.06	[-0.20, 0.04]	-1.11	.27

Note. Coefficient = *Regressions* beta value, *SE* = standard error, *CI* = confidence interval, *z* = *z*-statistic, *p* = *p*-value, c = c-path, b = b-path, a = a-path.

Table A.87.ii. *Defined model parameters (effects)*

Effect	Coefficient	<i>SE</i>	95% <i>CI</i>	<i>z</i>	<i>p</i>
Indirect (female)	-0.43	0.42	[-1.28, 0.43]	-1.03	.31
Total (female)	-0.99	0.80	[-2.55, 0.59]	-1.24	.22
Indirect (male)	-0.05	0.13	[-0.28, 0.28]	-0.37	.27
Total (male)	1.15	0.64	[-0.10, 2.42]	1.78	.08
Difference in indirect (male - female)	-0.38	0.44	[-1.30, 0.50]	-0.86	.39
Difference in indirect (male - female)	-2.13	1.03	[-4.17, -0.09]	-2.07	.04

Note. Coefficient = estimated model parameter, *SE* = standard error, *CI* = confidence interval, *z* = *z*-statistic, *p* = *p*-value.

Tables A.88.i & ii. Results of the mediation model with the predictor congener PCDF121, the mean DNA methylation of the CpGs in the promoter region of *AR*, and the predicted child's cognitive ability as outcome, controlling for confounders for the female and male subsample separately.

Table A.88.i. *Regressions*

	Coefficient	<i>SE</i>	95% <i>CI</i>	<i>z</i>	<i>p</i>
Child's cognitive ability ~ PCDF121 (c [female])	-0.44	0.69	[-1.78, 0.93]	-0.65	.52
Child's cognitive ability ~ DNAm AR (b [female])	1.18	1.76	[-5.09, 1.64]	0.67	.50
Child's cognitive ability ~ Mother's education level	0.38	0.31	[-0.23, 0.96]	1.25	.21
DNAm AR ~ PCDF121 (a [female])	-0.29	0.18	[-0.72, -0.03]	-1.59	.11
DNAm AR ~ Mother's education level	0.06	0.05	[-0.01, 0.18]	1.30	.19
Child's cognitive ability ~ PCDF121 (c [male])	1.36	0.67	[0.00, 2.65]	2.03	.04
Child's cognitive ability ~ DNAm AR (b [male])	-0.60	0.43	[-1.01, 0.27]	-1.40	.16
Child's cognitive ability ~ Mother's education level	0.58	0.32	[-0.03, 1.21]	1.83	.07
DNAm AR ~ PCDF121 (a [male])	0.18	0.15	[-0.11, 0.49]	1.20	.23
DNAm AR ~ Mother's education level	-0.08	0.07	[-0.22, 0.04]	-1.20	.23

Note. Coefficient = *Regressions* beta value, *SE* = standard error, *CI* = confidence interval, *z* = *z*-statistic, *p* = *p*-value, c = c-path, b = b-path, a = a-path.

Table A.88.ii. *Defined model parameters (effects)*

Effect	Coefficient	<i>SE</i>	95% <i>CI</i>	<i>z</i>	<i>p</i>
Indirect (female)	-0.34	0.35	[-1.03, 0.42]	-0.98	.33
Total (female)	-0.78	0.69	[-2.12, 0.63]	-1.13	.26
Indirect (male)	-0.11	0.11	[-0.34, 0.12]	-0.96	.34
Total (male)	1.25	0.67	[-0.08, 2.56]	1.86	.06
Difference in indirect (male - female)	-0.23	0.36	[-0.98, 0.55]	-0.63	.53
Difference in indirect (male - female)	-2.03	0.96	[-3.90, -0.12]	-2.12	.03

Note. Coefficient = estimated model parameter, *SE* = standard error, *CI* = confidence interval, *z* = *z*-statistic, *p* = *p*-value.

Tables A.89.i & ii. Results of the mediation model with the predictor congener PCDF130, the mean DNA methylation of the CpGs in the promoter region of *AR*, and the predicted child's cognitive ability as outcome, controlling for confounders for the female and male subsample separately.

Table A.89.i. *Regressions*

	Coefficient	SE	95% CI	z	p
Child's cognitive ability ~ PCDF130 (c [female])	0.16	0.57	[-0.98, 1.27]	0.28	.78
Child's cognitive ability ~ DNAm <i>AR</i> (b [female])	1.25	1.68	[-4.84, 1.69]	0.74	.46
Child's cognitive ability ~ Mother's education level	0.29	0.33	[-0.39, 0.92]	0.86	.39
DNAm <i>AR</i> ~ PCDF130 (a [female])	-0.07	0.07	[-0.22, 0.03]	-1.10	.27
DNAm <i>AR</i> ~ Mother's education level	0.04	0.04	[-0.02, 0.14]	1.06	.29
Child's cognitive ability ~ PCDF130 (c [male])	1.09	0.73	[-0.31, 2.56]	1.49	.14
Child's cognitive ability ~ DNAm <i>AR</i> (b [male])	-0.64	0.44	[-1.13, 0.25]	-1.46	.15
Child's cognitive ability ~ Mother's education level	0.54	0.32	[-0.06, 1.21]	1.67	.10
DNAm <i>AR</i> ~ PCDF130 (a [male])	0.20	0.12	[-0.02, 0.46]	1.70	.09
DNAm <i>AR</i> ~ Mother's education level	-0.09	0.07	[-0.26, 0.02]	-1.29	.20

Note. Coefficient = *Regressions* beta value, SE = standard error, CI = confidence interval, z = z-statistic, p = p-value, c = c-path, b = b-path, a = a-path.

Table A.89.ii. *Defined model parameters (effects)*

Effect	Coefficient	SE	95% CI	z	p
Indirect (female)	-0.09	0.11	[-0.34, 0.12]	-0.82	.41
Total (female)	0.07	0.57	[-1.06, 1.17]	0.12	.90
Indirect (male)	-0.13	0.12	[-0.41, 0.04]	-1.08	.28
Total (male)	0.96	0.72	[-0.42, 2.41]	1.33	.18
Difference in indirect (male - female)	0.04	0.16	[-0.28, 0.38]	0.24	.81
Difference in indirect (male - female)	-0.89	0.92	[-2.73, 0.85]	-0.97	.33

Note. Coefficient = estimated model parameter, SE = standard error, CI = confidence interval, z = z-statistic, p = p-value.

Tables A.90.i & ii. Results of the mediation model with the predictor congener PCDF131, the mean DNA methylation of the CpGs in the promoter region of *AR*, and the predicted child's cognitive ability as outcome, controlling for confounders for the female and male subsample separately.

Table A.90.i. *Regressions*

	Coefficient	SE	95% CI	z	p
Child's cognitive ability ~ PCDF131 (c [female])	-0.21	0.50	[-0.90, 1.14]	-0.42	.68
Child's cognitive ability ~ DNAm <i>AR</i> (b [female])	1.22	1.68	[-4.77, 1.66]	0.73	.47
Child's cognitive ability ~ Mother's education level	0.35	0.31	[-0.30, 0.93]	1.10	.27
DNAm <i>AR</i> ~ PCDF131 (a [female])	-0.05	0.07	[-0.25, 0.01]	-0.75	.45
DNAm <i>AR</i> ~ Mother's education level	0.03	0.03	[-0.02, 0.11]	1.00	.32
Child's cognitive ability ~ PCDF131 (c [male])	0.55	0.41	[-0.32, 1.30]	1.33	.18
Child's cognitive ability ~ DNAm <i>AR</i> (b [male])	-0.58	0.45	[-1.01, 0.38]	-1.28	.20
Child's cognitive ability ~ Mother's education level	0.65	0.29	[0.09, 1.25]	2.22	.03
DNAm <i>AR</i> ~ PCDF131 (a [male])	0.08	0.08	[-0.07, 0.27]	1.00	.32
DNAm <i>AR</i> ~ Mother's education level	-0.07	0.07	[-0.24, 0.06]	-0.96	.34

Note. Coefficient = *Regressions* beta value, SE = standard error, CI = confidence interval, z = z-statistic, p = p-value, c = c-path, b = b-path, a = a-path.

Table A.90.ii. *Defined model parameters (effects)*

Effect	Coefficient	SE	95% CI	z	p
Indirect (female)	-0.06	0.12	[-0.36, 0.17]	-0.52	.60
Total (female)	-0.27	0.47	[-0.94, 0.97]	-0.58	.56
Indirect (male)	-0.05	0.07	[-0.20, 0.06]	-0.69	.49
Total (male)	0.50	0.41	[-0.36, 1.25]	1.21	.23
Difference in indirect (male - female)	-0.02	0.14	[-0.35, 0.25]	-0.11	.91

Difference in indirect (male - female)	-0.77	0.63	[-1.79, 0.69]	-1.23	.22
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Note. Coefficient = estimated model parameter, SE = standard error, CI = confidence interval, z = z -statistic, p = p -value.

Tables A.91.i & ii. Results of the mediation model with the predictor congener PCB126, the mean DNA methylation of the CpGs in the promoter region of *ESR1*, and the predicted child's cognitive ability as outcome, controlling for confounders.

Table A.91.i. *Regressions*

	Coefficient	SE	95% CI	z	p
Child's cognitive ability ~ PCB126 (c)	-0.28	0.42	[-1.05, 0.64]	-0.65	.51
Child's cognitive ability ~ Sex	-3.64	0.48	[-4.60, -2.73]	-7.59	<.001
Child's cognitive ability ~ PCB126:Sex (c:Sex)	0.99	0.73	[-0.54, 2.38]	1.35	.18
Child's cognitive ability ~ DNAm <i>ESR1</i> (b)	0.84	0.81	[-0.23, 3.12]	1.03	.30
Child's cognitive ability ~ Birthweight	1.49x10 ⁻⁰³	5.18x10 ⁻⁰⁴	[0.00, 0.00]	2.87	.004
Child's cognitive ability ~ Mother's education level	0.40	0.22	[-0.02, 0.85]	1.82	.07
Child's cognitive ability ~ Mother's BMI before pregnancy	-0.19	0.06	[-0.30, -0.07]	-3.29	<.001
DNAm <i>ESR1</i> ~ PCB126 (a)	-0.02	0.04	[-0.12, 0.04]	-0.55	.59
DNAm <i>ESR1</i> ~ Sex	-0.03	0.06	[-0.16, 0.07]	-0.55	.58
DNAm <i>ESR1</i> ~ PCB126:Sex (a:Sex)	-0.21	0.15	[-0.52, 0.04]	-1.40	.16
DNAm <i>ESR1</i> ~ Birthweight	-3.64x10 ⁻⁰⁵	3.71x10 ⁻⁰⁵	[0.00, 0.00]	-0.98	.33
DNAm <i>ESR1</i> ~ Mother's education level	-3.41x10 ⁻⁰³	0.02	[-0.04, 0.04]	-0.16	.87
DNAm <i>ESR1</i> ~ Mother's BMI before pregnancy	6.19x10 ⁻⁰³	5.52x10 ⁻⁰³	[0.00, 0.02]	1.12	.26

Note. Coefficient = *Regressions* beta value, SE = standard error, CI = confidence interval, z = z -statistic, p = p -value, c = c-path, b = b-path, a = a-path.

Table A.91.ii. *Defined model parameters (effects)*

Effect	Coefficient	SE	95% CI	z	p
Indirect (female)	-0.02	0.05	[-0.13, 0.06]	-0.39	.70
Total (female)	-0.30	0.42	[-1.08, 0.61]	-0.70	.48
Indirect (male)	-0.19	0.17	[-0.57, 0.08]	-1.11	.27
Total (male)	0.52	0.63	[-0.72, 1.75]	0.83	.41
Difference in indirect (male - female)	0.17	0.17	[-0.10, 0.55]	1.01	.31
Difference in indirect (male - female)	-0.82	0.72	[-2.21, 0.65]	-1.13	.26

Note. Coefficient = estimated model parameter, SE = standard error, CI = confidence interval, z = z -statistic, p = p -value.

Tables A.92.i & ii. Results of the mediation model with the predictor congener PCB169, the mean DNA methylation of the CpGs in the promoter region of *ESR1*, and the predicted child's cognitive ability as outcome, controlling for confounders.

Table A.92.i. *Regressions*

	Coefficient	SE	95% CI	z	p
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Child's cognitive ability ~ PCB169 (c)	-0.04	0.59	[-1.31, 0.99]	-	.94
Child's cognitive ability ~ Sex	-3.62	0.48	[-4.59, - 2.73]	-	<
Child's cognitive ability ~ PCB169:Sex (c:Sex)	0.68	0.72	[-0.63, 2.19]	0.95	.34
Child's cognitive ability ~ DNAm <i>ESR1</i> (b)	0.72	0.82	[-0.30, 3.10]	0.88	.38
Child's cognitive ability ~ Birthweight	1.54x10 ⁻⁰³	5.16x10 ⁻⁰⁴	[0.00, 0.00]	2.98	.003
Child's cognitive ability ~ Mother's education level	0.37	0.22	[-0.05, 0.82]	1.66	.10
Child's cognitive ability ~ Mother's BMI before pregnancy	-0.18	0.06	[-0.30, - 0.07]	-	.001
DNAm <i>ESR1</i> ~ PCB169 (a)	-0.02	0.04	[-0.10, 0.07]	-	.64
DNAm <i>ESR1</i> ~ Sex	-0.03	0.06	[-0.17, 0.07]	-	.58
DNAm <i>ESR1</i> ~ PCB169:Sex (a:Sex)	-0.05	0.09	[-0.27, 0.10]	-	.59
DNAm <i>ESR1</i> ~ Birthweight	-5.62x10 ⁻⁰⁵	3.33x10 ⁻⁰⁵	[0.00, 0.00]	-	.09
DNAm <i>ESR1</i> ~ Mother's education level	-0.02	0.02	[-0.06, 0.02]	-	.37
DNAm <i>ESR1</i> ~ Mother's BMI before pregnancy	3.88x10 ⁻⁰³	4.99x10 ⁻⁰³	[-0.01, 0.01]	0.78	.44

Note. Coefficient = *Regressions* beta value, *SE* = standard error, *CI* = confidence interval, *z* = *z*-statistic, *p* = *p*-value, c = c-path, b = b-path, a = a-path.

Table A.92.ii. *Defined model parameters (effects)*

Effect	Coefficient	<i>SE</i>	95% <i>CI</i>	<i>z</i>	<i>p</i>
Indirect (female)	-0.01	0.05	[-0.15, 0.08]	-0.26	.79
Total (female)	-0.06	0.59	[-1.33, 0.98]	-0.10	.92
Indirect (male)	-0.05	0.08	[-0.25, 0.06]	-0.66	.51
Total (male)	0.59	0.48	[-0.36, 1.54]	1.23	.22
Difference in indirect (male - female)	0.04	0.10	[-0.16, 0.27]	0.38	.71
Difference in indirect (male - female)	-0.65	0.73	[-2.15, 0.69]	-0.89	.37

Note. Coefficient = estimated model parameter, *SE* = standard error, *CI* = confidence interval, *z* = *z*-statistic, *p* = *p*-value.

Tables A.93.i & ii. Results of the mediation model with the predictor congener PCB77, the mean DNA methylation of the CpGs in the promoter region of *ESR1*, and the predicted child's cognitive ability as outcome, controlling for confounders.

Table A.93.i. *Regressions*

	Coefficient	<i>SE</i>	95% <i>CI</i>	<i>z</i>	<i>p</i>
Child's cognitive ability ~ PCB77 (c)	0.90	0.79	[-0.54, 2.57]	1.15	.25
Child's cognitive ability ~ Sex	-3.63	0.47	[-4.59, - 2.71]	-	<
Child's cognitive ability ~ PCB77:Sex (c:Sex)	-2.35	1.10	[-4.48, - 0.17]	-	.03
Child's cognitive ability ~ DNAm <i>ESR1</i> (b)	0.69	0.83	[-0.29, 3.19]	0.84	.40
Child's cognitive ability ~ Birthweight	1.49x10 ⁻⁰³	5.26x10 ⁻⁰⁴	[0.00, 0.00]	2.84	.01
Child's cognitive ability ~ Mother's education level	0.42	0.20	[0.03, 0.82]	2.07	.04

Child's cognitive ability ~ Mother's BMI before pregnancy	-0.19	0.06	[-0.30, -0.08]	-	< .001
DNAm <i>ESR1</i> ~ PCB77 (a)	-0.03	0.07	[-0.15, 0.12]	-	.62
DNAm <i>ESR1</i> ~ Sex	-0.03	0.06	[-0.16, 0.07]	-	.62
DNAm <i>ESR1</i> ~ PCB77:Sex (a:Sex)	0.07	0.11	[-0.14, 0.28]	0.64	.52
DNAm <i>ESR1</i> ~ Birthweight	-5.56x10 ⁻⁰⁵	3.22x10 ⁻⁰⁵	[0.00, 0.00]	-	.09
DNAm <i>ESR1</i> ~ Mother's education level	-0.03	0.02	[-0.07, 0.01]	-	.21
DNAm <i>ESR1</i> ~ Mother's BMI before pregnancy	4.45x10 ⁻⁰³	4.96x10 ⁻⁰³	[0.00, 0.02]	0.90	.37

Note. Coefficient = *Regressions* beta value, *SE* = standard error, *CI* = confidence interval, *z* = *z*-statistic, *p* = *p*-value, c = c-path, b = b-path, a = a-path.

Table A.93.ii. *Defined model parameters (effects)*

Effect	Coefficient	<i>SE</i>	95% <i>CI</i>	<i>z</i>	<i>p</i>
Indirect (female)	-0.02	0.08	[-0.24, 0.11]	-0.28	.78
Total (female)	0.88	0.80	[-0.58, 2.57]	1.10	.27
Indirect (male)	0.02	0.09	[-0.14, 0.24]	0.26	.80
Total (male)	-1.43	0.79	[-2.84, 0.32]	-1.80	.07
Difference in indirect (male - female)	-0.05	0.13	[-0.36, 0.15]	-0.37	.71
Difference in indirect (male - female)	2.31	1.11	[0.08, 4.46]	2.08	.04

Note. Coefficient = estimated model parameter, *SE* = standard error, *CI* = confidence interval, *z* = *z*-statistic, *p* = *p*-value.

Tables A.94.i & ii. Results of the mediation model with the predictor congener PCB81, the mean DNA methylation of the CpGs in the promoter region of *ESR1*, and the predicted child's cognitive ability as outcome, controlling for confounders.

Table A.94.i. *Regressions*

	Coefficient	<i>SE</i>	95% <i>CI</i>	<i>z</i>	<i>p</i>
Child's cognitive ability ~ PCB81 (c)	-0.24	0.36	[-0.98, 0.46]	-	.50
Child's cognitive ability ~ Sex	-3.58	0.47	[-4.54, -2.69]	-	< .001
Child's cognitive ability ~ PCB81:Sex (c:Sex)	-0.61	0.61	[-1.74, 0.62]	-	.32
Child's cognitive ability ~ DNAm <i>ESR1</i> (b)	0.51	0.85	[-0.56, 3.00]	0.60	.55
Child's cognitive ability ~ Birthweight	1.54x10 ⁻⁰³	5.19x10 ⁻⁰⁴	[0.00, 0.00]	2.98	.003
Child's cognitive ability ~ Mother's education level	0.49	0.21	[0.10, 0.91]	2.35	.02
Child's cognitive ability ~ Mother's BMI before pregnancy	-0.18	0.06	[-0.29, -0.07]	-	.002
DNAm <i>ESR1</i> ~ PCB81 (a)	-0.03	0.03	[-0.09, 0.03]	-	.34
DNAm <i>ESR1</i> ~ Sex	-0.02	0.06	[-0.15, 0.08]	-	.70
DNAm <i>ESR1</i> ~ PCB81:Sex (a:Sex)	-0.07	0.08	[-0.24, 0.07]	-	.35
DNAm <i>ESR1</i> ~ Birthweight	-5.61x10 ⁻⁰⁵	3.27x10 ⁻⁰⁵	[0.00, 0.00]	-	.09

DNAm <i>ESR1</i> ~ Mother's education level	-0.02	0.02	[-0.07, 0.02]	-	.40
				0.84	
DNAm <i>ESR1</i> ~ Mother's BMI before pregnancy	4.97x10 ⁻⁰³	4.89x10 ⁻⁰³	[0.00, 0.02]	1.02	.31

Note. Coefficient = *Regressions* beta value, *SE* = standard error, CI = confidence interval, *z* = *z*-statistic, *p* = *p*-value, c = c-path, b = b-path, a = a-path.

Table A.94.ii. *Defined model parameters (effects)*

Effect	Coefficient	<i>SE</i>	95% CI	<i>z</i>	<i>p</i>
Indirect (female)	-0.02	0.04	[-0.14, 0.04]	-0.35	.73
Total (female)	-0.26	0.36	[-1.00, 0.45]	-0.72	.47
Indirect (male)	-0.05	0.07	[-0.18, 0.10]	-0.80	.43
Total (male)	-0.91	0.49	[-1.80, 0.14]	-1.85	.06
Difference in indirect (male - female)	0.04	0.07	[-0.13, 0.15]	0.55	.58
Difference in indirect (male - female)	0.65	0.61	[-0.60, 1.77]	1.07	.29

Note. Coefficient = estimated model parameter, *SE* = standard error, CI = confidence interval, *z* = *z*-statistic, *p* = *p*-value.

Tables A.95.i & ii. Results of the mediation model with the predictor congener PCDD48, the mean DNA methylation of the CpGs in the promoter region of *ESR1*, and the predicted child's cognitive ability as outcome, controlling for confounders.

Table A.95.i. *Regressions*

	Coefficient	<i>SE</i>	95% CI	<i>z</i>	<i>p</i>
Child's cognitive ability ~ PCDD48	-0.64	0.44	[-1.49, 0.24]	-	.14
(c)				1.47	
Child's cognitive ability ~ Sex	-3.67	0.47	[-4.64, -	-	<
			2.79]	7.72	.001
Child's cognitive ability ~ PCDD48:Sex	0.95	0.62	[-0.31, 2.13]	1.53	.13
(c:Sex)					
Child's cognitive ability ~ DNAm <i>ESR1</i>	0.67	0.81	[-0.33, 3.01]	0.84	.40
(b)					
Child's cognitive ability ~ Birthweight	1.48x10 ⁻⁰³	4.92x10 ⁻⁰⁴	[0.00, 0.00]	3.01	.003
Child's cognitive ability ~ Mother's education level	0.45	0.21	[0.06, 0.88]	2.16	.03
Child's cognitive ability ~ Mother's BMI before pregnancy	-0.19	0.06	[-0.30, -	-	<
			0.08]	3.31	.001
DNAm <i>ESR1</i> ~ PCDD48	-0.03	0.04	[-0.09, 0.05]	-	.46
(a)				0.74	
DNAm <i>ESR1</i> ~ Sex	-0.04	0.06	[-0.17, 0.07]	-	.57
				0.57	
DNAm <i>ESR1</i> ~ PCDD48:Sex	-0.07	0.10	[-0.30, 0.09]	-	.47
(a:Sex)				0.72	
DNAm <i>ESR1</i> ~ Birthweight	-5.88x10 ⁻⁰⁵	3.36x10 ⁻⁰⁵	[0.00, 0.00]	-	.08
				1.75	
DNAm <i>ESR1</i> ~ Mother's education level	-0.02	0.02	[-0.06, 0.02]	-	.37
				0.89	
DNAm <i>ESR1</i> ~ Mother's BMI before pregnancy	5.57x10 ⁻⁰³	5.55x10 ⁻⁰³	[0.00, 0.02]	1.00	.32

Note. Coefficient = *Regressions* beta value, *SE* = standard error, CI = confidence interval, *z* = *z*-statistic, *p* = *p*-value, c = c-path, b = b-path, a = a-path.

Table A.95.ii. *Defined model parameters (effects)*

Effect	Coefficient	<i>SE</i>	95% CI	<i>z</i>	<i>p</i>
Indirect (female)	-0.02	0.05	[-0.14, 0.05]	-0.38	.70
Total (female)	-0.66	0.44	[-1.49, 0.22]	-1.52	.13

Indirect (male)	-0.07	0.09	[-0.26, 0.10]	-0.76	.45
Total (male)	0.24	0.46	[-0.69, 1.14]	0.53	.60
Difference in indirect (male - female)	0.05	0.10	[-0.20, 0.25]	0.47	.64
Difference in indirect (male - female)	-0.90	0.62	[-2.09, 0.35]	-1.45	.15

Note. Coefficient = estimated model parameter, *SE* = standard error, CI = confidence interval, *z* = *z*-statistic, *p* = *p*-value.

Tables A.96.i & ii. Results of the mediation model with the predictor congener PCDD54, the mean DNA methylation of the CpGs in the promoter region of *ESR1*, and the predicted child's cognitive ability as outcome, controlling for confounders.

Table A.96.i. *Regressions*

	Coefficient	<i>SE</i>	95% CI	<i>z</i>	<i>p</i>
Child's cognitive ability ~ PCDD54	-0.56	0.72	[-2.00, 0.81]	-	.44
(c)				0.77	
Child's cognitive ability ~ Sex	-3.62	0.48	[-4.61, -2.68]	-	<
				7.48	.001
Child's cognitive ability ~ PCDD54:Sex	1.47	0.90	[-0.22, 3.28]	1.63	.10
(c:Sex)					
Child's cognitive ability ~ DNAm <i>ESR1</i>	0.74	0.82	[-0.28, 3.13]	0.90	.37
(b)					
Child's cognitive ability ~ Birthweight	1.50x10 ⁻⁰³	5.11x10 ⁻⁰⁴	[0.00, 0.00]	2.93	.003
Child's cognitive ability ~ Mother's education level	0.40	0.21	[-0.01, 0.83]	1.88	.06
Child's cognitive ability ~ Mother's BMI before pregnancy	-0.19	0.06	[-0.30, -0.08]	-	<
				3.53	.001
DNAm <i>ESR1</i> ~ PCDD54	1.84x10 ⁻⁰³	0.05	[-0.10, 0.11]	0.03	.97
(a)					
DNAm <i>ESR1</i> ~ Sex	-0.04	0.06	[-0.18, 0.07]	-	.57
				0.57	
DNAm <i>ESR1</i> ~ PCDD54:Sex	-0.09	0.12	[-0.38, 0.10]	-	.45
(a:Sex)				0.75	
DNAm <i>ESR1</i> ~ Birthweight	-5.55x10 ⁻⁰⁵	3.37x10 ⁻⁰⁵	[0.00, 0.00]	-	.10
				1.65	
DNAm <i>ESR1</i> ~ Mother's education level	-0.02	0.02	[-0.06, 0.02]	-	.29
				1.05	
DNAm <i>ESR1</i> ~ Mother's BMI before pregnancy	5.03x10 ⁻⁰³	5.17x10 ⁻⁰³	[0.00, 0.02]	0.97	.33

Note. Coefficient = *Regressions* beta value, *SE* = standard error, CI = confidence interval, *z* = *z*-statistic, *p* = *p*-value, c = c-path, b = b-path, a = a-path.

Table A.96.ii. *Defined model parameters (effects)*

Effect	Coefficient	<i>SE</i>	95% CI	<i>z</i>	<i>p</i>
Indirect (female)	1.36x10 ⁻⁰³	0.06	[-0.14, 0.13]	0.02	.98
Total (female)	-0.56	0.72	[-2.00, 0.83]	-0.77	.44
Indirect (male)	-0.07	0.11	[-0.33, 0.10]	-0.63	.53
Total (male)	0.84	0.54	[-0.24, 1.87]	1.57	.12
Difference in indirect (male - female)	0.07	0.13	[-0.17, 0.38]	0.52	.60
Difference in indirect (male - female)	-1.40	0.91	[-3.24, 0.34]	-1.54	.12

Note. Coefficient = estimated model parameter, *SE* = standard error, CI = confidence interval, *z* = *z*-statistic, *p* = *p*-value.

Tables A.97.i & ii. Results of the mediation model with the predictor congener PCDD66, the mean DNA methylation of the CpGs in the promoter region of *ESR1*, and the predicted child's cognitive ability as outcome, controlling for confounders.

Table A.97.i. *Regressions*

	Coefficient	SE	95% CI	z	p
Child's cognitive ability ~ PCDD66 (c)	-0.22	0.66	[-1.55, 1.08]	-0.34	.74
Child's cognitive ability ~ Sex	-3.61	0.48	[-4.60, -2.70]	-7.50	<.001
Child's cognitive ability ~ PCDD66:Sex (c:Sex)	1.31	0.83	[-0.26, 2.97]	1.57	0.12
Child's cognitive ability ~ DNAm <i>ESR1</i> (b)	0.82	0.81	[-0.19, 3.20]	1.02	.31
Child's cognitive ability ~ Birthweight	1.51x10 ⁻⁰³	5.06x10 ⁻⁰⁴	[0.00, 0.00]	2.98	.003
Child's cognitive ability ~ Mother's education level	0.34	0.21	[-0.06, 0.78]	1.60	.11
Child's cognitive ability ~ Mother's BMI before pregnancy	-0.19	0.05	[-0.30, -0.08]	-3.51	<.001
DNAm <i>ESR1</i> ~ PCDD66 (a)	-0.05	0.05	[-0.15, 0.07]	-0.90	.37
DNAm <i>ESR1</i> ~ Sex	-0.04	0.06	[-0.17, 0.07]	-0.62	.53
DNAm <i>ESR1</i> ~ PCDD66:Sex (a:Sex)	-0.08	0.11	[-0.33, 0.10]	-0.73	.47
DNAm <i>ESR1</i> ~ Birthweight	-5.53x10 ⁻⁰⁵	3.46x10 ⁻⁰⁵	[0.00, 0.00]	-1.60	.11
DNAm <i>ESR1</i> ~ Mother's education level	-0.01	0.02	[-0.05, 0.03]	-0.47	.64
DNAm <i>ESR1</i> ~ Mother's BMI before pregnancy	5.21x10 ⁻⁰³	5.21x10 ⁻⁰³	[0.00, 0.02]	1.00	.32

Note. Coefficient = *Regressions* beta value, SE = standard error, CI = confidence interval, z = z-statistic, p = p-value, c = c-path, b = b-path, a = a-path.

Table A.97.ii. *Defined model parameters (effects)*

Effect	Coefficient	SE	95% CI	z	p
Indirect (female)	-0.04	0.08	[-0.23, 0.08]	-0.54	.59
Total (female)	-0.26	0.67	[-1.59, 1.06]	-0.39	.69
Indirect (male)	-0.11	0.11	[-0.36, 0.06]	-1.01	.31
Total (male)	0.98	0.55	[-0.06, 2.11]	1.78	.08
Difference in indirect (male - female)	0.07	0.13	[-0.21, 0.35]	0.52	.60
Difference in indirect (male - female)	-1.24	0.83	[-2.89, 0.34]	-1.49	.14

Note. Coefficient = estimated model parameter, SE = standard error, CI = confidence interval, z = z-statistic, p = p-value.

Tables A.98.i & ii. Results of the mediation model with the predictor congener PCDD67, the mean DNA methylation of the CpGs in the promoter region of *ESR1*, and the predicted child's cognitive ability as outcome, controlling for confounders.

Table A.98.i. *Regressions*

	Coefficient	SE	95% CI	z	p
Child's cognitive ability ~ PCDD67 (c)	-0.32	0.76	[-2.02, 0.95]	-0.43	.67
Child's cognitive ability ~ Sex	-3.65	0.48	[-4.66, -2.75]	-7.57	<.001

Child's cognitive ability ~ PCDD67:Sex (c:Sex)	0.70	0.90	[-0.86, 2.68]	0.78	.44
Child's cognitive ability ~ DNAm <i>ESR1</i> (b)	0.69	0.84	[-0.33, 3.11]	0.83	.41
Child's cognitive ability ~ Birthweight	1.52x10 ⁻⁰³	5.07x10 ⁻⁰⁴	[0.00, 0.00]	3.00	.003
Child's cognitive ability ~ Mother's education level	0.42	0.22	[0.00, 0.84]	1.94	.05
Child's cognitive ability ~ Mother's BMI before pregnancy	-0.19	0.06	[-0.30, -0.08]	-	<
DNAm <i>ESR1</i> ~ PCDD67 (a)	-0.03	0.05	[-0.14, 0.07]	-	.52
DNAm <i>ESR1</i> ~ Sex	-0.04	0.06	[-0.17, 0.07]	-	.55
DNAm <i>ESR1</i> ~ PCDD67:Sex (a:Sex)	-0.06	0.10	[-0.29, 0.10]	-	.53
DNAm <i>ESR1</i> ~ Birthweight	-5.97x10 ⁻⁰⁵	3.39x10 ⁻⁰⁵	[0.00, 0.00]	-	.08
DNAm <i>ESR1</i> ~ Mother's education level	-0.02	0.02	[-0.06, 0.02]	-	.44
DNAm <i>ESR1</i> ~ Mother's BMI before pregnancy	4.37x10 ⁻⁰³	5.10x10 ⁻⁰³	[0.00, 0.02]	0.86	.39

Note. Coefficient = Regressions beta value, SE = standard error, CI = confidence interval, z = z-statistic, p = p-value, c = c-path, b = b-path, a = a-path.

Table A.98.ii. *Defined model parameters (effects)*

Effect	Coefficient	SE	95% CI	z	p
Indirect (female)	-0.02	0.07	[-0.21, 0.07]	-0.34	.74
Total (female)	-0.35	0.76	[-2.05, 0.93]	-0.45	.65
Indirect (male)	-0.07	0.08	[-0.26, 0.05]	-0.87	.39
Total (male)	0.31	0.52	[-0.65, 1.40]	0.60	.55
Difference in indirect (male - female)	0.04	0.10	[-0.18, 0.26]	0.43	.67
Difference in indirect (male - female)	-0.65	0.90	[-2.63, 0.91]	-0.72	.47

Note. Coefficient = estimated model parameter, SE = standard error, CI = confidence interval, z = z-statistic, p = p-value.

Tables A.99.i & ii. Results of the mediation model with the predictor congener PCDD70, the mean DNA methylation of the CpGs in the promoter region of *ESR1*, and the predicted child's cognitive ability as outcome, controlling for confounders.

Table A.99.i. *Regressions*

	Coefficient	SE	95% CI	z	p
Child's cognitive ability ~ PCDD70 (c)	-0.37	0.65	[-1.71, 0.87]	-	.57
Child's cognitive ability ~ Sex	-3.61	0.48	[-4.59, -2.70]	-	<
Child's cognitive ability ~ PCDD70:Sex (c:Sex)	1.58	0.89	[-0.15, 3.36]	1.78	.08
Child's cognitive ability ~ DNAm <i>ESR1</i> (b)	0.80	0.78	[-0.19, 3.02]	1.03	.30
Child's cognitive ability ~ Birthweight	1.46x10 ⁻⁰³	5.22x10 ⁻⁰⁴	[0.00, 0.00]	2.79	.01
Child's cognitive ability ~ Mother's education level	0.37	0.21	[-0.02, 0.80]	1.78	.08
Child's cognitive ability ~ Mother's BMI before pregnancy	-0.19	0.06	[-0.30, -0.08]	-	<
DNAm <i>ESR1</i> ~ PCDD70 (a)	-0.04	0.05	[-0.14, 0.06]	-	.40

DNAm <i>ESR1</i> ~ Sex	-0.04	0.06	[-0.18, 0.07]	-	.53
				0.62	
DNAm <i>ESR1</i> ~ PCDD70:Sex (a:Sex)	-0.10	0.13	[-0.39, 0.12]	-	.44
				0.77	
DNAm <i>ESR1</i> ~ Birthweight	-5.74x10 ⁻⁰⁵	3.53x10 ⁻⁰⁵	[0.00, 0.00]	-	.10
				1.62	
DNAm <i>ESR1</i> ~ Mother's education level	-0.02	0.02	[-0.06, 0.03]	-	.49
				0.69	
DNAm <i>ESR1</i> ~ Mother's BMI before pregnancy	5.24x10 ⁻⁰³	5.13x10 ⁻⁰³	[0.00, 0.02]	1.02	.31

Note. Coefficient = *Regressions* beta value, *SE* = standard error, CI = confidence interval, *z* = *z*-statistic, *p* = *p*-value, c = c-path, b = b-path, a = a-path.

Table A.99.ii. *Defined model parameters (effects)*

Effect	Coefficient	<i>SE</i>	95% CI	<i>z</i>	<i>p</i>
Indirect (female)	-0.03	0.07	[-0.22, 0.06]	-0.47	.64
Total (female)	-0.40	0.65	[-1.75, 0.84]	-0.62	.54
Indirect (male)	-0.11	0.11	[-0.33, 0.11]	-1.07	.28
Total (male)	1.10	0.61	[-0.14, 2.24]	1.80	.07
Difference in indirect (male - female)	0.08	0.13	[-0.25, 0.31]	0.60	.55
Difference in indirect (male - female)	-1.50	0.89	[-3.30, 0.21]	-1.69	.09

Note. Coefficient = estimated model parameter, *SE* = standard error, CI = confidence interval, *z* = *z*-statistic, *p* = *p*-value.

Tables A.100.i & ii. Results of the mediation model with the predictor congener PCDD73, the mean DNA methylation of the CpGs in the promoter region of *ESR1*, and the predicted child's cognitive ability as outcome, controlling for confounders.

Table A.100.i. *Regressions*

	Coefficient	<i>SE</i>	95% CI	<i>z</i>	<i>p</i>
Child's cognitive ability ~ PCDD73 (c)	0.01	0.51	[-1.01, 1.02]	0.02	.98
Child's cognitive ability ~ Sex	-3.60	0.48	[-4.57, -2.69]	-7.53	<.001
Child's cognitive ability ~ PCDD73:Sex (c:Sex)	0.70	0.67	[-0.63, 2.06]	1.04	.30
Child's cognitive ability ~ DNAm <i>ESR1</i> (b)	0.87	0.79	[-0.12, 3.22]	1.10	.27
Child's cognitive ability ~ Birthweight	1.50x10 ⁻⁰³	5.16x10 ⁻⁰⁴	[0.00, 0.00]	2.90	.004
Child's cognitive ability ~ Mother's education level	0.35	0.22	[-0.06, 0.79]	1.64	.10
Child's cognitive ability ~ Mother's BMI before pregnancy	-0.19	0.06	[-0.30, -0.08]	-3.42	<.001
DNAm <i>ESR1</i> ~ PCDD73 (a)	-0.07	0.05	[-0.16, 0.02]	-1.57	.12
DNAm <i>ESR1</i> ~ Sex	-0.04	0.06	[-0.18, 0.07]	-0.69	.49
				0.98	
DNAm <i>ESR1</i> ~ PCDD73:Sex (a:Sex)	-0.11	0.12	[-0.37, 0.08]	-	.33
				0.98	
DNAm <i>ESR1</i> ~ Birthweight	-4.38x10 ⁻⁰⁵	3.35x10 ⁻⁰⁵	[0.00, 0.00]	-	.19
				1.31	
DNAm <i>ESR1</i> ~ Mother's education level	6.01x10 ⁻⁰⁴	0.03	[-0.05, 0.05]	0.02	.98
DNAm <i>ESR1</i> ~ Mother's BMI before pregnancy	6.38x10 ⁻⁰³	5.47x10 ⁻⁰³	[0.00, 0.02]	1.17	.24

Note. Coefficient = *Regressions* beta value, *SE* = standard error, CI = confidence interval, *z* = *z*-statistic, *p* = *p*-value, c = c-path, b = b-path, a = a-path.

Table A.100.ii. *Defined model parameters (effects)*

Effect	Coefficient	SE	95% CI	z	p
Indirect (female)	-0.06	0.07	[-0.25, 0.03]	-0.87	.38
Total (female)	-0.05	0.51	[-1.07, 0.94]	-0.10	.92
Indirect (male)	-0.16	0.11	[-0.39, 0.06]	-1.42	.16
Total (male)	0.55	0.46	[-0.34, 1.47]	1.20	.23
Difference in indirect (male - female)	0.10	0.13	[-0.20, 0.33]	0.79	.43
Difference in indirect (male - female)	-0.60	0.66	[-1.93, 0.67]	-0.91	.36

Note. Coefficient = estimated model parameter, SE = standard error, CI = confidence interval, z = z-statistic, p = p-value.

Tables A.101.i & ii. Results of the mediation model with the predictor congener PCDD75, the mean DNA methylation of the CpGs in the promoter region of *ESR1*, and the predicted child's cognitive ability as outcome, controlling for confounders.

Table A.101.i. *Regressions*

	Coefficient	SE	95% CI	z	p
Child's cognitive ability ~ PCDD75	-0.51	0.67	[-1.94, 0.70]	-	.45
(c)				0.75	
Child's cognitive ability ~ Sex	-3.64	0.47	[-4.61, -2.76]	-7.69	<.001
Child's cognitive ability ~ PCDD75:Sex (c:Sex)	1.29	0.85	[-0.26, 3.06]	1.51	.13
Child's cognitive ability ~ DNAm <i>ESR1</i> (b)	0.79	0.81	[-0.27, 3.09]	0.97	.33
Child's cognitive ability ~ Birthweight	1.54x10 ⁻⁰³	5.02x10 ⁻⁰⁴	[0.00, 0.00]	3.08	.002
Child's cognitive ability ~ Mother's education level	0.41	0.20	[0.02, 0.82]	2.02	.04
Child's cognitive ability ~ Mother's BMI before pregnancy	-0.19	0.06	[-0.30, -0.08]	-3.29	.001
DNAm <i>ESR1</i> ~ PCDD75 (a)	-0.07	0.04	[-0.16, 0.01]	-1.65	.10
DNAm <i>ESR1</i> ~ Sex	-0.03	0.06	[-0.16, 0.07]	-0.57	.57
DNAm <i>ESR1</i> ~ PCDD75:Sex (a:Sex)	-0.10	0.13	[-0.40, 0.11]	-0.73	.47
DNAm <i>ESR1</i> ~ Birthweight	-5.80x10 ⁻⁰⁵	3.38x10 ⁻⁰⁵	[0.00, 0.00]	-1.71	.09
DNAm <i>ESR1</i> ~ Mother's education level	-0.01	0.02	[-0.05, 0.03]	-0.51	.61
DNAm <i>ESR1</i> ~ Mother's BMI before pregnancy	4.51x10 ⁻⁰³	5.06x10 ⁻⁰³	[0.00, 0.02]	0.89	.37

Note. Coefficient = *Regressions* beta value, SE = standard error, CI = confidence interval, z = z-statistic, p = p-value, c = c-path, b = b-path, a = a-path.

Table A.101.ii. *Defined model parameters (effects)*

Effect	Coefficient	SE	95% CI	z	p
Indirect (female)	-0.06	0.08	[-0.29, 0.03]	-0.70	.48
Total (female)	-0.57	0.67	[-2.01, 0.64]	-0.84	.40
Indirect (male)	-0.13	0.14	[-0.48, 0.05]	-0.96	.34
Total (male)	0.64	0.51	[-0.33, 1.72]	1.25	.21
Difference in indirect (male - female)	0.08	0.15	[-0.24, 0.40]	0.51	.61
Difference in indirect (male - female)	-1.21	0.85	[-3.01, 0.34]	-1.42	.16

Note. Coefficient = estimated model parameter, SE = standard error, CI = confidence interval, z = z-statistic, p = p-value.

Tables A.102.i & ii. Results of the mediation model with the predictor congener PCDF114, the mean DNA methylation of the CpGs in the promoter region of *ESR1*, and the predicted child's cognitive ability as outcome, controlling for confounders.

Table A.102.i. *Regressions*

	Coefficient	SE	95% CI	z	p
Child's cognitive ability ~ PCDF114 (c)	-1.13	0.66	[-2.43, 0.17]	-1.72	.09
Child's cognitive ability ~ Sex	-3.66	0.47	[-4.62, -2.75]	-7.70	<.001
Child's cognitive ability ~ PCDF114:Sex (c:Sex)	2.01	0.85	[0.42, 3.73]	2.36	.02
Child's cognitive ability ~ DNAm <i>ESR1</i> (b)	0.73	0.83	[-0.33, 3.09]	0.88	.38
Child's cognitive ability ~ Birthweight	1.54x10 ⁻⁰³	4.98x10 ⁻⁰⁴	[0.00, 0.00]	3.09	.002
Child's cognitive ability ~ Mother's education level	0.45	0.22	[0.05, 0.91]	2.06	.04
Child's cognitive ability ~ Mother's BMI before pregnancy	-0.20	0.05	[-0.30, -0.09]	-3.73	<.001
DNAm <i>ESR1</i> ~ PCDF114 (a)	-0.04	0.05	[-0.14, 0.07]	-0.79	.43
DNAm <i>ESR1</i> ~ Sex	-0.04	0.06	[-0.18, 0.07]	-0.62	.54
DNAm <i>ESR1</i> ~ PCDF114:Sex (a:Sex)	-0.09	0.13	[-0.40, 0.12]	-0.67	.50
DNAm <i>ESR1</i> ~ Birthweight	-5.83x10 ⁻⁰⁵	3.44x10 ⁻⁰⁵	[0.00, 0.00]	-1.70	.09
DNAm <i>ESR1</i> ~ Mother's education level	-0.01	0.02	[-0.05, 0.02]	-0.68	.50
DNAm <i>ESR1</i> ~ Mother's BMI before pregnancy	4.65x10 ⁻⁰³	5.21x10 ⁻⁰³	[0.00, 0.02]	0.89	.37

Note. Coefficient = *Regressions* beta value, SE = standard error, CI = confidence interval, z = z-statistic, p = p-value, c = c-path, b = b-path, a = a-path.

Table A.102.ii. *Defined model parameters (effects)*

Effect	Coefficient	SE	95% CI	z	p
Indirect (female)	-0.03	0.08	[-0.23, 0.08]	-0.41	.68
Total (female)	-1.16	0.65	[-2.44, 0.13]	-1.78	.08
Indirect (male)	-0.10	0.13	[-0.44, 0.05]	-0.74	.46
Total (male)	0.78	0.59	[-0.37, 1.95]	1.33	.18
Difference in indirect (male - female)	0.07	0.15	[-0.19, 0.43]	0.44	.66
Difference in indirect (male - female)	-1.94	0.85	[-3.65, -0.34]	-2.28	.02

Note. Coefficient = estimated model parameter, SE = standard error, CI = confidence interval, z = z-statistic, p = p-value.

Tables A.103.i & ii. Results of the mediation model with the predictor congener PCDF118, the mean DNA methylation of the CpGs in the promoter region of *ESR1*, and the predicted child's cognitive ability as outcome, controlling for confounders.

Table A.103.i. *Regressions*

	Coefficient	SE	95% CI	z	p
Child's cognitive ability ~ PCDF118 (c)	-0.88	0.72	[-2.28, 0.58]	-1.22	.22
Child's cognitive ability ~ Sex	-3.61	0.48	[-4.59, -2.72]	-7.57	<.001

Child's cognitive ability ~ PCDF118:Sex (c:Sex)	2.44	0.91	[0.63, 4.20]	2.67	.01
Child's cognitive ability ~ DNAm <i>ESRI</i> (b)	0.83	0.80	[-0.19, 3.12]	1.03	.30
Child's cognitive ability ~ Birthweight	1.53x10 ⁻⁰³	5.00x10 ⁻⁰⁴	[0.00, 0.00]	3.07	.002
Child's cognitive ability ~ Mother's education level	0.39	0.21	[0.00, 0.81]	1.88	.06
Child's cognitive ability ~ Mother's BMI before pregnancy	-0.19	0.05	[-0.30, -0.08]	-	<
DNAm <i>ESRI</i> ~ PCDF118 (a)	-0.06	0.06	[-0.17, 0.07]	-	.33
DNAm <i>ESRI</i> ~ Sex	-0.04	0.06	[-0.18, 0.07]	-	.53
DNAm <i>ESRI</i> ~ PCDF118:Sex (a:Sex)	-0.12	0.15	[-0.46, 0.12]	-	.42
DNAm <i>ESRI</i> ~ Birthweight	-5.86x10 ⁻⁰⁵	3.51x10 ⁻⁰⁵	[0.00, 0.00]	-	.10
DNAm <i>ESRI</i> ~ Mother's education level	-0.01	0.02	[-0.05, 0.03]	-	.48
DNAm <i>ESRI</i> ~ Mother's BMI before pregnancy	5.14x10 ⁻⁰³	5.22x10 ⁻⁰³	[0.00, 0.02]	0.99	.33

Note. Coefficient = Regressions beta value, SE = standard error, CI = confidence interval, z = z-statistic, p = p-value, c = c-path, b = b-path, a = a-path.

Table A.103.ii. Defined model parameters (effects)

Effect	Coefficient	SE	95% CI	z	p
Indirect (female)	-0.05	0.09	[-0.28, 0.08]	-0.55	.59
Total (female)	-0.93	0.72	[-2.31, 0.50]	-1.30	.19
Indirect (male)	-0.15	0.15	[-0.51, 0.07]	-1.00	.32
Total (male)	1.40	0.58	[0.22, 2.53]	2.41	.02
Difference in indirect (male - female)	0.10	0.17	[-0.24, 0.47]	0.58	.56
Difference in indirect (male - female)	-2.34	0.91	[-4.10, -0.56]	-2.57	.01

Note. Coefficient = estimated model parameter, SE = standard error, CI = confidence interval, z = z-statistic, p = p-value.

Tables A.104.i & ii. Results of the mediation model with the predictor congener PCDF121, the mean DNA methylation of the CpGs in the promoter region of *ESRI*, and the predicted child's cognitive ability as outcome, controlling for confounders.

Table A.104.i. Regressions

	Coefficient	SE	95% CI	z	p
Child's cognitive ability ~ PCDF121 (c)	-0.85	0.65	[-2.12, 0.43]	-	.19
Child's cognitive ability ~ Sex	-3.59	0.47	[-4.54, -2.70]	-	<
Child's cognitive ability ~ PCDF121:Sex (c:Sex)	2.49	0.86	[0.81, 4.17]	2.90	.004
Child's cognitive ability ~ DNAm <i>ESRI</i> (b)	0.81	0.78	[-0.19, 3.05]	1.04	.30
Child's cognitive ability ~ Birthweight	1.53x10 ⁻⁰³	4.98x10 ⁻⁰⁴	[0.00, 0.00]	3.08	.002
Child's cognitive ability ~ Mother's education level	0.39	0.21	[-0.01, 0.82]	1.83	.07
Child's cognitive ability ~ Mother's BMI before pregnancy	-0.20	0.06	[-0.30, -0.09]	-	<
DNAm <i>ESRI</i> ~ PCDF121 (a)	-0.04	0.06	[-0.14, 0.09]	-	.48

DNAm <i>ESR1</i> ~ Sex	-0.04	0.07	[-0.19, 0.07]	-	.52
				0.64	
DNAm <i>ESR1</i> ~ PCDF121:Sex (a:Sex)	-0.12	0.14	[-0.45, 0.11]	-	.41
				0.82	
DNAm <i>ESR1</i> ~ Birthweight	-5.82x10 ⁻⁰⁵	3.47x10 ⁻⁰⁵	[0.00, 0.00]	-	.09
				1.67	
DNAm <i>ESR1</i> ~ Mother's education level	-0.02	0.02	[-0.06, 0.03]	-	.46
				0.75	
DNAm <i>ESR1</i> ~ Mother's BMI before pregnancy	4.84x10 ⁻⁰³	5.15x10 ⁻⁰³	[0.00, 0.02]	0.94	.35

Note. Coefficient = *Regressions* beta value, *SE* = standard error, *CI* = confidence interval, *z* = *z*-statistic, *p* = *p*-value, c = c-path, b = b-path, a = a-path.

Table A.104.ii. *Defined model parameters (effects)*

Effect	Coefficient	<i>SE</i>	95% <i>CI</i>	<i>z</i>	<i>p</i>
Indirect (female)	-0.03	0.08	[-0.23, 0.10]	-0.43	.67
Total (female)	-0.89	0.64	[-2.13, 0.40]	-1.38	.17
Indirect (male)	-0.13	0.14	[-0.46, 0.07]	-0.93	.35
Total (male)	1.51	0.59	[0.33, 2.64]	2.58	.01
Difference in indirect (male - female)	0.10	0.16	[-0.21, 0.47]	0.59	.55
Difference in indirect (male - female)	-2.40	0.86	[-4.07, -0.70]	-2.78	.01

Note. Coefficient = estimated model parameter, *SE* = standard error, *CI* = confidence interval, *z* = *z*-statistic, *p* = *p*-value.

Tables A.105.i & ii. Results of the mediation model with the predictor congener PCDF130, the mean DNA methylation of the CpGs in the promoter region of *ESR1*, and the predicted child's cognitive ability as outcome, controlling for confounders.

Table A.105.i. *Regressions*

	Coefficient	<i>SE</i>	95% <i>CI</i>	<i>z</i>	<i>p</i>
Child's cognitive ability ~ PCDF130 (c)	0.03	0.52	[-0.99, 1.03]	0.05	.96
Child's cognitive ability ~ Sex	-3.61	0.47	[-4.58, -2.72]	-7.61	<.001
Child's cognitive ability ~ PCDF130:Sex (c:Sex)	1.12	0.77	[-0.35, 2.66]	1.45	.15
Child's cognitive ability ~ DNAm <i>ESR1</i> (b)	0.81	0.80	[-0.10, 3.28]	1.02	.31
Child's cognitive ability ~ Birthweight	1.48x10 ⁻⁰³	5.14x10 ⁻⁰⁴	[0.00, 0.00]	2.89	.004
Child's cognitive ability ~ Mother's education level	0.32	0.23	[-0.10, 0.78]	1.43	.15
Child's cognitive ability ~ Mother's BMI before pregnancy	-0.19	0.06	[-0.30, -0.08]	-3.38	<.001
DNAm <i>ESR1</i> ~ PCDF130 (a)	0.04	0.05	[-0.06, 0.12]	0.78	.44
DNAm <i>ESR1</i> ~ Sex	-0.03	0.06	[-0.17, 0.07]	-	.61
				0.52	
DNAm <i>ESR1</i> ~ PCDF130:Sex (a:Sex)	-0.15	0.10	[-0.38, 0.01]	-	.12
				1.56	
DNAm <i>ESR1</i> ~ Birthweight	-5.04x10 ⁻⁰⁵	3.34x10 ⁻⁰⁵	[0.00, 0.00]	-	.13
				1.51	
DNAm <i>ESR1</i> ~ Mother's education level	-0.02	0.02	[-0.07, 0.03]	-	.37
				0.89	
DNAm <i>ESR1</i> ~ Mother's BMI before pregnancy	4.53x10 ⁻⁰³	5.12x10 ⁻⁰³	[0.00, 0.02]	0.88	.38

Note. Coefficient = *Regressions* beta value, *SE* = standard error, *CI* = confidence interval, *z* = *z*-statistic, *p* = *p*-value, *c* = *c*-path, *b* = *b*-path, *a* = *a*-path.

Table A.105.ii. *Defined model parameters (effects)*

Effect	Coefficient	SE	95% CI	<i>z</i>	<i>p</i>
Indirect (female)	0.03	0.06	[-0.05, 0.20]	0.45	.66
Total (female)	0.06	0.52	[-0.97, 1.09]	0.11	.92
Indirect (male)	-0.10	0.07	[-0.24, 0.07]	-1.28	.20
Total (male)	1.05	0.65	[-0.20, 2.34]	1.61	.11
Difference in indirect (male - female)	0.12	0.10	[-0.05, 0.34]	1.26	.21
Difference in indirect (male - female)	-0.99	0.78	[-2.54, 0.50]	-1.28	.20

Note. Coefficient = estimated model parameter, *SE* = standard error, *CI* = confidence interval, *z* = *z*-statistic, *p* = *p*-value.

Tables A.106.i & ii. Results of the mediation model with the predictor congener PCDF131, the mean DNA methylation of the CpGs in the promoter region of *ESR1*, and the predicted child's cognitive ability as outcome, controlling for confounders.

Table A.106.i. *Regressions*

	Coefficient	SE	95% CI	<i>z</i>	<i>p</i>
Child's cognitive ability ~ PCDF131 (c)	-0.51	0.45	[-1.13, 0.64]	- 1.12	.26
Child's cognitive ability ~ Sex	-3.65	0.47	[-4.61, - 2.74]	- 7.69	< .001
Child's cognitive ability ~ PCDF131:Sex (c:Sex)	1.04	0.58	[-0.33, 1.95]	1.79	.07
Child's cognitive ability ~ DNAm <i>ESR1</i> (b)	0.81	0.84	[-0.34, 3.05]	0.96	.34
Child's cognitive ability ~ Birthweight	1.56x10 ⁻⁰³	5.14x10 ⁻⁰⁴	[0.00, 0.00]	3.04	.002
Child's cognitive ability ~ Mother's education level	0.41	0.21	[0.02, 0.84]	1.95	.05
Child's cognitive ability ~ Mother's BMI before pregnancy	-0.18	0.06	[-0.30, - 0.07]	- 3.24	.001
DNAm <i>ESR1</i> ~ PCDF131 (a)	-0.02	0.03	[-0.08, 0.05]	- 0.76	.45
DNAm <i>ESR1</i> ~ Sex	-0.03	0.06	[-0.15, 0.08]	- 0.48	.63
DNAm <i>ESR1</i> ~ PCDF131:Sex (a:Sex)	-0.13	0.14	[-0.42, 0.08]	- 0.89	.37
DNAm <i>ESR1</i> ~ Birthweight	-4.92x10 ⁻⁰⁵	3.36x10 ⁻⁰⁵	[0.00, 0.00]	- 1.47	.14
DNAm <i>ESR1</i> ~ Mother's education level	-0.01	0.02	[-0.05, 0.02]	- 0.84	.40
DNAm <i>ESR1</i> ~ Mother's BMI before pregnancy	2.48x10 ⁻⁰³	4.39x10 ⁻⁰³	[-0.01, 0.01]	0.56	.57

Note. Coefficient = *Regressions* beta value, *SE* = standard error, *CI* = confidence interval, *z* = *z*-statistic, *p* = *p*-value, *c* = *c*-path, *b* = *b*-path, *a* = *a*-path.

Table A.106.ii. *Defined model parameters (effects)*

Effect	Coefficient	SE	95% CI	<i>z</i>	<i>p</i>
Indirect (female)	-0.02	0.04	[-0.12, 0.06]	-0.45	.65
Total (female)	-0.53	0.46	[-1.16, 0.63]	-1.14	.25
Indirect (male)	-0.12	0.17	[-0.57, 0.08]	-0.70	.49
Total (male)	0.41	0.39	[-0.38, 1.14]	1.07	.29
Difference in indirect (male - female)	0.10	0.18	[-0.16, 0.55]	0.58	.56
Difference in indirect (male - female)	-0.94	0.60	[-1.90, 0.44]	-1.57	.12

Note. Coefficient = estimated model parameter, *SE* = standard error, *CI* = confidence interval, *z* = *z*-statistic, *p* = *p*-value.

Tables A.107.i & ii. Results of the mediation model with the predictor congener PCB126, the mean DNA methylation of the CpGs in the promoter region of *ESR2*, and the predicted child's cognitive ability as outcome, controlling for confounders.

Table A.107.i. *Regressions*

	Coefficient	<i>SE</i>	95% CI	<i>z</i>	<i>p</i>
Child's cognitive ability ~ PCB126 (c)	-0.28	0.40	[-1.02, 0.60]	-0.70	.48
Child's cognitive ability ~ Sex	-3.58	0.48	[-4.53, -2.63]	-7.45	<.001
Child's cognitive ability ~ PCB126:Sex (c:Sex)	0.88	0.72	[-0.58, 2.23]	1.22	.22
Child's cognitive ability ~ DNAm <i>ESR2</i> (b)	1.98	1.07	[0.07, 4.22]	1.86	.06
Child's cognitive ability ~ Birthweight	1.47x10 ⁻⁰³	5.11x10 ⁻⁰⁴	[0.00, 0.00]	2.88	.004
Child's cognitive ability ~ Mother's education level	0.41	0.22	[-0.01, 0.87]	1.83	.07
Child's cognitive ability ~ Mother's BMI before pregnancy	-0.19	0.06	[-0.30, -0.08]	-3.41	<.001
DNAm <i>ESR2</i> ~ PCB126 (a)	-7.07x10 ⁻⁰³	0.03	[-0.07, 0.06]	-0.21	.83
DNAm <i>ESR2</i> ~ Sex	-0.05	0.04	[-0.12, 0.03]	-1.32	.19
DNAm <i>ESR2</i> ~ PCB126:Sex (a:Sex)	-0.03	0.07	[-0.18, 0.10]	-0.47	.64
DNAm <i>ESR2</i> ~ Birthweight	-8.52x10 ⁻⁰⁶	3.66x10 ⁻⁰⁵	[0.00, 0.00]	-0.23	.82
DNAm <i>ESR2</i> ~ Mother's education level	-1.97x10 ⁻⁰³	0.02	[-0.04, 0.03]	-0.11	.92
DNAm <i>ESR2</i> ~ Mother's BMI before pregnancy	3.89x10 ⁻⁰³	4.01x10 ⁻⁰³	[0.00, 0.01]	0.97	.33

Note. Coefficient = *Regressions* beta value, *SE* = standard error, *CI* = confidence interval, *z* = *z*-statistic, *p* = *p*-value, c = c-path, b = b-path, a = a-path.

Table A.107.ii. *Defined model parameters (effects)*

Effect	Coefficient	<i>SE</i>	95% CI	<i>z</i>	<i>p</i>
Indirect (female)	-0.01	0.08	[-0.17, 0.15]	-0.18	.85
Total (female)	-0.30	0.42	[-1.06, 0.62]	-0.71	.48
Indirect (male)	-0.08	0.15	[-0.37, 0.26]	-0.54	.59
Total (male)	0.51	0.63	[-0.74, 1.75]	0.81	.42
Difference in indirect (male - female)	0.07	0.15	[-0.30, 0.35]	0.44	.66
Difference in indirect (male - female)	-0.81	0.72	[-2.22, 0.64]	-1.12	.26

Note. Coefficient = estimated model parameter, *SE* = standard error, *CI* = confidence interval, *z* = *z*-statistic, *p* = *p*-value.

Tables A.108.i & ii. Results of the mediation model with the predictor congener PCB169, the mean DNA methylation of the CpGs in the promoter region of *ESR2*, and the predicted child's cognitive ability as outcome, controlling for confounders.

Table A.108.i. *Regressions*

	Coefficient	<i>SE</i>	95% CI	<i>z</i>	<i>p</i>
Child's cognitive ability ~ PCB169 (c)	0.02	0.56	[-1.20, 1.00]	0.03	.97

Child's cognitive ability ~ Sex	-3.56	0.48	[-4.55, -2.66]	-7.39	<.001
Child's cognitive ability ~ PCB169:Sex (c:Sex)	0.52	0.71	[-0.77, 2.00]	0.73	.46
Child's cognitive ability ~ DNAm <i>ESR2</i> (b)	1.86	1.11	[-0.07, 4.25]	1.67	.09
Child's cognitive ability ~ Birthweight	1.52x10 ⁻⁰³	5.13x10 ⁻⁰⁴	[0.00, 0.00]	2.95	.003
Child's cognitive ability ~ Mother's education level	0.36	0.22	[-0.05, 0.81]	1.65	.10
Child's cognitive ability ~ Mother's BMI before pregnancy	-0.19	0.06	[-0.29, -0.07]	-3.30	<.001
DNAm <i>ESR2</i> ~ PCB169 (a)	-0.04	0.04	[-0.12, 0.02]	-1.16	.24
DNAm <i>ESR2</i> ~ Sex	-0.05	0.04	[-0.12, 0.02]	-1.30	.20
DNAm <i>ESR2</i> ~ PCB169:Sex (a:Sex)	0.06	0.06	[-0.05, 0.18]	1.14	.25
DNAm <i>ESR2</i> ~ Birthweight	-1.23x10 ⁻⁰⁵	3.93x10 ⁻⁰⁵	[0.00, 0.00]	-0.31	.75
DNAm <i>ESR2</i> ~ Mother's education level	-4.12x10 ⁻⁰³	0.02	[-0.04, 0.03]	-0.24	.81
DNAm <i>ESR2</i> ~ Mother's BMI before pregnancy	2.78x10 ⁻⁰³	3.74x10 ⁻⁰³	[0.00, 0.01]	0.74	.46

Note. Coefficient = *Regressions* beta value, *SE* = standard error, *CI* = confidence interval, *z* = *z*-statistic, *p* = *p*-value, *c* = *c*-path, *b* = *b*-path, *a* = *a*-path.

Table A.108.ii. *Defined model parameters (effects)*

Effect	Coefficient	<i>SE</i>	95% <i>CI</i>	<i>z</i>	<i>p</i>
Indirect (female)	-0.08	0.09	[-0.29, 0.05]	-0.91	.37
Total (female)	-0.06	0.59	[-1.32, 0.97]	-0.10	.92
Indirect (male)	0.04	0.11	[-0.14, 0.31]	0.39	.70
Total (male)	0.58	0.47	[-0.32, 1.53]	1.23	.22
Difference in indirect (male - female)	-0.12	0.14	[-0.48, 0.08]	-0.83	.41
Difference in indirect (male - female)	-0.64	0.72	[-2.17, 0.68]	-0.88	.38

Note. Coefficient = estimated model parameter, *SE* = standard error, *CI* = confidence interval, *z* = *z*-statistic, *p* = *p*-value.

Tables A.109.i & ii. Results of the mediation model with the predictor congener PCB77, the mean DNA methylation of the CpGs in the promoter region of *ESR2*, and the predicted child's cognitive ability as outcome, controlling for confounders.

Table A.109.i. *Regressions*

	Coefficient	<i>SE</i>	95% <i>CI</i>	<i>z</i>	<i>p</i>
Child's cognitive ability ~ PCB77 (c)	0.91	0.78	[-0.53, 2.55]	1.17	.24
Child's cognitive ability ~ Sex	-3.55	0.48	[-4.48, -2.64]	-7.47	<.001
Child's cognitive ability ~ PCB77:Sex (c:Sex)	-2.54	1.10	[-4.71, -0.37]	-2.30	.02
Child's cognitive ability ~ DNAm <i>ESR2</i> (b)	2.17	1.07	[0.27, 4.49]	2.03	.04
Child's cognitive ability ~ Birthweight	1.47x10 ⁻⁰³	5.04x10 ⁻⁰⁴	[0.00, 0.00]	2.92	.003
Child's cognitive ability ~ Mother's education level	0.41	0.20	[0.04, 0.81]	2.10	.04
Child's cognitive ability ~ Mother's BMI before pregnancy	-0.20	0.06	[-0.31, -0.09]	-3.49	<.001

DNAm <i>ESR2</i> ~ PCB77 (a)	-0.01	0.04	[-0.09, 0.09]	-	.79
DNAm <i>ESR2</i> ~ Sex	-0.05	0.04	[-0.12, 0.02]	-	.17
DNAm <i>ESR2</i> ~ PCB77:Sex (a:Sex)	0.11	0.11	[-0.09, 0.34]	0.96	.34
DNAm <i>ESR2</i> ~ Birthweight	-1.01x10 ⁻⁰⁵	4.00x10 ⁻⁰⁵	[0.00, 0.00]	-	.80
DNAm <i>ESR2</i> ~ Mother's education level	-6.73x10 ⁻⁰³	0.01	[-0.03, 0.02]	-	.63
DNAm <i>ESR2</i> ~ Mother's BMI before pregnancy	4.11x10 ⁻⁰³	3.78x10 ⁻⁰³	[0.00, 0.01]	1.09	.28

Note. Coefficient = Regressions beta value, SE = standard error, CI = confidence interval, z = z -statistic, p = p -value, c = c-path, b = b-path, a = a-path.

Table A.109.ii. *Defined model parameters (effects)*

Effect	Coefficient	SE	95% CI	z	p
Indirect (female)	-0.03	0.11	[-0.23, 0.22]	-0.23	.81
Total (female)	0.88	0.80	[-0.58, 2.62]	1.10	.27
Indirect (male)	0.20	0.27	[-0.19, 0.90]	0.75	.45
Total (male)	-1.43	0.79	[-2.84, 0.32]	-1.80	.07
Difference in indirect (male - female)	-0.23	0.30	[-0.96, 0.23]	-0.78	.44
Difference in indirect (male - female)	2.31	1.11	[0.07, 4.47]	2.07	.04

Note. Coefficient = estimated model parameter, SE = standard error, CI = confidence interval, z = z -statistic, p = p -value.

Tables A.110.i & ii. Results of the mediation model with the predictor congener PCB81, the mean DNA methylation of the CpGs in the promoter region of *ESR2*, and the predicted child's cognitive ability as outcome, controlling for confounders.

Table A.110.i. *Regressions*

	Coefficient	SE	95% CI	z	p
Child's cognitive ability ~ PCB81 (c)	-0.26	0.35	[-0.96, 0.44]	-	.45
Child's cognitive ability ~ Sex	-3.52	0.48	[-4.49, -2.59]	-	<
Child's cognitive ability ~ PCB81:Sex (c:Sex)	-0.55	0.60	[-1.71, 0.67]	-	.36
Child's cognitive ability ~ DNAm <i>ESR2</i> (b)	1.76	1.14	[-0.21, 4.24]	1.55	.12
Child's cognitive ability ~ Birthweight	1.53x10 ⁻⁰³	5.11x10 ⁻⁰⁴	[0.00, 0.00]	3.00	.003
Child's cognitive ability ~ Mother's education level	0.49	0.21	[0.09, 0.90]	2.37	.02
Child's cognitive ability ~ Mother's BMI before pregnancy	-0.18	0.06	[-0.29, -0.07]	-	.001
DNAm <i>ESR2</i> ~ PCB81 (a)	2.10x10 ⁻⁰³	0.03	[-0.06, 0.06]	0.07	.95
DNAm <i>ESR2</i> ~ Sex	-0.04	0.04	[-0.12, 0.02]	-	.21
DNAm <i>ESR2</i> ~ PCB81:Sex (a:Sex)	-0.06	0.07	[-0.18, 0.08]	-	.41
DNAm <i>ESR2</i> ~ Birthweight	-1.28x10 ⁻⁰⁵	3.96x10 ⁻⁰⁵	[0.00, 0.00]	-	.75
DNAm <i>ESR2</i> ~ Mother's education level	-4.04x10 ⁻⁰³	0.02	[-0.03, 0.03]	-	.80

DNAm <i>ESR2</i> ~ Mother's BMI before pregnancy	3.74x10 ⁻⁰³	3.87x10 ⁻⁰³	[0.00, 0.01]	0.97	.33
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Note. Coefficient = *Regressions* beta value, *SE* = standard error, *CI* = confidence interval, *z* = *z*-statistic, *p* = *p*-value, *c* = *c*-path, *b* = *b*-path, *a* = *a*-path.

Table A.110.ii. *Defined model parameters (effects)*

Effect	Coefficient	<i>SE</i>	95% <i>CI</i>	<i>z</i>	<i>p</i>
Indirect (female)	3.70e10 ⁻⁰³	0.07	[-0.13, 0.15]	0.06	.96
Total (female)	-0.26	0.36	[-0.98, 0.45]	-0.72	.47
Indirect (male)	-0.09	0.13	[-0.34, 0.18]	-0.75	.45
Total (male)	-0.90	0.49	[-1.79, 0.13]	-1.85	.06
Difference in indirect (male - female)	0.10	0.14	[-0.19, 0.39]	0.70	.48
Difference in indirect (male - female)	0.64	0.60	[-0.62, 1.79]	1.06	.29

Note. Coefficient = estimated model parameter, *SE* = standard error, *CI* = confidence interval, *z* = *z*-statistic, *p* = *p*-value.

Tables A.111.i & ii. Results of the mediation model with the predictor congener PCDD48, the mean DNA methylation of the CpGs in the promoter region of *ESR2*, and the predicted child's cognitive ability as outcome, controlling for confounders.

Table A.111.i. *Regressions*

	Coefficient	<i>SE</i>	95% <i>CI</i>	<i>z</i>	<i>p</i>
Child's cognitive ability ~ PCDD48 (c)	-0.57	0.44	[-1.40, 0.35]	- 1.30	.19
Child's cognitive ability ~ Sex	-3.60	0.47	[-4.57, - 2.71]	- 7.62	< .001
Child's cognitive ability ~ PCDD48:Sex (c:Sex)	0.82	0.64	[-0.50, 2.02]	1.28	.20
Child's cognitive ability ~ DNAm <i>ESR2</i> (b)	1.76	1.08	[-0.11, 4.11]	1.64	.10
Child's cognitive ability ~ Birthweight	1.47x10 ⁻⁰³	4.88x10 ⁻⁰⁴	[0.00, 0.00]	3.00	.003
Child's cognitive ability ~ Mother's education level	0.45	0.21	[0.06, 0.87]	2.15	.03
Child's cognitive ability ~ Mother's BMI before pregnancy	-0.19	0.06	[-0.30, - 0.08]	- 3.47	< .001
DNAm <i>ESR2</i> ~ PCDD48 (a)	-0.05	0.03	[-0.11, 0.00]	- 1.88	.06
DNAm <i>ESR2</i> ~ Sex	-0.05	0.04	[-0.12, 0.02]	- 1.34	.18
DNAm <i>ESR2</i> ~ PCDD48:Sex (a:Sex)	0.05	0.05	[-0.06, 0.15]	0.93	.35
DNAm <i>ESR2</i> ~ Birthweight	-1.66x10 ⁻⁰⁵	3.93x10 ⁻⁰⁵	[0.00, 0.00]	- 0.42	.67
DNAm <i>ESR2</i> ~ Mother's education level	-2.58x10 ⁻⁰³	0.02	[-0.03, 0.03]	- 0.16	.87
DNAm <i>ESR2</i> ~ Mother's BMI before pregnancy	3.47x10 ⁻⁰³	4.01x10 ⁻⁰³	[0.00, 0.01]	0.87	.39

Note. Coefficient = *Regressions* beta value, *SE* = standard error, *CI* = confidence interval, *z* = *z*-statistic, *p* = *p*-value, *c* = *c*-path, *b* = *b*-path, *a* = *a*-path.

Table A.111.ii. *Defined model parameters (effects)*

Effect	Coefficient	<i>SE</i>	95% <i>CI</i>	<i>z</i>	<i>p</i>
Indirect (female)	-0.09	0.08	[-0.30, 0.01]	-1.11	.27
Total (female)	-0.66	0.44	[-1.52, 0.23]	-1.51	.13
Indirect (male)	-7.89x10 ⁻⁰³	0.09	[-0.17, 0.21]	-0.09	.93
Total (male)	0.24	0.46	[-0.67, 1.13]	0.52	.61

Difference in indirect (male - female)	-0.08	0.13	[-0.43, 0.07]	-0.65	.52
Difference in indirect (male - female)	-0.90	0.63	[-2.12, 0.37]	-1.43	.15

Note. Coefficient = estimated model parameter, *SE* = standard error, *CI* = confidence interval, *z* = *z*-statistic, *p* = *p*-value.

Tables A.112.i & ii. Results of the mediation model with the predictor congener PCDD54, the mean DNA methylation of the CpGs in the promoter region of *ESR2*, and the predicted child's cognitive ability as outcome, controlling for confounders.

Table A.112.i. *Regressions*

	Coefficient	<i>SE</i>	95% CI	<i>z</i>	<i>p</i>
Child's cognitive ability ~ PCDD54	-0.50	0.69	[-1.90, 0.79]	-	.46
(c)				0.73	
Child's cognitive ability ~ Sex	-3.56	0.48	[-4.53, -2.63]	-	<
				7.36	.001
Child's cognitive ability ~ PCDD54:Sex	1.37	0.87	[-0.34, 3.09]	1.57	.12
(c:Sex)					
Child's cognitive ability ~ DNAm <i>ESR2</i>	1.91	1.08	[-0.03, 4.22]	1.78	.08
(b)					
Child's cognitive ability ~ Birthweight	1.48x10 ⁻⁰³	4.98x10 ⁻⁰⁴	[0.00, 0.00]	2.97	.003
Child's cognitive ability ~ Mother's education level	0.39	0.21	[-0.01, 0.82]	1.87	.06
Child's cognitive ability ~ Mother's BMI before pregnancy	-0.20	0.05	[-0.30, -0.09]	-	<
				3.63	.001
DNAm <i>ESR2</i> ~ PCDD54	-0.03	0.05	[-0.13, 0.05]	-	.55
(a)				0.61	
DNAm <i>ESR2</i> ~ Sex	-0.05	0.04	[-0.13, 0.02]	-	.19
				1.31	
DNAm <i>ESR2</i> ~ PCDD54:Sex	0.01	0.08	[-0.15, 0.17]	0.18	.85
(a:Sex)					
DNAm <i>ESR2</i> ~ Birthweight	-1.33x10 ⁻⁰⁵	4.02x10 ⁻⁰⁵	[0.00, 0.00]	-	.74
				0.33	
DNAm <i>ESR2</i> ~ Mother's education level	-3.90x10 ⁻⁰³	0.02	[-0.04, 0.03]	-	.82
				0.23	
DNAm <i>ESR2</i> ~ Mother's BMI before pregnancy	3.45x10 ⁻⁰³	3.99x10 ⁻⁰³	[0.00, 0.01]	0.86	.39

Note. Coefficient = *Regressions* beta value, *SE* = standard error, *CI* = confidence interval, *z* = *z*-statistic, *p* = *p*-value, c = c-path, b = b-path, a = a-path.

Table A.112.ii. *Defined model parameters (effects)*

Effect	Coefficient	<i>SE</i>	95% CI	<i>z</i>	<i>p</i>
Indirect (female)	-0.05	0.10	[-0.29, 0.12]	-0.52	.60
Total (female)	-0.56	0.72	[-2.02, 0.80]	-0.78	.44
Indirect (male)	-0.02	0.15	[-0.32, 0.32]	-0.16	.87
Total (male)	0.84	0.53	[-0.25, 1.85]	1.58	.11
Difference in indirect (male - female)	-0.03	0.18	[-0.46, 0.28]	-0.16	.87
Difference in indirect (male - female)	-1.40	0.89	[-3.18, 0.35]	-1.57	.12

Note. Coefficient = estimated model parameter, *SE* = standard error, *CI* = confidence interval, *z* = *z*-statistic, *p* = *p*-value.

Tables A.113.i & ii. Results of the mediation model with the predictor congener PCDD66, the mean DNA methylation of the CpGs in the promoter region of *ESR2*, and the predicted child's cognitive ability as outcome, controlling for confounders.

Table A.113.i. *Regressions*

	Coefficient	<i>SE</i>	95% CI	<i>z</i>	<i>p</i>
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Child's cognitive ability ~ PCDD66 (c)	-0.20	0.65	[-1.51, 1.04]	- 0.31	.76
Child's cognitive ability ~ Sex	-3.54	0.48	[-4.51, - 2.64]	- 7.40	< .001
Child's cognitive ability ~ PCDD66:Sex (c:Sex)	1.22	0.84	[-0.40, 2.92]	1.45	.15
Child's cognitive ability ~ DNAm <i>ESR2</i> (b)	1.97	1.04	[0.07, 4.18]	1.90	.06
Child's cognitive ability ~ Birthweight	1.49x10 ⁻⁰³	4.99x10 ⁻⁰⁴	[0.00, 0.00]	2.98	.003
Child's cognitive ability ~ Mother's education level	0.34	0.21	[-0.06, 0.77]	1.58	.11
Child's cognitive ability ~ Mother's BMI before pregnancy	-0.19	0.05	[-0.30, - 0.09]	- 3.56	< .001
DNAm <i>ESR2</i> ~ PCDD66 (a)	-0.03	0.04	[-0.12, 0.05]	- 0.75	.46
DNAm <i>ESR2</i> ~ Sex	-0.05	0.04	[-0.12, 0.02]	- 1.35	.18
DNAm <i>ESR2</i> ~ PCDD66:Sex (a:Sex)	0.01	0.07	[-0.14, 0.15]	0.15	.88
DNAm <i>ESR2</i> ~ Birthweight	-1.28x10 ⁻⁰⁵	3.83x10 ⁻⁰⁵	[0.00, 0.00]	- 0.33	.74
DNAm <i>ESR2</i> ~ Mother's education level	-1.63x10 ⁻⁰³	0.02	[-0.04, 0.04]	- 0.09	.93
DNAm <i>ESR2</i> ~ Mother's BMI before pregnancy	3.67x10 ⁻⁰³	3.85x10 ⁻⁰³	[0.00, 0.01]	0.95	.34

Note. Coefficient = *Regressions* beta value, *SE* = standard error, *CI* = confidence interval, *z* = *z*-statistic, *p* = *p*-value, *c* = *c*-path, *b* = *b*-path, *a* = *a*-path.

Table A.113.ii. *Defined model parameters (effects)*

Effect	Coefficient	<i>SE</i>	95% <i>CI</i>	<i>z</i>	<i>p</i>
Indirect (female)	-0.06	0.10	[-0.29, 0.13]	-0.64	.52
Total (female)	-0.26	0.66	[-1.59, 1.03]	-0.40	.69
Indirect (male)	-0.04	0.15	[-0.34, 0.29]	-0.29	.77
Total (male)	0.98	0.55	[-0.05, 2.11]	1.78	.08
Difference in indirect (male - female)	-0.02	0.16	[-0.41, 0.27]	-0.13	.89
Difference in indirect (male - female)	-1.24	0.83	[-2.94, 0.36]	-1.49	.14

Note. Coefficient = estimated model parameter, *SE* = standard error, *CI* = confidence interval, *z* = *z*-statistic, *p* = *p*-value.

Tables A.114.i & ii. Results of the mediation model with the predictor congener PCDD67, the mean DNA methylation of the CpGs in the promoter region of *ESR2*, and the predicted child's cognitive ability as outcome, controlling for confounders.

Table A.114.i. *Regressions*

	Coefficient	<i>SE</i>	95% <i>CI</i>	<i>z</i>	<i>p</i>
Child's cognitive ability ~ PCDD67 (c)	-0.27	0.72	[-1.84, 0.98]	- 0.37	.71
Child's cognitive ability ~ Sex	-3.58	0.49	[-4.57, - 2.66]	- 7.35	< .001
Child's cognitive ability ~ PCDD67:Sex (c:Sex)	0.58	0.88	[-1.01, 2.46]	0.65	.51
Child's cognitive ability ~ DNAm <i>ESR2</i> (b)	1.89	1.11	[-0.08, 4.27]	1.70	.09
Child's cognitive ability ~ Birthweight	1.50x10 ⁻⁰³	5.04x10 ⁻⁰⁴	[0.00, 0.00]	2.98	.003
Child's cognitive ability ~ Mother's education level	0.41	0.21	[0.00, 0.84]	1.93	.05

Child's cognitive ability ~ Mother's BMI before pregnancy	-0.19	0.06	[-0.30, -0.08]	-	<
DNAm <i>ESR2</i> ~ PCDD67	-0.04	0.05	[-0.15, 0.04]	-	.39
(a)				0.85	
DNAm <i>ESR2</i> ~ Sex	-0.05	0.04	[-0.12, 0.02]	-	.18
				1.34	
DNAm <i>ESR2</i> ~ PCDD67:Sex	0.04	0.07	[-0.09, 0.18]	0.57	.57
(a:Sex)					
DNAm <i>ESR2</i> ~ Birthweight	-1.47x10 ⁻⁰⁵	4.02x10 ⁻⁰⁵	[0.00, 0.00]	-	.71
				0.37	
DNAm <i>ESR2</i> ~ Mother's education level	-3.25x10 ⁻⁰³	0.02	[-0.03, 0.03]	-	.85
				0.19	
DNAm <i>ESR2</i> ~ Mother's BMI before pregnancy	3.15x10 ⁻⁰³	3.75x10 ⁻⁰³	[0.00, 0.01]	0.84	.40

Note. Coefficient = *Regressions* beta value, *SE* = standard error, *CI* = confidence interval, *z* = *z*-statistic, *p* = *p*-value, c = c-path, b = b-path, a = a-path.

Table A.114.ii. *Defined model parameters (effects)*

Effect	Coefficient	<i>SE</i>	95% <i>CI</i>	<i>z</i>	<i>p</i>
Indirect (female)	-0.08	0.11	[-0.35, 0.10]	-0.73	.47
Total (female)	-0.35	0.75	[-2.00, 0.96]	-0.46	.64
Indirect (male)	-5.71x10 ⁻⁰³	0.12	[-0.22, 0.28]	-0.05	.96
Total (male)	0.30	0.52	[-0.69, 1.36]	0.58	.56
Difference in indirect (male - female)	-0.07	0.16	[-0.48, 0.16]	-0.47	.64
Difference in indirect (male - female)	-0.65	0.90	[-2.59, 0.94]	-0.72	.47

Note. Coefficient = estimated model parameter, *SE* = standard error, *CI* = confidence interval, *z* = *z*-statistic, *p* = *p*-value.

Tables A.115.i & ii. Results of the mediation model with the predictor congener PCDD70, the mean DNA methylation of the CpGs in the promoter region of *ESR2*, and the predicted child's cognitive ability as outcome, controlling for confounders.

Table A.115.i. *Regressions*

	Coefficient	<i>SE</i>	95% <i>CI</i>	<i>z</i>	<i>p</i>
Child's cognitive ability ~ PCDD70	-0.38	0.64	[-1.67, 0.82]	-	.55
(c)				0.60	
Child's cognitive ability ~ Sex	-3.56	0.48	[-4.52, -2.66]	-	<
				7.44	.001
Child's cognitive ability ~ PCDD70:Sex	1.47	0.89	[-0.29, 3.20]	1.64	.10
(c:Sex)					
Child's cognitive ability ~ DNAm <i>ESR2</i>	1.89	1.04	[0.06, 4.14]	1.81	.07
(b)					
Child's cognitive ability ~ Birthweight	1.43x10 ⁻⁰³	5.04x10 ⁻⁰⁴	[0.00, 0.00]	2.84	.004
Child's cognitive ability ~ Mother's education level	0.37	0.21	[-0.02, 0.80]	1.80	.07
Child's cognitive ability ~ Mother's BMI before pregnancy	-0.19	0.05	[-0.30, -0.08]	-	<
				3.54	.001
DNAm <i>ESR2</i> ~ PCDD70	-0.01	0.04	[-0.10, 0.07]	-	.78
(a)				0.28	
DNAm <i>ESR2</i> ~ Sex	-0.05	0.04	[-0.12, 0.03]	-	.21
				1.25	
DNAm <i>ESR2</i> ~ PCDD70:Sex	0.02	0.08	[-0.15, 0.17]	0.24	.81
(a:Sex)					
DNAm <i>ESR2</i> ~ Birthweight	-1.39x10 ⁻⁰⁵	3.93x10 ⁻⁰⁵	[0.00, 0.00]	-	.72
				0.35	

DNAm <i>ESR2</i> ~ Mother's education level	-6.60x10 ⁻⁰³	0.02	[-0.04, 0.03]	-	.70
				0.39	
DNAm <i>ESR2</i> ~ Mother's BMI before pregnancy	3.52x10 ⁻⁰³	3.92x10 ⁻⁰³	[0.00, 0.01]	0.90	.37

Note. Coefficient = *Regressions* beta value, *SE* = standard error, CI = confidence interval, *z* = *z*-statistic, *p* = *p*-value, c = c-path, b = b-path, a = a-path.

Table A.115.ii. *Defined model parameters (effects)*

Effect	Coefficient	<i>SE</i>	95% CI	<i>z</i>	<i>p</i>
Indirect (female)	-0.02	0.09	[-0.21, 0.16]	-0.25	.80
Total (female)	-0.40	0.65	[-1.72, 0.83]	-0.62	.54
Indirect (male)	0.01	0.17	[-0.29, 0.43]	0.08	.94
Total (male)	1.10	0.61	[-0.13, 2.27]	1.82	.07
Difference in indirect (male - female)	-0.04	0.18	[-0.48, 0.27]	-0.20	.84
Difference in indirect (male - female)	-1.50	0.89	[-3.28, 0.21]	-1.68	.09

Note. Coefficient = estimated model parameter, *SE* = standard error, CI = confidence interval, *z* = *z*-statistic, *p* = *p*-value.

Tables A.116.i & ii. Results of the mediation model with the predictor congener PCDD73, the mean DNA methylation of the CpGs in the promoter region of *ESR2*, and the predicted child's cognitive ability as outcome, controlling for confounders.

Table A.116.i. *Regressions*

	Coefficient	<i>SE</i>	95% CI	<i>z</i>	<i>p</i>
Child's cognitive ability ~ PCDD73 (c)	0.04	0.52	[-0.99, 1.05]	0.07	.94
Child's cognitive ability ~ Sex	-3.55	0.48	[-4.52, -2.66]	-7.44	<.001
Child's cognitive ability ~ PCDD73:Sex (c:Sex)	0.56	0.67	[-0.75, 1.90]	0.83	.41
Child's cognitive ability ~ DNAm <i>ESR2</i> (b)	1.98	1.07	[0.10, 4.34]	1.84	.07
Child's cognitive ability ~ Birthweight	1.48x10 ⁻⁰³	5.06x10 ⁻⁰⁴	[0.00, 0.00]	2.92	.004
Child's cognitive ability ~ Mother's education level	0.35	0.21	[-0.05, 0.79]	1.65	.10
Child's cognitive ability ~ Mother's BMI before pregnancy	-0.19	0.06	[-0.30, -0.08]	-3.47	<.001
DNAm <i>ESR2</i> ~ PCDD73 (a)	-0.04	0.04	[-0.12, 0.03]	-1.22	.22
DNAm <i>ESR2</i> ~ Sex	-0.05	0.04	[-0.12, 0.02]	-1.40	.16
DNAm <i>ESR2</i> ~ PCDD73:Sex (a:Sex)	0.02	0.06	[-0.10, 0.12]	0.39	.70
DNAm <i>ESR2</i> ~ Birthweight	-1.10x10 ⁻⁰⁵	3.77x10 ⁻⁰⁵	[0.00, 0.00]	-0.29	.77
DNAm <i>ESR2</i> ~ Mother's education level	1.01x10 ⁻⁰³	0.02	[-0.03, 0.04]	0.06	.95
DNAm <i>ESR2</i> ~ Mother's BMI before pregnancy	4.18x10 ⁻⁰³	3.99x10 ⁻⁰³	[0.00, 0.01]	1.05	.30

Note. Coefficient = *Regressions* beta value, *SE* = standard error, CI = confidence interval, *z* = *z*-statistic, *p* = *p*-value, c = c-path, b = b-path, a = a-path.

Table A.116.ii. *Defined model parameters (effects)*

Effect	Coefficient	<i>SE</i>	95% CI	<i>z</i>	<i>p</i>
Indirect (female)	-0.09	0.09	[-0.30, 0.06]	-0.97	.33
Total (female)	-0.05	0.52	[-1.10, 0.97]	-0.10	.92
Indirect (male)	-0.05	0.11	[-0.26, 0.18]	-0.43	.67

Total (male)	0.55	0.45	[-0.34, 1.46]	1.21	.23
Difference in indirect (male - female)	-0.04	0.13	[-0.35, 0.19]	-0.33	.74
Difference in indirect (male - female)	-0.60	0.67	[-1.94, 0.69]	-0.90	.37

Note. Coefficient = estimated model parameter, *SE* = standard error, CI = confidence interval, *z* = *z*-statistic, *p* = *p*-value.

Tables A.117.i & ii. Results of the mediation model with the predictor congener PCDD75, the mean DNA methylation of the CpGs in the promoter region of *ESR2*, and the predicted child's cognitive ability as outcome, controlling for confounders.

Table A.117.i. *Regressions*

	Coefficient	<i>SE</i>	95% CI	<i>z</i>	<i>p</i>
Child's cognitive ability ~ PCDD75	-0.48	0.64	[-1.86, 0.63]	-	.45
(c)				0.75	
Child's cognitive ability ~ Sex	-3.58	0.48	[-4.58, -2.70]	-	<
				7.44	.001
Child's cognitive ability ~ PCDD75:Sex	1.13	0.84	[-0.39, 2.88]	1.35	.18
(c:Sex)					
Child's cognitive ability ~ DNAm <i>ESR2</i>	1.85	1.08	[-0.09, 4.17]	1.72	.09
(b)					
Child's cognitive ability ~ Birthweight	1.52x10 ⁻⁰³	5.07x10 ⁻⁰⁴	[0.00, 0.00]	2.99	.003
Child's cognitive ability ~ Mother's education level	0.41	0.20	[0.03, 0.82]	2.03	.04
Child's cognitive ability ~ Mother's BMI before pregnancy	-0.19	0.06	[-0.30, -0.08]	-	<
				3.34	.001
DNAm <i>ESR2</i> ~ PCDD75	-0.05	0.04	[-0.12, 0.03]	-	.24
(a)				1.19	
DNAm <i>ESR2</i> ~ Sex	-0.05	0.04	[-0.12, 0.02]	-	.19
				1.33	
DNAm <i>ESR2</i> ~ PCDD75:Sex	0.04	0.06	[-0.09, 0.15]	0.71	.48
(a:Sex)					
DNAm <i>ESR2</i> ~ Birthweight	-1.26x10 ⁻⁰⁵	3.89x10 ⁻⁰⁵	[0.00, 0.00]	-	.75
				0.32	
DNAm <i>ESR2</i> ~ Mother's education level	-3.40x10 ⁻⁰³	0.02	[-0.03, 0.03]	-	.83
				0.21	
DNAm <i>ESR2</i> ~ Mother's BMI before pregnancy	3.41x10 ⁻⁰³	3.79x10 ⁻⁰³	[0.00, 0.01]	0.90	.37

Note. Coefficient = *Regressions* beta value, *SE* = standard error, CI = confidence interval, *z* = *z*-statistic, *p* = *p*-value, c = c-path, b = b-path, a = a-path.

Table A.117.ii. *Defined model parameters (effects)*

Effect	Coefficient	<i>SE</i>	95% CI	<i>z</i>	<i>p</i>
Indirect (female)	-0.08	0.09	[-0.30, 0.06]	-0.93	.35
Total (female)	-0.57	0.66	[-1.97, 0.60]	-0.85	.39
Indirect (male)	-5.09x10 ⁻⁰³	0.11	[-0.20, 0.25]	-0.05	.96
Total (male)	0.64	0.52	[-0.33, 1.70]	1.25	.21
Difference in indirect (male - female)	-0.08	0.14	[-0.44, 0.14]	-0.56	.58
Difference in indirect (male - female)	-1.21	0.85	[-2.98, 0.34]	-1.43	.15

Note. Coefficient = estimated model parameter, *SE* = standard error, CI = confidence interval, *z* = *z*-statistic, *p* = *p*-value.

Tables A.118.i & ii. Results of the mediation model with the predictor congener PCDF114, the mean DNA methylation of the CpGs in the promoter region of *ESR2*, and the predicted child's cognitive ability as outcome, controlling for confounders.

Table A.118.i. *Regressions*

	Coefficient	SE	95% CI	z	p
Child's cognitive ability ~ PCDF114 (c)	-1.05	0.64	[-2.30, 0.17]	- 1.66	.10
Child's cognitive ability ~ Sex	-3.60	0.48	[-4.55, - 2.71]	- 7.56	< .001
Child's cognitive ability ~ PCDF114:Sex (c:Sex)	1.84	0.85	[0.20, 3.53]	2.16	.03
Child's cognitive ability ~ DNAm <i>ESR2</i> (b)	1.76	1.07	[-0.15, 4.10]	1.64	.10
Child's cognitive ability ~ Birthweight	1.51x10 ⁻⁰³	4.86x10 ⁻⁰⁴	[0.00, 0.00]	3.11	.002
Child's cognitive ability ~ Mother's education level	0.45	0.22	[0.03, 0.89]	2.04	.04
Child's cognitive ability ~ Mother's BMI before pregnancy	-0.20	0.05	[-0.30, - 0.09]	- 3.78	< .001
DNAm <i>ESR2</i> ~ PCDF114 (a)	-0.06	0.04	[-0.14, 0.02]	- 1.50	.13
DNAm <i>ESR2</i> ~ Sex	-0.05	0.04	[-0.13, 0.02]	- 1.35	.18
DNAm <i>ESR2</i> ~ PCDF114:Sex (a:Sex)	0.06	0.07	[-0.09, 0.19]	0.78	.43
DNAm <i>ESR2</i> ~ Birthweight	-1.28x10 ⁻⁰⁵	3.93x10 ⁻⁰⁵	[0.00, 0.00]	- 0.33	.75
DNAm <i>ESR2</i> ~ Mother's education level	-1.18x10 ⁻⁰³	0.02	[-0.03, 0.03]	- 0.07	.95
DNAm <i>ESR2</i> ~ Mother's BMI before pregnancy	3.10x10 ⁻⁰³	3.81x10 ⁻⁰³	[0.00, 0.01]	0.81	.42

Note. Coefficient = *Regressions* beta value, SE = standard error, CI = confidence interval, z = z-statistic, p = p-value, c = c-path, b = b-path, a = a-path.

Table A.118.ii. *Defined model parameters (effects)*

Effect	Coefficient	SE	95% CI	z	p
Indirect (female)	-0.11	0.10	[-0.34, 0.04]	-1.07	.28
Total (female)	-1.16	0.65	[-2.42, 0.10]	-1.79	.07
Indirect (male)	-8.38x10 ⁻⁰³	0.13	[-0.25, 0.29]	-0.07	.95
Total (male)	0.78	0.59	[-0.37, 2.01]	1.31	.19
Difference in indirect (male - female)	-0.10	0.16	[-0.50, 0.15]	-0.60	.55
Difference in indirect (male - female)	-1.94	0.86	[-3.63, -0.30]	-2.26	.02

Note. Coefficient = estimated model parameter, SE = standard error, CI = confidence interval, z = z-statistic, p = p-value.

Tables A.119.i & ii. Results of the mediation model with the predictor congener PCDF118, the mean DNA methylation of the CpGs in the promoter region of *ESR2*, and the predicted child's cognitive ability as outcome, controlling for confounders.

Table A.119.i. *Regressions*

	Coefficient	SE	95% CI	z	p
Child's cognitive ability ~ PCDF118 (c)	-0.84	0.72	[-2.25, 0.56]	- 1.16	.24
Child's cognitive ability ~ Sex	-3.56	0.48	[-4.51, - 2.63]	- 7.36	< .001
Child's cognitive ability ~ PCDF118:Sex (c:Sex)	2.22	0.93	[0.40, 4.03]	2.39	.02
Child's cognitive ability ~ DNAm <i>ESR2</i> (b)	1.80	1.05	[-0.07, 4.00]	1.72	.09
Child's cognitive ability ~ Birthweight	1.50x10 ⁻⁰³	4.89x10 ⁻⁰⁴	[0.00, 0.00]	3.08	.002

Child's cognitive ability ~ Mother's education level	0.39	0.21	[-0.02, 0.81]	1.82	.07
Child's cognitive ability ~ Mother's BMI before pregnancy	-0.19	0.05	[-0.29, -0.09]	-	<
DNAm <i>ESR2</i> ~ PCDF118 (a)	-0.05	0.05	[-0.14, 0.04]	-	.25
DNAm <i>ESR2</i> ~ Sex	-0.05	0.04	[-0.13, 0.02]	-	.19
DNAm <i>ESR2</i> ~ PCDF118:Sex (a:Sex)	0.07	0.08	[-0.11, 0.22]	0.77	.44
DNAm <i>ESR2</i> ~ Birthweight	-1.36x10 ⁻⁰⁵	3.96x10 ⁻⁰⁵	[0.00, 0.00]	-	.73
DNAm <i>ESR2</i> ~ Mother's education level	-4.24x10 ⁻⁰³	0.02	[-0.03, 0.03]	-	.79
DNAm <i>ESR2</i> ~ Mother's BMI before pregnancy	3.52x10 ⁻⁰³	3.75x10 ⁻⁰³	[0.00, 0.01]	0.94	.35

Note. Coefficient = *Regressions* beta value, *SE* = standard error, *CI* = confidence interval, *z* = *z*-statistic, *p* = *p*-value, *c* = *c*-path, *b* = *b*-path, *a* = *a*-path.

Table A.119.ii. *Defined model parameters (effects)*

Effect	Coefficient	<i>SE</i>	95% <i>CI</i>	<i>z</i>	<i>p</i>
Indirect (female)	-0.10	0.11	[-0.35, 0.08]	-0.90	.37
Total (female)	-0.93	0.73	[-2.37, 0.48]	-1.29	.20
Indirect (male)	0.02	0.16	[-0.26, 0.40]	0.12	.91
Total (male)	1.41	0.58	[0.27, 2.57]	2.42	.02
Difference in indirect (male - female)	-0.12	0.20	[-0.61, 0.18]	-0.59	.55
Difference in indirect (male - female)	-2.34	0.93	[-4.13, -0.54]	-2.52	.01

Note. Coefficient = estimated model parameter, *SE* = standard error, *CI* = confidence interval, *z* = *z*-statistic, *p* = *p*-value.

Tables A.120.i & ii. Results of the mediation model with the predictor congener PCDF121, the mean DNA methylation of the CpGs in the promoter region of *ESR2*, and the predicted child's cognitive ability as outcome, controlling for confounders.

Table A.120.i. *Regressions*

	Coefficient	<i>SE</i>	95% <i>CI</i>	<i>z</i>	<i>p</i>
Child's cognitive ability ~ PCDF121 (c)	-0.83	0.62	[-2.03, 0.43]	-	.18
Child's cognitive ability ~ Sex	-3.55	0.47	[-4.51, -2.66]	-	<
Child's cognitive ability ~ PCDF121:Sex (c:Sex)	2.27	0.86	[0.53, 3.90]	2.64	.01
Child's cognitive ability ~ DNAm <i>ESR2</i> (b)	1.73	1.06	[-0.17, 4.06]	1.63	.10
Child's cognitive ability ~ Birthweight	1.51x10 ⁻⁰³	4.93x10 ⁻⁰⁴	[0.00, 0.00]	3.05	.002
Child's cognitive ability ~ Mother's education level	0.39	0.21	[-0.02, 0.81]	1.82	.07
Child's cognitive ability ~ Mother's BMI before pregnancy	-0.20	0.05	[-0.30, -0.09]	-	<
DNAm <i>ESR2</i> ~ PCDF121 (a)	-0.03	0.04	[-0.12, 0.05]	-	.48
DNAm <i>ESR2</i> ~ Sex	-0.05	0.04	[-0.12, 0.03]	-	.21
DNAm <i>ESR2</i> ~ PCDF121:Sex (a:Sex)	0.08	0.08	[-0.09, 0.23]	0.96	.34
DNAm <i>ESR2</i> ~ Birthweight	-1.29x10 ⁻⁰⁵	3.97x10 ⁻⁰⁵	[0.00, 0.00]	-	.75

DNAm <i>ESR2</i> ~ Mother's education level	-7.43x10 ⁻⁰³	0.02	[-0.04, 0.03]	-	.64
				0.47	
DNAm <i>ESR2</i> ~ Mother's BMI before pregnancy	3.23x10 ⁻⁰³	3.78x10 ⁻⁰³	[0.00, 0.01]	0.85	.39

Note. Coefficient = *Regressions* beta value, *SE* = standard error, CI = confidence interval, *z* = *z*-statistic, *p* = *p*-value, c = c-path, b = b-path, a = a-path.

Table A.120.ii. *Defined model parameters (effects)*

Effect	Coefficient	<i>SE</i>	95% CI	<i>z</i>	<i>p</i>
Indirect (female)	-0.05	0.09	[-0.28, 0.11]	-0.57	.57
Total (female)	-0.89	0.64	[-2.11, 0.40]	-1.40	.16
Indirect (male)	0.08	0.16	[-0.18, 0.48]	0.49	.63
Total (male)	1.51	0.59	[0.30, 2.63]	2.54	.01
Difference in indirect (male - female)	-0.13	0.19	[-0.62, 0.14]	-0.70	.49
Difference in indirect (male - female)	-2.40	0.86	[-4.04, -0.66]	-2.80	.01

Note. Coefficient = estimated model parameter, *SE* = standard error, CI = confidence interval, *z* = *z*-statistic, *p* = *p*-value.

Tables A.121.i & ii. Results of the mediation model with the predictor congener PCDF130, the mean DNA methylation of the CpGs in the promoter region of *ESR2*, and the predicted child's cognitive ability as outcome, controlling for confounders.

Table A.121.i. *Regressions*

	Coefficient	<i>SE</i>	95% CI	<i>z</i>	<i>p</i>
Child's cognitive ability ~ PCDF130 (c)	0.04	0.51	[-0.98, 1.04]	0.09	.93
Child's cognitive ability ~ Sex	-3.56	0.48	[-4.52, -2.63]	-7.40	<.001
Child's cognitive ability ~ PCDF130:Sex (c:Sex)	0.97	0.77	[-0.48, 2.57]	1.26	.21
Child's cognitive ability ~ DNAm <i>ESR2</i> (b)	1.86	1.08	[-0.03, 4.21]	1.73	.08
Child's cognitive ability ~ Birthweight	1.46x10 ⁻⁰³	5.08x10 ⁻⁰⁴	[0.00, 0.00]	2.88	.004
Child's cognitive ability ~ Mother's education level	0.32	0.22	[-0.10, 0.78]	1.46	.15
Child's cognitive ability ~ Mother's BMI before pregnancy	-0.19	0.06	[-0.30, -0.08]	-3.49	<.001
DNAm <i>ESR2</i> ~ PCDF130 (a)	5.60x10 ⁻⁰³	0.03	[-0.06, 0.07]	0.18	.86
DNAm <i>ESR2</i> ~ Sex	-0.05	0.04	[-0.12, 0.02]	-1.29	.20
DNAm <i>ESR2</i> ~ PCDF130:Sex (a:Sex)	0.01	0.06	[-0.11, 0.12]	0.22	.83
DNAm <i>ESR2</i> ~ Birthweight	-1.35x10 ⁻⁰⁵	3.85x10 ⁻⁰⁵	[0.00, 0.00]	-0.35	.73
DNAm <i>ESR2</i> ~ Mother's education level	-9.04x10 ⁻⁰³	0.02	[-0.04, 0.02]	-0.58	.56
DNAm <i>ESR2</i> ~ Mother's BMI before pregnancy	3.43x10 ⁻⁰³	3.82x10 ⁻⁰³	[0.00, 0.01]	0.90	.37

Note. Coefficient = *Regressions* beta value, *SE* = standard error, CI = confidence interval, *z* = *z*-statistic, *p* = *p*-value, c = c-path, b = b-path, a = a-path.

Table A.121.ii. *Defined model parameters (effects)*

Effect	Coefficient	<i>SE</i>	95% CI	<i>z</i>	<i>p</i>
Indirect (female)	0.01	0.07	[-0.12, 0.16]	0.16	.88
Total (female)	0.05	0.53	[-0.99, 1.09]	0.10	.92

Indirect (male)	0.03	0.12	[-0.17, 0.32]	0.29	.77
Total (male)	1.05	0.64	[-0.18, 2.37]	1.63	.10
Difference in indirect (male - female)	-0.02	0.12	[-0.32, 0.21]	-0.19	.85
Difference in indirect (male - female)	-0.99	0.78	[-2.60, 0.49]	-1.28	.20

Note. Coefficient = estimated model parameter, *SE* = standard error, CI = confidence interval, *z* = *z*-statistic, *p* = *p*-value.

Tables A.122.i & ii. Results of the mediation model with the predictor congener PCDF131, the mean DNA methylation of the CpGs in the promoter region of *ESR2*, and the predicted child's cognitive ability as outcome, controlling for confounders.

Table A.122.i. *Regressions*

	Coefficient	<i>SE</i>	95% CI	<i>z</i>	<i>p</i>
Child's cognitive ability ~ PCDF131	-0.52	0.46	[-1.14, 0.66]	-	.26
(c)				1.12	
Child's cognitive ability ~ Sex	-3.59	0.49	[-4.59, -2.70]	-	<
				7.38	.001
Child's cognitive ability ~ PCDF131:Sex	0.83	0.60	[-0.58, 1.79]	1.39	.16
(c:Sex)					
Child's cognitive ability ~ DNAm <i>ESR2</i>	1.80	1.11	[-0.17, 4.19]	1.61	.11
(b)					
Child's cognitive ability ~ Birthweight	1.55x10 ⁻⁰³	5.08x10 ⁻⁰⁴	[0.00, 0.00]	3.04	.002
Child's cognitive ability ~ Mother's education level	0.42	0.21	[0.03, 0.84]	2.05	.04
Child's cognitive ability ~ Mother's BMI before pregnancy	-0.19	0.06	[-0.30, -0.08]	-	<
				3.30	.001
DNAm <i>ESR2</i> ~ PCDF131	-3.86x10 ⁻⁰³	0.03	[-0.07, 0.05]	-	.90
(a)				0.13	
DNAm <i>ESR2</i> ~ Sex	-0.05	0.04	[-0.12, 0.02]	-	.19
				1.31	
DNAm <i>ESR2</i> ~ PCDF131:Sex	0.06	0.05	[-0.03, 0.15]	1.26	.21
(a:Sex)					
DNAm <i>ESR2</i> ~ Birthweight	-1.41x10 ⁻⁰⁵	3.96x10 ⁻⁰⁵	[0.00, 0.00]	-	.72
				0.36	
DNAm <i>ESR2</i> ~ Mother's education level	-0.01	0.01	[-0.04, 0.02]	-	.43
				0.79	
DNAm <i>ESR2</i> ~ Mother's BMI before pregnancy	4.10x10 ⁻⁰³	3.64x10 ⁻⁰³	[0.00, 0.01]	1.12	.26

Note. Coefficient = *Regressions* beta value, *SE* = standard error, CI = confidence interval, *z* = *z*-statistic, *p* = *p*-value, c = c-path, b = b-path, a = a-path.

Table A.122.ii. *Defined model parameters (effects)*

Effect	Coefficient	<i>SE</i>	95% CI	<i>z</i>	<i>p</i>
Indirect (female)	-6.95x10 ⁻⁰³	0.06	[-0.14, 0.12]	-0.11	.91
Total (female)	-0.52	0.46	[-1.16, 0.63]	-1.15	.25
Indirect (male)	0.10	0.10	[-0.03, 0.35]	0.97	.33
Total (male)	0.41	0.39	[-0.43, 1.14]	1.05	.29
Difference in indirect (male - female)	-0.10	0.12	[-0.41, 0.06]	-0.87	.39
Difference in indirect (male - female)	-0.94	0.59	[-1.90, 0.43]	-1.58	.11

Note. Coefficient = estimated model parameter, *SE* = standard error, CI = confidence interval, *z* = *z*-statistic, *p* = *p*-value.

Tables A.123.i & ii. Results of the mediation model with the predictor congener PCDF121, the mean DNA methylation of the CpGs in the promoter region of *AR*, and the predicted mental development index (MDI) of the Bayley Scale (Bayley,1993) as outcome, controlling for confounders for the female and male subsample separately.

Table A.123.i. *Regressions*

	Coefficient	SE	95% CI	z	p
MDI (24m) ~ PCDF121 (c [female])	3.92	3.50	[-2.92, 10.79]	1.12	.26
MDI (24m) ~ DNAm <i>AR</i> (b [female])	2.82	4.12	[-10.57, 6.74]	0.68	.49
MDI (24m) ~ MDI (12m)	0.33	0.10	[0.11, 0.51]	3.23	.001
DNAm <i>AR</i> ~ PCDF121 (a [female])	-0.23	0.14	[-0.55, -0.01]	-1.59	.11
MDI (24m) ~ PCDF121 (c [male])	10.85	3.20	[4.36, 16.96]	3.39	< .001
MDI (24m) ~ DNAm <i>AR</i> (b [male])	-2.21	1.62	[-4.61, 1.16]	-1.36	0.17
MDI (24m) ~ MDI (12m)	0.47	0.11	[0.26, 0.68]	4.41	< .001
DNAm <i>AR</i> ~ PCDF121 (a [male])	0.11	0.17	[-0.25, 0.41]	0.64	.53

Note. Coefficient = *Regressions* beta value, SE = standard error, CI = confidence interval, z = z-statistic, p = p-value, c = c-path, b = b-path, a = a-path.

Table A.123.ii. *Defined model parameters (effects)*

Effect	Coefficient	SE	95% CI	z	p
Indirect (female)	-0.64	0.80	[-2.50, 0.70]	-0.80	.42
Total (female)	3.28	3.45	[-3.64, 10.02]	0.95	.34
Indirect (male)	-0.24	0.42	[-0.95, 0.81]	-0.56	.58
Total (male)	10.61	3.13	[4.42, 16.69]	3.39	< .001
difference in indirect (male - female)	-0.40	0.90	[-2.52, 1.05]	-0.45	.65
difference in Total (male - female)	-7.34	4.68	[-16.75, 1.90]	-1.57	.12

Note. Coefficient = estimated model parameter, SE = standard error, CI = confidence interval, z = z-statistic, p = p-value.

Tables A.124.i & ii. Results of the mediation model with the predictor congener PCDF118, the mean DNA methylation of the CpGs in the promoter region of *ESR1*, and the mental development scale (MDI) of the Bayley Scale of Infant Development (Bayley, 1993) as outcome, controlling for confounders.

Table A.124.i. *Regressions*

	Coefficient	SE	95% CI	z	p
MDI (24m) ~ PCDF118 (c)	5.53	3.59	[-1.52, 12.38]	1.54	.12
MDI (24m) ~ Sex	-3.16	2.31	[-7.72, 1.29]	-1.37	.17
MDI (24m) ~ PCDF118:Sex (c*Sex)	4.51	4.60	[-4.23, 13.80]	0.98	.33
MDI (24m) ~ DNAm <i>ESR1</i> (b)	0.72	4.16	[-7.33, 8.81]	0.17	.86
MDI (24m) ~ MDI (12m)	0.42	0.07	[0.28, 0.55]	6.18	< .001
DNAm <i>ESR1</i> ~ PCDF118 (a)	-0.07	0.06	[-0.18, 0.04]	-1.33	.19
DNAm <i>ESR1</i> ~ Sex	-0.04	0.06	[-0.17, 0.07]	-0.63	.53
DNAm <i>ESR1</i> ~ PCDF118:Sex (a*Sex)	-0.12	0.15	[-0.46, 0.12]	-0.81	.42

Note. Coefficient = *Regressions* beta value, SE = standard error, CI = confidence interval, z = z-statistic, p = p-value, c = c-path, b = b-path, a = a-path.

Table A.124.ii. *Defined model parameters (effects)*

Effect	Coefficient	SE	95% CI	z	p
Indirect (female)	-0.05	0.37	[-0.89, 0.68]	-0.14	.89
Total (female)	5.48	3.56	[-1.56, 12.32]	1.54	.12
Indirect (male)	-0.14	0.78	[-2.15, 1.06]	-0.18	.86
Total (male)	9.90	2.94	[4.08, 15.74]	3.37	< .001
Difference in indirect (male - female)	0.09	0.65	[-0.92, 1.78]	0.13	.90
Difference in Total (male - female)	-4.43	4.60	[-13.58, 4.37]	-0.96	.34

Note. Coefficient = estimated model parameter, SE = standard error, CI = confidence interval, z = z-statistic, p = p-value.

Tables A.125.i & ii. Results of the mediation model with the predictor congener PCDF121, the mean DNA methylation of the CpGs in the promoter region of *ESR1*, and the mental development scale (MDI) of the Bayley Scale of Infant Development (Bayley, 1993) as outcome, controlling for confounders.

Table A.125.i. *Regressions*

	Coefficient	SE	95% CI	z	p
MDI (24m) ~ PCDF121	3.67	3.30	[-2.76, 10.33]	1.11	.27
(c)					
MDI (24m) ~ Sex	-3.04	2.35	[-7.65, 1.64]	-1.29	.20
MDI (24m) ~ PCDF121:Sex	7.22	4.55	[-1.65, 16.17]	1.59	.11
(c*Sex)					
MDI (24m) ~ DNAm <i>ESR1</i>	0.58	4.11	[-7.34, 8.41]	0.14	.89
(b)					
MDI (24m) ~ MDI (12m)	0.41	0.07	[0.27, 0.54]	6.02	< .001
DNAm <i>ESR1</i> ~ PCDF121	-0.06	0.05	[-0.15, 0.05]	-1.18	.24
(a)					
DNAm <i>ESR1</i> ~ Sex	-0.04	0.06	[-0.18, 0.07]	-0.65	.52
DNAm <i>ESR1</i> ~ PCDF121:Sex	-0.12	0.14	[-0.43, 0.11]	-0.84	.40
(a*Sex)					

Note. Coefficient = *Regressions* beta value, SE = standard error, CI = confidence interval, z = z-statistic, p = p-value, c = c-path, b = b-path, a = a-path.

Table A.125.ii. *Defined model parameters (effects)*

Effect	Coefficient	SE	95% CI	z	p
Indirect (female)	-0.04	0.32	[-0.79, 0.57]	-0.11	.91
Total (female)	3.63	3.29	[-2.73, 10.23]	1.10	.27
Indirect (male)	-0.10	0.72	[-1.86, 1.00]	-0.14	.89
Total (male)	10.79	3.13	[4.65, 16.99]	3.44	< .001
Difference in indirect (male - female)	0.07	0.60	[-0.95, 1.60]	0.11	.91
Difference in Total (male - female)	-7.16	4.54	[-16.15, 1.74]	-1.57	.12

Note. Coefficient = estimated model parameter, SE = standard error, CI = confidence interval, z = z-statistic, p = p-value.

Outcome: longitudinal pubertal development

Tables A.126.i & ii. Results of the mediation model with the predictor congener PCDD67, the DNA methylation of the DMR annotated for the gene *PDE6B* as mediator, and the predicted slope of longitudinal pubertal development as outcome, controlling for confounders.

Table A.126.i. *Regressions*

	Coefficient	SE	95% CI	z	p
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Slope of lpd ~ PCDD67 (c)	-8.28x10 ⁻⁰³	4.10x10 ⁻⁰³	[-0.02, 0.00]	-2.02	.04
Slope of lpd ~ Sex	-0.09	4.29x10 ⁻⁰³	[-0.10, -0.08]	-21.15	< .001
Slope of lpd ~ PCDD67:Sex (c:Sex)	0.01	7.64x10 ⁻⁰³	[0.00, 0.03]	1.85	.06
Slope of lpd ~ DNAm DMR (<i>PDE6B</i>) (b)	3.41x10 ⁻⁰³	5.09x10 ⁻⁰³	[-0.01, 0.01]	0.67	.50
Slope of lpd ~ NK	-0.05	0.05	[-0.14, 0.05]	-1.10	.27
DNAm DMR (<i>PDE6B</i>) ~ PCDD67 (a)	0.03	0.09	[-0.14, 0.22]	0.35	.72
DNAm DMR (<i>PDE6B</i>) ~ Sex	0.01	0.06	[-0.11, 0.13]	0.20	.84
DNAm DMR (<i>PDE6B</i>) ~ PCDD67:Sex (a:Sex)	-0.03	0.11	[-0.27, 0.18]	-0.29	.77
DNAm DMR (<i>PDE6B</i>) ~ NK	2.43	0.94	[0.61, 4.31]	2.58	.01

Note. Coefficient = *Regressions* beta value, *SE* = standard error, *CI* = confidence interval, *z* = *z*-statistic, *p* = *p*-value, lpd = longitudinal pubertal development, c = c-path, b = b-path, a = a-path.

Table A.126.ii. *Defined model parameters (effects)*

Effect	Coefficient	<i>SE</i>	95% <i>CI</i>	<i>z</i>	<i>p</i>
Indirect (female)	1.10x10 ⁻⁰⁴	5.70x10 ⁻⁰⁴	[0.00, 0.00]	0.19	.85
Total (female)	-8.17x10 ⁻⁰³	4.10x10 ⁻⁰³	[-0.02, 0.00]	-1.99	.05
Indirect (male)	-3.22x10 ⁻⁰⁶	4.21x10 ⁻⁰⁴	[0.00, 0.00]	-7.65x10 ⁻⁰³	.99
Total (male)	5.88x10 ⁻⁰³	6.25x10 ⁻⁰³	[-0.01, 0.02]	0.94	.35
Difference in indirect (male - female)	1.13x10 ⁻⁰⁴	7.26x10 ⁻⁰⁴	[0.00, 0.00]	0.16	.88
Difference in total (male - female)	-0.01	7.60x10 ⁻⁰³	[-0.03, 0.00]	-1.85	.07

Note. Coefficient = estimated model parameter, *SE* = standard error, *CI* = confidence interval, *z* = *z*-statistic, *p* = *p*-value.

Tables A.127.i & ii. Results of the mediation model with the predictor congener PCDF130, the hubCpG of the *lightcyan1* module as mediator, and the predicted slope of longitudinal pubertal development as outcome, controlling for confounders.

Table A.127.i. *Regressions*

	Coefficient	<i>SE</i>	95% <i>CI</i>	<i>z</i>	<i>p</i>
Slope of lpd ~ PCDF130 (c)	-5.38x10 ⁻⁰⁴	4.00x10 ⁻⁰³	[-0.01, 0.01]	-0.13	.89
Slope of lpd ~ Sex	-0.09	4.21x10 ⁻⁰³	[-0.10, -0.08]	-21.46	< .001
Slope of lpd ~ PCDF130:Sex (c:Sex)	0.01	8.15x10 ⁻⁰³	[0.00, 0.03]	1.42	.16
Slope of lpd ~ hubCpG (<i>lightcyan1</i> module) (b)	4.93x10 ⁻⁰⁴	5.17x10 ⁻⁰³	[-0.01, 0.01]	0.10	.92
Slope of lpd ~ CD4T	9.20x10 ⁻⁰³	0.05	[-0.09, 0.10]	0.20	.84
Slope of lpd ~ B-cells	-0.04	0.06	[-0.16, 0.09]	-0.64	.52
hubCpG (<i>lightcyan1</i> module) ~ PCDF130 (a)	-0.11	0.06	[-0.23, 0.00]	-1.87	.06
hubCpG (<i>lightcyan1</i> module) ~ Sex	1.53x10 ⁻⁰³	0.05	[-0.11, 0.11]	0.03	.98
hubCpG (<i>lightcyan1</i> module) ~ PCDF130:Sex (a:Sex)	0.09	0.08	[-0.07, 0.24]	1.09	.28
hubCpG (<i>lightcyan1</i> module) ~ CD4T	1.61	0.63	[0.40, 2.88]	2.57	.01
hubCpG (<i>lightcyan1</i> module) ~ B-cells	3.58	1.35	[0.99, 6.27]	2.66	.01

Note. Coefficient = *Regressions* beta value, *SE* = standard error, *CI* = confidence interval, *z* = *z*-statistic, *p* = *p*-value, lpd = longitudinal pubertal development, c = c-path, b = b-path, a = a-path.

Table A.127.ii. *Defined model parameters (effects)*

Effect	Coefficient	<i>SE</i>	95% <i>CI</i>	<i>z</i>	<i>p</i>
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Indirect (female)	-5.48x10 ⁻⁰⁵	6.47x10 ⁻⁰⁴	[0.00, 0.00]	-0.08	.93
Total (female)	-5.93x10 ⁻⁰⁴	3.98x10 ⁻⁰³	[-0.01, 0.01]	-0.15	.88
Indirect (male)	-1.12x10 ⁻⁰⁵	3.18x10 ⁻⁰⁴	[0.00, 0.00]	-0.04	.97
Total (male)	0.01	7.26x10 ⁻⁰³	[0.00, 0.03]	1.52	.13
Difference in indirect (male - female)	-4.36x10 ⁻⁰⁵	6.32x10 ⁻⁰⁴	[0.00, 0.00]	-0.07	.95
Difference in total (male - female)	-0.01	8.21x10 ⁻⁰³	[-0.03, 0.00]	-1.41	.16

Note. Coefficient = estimated model parameter, *SE* = standard error, CI = confidence interval, *z* = *z*-statistic, *p* = *p*-value.

Tables A.128.i & ii. Results of the mediation model with the predictor congener PCDF130, the EigenCpG of the salmon module as mediator, and the predicted slope of longitudinal pubertal development as outcome, controlling for confounders in the female subsample.

Table A.128.i. *Regressions*

	Coefficient	<i>SE</i>	95% CI	<i>z</i>	<i>p</i>
Slope of lpd ~ PCDF130	-9.65x10 ⁻⁰⁴	4.14x10 ⁻⁰³	[-0.01, 0.01]	-0.23	.82
(c)					
Slope of lpd ~ EigenCpG (salmon module)	3.00x10 ⁻⁰³	0.03	[-0.07, 0.06]	0.09	.93
(b)					
Slope of lpd ~ B-cells	-0.03	0.06	[-0.13, 0.09]	-0.52	.61
Slope of lpd ~ EPIC array plate	-5.85x10 ⁻⁰³	6.62x10 ⁻⁰³	[-0.02, 0.01]	-0.88	.38
EigenCpG (salmon module) ~ PCDF130	0.02	0.02	[-0.01, 0.06]	1.25	.21
(a)					
EigenCpG (salmon module) ~ B-cells	-1.26	0.34	[-1.81, -0.51]	-3.74	< .001
EigenCpG (salmon module) ~ EPIC array plate	0.13	0.02	[0.09, 0.17]	6.86	< .001

Note. Coefficient = *Regressions* beta value, *SE* = standard error, CI = confidence interval, *z* = *z*-statistic, *p* = *p*-value, lpd = longitudinal pubertal development, c = c-path, b = b-path, a = a-path.

Table A.128.ii. *Defined model parameters (effects)*

Effect	Coefficient	<i>SE</i>	95% CI	<i>z</i>	<i>p</i>
indirect	6.82x10 ⁻⁰⁵	1.06x10 ⁻⁰³	[0.00, 0.00]	0.06	.95
total	-8.97x10 ⁻⁰⁴	4.21x10 ⁻⁰³	[-0.01, 0.01]	-0.21	.83

Note. Coefficient = estimated model parameter, *SE* = standard error, CI = confidence interval, *z* = *z*-statistic, *p* = *p*-value.

Tables A.129.i & ii. Results of the mediation model with the predictor congener PCDF130, the mean DNA methylation of the CpGs in the promoter region of *AR*, and the predicted slope of longitudinal pubertal development as outcome, for the female and male subsample separately.

Table A.129.i. *Regressions*

	Coefficient	<i>SE</i>	95% CI	<i>z</i>	<i>p</i>
Slope of lpd ~ PCDF130 (c [female])	-5.59x10 ⁻⁰⁴	3.88x10 ⁻⁰³	[-0.01, 0.01]	-0.14	.89
Slope of lpd ~ DNAm <i>AR</i> (b [female])	6.03x10 ⁻⁰³	7.29x10 ⁻⁰³	[-0.01, 0.01]	0.83	.41
DNAm <i>AR</i> ~ PCDF130 (a [female])	-0.03	0.04	[-0.13, 0.05]	-0.78	.43
Slope of lpd ~ PCDF130 (c [male])	9.31x10 ⁻⁰³	6.82x10 ⁻⁰³	[0.00, 0.02]	1.37	.17
Slope of lpd ~ DNAm <i>AR</i> (b [male])	2.01x10 ⁻⁰³	0.02	[-0.01, 0.05]	0.13	.90
DNAm <i>AR</i> ~ PCDF130 (a [male])	0.13	0.11	[-0.08, 0.34]	1.21	.23

Note. Coefficient = *Regressions* beta value, *SE* = standard error, CI = confidence interval, *z* = *z*-statistic, *p* = *p*-value, lpd = longitudinal pubertal development, c = c-path, b = b-path, a = a-path.

Table A.129.ii. *Defined model parameters (effects)*

Effect	Coefficient	<i>SE</i>	95% CI	<i>z</i>	<i>p</i>
Indirect (female)	-2.11x10 ⁻⁰⁴	3.68x10 ⁻⁰⁴	[0.00, 0.00]	-0.57	.57
Total (female)	-7.70x10 ⁻⁰⁴	3.85x10 ⁻⁰³	[-0.01, 0.01]	-0.20	.84
Indirect (male)	2.58x10 ⁻⁰⁴	1.74x10 ⁻⁰³	[0.00, 0.00]	0.15	.88

Total (male)	9.57x10 ⁻⁰³	6.80x10 ⁻⁰³	[0.00, 0.02]	1.41	.16
Difference in indirect (male - female)	-4.69x10 ⁻⁰⁴	1.78x10 ⁻⁰³	[-0.01, 0.00]	-0.26	.79
Difference in total (male - female)	-0.01	7.76x10 ⁻⁰³	[-0.03, 0.00]	-1.33	.18

Note. Coefficient = estimated model parameter, SE = standard error, CI = confidence interval, $z = z$ -statistic, $p = p$ -value.

Tables A.130.i & ii. Results of the mediation model with the predictor congener PCDD70, the mean DNA methylation of the CpGs in the promoter region of *ESR2*, and the predicted slope of longitudinal pubertal development as outcome.

Table A.130.i. *Regressions*

	Coefficient	SE	95% CI	z	p
Slope of lpd ~ PCDD70	-0.01	3.66x10 ⁻⁰³	[-0.02, 0.00]	-2.89	.004
(c)					
Slope of lpd ~ Sex	-0.09	3.79x10 ⁻⁰³	[-0.10, -0.08]	-23.39	< .001
Slope of lpd ~ PCDD70:Sex	0.02	6.90x10 ⁻⁰³	[0.00, 0.03]	2.21	.03
(c:Sex)					
Slope of lpd ~ DNAm <i>ESR2</i>	0.02	7.23x10 ⁻⁰³	[0.01, 0.03]	2.47	.013
(b)					
DNAm <i>ESR2</i> ~ PCDD70	-0.01	0.04	[-0.09, 0.06]	-0.36	.72
(a)					
DNAm <i>ESR2</i> ~ Sex	-0.05	0.04	[-0.12, 0.02]	-1.27	.20
DNAm <i>ESR2</i> ~ PCDD70:Sex	0.02	0.08	[-0.16, 0.17]	0.20	.84
(a:Sex)					

Note. Coefficient = *Regressions* beta value, SE = standard error, CI = confidence interval, $z = z$ -statistic, $p = p$ -value, lpd = longitudinal pubertal development, c = c-path, b = b-path, a = a-path.

Table A.130.ii. *Defined model parameters (effects)*

Effect	Coefficient	SE	95% CI	z	p
Indirect (female)	-2.50x10 ⁻⁰⁴	7.77x10 ⁻⁰⁴	[0.00, 0.00]	-0.32	.75
Total (female)	-0.01	3.77x10 ⁻⁰³	[-0.02, 0.00]	-2.88	.004
Indirect (male)	5.23x10 ⁻⁰⁵	1.49x10 ⁻⁰³	[0.00, 0.00]	0.04	.97
Total (male)	4.73x10 ⁻⁰³	5.78x10 ⁻⁰³	[-0.01, 0.02]	0.82	.41
Difference in indirect (male - female)	-3.02x10 ⁻⁰⁴	1.71x10 ⁻⁰³	[0.00, 0.00]	-0.18	.86
Difference in total (male - female)	-0.02	6.88x10 ⁻⁰³	[-0.03, 0.00]	-2.26	.02

Note. Coefficient = estimated model parameter, SE = standard error, CI = confidence interval, $z = z$ -statistic, $p = p$ -value.

Tables A.131.i & ii. Results of the mediation model with the predictor congener PCDF131, the mean DNA methylation of the CpGs in the promoter region of *ESR2*, and the predicted slope of longitudinal pubertal development as outcome.

Table A.131.i. *Regressions*

	Coefficient	SE	95% CI	z	p
Slope of lpd ~ PCDF131	-2.94x10 ⁻⁰³	2.70x10 ⁻⁰³	[-0.01, 0.00]	-1.09	.28
(c)					
Slope of lpd ~ Sex	-0.09	3.87x10 ⁻⁰³	[-0.09, -0.08]	-22.47	< .001
Slope of lpd ~ PCDF131:Sex	4.84x10 ⁻⁰³	4.95x10 ⁻⁰³	[0.00, 0.02]	0.98	.33
(c:Sex)					
Slope of lpd ~ DNAm <i>ESR2</i>	0.02	7.73x10 ⁻⁰³	[0.00, 0.04]	2.32	.02
(b)					
DNAm <i>ESR2</i> ~ PCDF131	-0.01	0.03	[-0.07, 0.05]	-0.38	.70
(a)					
DNAm <i>ESR2</i> ~ Sex	-0.05	0.04	[-0.12, 0.02]	-1.29	.20
DNAm <i>ESR2</i> ~ PCDF131:Sex	0.06	0.05	[-0.03, 0.15]	1.23	.22
(a:Sex)					

Note. Coefficient = *Regressions* beta value, *SE* = standard error, *CI* = confidence interval, *z* = *z*-statistic, *p* = *p*-value, *lpd* = longitudinal pubertal development, *c* = *c*-path, *b* = *b*-path, *a* = *a*-path.

Table A.131.ii. *Defined model parameters (effects)*

Effect	Coefficient	<i>SE</i>	95% <i>CI</i>	<i>z</i>	<i>p</i>
Indirect (female)	-2.03x10 ⁻⁰⁴	5.97x10 ⁻⁰⁴	[0.00, 0.00]	-0.34	.73
Total (female)	-3.14x10 ⁻⁰³	2.87x10 ⁻⁰³	[-0.01, 0.00]	-1.10	.27
Indirect (male)	8.05x10 ⁻⁰⁴	8.11x10 ⁻⁰⁴	[0.00, 0.00]	0.99	.32
Total (male)	2.71x10 ⁻⁰³	4.18x10 ⁻⁰³	[0.00, 0.01]	0.65	.52
Difference in indirect (male - female)	-1.01x10 ⁻⁰³	1.06x10 ⁻⁰³	[0.00, 0.00]	-0.96	.34
Difference in total (male - female)	-5.85x10 ⁻⁰³	5.03x10 ⁻⁰³	[-0.02, 0.00]	-1.16	.24

Note. Coefficient = estimated model parameter, *SE* = standard error, *CI* = confidence interval, *z* = *z*-statistic, *p* = *p*-value.

Tables A.132.i & ii. Results of the mediation model with the predictor congener PCB126, the DNA methylation of the DMR annotated for the gene *RNF19A* as mediator, and the predicted difference in PDS score between baseline (t0) & last follow-up (t5) as outcome, controlling for confounders.

Table A.132.i. *Regressions*

	Coefficient	<i>SE</i>	95% <i>CI</i>	<i>z</i>	<i>p</i>
PDS score (t5-t0) ~ PCB126	0.02	0.03	[-0.05, 0.06]	0.60	.55
(c)					
PDS score (t5-t0) ~ Sex	-0.80	0.04	[-0.88, -0.72]	-18.98	< .001
PDS score (t5-t0) ~ PCB126:Sex	0.06	0.08	[-0.13, 0.19]	0.75	.46
(c:Sex)					
PDS score (t5-t0) ~ DNAm DMP (<i>RNF19A</i>)	0.07	0.06	[-0.06, 0.18]	1.07	.28
(b)					
PDS score (t5-t0) ~ CD4T	-0.15	0.38	[-0.97, 0.50]	-0.40	.69
PDS score (t5-t0) ~ CD8T	0.37	0.88	[-1.46, 1.99]	0.42	.67
PDS score (t5-t0) ~ NK	-0.80	0.53	[-1.75, 0.34]	-1.53	.13
DNAm DMP (<i>RNF19A</i>) ~ PCB126	-0.06	0.03	[-0.13, 0.01]	-1.69	.09
(a)					
DNAm DMP (<i>RNF19A</i>) ~ Sex	0.09	0.05	[-0.01, 0.19]	1.66	.10
DNAm DMP (<i>RNF19A</i>) ~ PCB126:Sex	0.04	0.10	[-0.15, 0.23]	0.38	.71
(a:Sex)					
DNAm DMP (<i>RNF19A</i>) ~ CD4T	1.19	0.46	[0.28, 2.06]	2.58	.01
DNAm DMP (<i>RNF19A</i>) ~ CD8T	2.28	1.10	[0.15, 4.44]	2.08	.04
DNAm DMP (<i>RNF19A</i>) ~ NK	1.68	0.76	[0.16, 3.15]	2.21	.03

Note. Coefficient = *Regressions* beta value, *SE* = standard error, *CI* = confidence interval, *z* = *z*-statistic, *p* = *p*-value, *c* = *c*-path, *b* = *b*-path, *a* = *a*-path.

Table A.132.ii. *Defined model parameters (effects)*

Effect	Coefficient	<i>SE</i>	95% <i>CI</i>	<i>z</i>	<i>p</i>
Indirect (female)	-3.77x10 ⁻⁰³	4.60x10 ⁻⁰³	[-0.01, 0.00]	-0.82	.41
Total (female)	0.01	0.03	[-0.05, 0.05]	0.45	.65
Indirect (male)	-1.36x10 ⁻⁰³	8.13x10 ⁻⁰³	[-0.02, 0.01]	-0.17	.87
Total (male)	0.07	0.08	[-0.11, 0.19]	0.98	.33
Difference in indirect (male - female)	-2.41x10 ⁻⁰³	8.41x10 ⁻⁰³	[-0.02, 0.01]	-0.29	.78
Difference in total (male - female)	-0.06	0.08	[-0.19, 0.12]	-0.78	.43

Note. Coefficient = estimated model parameter, *SE* = standard error, *CI* = confidence interval, *z* = *z*-statistic, *p* = *p*-value.

Tables A.133.i & ii. Results of the mediation model with the predictor congener PCB169, the DNA methylation of the DMP annotated for the gene *CRYBG3* as mediator, and the predicted difference in PDS score between baseline (t0) & last follow-up (t5) as outcome.

Table A.133.i. *Regressions*

	Coefficient	SE	95% CI	z	p
PDS score (t5-t0) ~ PCB169 (c)	-0.04	0.04	[-0.12, 0.04]	-0.98	.33
PDS score (t5-t0) ~ Sex	-0.79	0.04	[-0.86, -0.71]	-20.96	< .001
PDS score (t5-t0) ~ PCB169:Sex (c:Sex)	0.20	0.06	[0.08, 0.32]	3.25	.001
PDS score (t5-t0) ~ DNAm DMP (<i>CRYBG3</i>) (b)	0.01	0.06	[-0.09, 0.13]	0.19	.85
DNAm DMP (<i>CRYBG3</i>) ~ PCB169 (a)	0.13	0.06	[0.02, 0.24]	2.32	.02
DNAm DMP (<i>CRYBG3</i>) ~ Sex	-0.06	0.05	[-0.17, 0.04]	-1.22	.22
DNAm DMP (<i>CRYBG3</i>) ~ PCB169:Sex (a:Sex)	-0.19	0.07	[-0.33, -0.05]	-2.70	.01

Note. Coefficient = *Regressions* beta value, SE = standard error, CI = confidence interval, z = z-statistic, p = p-value, c = c-path, b = b-path, a = a-path.

Table A.133.ii. *Defined model parameters (effects)*

Effect	Coefficient	SE	95% CI	z	p
Indirect (female)	1.41x10 ⁻⁰³	8.00x10 ⁻⁰³	[-0.01, 0.02]	0.18	.86
Total (female)	-0.04	0.04	[-0.11, 0.03]	-1.01	.31
Indirect (male)	-6.86x10 ⁻⁰⁴	4.34x10 ⁻⁰³	[-0.01, 0.01]	-0.16	.87
Total (male)	0.16	0.05	[0.06, 0.24]	3.43	< .001
Difference in indirect (male - female)	2.10x10 ⁻⁰³	0.01	[-0.02, 0.03]	0.18	.86
Difference in total (male - female)	-0.19	0.06	[-0.31, -0.08]	-3.31	< .001

Note. Coefficient = estimated model parameter, SE = standard error, CI = confidence interval, z = z-statistic, p = p-value.

Tables A.134.i & ii. Results of the mediation model with the predictor congener PCDD66, the DNA methylation of the DMR annotated for the gene *EIF2AK4* as mediator, and the predicted difference in PDS score between baseline (t0) & last follow-up (t5) as outcome, controlling for confounders.

Table A.134.i. *Regressions*

	Coefficient	SE	95% CI	z	p
PDS score (t5-t0) ~ PCDD66 (c)	-0.03	0.05	[-0.12, 0.06]	-0.68	.50
PDS score (t5-t0) ~ Sex	-0.77	0.04	[-0.85, -0.69]	-17.85	< .001
PDS score (t5-t0) ~ PCDD66:Sex (c:Sex)	0.12	0.07	[-0.03, 0.26]	1.58	.11
PDS score (t5-t0) ~ DNAm DMR (<i>EIF2AK4</i>) (b)	0.07	0.04	[0.00, 0.15]	1.84	.07
PDS score (t5-t0) ~ Mother's BMI before pregnancy	2.64x10 ⁻⁰³	3.31x10 ⁻⁰³	[0.00, 0.01]	0.80	.43
DNAm DMR (<i>EIF2AK4</i>) ~ PCDD66 (a)	-0.13	0.09	[-0.30, 0.04]	-1.47	.14
DNAm DMR (<i>EIF2AK4</i>) ~ Sex	-0.16	0.08	[-0.31, -0.01]	-2.02	.04
DNAm DMR (<i>EIF2AK4</i>) ~ PCDD66:Sex (a:Sex)	-0.03	0.17	[-0.36, 0.32]	-0.15	.88
DNAm DMR (<i>EIF2AK4</i>) ~ Mother's BMI before pregnancy	-0.02	7.72x10 ⁻⁰³	[-0.04, 0.00]	-2.75	.01

Note. Coefficient = *Regressions* beta value, *SE* = standard error, *CI* = confidence interval, *z* = *z*-statistic, *p* = *p*-value, *c* = *c*-path, *b* = *b*-path, *a* = *a*-path.

Table A.134.ii. *Defined model parameters (effects)*

Effect	Coefficient	<i>SE</i>	95% CI	<i>z</i>	<i>p</i>
Indirect (female)	-9.34x10 ⁻⁰³	9.35x10 ⁻⁰³	[-0.03, 0.00]	-1.00	.32
Total (female)	-0.04	0.05	[-0.13, 0.05]	-0.90	.37
Indirect (male)	-0.01	0.01	[-0.05, 0.01]	-0.80	.42
Total (male)	0.08	0.06	[-0.05, 0.20]	1.25	.21
Difference in indirect (male - female)	1.89x10 ⁻⁰³	0.01	[-0.03, 0.03]	0.13	.90
Difference in total (male - female)	-0.12	0.08	[-0.26, 0.03]	-1.54	.12

Note. Coefficient = estimated model parameter, *SE* = standard error, *CI* = confidence interval, *z* = *z*-statistic, *p* = *p*-value.

Tables A.135.i & ii. Results of the mediation model with the predictor congener PCDD67, the DNA methylation of the DMR annotated for the gene *PDE6B* as mediator, and the predicted difference in PDS score between baseline (t0) & last follow-up (t5) as outcome, controlling for confounders.

Table A.135.i. *Regressions*

	Coefficient	<i>SE</i>	95% CI	<i>z</i>	<i>p</i>
PDS score (t5-t0) ~ PCDD67	-0.03	0.05	[-0.12, 0.07]	-0.70	.49
(c)					
PDS score (t5-t0) ~ Sex	-0.80	0.04	[-0.88, -0.72]	-19.97	< .001
PDS score (t5-t0) ~ PCDD67:Sex	0.12	0.09	[-0.06, 0.27]	1.43	.15
(c:Sex)					
PDS score (t5-t0) ~ DNAm DMR (<i>PDE6B</i>)	0.01	0.06	[-0.11, 0.13]	0.24	.81
(b)					
PDS score (t5-t0) ~ NK	-0.80	0.55	[-1.79, 0.38]	-1.46	.14
DNAm DMR (<i>PDE6B</i>) ~ PCDD67	0.03	0.09	[-0.14, 0.22]	0.35	.73
(a)					
DNAm DMR (<i>PDE6B</i>) ~ Sex	0.01	0.06	[-0.11, 0.13]	0.20	.84
DNAm DMR (<i>PDE6B</i>) ~ PCDD67:Sex	-0.03	0.11	[-0.26, 0.18]	-0.29	.77
(a:Sex)					
DNAm DMR (<i>PDE6B</i>) ~ NK	2.43	0.95	[0.70, 4.40]	2.55	.01

Note. Coefficient = *Regressions* beta value, *SE* = standard error, *CI* = confidence interval, *z* = *z*-statistic, *p* = *p*-value, *c* = *c*-path, *b* = *b*-path, *a* = *a*-path.

Table A.135.ii. *Defined model parameters (effects)*

Effect	Coefficient	<i>SE</i>	95% CI	<i>z</i>	<i>p</i>
Indirect (female)	4.71x10 ⁻⁰⁴	5.95x10 ⁻⁰³	[-0.01, 0.01]	0.08	.94
Total (female)	-0.03	0.05	[-0.12, 0.07]	-0.70	.49
Indirect (male)	-1.38x10 ⁻⁰⁵	4.24x10 ⁻⁰³	[-0.01, 0.01]	-3.26x10 ⁻⁰³	.997
Total (male)	0.09	0.07	[-0.06, 0.21]	1.30	.20
Difference in indirect (male - female)	4.85x10 ⁻⁰⁴	7.18x10 ⁻⁰³	[-0.01, 0.02]	0.07	.95
Difference in total (male - female)	-0.12	0.08	[-0.27, 0.06]	-1.44	.15

Note. Coefficient = estimated model parameter, *SE* = standard error, *CI* = confidence interval, *z* = *z*-statistic, *p* = *p*-value.

Tables A.136.i & ii. Results of the mediation model with the predictor congener PCDD70, the DNA methylation of the DMP annotated for the gene *H2BC5* as mediator, and the predicted difference in PDS score between baseline (t0) & last follow-up (t5) as outcome, controlling for confounders.

Table A.136.i. *Regressions*

	Coefficient	<i>SE</i>	95% CI	<i>z</i>	<i>p</i>
PDS score (t5-t0) ~ PCDD70	-0.02	0.04	[-0.09, 0.07]	-0.44	.66
(c)					

PDS score (t5-t0) ~ Sex	-0.77	0.04	[-0.85, -0.69]	-19.31	< .001
PDS score (t5-t0) ~ PCDD70:Sex (c:Sex)	0.09	0.08	[-0.08, 0.22]	1.15	.25
PDS score (t5-t0) ~ DNAm DMP (<i>H2BC5</i>) (b)	-0.05	0.05	[-0.14, 0.07]	-0.88	.38
PDS score (t5-t0) ~ Gestational length	0.02	0.02	[-0.02, 0.04]	0.90	.37
DNAm DMP (<i>H2BC5</i>) ~ PCDD70 (a)	0.16	0.11	[-0.04, 0.37]	1.48	.14
DNAm DMP (<i>H2BC5</i>) ~ Sex	0.01	0.10	[-0.19, 0.19]	0.11	.92
DNAm DMP (<i>H2BC5</i>) ~ PCDD70:Sex (a:Sex)	0.20	0.32	[-0.31, 0.93]	0.62	.53
DNAm DMP (<i>H2BC5</i>) ~ Gestational length	0.10	0.04	[0.04, 0.18]	2.77	.01

Note. Coefficient = *Regressions* beta value, *SE* = standard error, CI = confidence interval, *z* = *z*-statistic, *p* = *p*-value, c = c-path, b = b-path, a = a-path.

Table A.136.ii. *Defined model parameters (effects)*

Effect	Coefficient	<i>SE</i>	95% CI	<i>z</i>	<i>p</i>
Indirect (female)	-7.42x10 ⁻⁰³	0.01	[-0.03, 0.01]	-0.69	.49
Total (female)	-0.03	0.04	[-0.10, 0.07]	-0.61	.54
Indirect (male)	-0.02	0.03	[-0.08, 0.03]	-0.60	.55
Total (male)	0.05	0.07	[-0.09, 0.17]	0.78	.44
Difference in indirect (male - female)	9.50x10 ⁻⁰³	0.02	[-0.03, 0.07]	0.40	.69
Difference in total (male - female)	-0.08	0.08	[-0.22, 0.10]	-0.97	.33

Note. Coefficient = estimated model parameter, *SE* = standard error, CI = confidence interval, *z* = *z*-statistic, *p* = *p*-value.

Tables A.137.i & ii. Results of the mediation model with the predictor congener PCDD75, the DNA methylation of the DMP annotated for the gene *LNFG* as mediator, and the predicted difference in PDS score between baseline (t0) & last follow-up (t5) as outcome.

Table A.137.i. *Regressions*

	Coefficient	<i>SE</i>	95% CI	<i>z</i>	<i>p</i>
PDS score (t5-t0) ~ PCDD75 (c)	-0.03	0.04	[-0.12, 0.05]	-0.76	.50
PDS score (t5-t0) ~ Sex	-0.78	0.04	[-0.85, -0.69]	-19.46	< .001
PDS score (t5-t0) ~ PCDD75:Sex (c:Sex)	0.15	0.07	[0.02, 0.29]	2.22	.03
PDS score (t5-t0) ~ DNAm DMP (<i>LNFG</i>) (b)	-0.12	0.10	[-0.35, 0.04]	-1.20	.23
DNAm DMP (<i>LNFG</i>) ~ PCDD75 (a)	0.01	0.07	[-0.15, 0.14]	0.14	.89
DNAm DMP (<i>LNFG</i>) ~ Sex	0.05	0.10	[-0.13, 0.26]	0.48	.63
DNAm DMP (<i>LNFG</i>) ~ PCDD75:Sex (a:Sex)	0.21	0.21	[-0.12, 0.67]	1.02	.31

Note. Coefficient = *Regressions* beta value, *SE* = standard error, CI = confidence interval, *z* = *z*-statistic, *p* = *p*-value, c = c-path, b = b-path, a = a-path.

Table A.137.ii. *Defined model parameters (effects)*

Effect	Coefficient	<i>SE</i>	95% CI	<i>z</i>	<i>p</i>
Indirect (female)	-1.22x10 ⁻⁰³	0.01	[-0.03, 0.03]	-0.10	.92
Total (female)	-0.03	0.04	[-0.11, 0.05]	-0.81	.42
Indirect (male)	-0.03	0.04	[-0.13, 0.02]	-0.69	.49
Total (male)	0.09	0.06	[-0.05, 0.21]	1.44	.15
Difference in indirect (male - female)	0.03	0.04	[-0.02, 0.14]	0.63	.53
Difference in total (male - female)	-0.13	0.08	[-0.27, 0.05]	-1.59	.11

Note. Coefficient = estimated model parameter, *SE* = standard error, *CI* = confidence interval, *z* = *z*-statistic, *p* = *p*-value.

Tables A.138.i & ii. Results of the mediation model with the predictor congener PCDF130, the DNA methylation of the hubCpG of the salmon module as mediator, and the predicted difference in PDS score between baseline (t0) & last follow-up (t5) as outcome, controlling for confounders.

Table A.138.i. *Regressions*

	Coefficient	<i>SE</i>	95% CI	<i>z</i>	<i>p</i>
PDS score (t5-t0) ~ PCDF130 (c)	-0.03	0.03	[-0.10, 0.02]	-0.96	.34
PDS score (t5-t0) ~ Sex	-0.81	0.04	[-0.88, -0.74]	-21.76	< .001
PDS score (t5-t0) ~ PCDF130:Sex (c:Sex)	0.11	0.06	[0.01, 0.24]	1.96	.05
PDS score (t5-t0) ~ hubCpG (salmon module) (b)	0.03	0.06	[-0.08, 0.14]	0.57	.57
PDS score (t5-t0) ~ Mother's age at birth	8.69x10 ⁻⁰³	4.42x10 ⁻⁰³	[0.00, 0.02]	1.97	.05
PDS score (t5-t0) ~ EPIC array plate	-0.15	0.04	[-0.22, -0.08]	-4.06	< .001
hubCpG (salmon module) ~ PCDF130 (a)	0.03	0.05	[-0.07, 0.14]	0.55	.58
hubCpG (salmon module) ~ Sex	0.16	0.05	[0.07, 0.26]	3.19	.001
hubCpG (salmon module) ~ PCDF130:Sex (a:Sex)	-0.08	0.08	[-0.24, 0.08]	-0.93	.35
hubCpG (salmon module) ~ Mother's age at birth	0.01	5.44x10 ⁻⁰³	[0.00, 0.02]	1.96	.05
hubCpG (salmon module) ~ EPIC array plate	0.24	0.05	[0.15, 0.34]	4.94	< .001

Note. Coefficient = *Regressions* beta value, *SE* = standard error, *CI* = confidence interval, *z* = *z*-statistic, *p* = *p*-value, c = c-path, b = b-path, a = a-path.

Table A.138.ii. *Defined model parameters (effects)*

Effect	Coefficient	<i>SE</i>	95% CI	<i>z</i>	<i>p</i>
Indirect (female)	9.24x10 ⁻⁰⁴	3.78x10 ⁻⁰³	[-0.01, 0.01]	0.24	.81
Total (female)	-0.03	0.03	[-0.10, 0.02]	-0.93	.35
Indirect (male)	-1.45x10 ⁻⁰³	4.71x10 ⁻⁰³	[-0.01, 0.01]	-0.31	.76
Total (male)	0.08	0.05	[-0.02, 0.19]	1.59	.11
Difference in indirect (male - female)	2.37x10 ⁻⁰³	6.65x10 ⁻⁰³	[-0.01, 0.02]	0.36	.72
Difference in total (male - female)	-0.11	0.06	[-0.24, 0.00]	-1.93	.05

Note. Coefficient = estimated model parameter, *SE* = standard error, *CI* = confidence interval, *z* = *z*-statistic, *p* = *p*-value.

Tables A.139.i & ii. Results of the mediation model with the predictor congener PCDF130, the DNA methylation of the hubCpG of the brown module as mediator, and the predicted difference in PDS score between baseline (t0) & last follow-up (t5) as outcome, controlling for confounders.

Table A.139.i. *Regressions*

	Coefficient	<i>SE</i>	95% CI	<i>z</i>	<i>p</i>
PDS score (t5-t0) ~ PCDF130 (c)	2.51x10 ⁻⁰³	0.03	[-0.06, 0.06]	0.08	.94
PDS score (t5-t0) ~ Sex	-0.78	0.04	[-0.86, -0.71]	-19.42	< .001
PDS score (t5-t0) ~ PCDF130:Sex (c:Sex)	0.12	0.07	[-0.02, 0.26]	1.68	.09
PDS score (t5-t0) ~ hubCpG (brown module) (b)	-0.04	0.04	[-0.11, 0.03]	-1.05	.29
PDS score (t5-t0) ~ B-cells	-1.28	0.69	[-2.43, 0.20]	-1.85	.06

hubCpG (brown module) ~ PCDF130 (a)	0.10	0.11	[-0.13, 0.32]	0.84	.40
hubCpG (brown module) ~ Sex	0.18	0.10	[-0.01, 0.38]	1.80	.07
hubCpG (brown module) ~ PCDF130:Sex (a:Sex)	-0.23	0.15	[-0.53, 0.05]	-1.58	.12
hubCpG (brown module) ~ B-cells	-6.55	2.25	[-11.00, -2.22]	-2.92	.004

Note. Coefficient = *Regressions* beta value, *SE* = standard error, CI = confidence interval, *z* = *z*-statistic, *p* = *p*-value, c = c-path, b = b-path, a = a-path.

Table A.139.ii. *Defined model parameters (effects)*

Effect	Coefficient	<i>SE</i>	95% CI	<i>z</i>	<i>p</i>
Indirect (female)	-3.76x10 ⁻⁰³	7.76x10 ⁻⁰³	[-0.03, 0.01]	-0.48	.63
Total (female)	-1.25x10 ⁻⁰³	0.03	[-0.07, 0.05]	-0.04	.97
Indirect (male)	5.26x10 ⁻⁰³	7.30x10 ⁻⁰³	[0.00, 0.02]	0.72	.47
Total (male)	0.13	0.06	[0.00, 0.24]	2.05	.04
Difference in indirect (male - female)	-9.02x10 ⁻⁰³	0.01	[-0.04, 0.01]	-0.70	.48
Difference in total (male - female)	-0.13	0.07	[-0.27, 0.01]	-1.83	.07

Note. Coefficient = estimated model parameter, *SE* = standard error, CI = confidence interval, *z* = *z*-statistic, *p* = *p*-value.

Tables A.140.i & ii. Results of the mediation model with the predictor congener PCDF130, the DNA methylation of the hubCpG of the yellow module as mediator, and the predicted difference in PDS score between baseline (t0) & last follow-up (t5) as outcome, controlling for confounders.

Table A.140.i. *Regressions*

	Coefficient	<i>SE</i>	95% CI	<i>z</i>	<i>p</i>
PDS score (t5-t0) ~ PCDF130 (c)	-8.71x10 ⁻⁰³	0.04	[-0.09, 0.05]	-0.24	.81
PDS score (t5-t0) ~ Sex	-0.79	0.03	[-0.86, -0.72]	-22.55	< .001
PDS score (t5-t0) ~ PCDF130:Sex (c:Sex)	0.10	0.07	[-0.03, 0.23]	1.40	.16
PDS score (t5-t0) ~ hubCpG (yellow module) (b)	-0.06	0.06	[-0.18, 0.04]	-1.09	.28
PDS score (t5-t0) ~ B-cells	-1.15	0.63	[-2.30, 0.15]	-1.81	.07
PDS score (t5-t0) ~ EPIC array plate	-0.12	0.03	[-0.19, -0.05]	-3.55	< .001
hubCpG (yellow module) ~ PCDF130 (a)	-0.05	0.08	[-0.22, 0.10]	-0.65	.51
hubCpG (yellow module) ~ Sex	0.02	0.06	[-0.09, 0.14]	0.42	.67
hubCpG (yellow module) ~ PCDF130:Sex (a:Sex)	0.05	0.10	[-0.14, 0.25]	0.48	.63
hubCpG (yellow module) ~ B-cells	-2.94	1.08	[-5.21, -0.96]	-2.72	.01
hubCpG (yellow module) ~ EPIC array plate	-0.14	0.06	[-0.26, -0.03]	-2.33	.02

Note. Coefficient = *Regressions* beta value, *SE* = standard error, CI = confidence interval, *z* = *z*-statistic, *p* = *p*-value, c = c-path, b = b-path, a = a-path.

Table A.140.ii. *Defined model parameters (effects)*

Effect	Coefficient	<i>SE</i>	95% CI	<i>z</i>	<i>p</i>
Indirect (female)	3.28x10 ⁻⁰³	8.45x10 ⁻⁰³	[-0.01, 0.03]	0.39	.70
Total (female)	-5.43x10 ⁻⁰³	0.04	[-0.08, 0.06]	-0.15	.88
Indirect (male)	3.92x10 ⁻⁰⁴	4.85x10 ⁻⁰³	[-0.01, 0.01]	0.08	.94
Total (male)	0.09	0.06	[-0.03, 0.21]	1.46	.14
Difference in indirect (male - female)	2.89x10 ⁻⁰³	9.48x10 ⁻⁰³	[-0.01, 0.03]	0.31	.76
Difference in total (male - female)	-0.09	0.07	[-0.23, 0.04]	-1.37	.17

Note. Coefficient = estimated model parameter, *SE* = standard error, CI = confidence interval, *z* = *z*-statistic, *p* = *p*-value.

Tables A.141.i & ii. Results of the mediation model with the predictor congener PCDF130, the DNA methylation of the hubCpG of the white module as mediator, and the predicted difference in PDS score between baseline (t0) & last follow-up (t5) as outcome, controlling for confounders.

Table A.141.i. *Regressions*

	Coefficient	SE	95% CI	z	p
PDS score (t5-t0) ~ PCDF130 (c)	0.01	0.04	[-0.07, 0.09]	0.30	.77
PDS score (t5-t0) ~ Sex	-0.80	0.03	[-0.87, -0.73]	-23.15	< .001
PDS score (t5-t0) ~ PCDF130:Sex (c:Sex)	0.10	0.07	[-0.03, 0.23]	1.48	.14
PDS score (t5-t0) ~ hubCpG (white module) (b)	0.08	0.07	[-0.04, 0.22]	1.20	.23
PDS score (t5-t0) ~ Mother's education level	-0.02	0.02	[-0.06, 0.01]	-1.44	.15
PDS score (t5-t0) ~ B-cells	-1.15	0.63	[-2.35, 0.11]	-1.83	.07
PDS score (t5-t0) ~ EPIC array plate	-0.11	0.03	[-0.18, -0.04]	-3.21	.001
hubCpG (white module) ~ PCDF130 (a)	-0.04	0.07	[-0.18, 0.11]	-0.51	.61
hubCpG (white module) ~ Sex	0.01	0.06	[-0.10, 0.13]	0.26	.79
hubCpG (white module) ~ PCDF130:Sex (a:Sex)	-0.08	0.10	[-0.27, 0.11]	-0.81	.42
hubCpG (white module) ~ Mother's education level	0.06	0.02	[0.01, 0.10]	2.44	.02
hubCpG (white module) ~ B-cells	2.98	1.16	[0.78, 5.34]	2.56	.01
hubCpG (white module) ~ EPIC array plate	0.10	0.06	[-0.01, 0.21]	1.68	.09

Note. Coefficient = *Regressions* beta value, SE = standard error, CI = confidence interval, z = z-statistic, p = p-value, c = c-path, b = b-path, a = a-path.

Table A.141.ii. *Defined model parameters (effects)*

Effect	Coefficient	SE	95% CI	z	p
Indirect (female)	-2.95x10 ⁻⁰³	7.98x10 ⁻⁰³	[-0.02, 0.01]	-0.37	.71
Total (female)	8.85x10 ⁻⁰³	0.04	[-0.07, 0.08]	0.23	.82
Indirect (male)	-9.01x10 ⁻⁰³	9.78x10 ⁻⁰³	[-0.03, 0.00]	-0.92	.36
Total (male)	0.10	0.06	[-0.01, 0.21]	1.76	.08
Difference in indirect (male - female)	6.06x10 ⁻⁰³	0.01	[-0.01, 0.04]	0.53	.60
Difference in total (male - female)	-0.09	0.07	[-0.23, 0.04]	-1.38	.17

Note. Coefficient = estimated model parameter, SE = standard error, CI = confidence interval, z = z-statistic, p = p-value.

Tables A.142.i & ii. Results of the mediation model with the predictor congener PCDF130, the DNA methylation of the hubCpG of the lightcyan1 module as mediator, and the predicted difference in PDS score between baseline (t0) & last follow-up (t5) as outcome, controlling for confounders.

Table A.143.i. *Regressions*

	Coefficient	SE	95% CI	z	p
PDS score (t5-t0) ~ PCDF130 (c)	-1.75x10 ⁻⁰³	0.03	[-0.07, 0.05]	-0.05	.96
PDS score (t5-t0) ~ Sex	-0.79	0.04	[-0.87, -0.72]	-20.47	< .001
PDS score (t5-t0) ~ PCDF130:Sex (c:Sex)	0.13	0.07	[-0.01, 0.27]	1.89	.06
PDS score (t5-t0) ~ hubCpG (lightcyan1 module) (b)	-8.69x10 ⁻⁰⁴	0.06	[-0.10, 0.13]	-0.01	.99
PDS score (t5-t0) ~ CD4T	0.19	0.42	[-0.73, 0.94]	0.44	.66
PDS score (t5-t0) ~ B-cells	-1.22	0.80	[-2.67, 0.41]	-1.51	.13
hubCpG (lightcyan1 module) ~ PCDF130 (a)	-0.11	0.06	[-0.23, 0.00]	-1.90	.06
hubCpG (lightcyan1 module) ~ Sex	1.52x10 ⁻⁰³	0.05	[-0.11, 0.11]	0.03	.98

hubCpG (lightcyan1 module) ~ PCDF130:Sex (a:Sex)	0.09	0.08	[-0.07, 0.24]	1.09	.27
hubCpG (lightcyan1 module) ~ CD4T	1.61	0.63	[0.40, 2.89]	2.54	.01
hubCpG (lightcyan1 module) ~ B-cells	3.58	1.32	[1.02, 6.15]	2.70	.01

Note. Coefficient = *Regressions* beta value, *SE* = standard error, CI = confidence interval, *z* = *z*-statistic, *p* = *p*-value, c = c-path, b = b-path, a = a-path.

Table A.142.ii. *Defined model parameters (effects)*

Effect	Coefficient	<i>SE</i>	95% CI	<i>z</i>	<i>p</i>
Indirect (female)	9.66x10 ⁻⁰⁵	7.60x10 ⁻⁰³	[-0.02, 0.02]	0.01	.99
Total (female)	-1.66x10 ⁻⁰³	0.03	[-0.07, 0.05]	-0.05	.96
Indirect (male)	1.98x10 ⁻⁰⁵	3.66x10 ⁻⁰³	[-0.01, 0.01]	5.40x10 ⁻⁰³	.996
Total (male)	0.13	0.06	[0.00, 0.25]	2.06	.04
Difference in indirect (male - female)	7.68x10 ⁻⁰⁵	7.33x10 ⁻⁰³	[-0.02, 0.01]	0.01	.99
Difference in total (male - female)	-0.13	0.07	[-0.27, 0.01]	-1.88	.06

Note. Coefficient = estimated model parameter, *SE* = standard error, CI = confidence interval, *z* = *z*-statistic, *p* = *p*-value.

Tables A.143.i & ii. Results of the mediation model with the predictor congener PCDF130, the DNA methylation of the hubCpG of the red module as mediator, and the predicted difference in PDS score between baseline (t0) & last follow-up (t5) as outcome, controlling for confounders.

Table A.143.i. *Regressions*

	Coefficient	<i>SE</i>	95% CI	<i>z</i>	<i>p</i>
PDS score (t5-t0) ~ PCDF130 (c)	-0.03	0.03	[-0.10, 0.03]	-0.83	.41
PDS score (t5-t0) ~ Sex	-0.80	0.03	[-0.87, -0.74]	-23.43	<.001
PDS score (t5-t0) ~ PCDF130:Sex (c:Sex)	0.11	0.06	[0.00, 0.23]	1.89	.06
PDS score (t5-t0) ~ hubCpG (red module) (b)	0.03	0.04	[-0.06, 0.11]	0.62	.54
PDS score (t5-t0) ~ Mother's age at birth	8.68x10 ⁻⁰³	4.43x10 ⁻⁰³	[0.00, 0.02]	1.96	.05
PDS score (t5-t0) ~ EPIC array plate	-0.14	0.04	[-0.21, -0.07]	-4.10	<.001
hubCpG (red module) ~ PCDF130 (a)	-0.04	0.11	[-0.25, 0.17]	-0.33	.74
hubCpG (red module) ~ Sex	0.12	0.08	[-0.04, 0.27]	1.47	.14
hubCpG (red module) ~ PCDF130:Sex (a:Sex)	9.75x10 ⁻⁰⁴	0.13	[-0.27, 0.25]	7.34x10 ⁻⁰³	.99
hubCpG (red module) ~ Mother's age at birth	0.02	8.54x10 ⁻⁰³	[0.00, 0.03]	1.79	.07
hubCpG (red module) ~ EPIC array plate	0.25	0.07	[0.11, 0.40]	3.43	<.001

Note. Coefficient = *Regressions* beta value, *SE* = standard error, CI = confidence interval, *z* = *z*-statistic, *p* = *p*-value, c = c-path, b = b-path, a = a-path.

Table A.143.ii. *Defined model parameters (effects)*

Effect	Coefficient	<i>SE</i>	95% CI	<i>z</i>	<i>p</i>
Indirect (female)	-9.64x10 ⁻⁰⁴	5.56x10 ⁻⁰³	[-0.01, 0.01]	-0.17	.86
Total (female)	-0.03	0.03	[-0.10, 0.03]	-0.87	.38
Indirect (male)	-9.38x10 ⁻⁰⁴	4.75x10 ⁻⁰³	[-0.01, 0.01]	-0.20	.84
Total (male)	0.08	0.05	[-0.01, 0.18]	1.60	.11
Difference in indirect (male - female)	-2.64x10 ⁻⁰⁵	7.06x10 ⁻⁰³	[-0.01, 0.02]	-3.74x10 ⁻⁰³	.997

Difference in total (male - female)	-0.11	0.06	[-0.23, 0.00]	-1.90	.06
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Note. Coefficient = estimated model parameter, SE = standard error, CI = confidence interval, z = z -statistic, p = p -value.

Tables A.144.i & ii. Results of the mediation model with the predictor congener PCDF130, the EigenCpG of the brown module as mediator, and the predicted difference in PDS score between baseline (t0) & last follow-up (t5) as outcome, controlling for confounders in the female subsample.

Table A.144.i. *Regressions*

	Coefficient	SE	95% CI	z	p
PDS score (t5-t0) ~ PCDF130 (c)	-2.97x10 ⁻⁰³	0.03	[-0.08, 0.06]	-0.09	.93
PDS score (t5-t0) ~ EigenCpG (brown module) (b)	0.57	0.33	[-0.15, 1.14]	1.75	.08
PDS score (t5-t0) ~ B-cells	0.03	0.80	[-1.55, 1.62]	0.04	.97
PDS score (t5-t0) ~ EPIC array plate	-0.14	0.05	[-0.23, -0.03]	-2.84	.004
EigenCpG (brown module) ~ PCDF130 (a)	3.80x10 ⁻⁰³	0.01	[-0.02, 0.03]	0.29	.77
EigenCpG (brown module) ~ B-cells	-2.62	0.34	[-3.14, -1.80]	-7.61	< .001
EigenCpG (brown module) ~ EPIC array plate	0.06	0.02	[0.03, 0.10]	3.82	< .001

Note. Coefficient = *Regressions* beta value, SE = standard error, CI = confidence interval, z = z -statistic, p = p -value, c = c-path, b = b-path, a = a-path.

Table A.144.ii. *Defined model parameters (effects)*

Effect	Coefficient	SE	95% CI	z	p
indirect	2.17x10 ⁻⁰³	8.11x10 ⁻⁰³	[-0.02, 0.02]	0.27	.79
total	-7.95x10 ⁻⁰⁴	0.03	[-0.08, 0.06]	-0.02	.98

Note. Coefficient = estimated model parameter, SE = standard error, CI = confidence interval, z = z -statistic, p = p -value.

Tables A.145.i & ii. Results of the mediation model with the predictor congener PCDF130, the EigenCpG of the lightcyan1 module as mediator, and the predicted difference in PDS score between baseline (t0) & last follow-up (t5) as outcome, controlling for confounders in the female subsample.

Table A.145.i. *Regressions*

	Coefficient	SE	95% CI	z	p
PDS score (t5-t0) ~ PCDF130 (c)	5.93x10 ⁻⁰³	0.03	[-0.06, 0.06]	0.20	.84
PDS score (t5-t0) ~ EigenCpG (lightcyan1 module) (b)	0.19	0.52	[-0.77, 1.26]	0.36	.72
PDS score (t5-t0) ~ CD4T	0.02	0.77	[-1.70, 1.35]	0.03	.98
PDS score (t5-t0) ~ NK	-1.40	1.10	[-3.84, 0.56]	-1.27	.20
PDS score (t5-t0) ~ Granulocytes	-0.55	0.52	[-1.60, 0.42]	-1.06	.29
PDS score (t5-t0) ~ B-cells	-2.48	1.20	[-4.69, 0.05]	-2.08	.04
EigenCpG (lightcyan1 module) ~ PCDF130 (a)	-5.65x10 ⁻⁰³	7.99x10 ⁻⁰³	[-0.02, 0.01]	-0.71	.48
EigenCpG (lightcyan1 module) ~ CD4T	1.07	0.15	[0.78, 1.38]	7.05	< .001
EigenCpG (lightcyan1 module) ~ NK	0.94	0.25	[0.47, 1.48]	3.70	< .001
EigenCpG (lightcyan1 module) ~ Granulocytes	0.36	0.15	[0.14, 0.73]	2.38	.02
EigenCpG (lightcyan1 module) ~ B-cells	2.41	0.23	[1.87, 2.77]	10.62	< .001

Note. Coefficient = *Regressions* beta value, SE = standard error, CI = confidence interval, z = z -statistic, p = p -value, c = c-path, b = b-path, a = a-path.

Table A.145.ii. *Defined model parameters (effects)*

Effect	Coefficient	SE	95% CI	z	p
indirect	-1.07x10 ⁻⁰³	5.80x10 ⁻⁰³	[-0.02, 0.01]	-0.18	.85

total	4.86x10 ⁻⁰³	0.03	[-0.06, 0.05]	0.17	.87
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Note. Coefficient = estimated model parameter, SE = standard error, CI = confidence interval, z = z-statistic, p = p-value.

Tables A.146.i & ii. Results of the mediation model with the predictor congener PCDF130, the EigenCpG of the red module as mediator, and the predicted difference in PDS score between baseline (t0) & last follow-up (t5) as outcome, controlling for confounders in the female subsample.

Table A.146.i. *Regressions*

	Coefficient	SE	95% CI	z	p
PDS score (t5-t0) ~ PCDF130 (c)	-0.01	0.04	[-0.11, 0.04]	-0.35	.73
PDS score (t5-t0) ~ EigenCpG (red module) (b)	0.04	0.34	[-0.52, 0.81]	0.11	.91
PDS score (t5-t0) ~ EPIC array plate	-0.11	0.05	[-0.21, -0.02]	-2.25	.03
EigenCpG (red module) ~ PCDF130 (a)	0.01	0.02	[-0.03, 0.06]	0.66	.51
EigenCpG (red module) ~ EPIC array plate	0.09	0.02	[0.05, 0.13]	4.04	< .001

Note. Coefficient = *Regressions* beta value, SE = standard error, CI = confidence interval, z = z-statistic, p = p-value, c = c-path, b = b-path, a = a-path.

Table A.146.ii. *Defined model parameters (effects)*

Effect	Coefficient	SE	95% CI	z	p
indirect	5.31x10 ⁻⁰⁴	0.01	[-0.01, 0.03]	0.05	.96
total	-0.01	0.04	[-0.11, 0.04]	-0.34	.73

Note. Coefficient = estimated model parameter, SE = standard error, CI = confidence interval, z = z-statistic, p = p-value.

Tables A.147.i & ii. Results of the mediation model with the predictor congener PCDF130, the EigenCpG of the salmon module as mediator, and the predicted difference in PDS score between baseline (t0) & last follow-up (t5) as outcome, controlling for confounders in the female subsample.

Table A.147.i. *Regressions*

	Coefficient	SE	95% CI	z	p
PDS score (t5-t0) ~ PCDF130 (c)	-8.09x10 ⁻⁰³	0.04	[-0.09, 0.05]	-0.22	.83
PDS score (t5-t0) ~ EigenCpG (salmon module) (b)	0.39	0.28	[-0.26, 0.87]	1.38	.17
PDS score (t5-t0) ~ B-cells	-0.90	0.58	[-1.93, 0.38]	-1.54	.12
PDS score (t5-t0) ~ EPIC array plate	-0.15	0.06	[-0.26, -0.01]	-2.42	.02
EigenCpG (salmon module) ~ PCDF130 (a)	0.02	0.02	[-0.01, 0.06]	1.24	.21
EigenCpG (salmon module) ~ B-cells	-1.26	0.33	[-1.82, -0.51]	-3.77	< .001
EigenCpG (salmon module) ~ EPIC array plate	0.13	0.02	[0.09, 0.17]	6.81	< .001

Note. Coefficient = *Regressions* beta value, SE = standard error, CI = confidence interval, z = z-statistic, p = p-value, c = c-path, b = b-path, a = a-path.

Table A.147.ii. *Defined model parameters (effects)*

Effect	Coefficient	SE	95% CI	z	p
indirect	8.94x10 ⁻⁰³	0.01	[-0.01, 0.03]	0.84	.40
total	8.51x10 ⁻⁰⁴	0.04	[-0.08, 0.06]	0.02	.98

Note. Coefficient = estimated model parameter, SE = standard error, CI = confidence interval, z = z-statistic, p = p-value.

Tables A.148.i & ii. Results of the mediation model with the predictor congener PCDF130, the EigenCpG of the white module as mediator, and the predicted difference in PDS score between baseline (t0) & last follow-up (t5) as outcome, controlling for confounders in the female subsample.

Table A.148.i. *Regressions*

	Coefficient	SE	95% CI	z	p
PDS score (t5-t0) ~ PCDF130	4.96x10 ⁻⁰⁴	0.03	[-0.07, 0.05]	0.02	.99
(c)					
PDS score (t5-t0) ~ EigenCpG (white module)	0.19	0.25	[-0.38, 0.63]	0.76	.45
(b)					
PDS score (t5-t0) ~ CD4T	0.76	0.46	[-0.34, 1.50]	1.65	.10
PDS score (t5-t0) ~ B-cells	-1.73	0.87	[-3.39, 0.05]	-1.99	.05
EigenCpG (white module) ~ PCDF130	-0.02	0.02	[-0.06, 0.02]	-0.96	.34
(a)					
EigenCpG (white module) ~ CD4T	-0.52	0.22	[-0.94, -0.09]	-2.40	.02
EigenCpG (white module) ~ B-cells	-1.21	0.31	[-1.77, -0.52]	-3.86	< .001

Note. Coefficient = *Regressions* beta value, SE = standard error, CI = confidence interval, z = z-statistic, p = p-value, c = c-path, b = b-path, a = a-path.

Table A.148.ii. *Defined model parameters (effects)*

Effect	Coefficient	SE	95% CI	z	p
indirect	-4.02x10 ⁻⁰³	8.35x10 ⁻⁰³	[-0.02, 0.01]	-0.48	.63
total	-3.52x10 ⁻⁰³	0.03	[-0.07, 0.05]	-0.11	.91

Note. Coefficient = estimated model parameter, SE = standard error, CI = confidence interval, z = z-statistic, p = p-value.

Tables A.149.i & ii. Results of the mediation model with the predictor congener PCDF130, the EigenCpG of the yellow module as mediator, and the predicted difference in PDS score between baseline (t0) & last follow-up (t5) as outcome, controlling for confounders in the female subsample.

Table A.149.i. *Regressions*

	Coefficient	SE	95% CI	z	p
PDS score (t5-t0) ~ PCDF130	2.32x10 ⁻⁰³	0.03	[-0.07, 0.05]	0.08	.94
(c)					
PDS score (t5-t0) ~ EigenCpG (yellow module)	0.23	0.24	[-0.26, 0.70]	0.96	.34
(b)					
PDS score (t5-t0) ~ B-cells	-0.97	0.83	[-2.57, 0.70]	-1.17	.24
EigenCpG (yellow module) ~ PCDF130	-0.02	0.02	[-0.06, 0.02]	-0.90	.37
(a)					
EigenCpG (yellow module) ~ B-cells	-2.06	0.32	[-2.57, -1.33]	-6.54	< .001

Note. Coefficient = *Regressions* beta value, SE = standard error, CI = confidence interval, z = z-statistic, p = p-value, c = c-path, b = b-path, a = a-path.

Table A.149.ii. *Defined model parameters (effects)*

Effect	Coefficient	SE	95% CI	z	p
indirect	-4.27x10 ⁻⁰³	7.64x10 ⁻⁰³	[-0.02, 0.01]	-0.56	.58
total	-1.95x10 ⁻⁰³	0.03	[-0.07, 0.05]	-0.06	.95

Note. Coefficient = estimated model parameter, SE = standard error, CI = confidence interval, z = z-statistic, p = p-value.

Tables A.150.i & ii. Results of the mediation model with the predictor congener PCB126, the mean DNA methylation of the CpGs in the promoter region of AR, and the predicted difference in PDS score between baseline (t0) & last follow-up (t5) as outcome, for the female and male subsample separately.

Table A.150.i. *Regressions*

	Coefficient	SE	95% CI	z	p
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PDS score (t5-t0) ~ PCB126 (c [female])	2.38x10 ⁻⁰³	0.03	[-0.08, 0.04]	0.08	.94
PDS score (t5-t0) ~ DNAm AR (b [female])	0.03	0.10	[-0.28, 0.06]	0.27	.79
DNAm AR ~ PCB126 (a [female])	-0.09	0.10	[-0.32, 0.05]	-0.95	.34
PDS score (t5-t0) ~ PCB126 (c [male])	0.06	0.07	[-0.10, 0.16]	0.86	.39
PDS score (t5-t0) ~ DNAm AR (b [male])	3.19x10 ⁻⁰³	0.15	[-0.07, 0.39]	0.02	.98
DNAm AR ~ PCB126 (a [male])	-0.06	0.14	[-0.36, 0.18]	-0.42	.68

Note. Coefficient = *Regressions* beta value, *SE* = standard error, *CI* = confidence interval, *z* = *z*-statistic, *p* = *p*-value, c = c-path, b = b-path, a = a-path.

Table A.150.ii. *Defined model parameters (effects)*

Effect	Coefficient	<i>SE</i>	95% CI	<i>z</i>	<i>p</i>
Indirect (female)	-2.64x10 ⁻⁰³	5.76x10 ⁻⁰³	[-0.01, 0.01]	-0.46	.65
Total (female)	-2.59x10 ⁻⁰⁴	0.03	[-0.08, 0.03]	-8.87x10 ⁻⁰³	.99
Indirect (male)	-1.83x10 ⁻⁰⁴	0.03	[-0.09, 0.02]	-6.69x10 ⁻⁰³	.995
Total (male)	0.06	0.07	[-0.13, 0.16]	0.75	.45
Difference in indirect (male - female)	-2.45x10 ⁻⁰³	0.03	[-0.02, 0.09]	-0.09	.93
Difference in total (male - female)	-0.06	0.08	[-0.18, 0.13]	-0.70	.48

Note. Coefficient = estimated model parameter, *SE* = standard error, *CI* = confidence interval, *z* = *z*-statistic, *p* = *p*-value.

Tables A.151.i & ii. Results of the mediation model with the predictor congener PCB169, the mean DNA methylation of the CpGs in the promoter region of *AR*, and the predicted difference in PDS score between baseline (t0) & last follow-up (t5) as outcome, for the female and male subsample separately.

Table A.151.i. *Regressions*

	Coefficient	<i>SE</i>	95% CI	<i>z</i>	<i>p</i>
PDS score (t5-t0) ~ PCB169 (c [female])	-0.04	0.04	[-0.12, 0.03]	-0.94	.35
PDS score (t5-t0) ~ DNAm AR (b [female])	0.02	0.11	[-0.30, 0.05]	0.19	.85
DNAm AR ~ PCB169 (a [female])	-0.15	0.10	[-0.39, 0.01]	-1.45	.15
PDS score (t5-t0) ~ PCB169 (c [male])	0.13	0.05	[0.02, 0.22]	2.68	.01
PDS score (t5-t0) ~ DNAm AR (b [male])	-0.02	0.14	[-0.09, 0.36]	-0.12	.91
DNAm AR ~ PCB169 (a [male])	0.04	0.19	[-0.37, 0.37]	0.20	.84

Note. Coefficient = *Regressions* beta value, *SE* = standard error, *CI* = confidence interval, *z* = *z*-statistic, *p* = *p*-value, c = c-path, b = b-path, a = a-path.

Table A.151.ii. *Defined model parameters (effects)*

Effect	Coefficient	<i>SE</i>	95% CI	<i>z</i>	<i>p</i>
Indirect (female)	-3.15x10 ⁻⁰³	0.01	[-0.01, 0.04]	-0.22	.83
Total (female)	-0.04	0.04	[-0.11, 0.03]	-1.05	.30
Indirect (male)	-6.38x10 ⁻⁰⁴	0.03	[-0.07, 0.05]	-0.02	.98
Total (male)	0.13	0.06	[0.00, 0.22]	2.34	.02
Difference in indirect (male - female)	-2.51x10 ⁻⁰³	0.03	[-0.06, 0.08]	-0.08	.94
Difference in total (male - female)	-0.17	0.07	[-0.29, -0.02]	-2.53	.01

Note. Coefficient = estimated model parameter, *SE* = standard error, *CI* = confidence interval, *z* = *z*-statistic, *p* = *p*-value.

Tables A.152.i & ii. Results of the mediation model with the predictor congener PCB77, the mean DNA methylation of the CpGs in the promoter region of *AR*, and the predicted difference in PDS score between baseline (t0) & last follow-up (t5) as outcome, for the female and male subsample separately.

Table A.151.i. *Regressions*

	Coefficient	<i>SE</i>	95% CI	<i>z</i>	<i>p</i>
PDS score (t5-t0) ~ PCB77 (c [female])	-1.14x10 ⁻⁰³	0.05	[-0.09, 0.12]	-0.02	.98
PDS score (t5-t0) ~ DNAm AR (b [female])	0.03	0.10	[-0.26, 0.06]	0.28	.78
DNAm AR ~ PCB77 (a [female])	0.02	0.10	[-0.16, 0.25]	0.16	.87
PDS score (t5-t0) ~ PCB77 (c [male])	0.14	0.07	[0.01, 0.31]	1.94	.05

PDS score (t5-t0) ~ DNAm AR (b [male])	0.02	0.15	[-0.05, 0.41]	0.14	.89
DNAm AR ~ PCB77 (a [male])	0.32	0.32	[-0.13, 1.05]	1.01	.31

Note. Coefficient = *Regressions* beta value, SE = standard error, CI = confidence interval, z = z -statistic, p = p -value, c = c-path, b = b-path, a = a-path.

Table A.151.ii. *Defined model parameters (effects)*

Effect	Coefficient	SE	95% CI	z	p
Indirect (female)	4.58×10^{-04}	8.33×10^{-03}	[0.00, 0.03]	0.06	.96
Total (female)	-6.80×10^{-04}	0.05	[-0.08, 0.13]	-0.01	.99
Indirect (male)	6.88×10^{-03}	0.08	[-0.03, 0.27]	0.09	.93
Total (male)	0.15	0.10	[0.02, 0.44]	1.43	.15
Difference in indirect (male - female)	-6.42×10^{-03}	0.08	[-0.26, 0.04]	-0.08	.94
Difference in total (male - female)	-0.15	0.12	[-0.44, 0.03]	-1.28	.20

Note. Coefficient = estimated model parameter, SE = standard error, CI = confidence interval, z = z -statistic, p = p -value.

Tables A.153.i & ii. Results of the mediation model with the predictor congener PCB81, the mean DNA methylation of the CpGs in the promoter region of AR, and the predicted difference in PDS score between baseline (t0) & last follow-up (t5) as outcome, for the female and male subsample separately.

Table A.153.i. *Regressions*

	Coefficient	SE	95% CI	z	p
PDS score (t5-t0) ~ PCB81 (c [female])	-0.04	0.03	[-0.09, 0.03]	-1.36	.17
PDS score (t5-t0) ~ DNAm AR (b [female])	0.03	0.11	[-0.28, 0.06]	0.29	.77
DNAm AR ~ PCB81 (a [female])	-0.02	0.04	[-0.10, 0.06]	-0.59	.55
PDS score (t5-t0) ~ PCB81 (c [male])	6.66×10^{-03}	0.07	[-0.12, 0.13]	0.10	.92
PDS score (t5-t0) ~ DNAm AR (b [male])	0.02	0.15	[-0.06, 0.42]	0.12	.90
DNAm AR ~ PCB81 (a [male])	0.08	0.13	[-0.15, 0.35]	0.65	.52

Note. Coefficient = *Regressions* beta value, SE = standard error, CI = confidence interval, z = z -statistic, p = p -value, c = c-path, b = b-path, a = a-path.

Table A.153.ii. *Defined model parameters (effects)*

Effect	Coefficient	SE	95% CI	z	p
Indirect (female)	-7.19×10^{-04}	5.52×10^{-03}	[0.00, 0.02]	-0.13	.90
Total (female)	-0.04	0.03	[-0.09, 0.03]	-1.38	.17
Indirect (male)	1.56×10^{-03}	0.02	[-0.04, 0.06]	0.07	.95
Total (male)	8.22×10^{-03}	0.07	[-0.12, 0.15]	0.12	.90
Difference in indirect (male - female)	-2.28×10^{-03}	0.02	[-0.06, 0.04]	-0.10	.92
Difference in total (male - female)	-0.05	0.07	[-0.20, 0.09]	-0.69	.49

Note. Coefficient = estimated model parameter, SE = standard error, CI = confidence interval, z = z -statistic, p = p -value.

Tables A.154.i & ii. Results of the mediation model with the predictor congener PCDD48, the mean DNA methylation of the CpGs in the promoter region of AR, and the predicted difference in PDS score between baseline (t0) & last follow-up (t5) as outcome, for the female and male subsample separately.

Table A.154.i. *Regressions*

	Coefficient	SE	95% CI	z	p
PDS score (t5-t0) ~ PCDD48 (c [female])	-0.04	0.03	[-0.11, 0.02]	-1.44	.15
PDS score (t5-t0) ~ DNAm AR (b [female])	0.02	0.11	[-0.31, 0.05]	0.16	.87
DNAm AR ~ PCDD48 (a [female])	-0.12	0.08	[-0.31, 0.01]	-1.41	.16
PDS score (t5-t0) ~ PCDD48 (c [male])	0.03	0.05	[-0.09, 0.12]	0.52	.60
PDS score (t5-t0) ~ DNAm AR (b [male])	0.01	0.15	[-0.06, 0.41]	0.10	.92
DNAm AR ~ PCDD48 (a [male])	0.08	0.10	[-0.11, 0.29]	0.83	.41

Note. Coefficient = *Regressions* beta value, SE = standard error, CI = confidence interval, z = z -statistic, p = p -value, c = c-path, b = b-path, a = a-path.

Table A.154.ii. *Defined model parameters (effects)*

Effect	Coefficient	SE	95% CI	z	p
Indirect (female)	-2.13x10 ⁻⁰³	0.01	[-0.01, 0.03]	-0.20	.84
Total (female)	-0.05	0.03	[-0.10, 0.01]	-1.57	.12
Indirect (male)	1.20x10 ⁻⁰³	0.02	[-0.02, 0.05]	0.07	.95
Total (male)	0.03	0.06	[-0.09, 0.13]	0.52	.60
Difference in indirect (male - female)	-3.33x10 ⁻⁰³	0.02	[-0.05, 0.04]	-0.16	.88
Difference in total (male - female)	-0.08	0.06	[-0.19, 0.06]	-1.19	.24

Note. Coefficient = estimated model parameter, SE = standard error, CI = confidence interval, z = z-statistic, p = p-value.

Tables A.155.i & ii. Results of the mediation model with the predictor congener PCDD54, the mean DNA methylation of the CpGs in the promoter region of AR, and the predicted difference in PDS score between baseline (t0) & last follow-up (t5) as outcome, for the female and male subsample separately.

Table A.155.i. *Regressions*

	Coefficient	SE	95% CI	z	p
PDS score (t5-t0) ~ PCDD54 (c [female])	-0.02	0.05	[-0.12, 0.07]	-0.39	.70
PDS score (t5-t0) ~ DNAm AR (b [female])	0.02	0.11	[-0.29, 0.06]	0.22	.82
DNAm AR ~ PCDD54 (a [female])	-0.24	0.16	[-0.60, -0.01]	-1.51	.13
PDS score (t5-t0) ~ PCDD54 (c [male])	0.07	0.07	[-0.08, 0.19]	1.06	.29
PDS score (t5-t0) ~ DNAm AR (b [male])	7.53x10 ⁻⁰³	0.15	[-0.06, 0.40]	0.05	.96
DNAm AR ~ PCDD54 (a [male])	0.02	0.17	[-0.34, 0.32]	0.12	.90

Note. Coefficient = *Regressions* beta value, SE = standard error, CI = confidence interval, z = z-statistic, p = p-value, c = c-path, b = b-path, a = a-path.

Table A.155.ii. *Defined model parameters (effects)*

Effect	Coefficient	SE	95% CI	z	p
Indirect (female)	-5.64x10 ⁻⁰³	0.02	[-0.03, 0.04]	-0.33	.74
Total (female)	-0.02	0.05	[-0.11, 0.07]	-0.54	.59
Indirect (male)	1.53x10 ⁻⁰⁴	0.03	[-0.08, 0.05]	5.25x10 ⁻⁰³	.996
Total (male)	0.07	0.07	[-0.10, 0.19]	0.98	.33
Difference in indirect (male - female)	-5.79x10 ⁻⁰³	0.03	[-0.06, 0.08]	-0.17	.86
Difference in total (male - female)	-0.09	0.08	[-0.24, 0.09]	-1.12	.26

Note. Coefficient = estimated model parameter, SE = standard error, CI = confidence interval, z = z-statistic, p = p-value.

Tables A.156.i & ii. Results of the mediation model with the predictor congener PCDD66, the mean DNA methylation of the CpGs in the promoter region of AR, and the predicted difference in PDS score between baseline (t0) & last follow-up (t5) as outcome, for the female and male subsample separately.

Table A.156.i. *Regressions*

	Coefficient	SE	95% CI	z	p
PDS score (t5-t0) ~ PCDD66 (c [female])	-0.04	0.05	[-0.14, 0.05]	-0.84	.40
PDS score (t5-t0) ~ DNAm AR (b [female])	0.02	0.12	[-0.32, 0.06]	0.18	.86
DNAm AR ~ PCDD66 (a [female])	-0.23	0.14	[-0.55, 0.00]	-1.60	.11
PDS score (t5-t0) ~ PCDD66 (c [male])	0.06	0.06	[-0.07, 0.17]	1.06	.29
PDS score (t5-t0) ~ DNAm AR (b [male])	7.22x10 ⁻⁰³	0.15	[-0.07, 0.40]	0.05	.96
DNAm AR ~ PCDD66 (a [male])	-3.25x10 ⁻⁰⁴	0.18	[-0.39, 0.30]	-1.85x10 ⁻⁰³	.999

Note. Coefficient = *Regressions* beta value, SE = standard error, CI = confidence interval, z = z-statistic, p = p-value, c = c-path, b = b-path, a = a-path.

Table A.156.ii. *Defined model parameters (effects)*

Effect	Coefficient	SE	95% CI	z	p
Indirect (female)	-4.69x10 ⁻⁰³	0.02	[-0.02, 0.07]	-0.19	.85
Total (female)	-0.05	0.05	[-0.14, 0.05]	-0.98	.33
Indirect (male)	-2.35x10 ⁻⁰⁶	0.03	[-0.09, 0.05]	-7.52x10 ⁻⁰⁵	> .999
Total (male)	0.06	0.07	[-0.11, 0.18]	0.92	.36
Difference in indirect (male - female)	-4.69x10 ⁻⁰³	0.04	[-0.05, 0.12]	-0.12	.91
Difference in total (male - female)	-0.11	0.08	[-0.25, 0.09]	-1.32	.19

Note. Coefficient = estimated model parameter, SE = standard error, CI = confidence interval, z = z-statistic, p = p-value.

Tables A.157.i & ii. Results of the mediation model with the predictor congener PCDD67, the mean DNA methylation of the CpGs in the promoter region of AR, and the predicted difference in PDS score between baseline (t0) & last follow-up (t5) as outcome, for the female and male subsample separately.

Table A.157.i. *Regressions*

	Coefficient	SE	95% CI	z	p
PDS score (t5-t0) ~ PCDD67 (c [female])	-0.03	0.05	[-0.13, 0.06]	-0.70	.49
PDS score (t5-t0) ~ DNAm AR (b [female])	0.02	0.11	[-0.31, 0.06]	0.19	.85
DNAm AR ~ PCDD67 (a [female])	-0.24	0.16	[-0.60, 0.01]	-1.49	.14
PDS score (t5-t0) ~ PCDD67 (c [male])	0.08	0.07	[-0.08, 0.18]	1.18	.24
PDS score (t5-t0) ~ DNAm AR (b [male])	5.91x10 ⁻⁰³	0.15	[-0.07, 0.40]	0.04	.97
DNAm AR ~ PCDD67 (a [male])	0.04	0.15	[-0.29, 0.32]	0.25	.80

Note. Coefficient = *Regressions* beta value, SE = standard error, CI = confidence interval, z = z-statistic, p = p-value, c = c-path, b = b-path, a = a-path.

Table A.157.ii. *Defined model parameters (effects)*

Effect	Coefficient	SE	95% CI	z	p
Indirect (female)	-4.96x10 ⁻⁰³	0.02	[-0.03, 0.06]	-0.22	.82
Total (female)	-0.04	0.05	[-0.13, 0.06]	-0.82	.41
Indirect (male)	2.28x10 ⁻⁰⁴	0.03	[-0.06, 0.05]	9.06x10 ⁻⁰³	.99
Total (male)	0.08	0.07	[-0.09, 0.19]	1.11	.27
Difference in indirect (male - female)	-5.19x10 ⁻⁰³	0.03	[-0.06, 0.09]	-0.16	.88
Difference in total (male - female)	-0.12	0.08	[-0.25, 0.08]	-1.37	.17

Note. Coefficient = estimated model parameter, SE = standard error, CI = confidence interval, z = z-statistic, p = p-value.

Tables A.158.i & ii. Results of the mediation model with the predictor congener PCDD70, the mean DNA methylation of the CpGs in the promoter region of AR, and the predicted difference in PDS score between baseline (t0) & last follow-up (t5) as outcome, for the female and male subsample separately.

Table A.158.i. *Regressions*

	Coefficient	SE	95% CI	z	p
PDS score (t5-t0) ~ PCDD70 (c [female])	-0.04	0.04	[-0.12, 0.05]	-0.84	.40
PDS score (t5-t0) ~ DNAm AR (b [female])	0.02	0.10	[-0.28, 0.06]	0.19	.85
DNAm AR ~ PCDD70 (a [female])	-0.22	0.16	[-0.58, 0.02]	-1.39	.16
PDS score (t5-t0) ~ PCDD70 (c [male])	0.06	0.06	[-0.08, 0.16]	1.00	.32
PDS score (t5-t0) ~ DNAm AR (b [male])	7.62x10 ⁻⁰³	0.15	[-0.07, 0.41]	0.05	.96
DNAm AR ~ PCDD70 (a [male])	0.05	0.16	[-0.30, 0.33]	0.28	.78

Note. Coefficient = *Regressions* beta value, SE = standard error, CI = confidence interval, z = z-statistic, p = p-value, c = c-path, b = b-path, a = a-path.

Table A.158.ii. *Defined model parameters (effects)*

Effect	Coefficient	SE	95% CI	z	p
Indirect (female)	-4.38x10 ⁻⁰³	0.02	[-0.03, 0.04]	-0.29	.77
Total (female)	-0.04	0.04	[-0.12, 0.05]	-0.98	.33
Indirect (male)	3.43x10 ⁻⁰⁴	0.03	[-0.07, 0.05]	0.01	.99

Total (male)	0.06	0.07	[-0.10, 0.16]	0.91	.36
Difference in indirect (male - female)	-4.72x10 ⁻⁰³	0.03	[-0.06, 0.08]	-0.15	.88
Difference in total (male - female)	-0.10	0.08	[-0.23, 0.08]	-1.30	.19

Note. Coefficient = estimated model parameter, SE = standard error, CI = confidence interval, z = z -statistic, p = p -value.

Tables A.159.i & ii. Results of the mediation model with the predictor congener PCDD73, the mean DNA methylation of the CpGs in the promoter region of AR, and the predicted difference in PDS score between baseline (t0) & last follow-up (t5) as outcome, for the female and male subsample separately.

Table A.159.i. *Regressions*

	Coefficient	SE	95% CI	z	p
PDS score (t5-t0) ~ PCDD73 (c [female])	-0.05	0.04	[-0.15, 0.01]	-1.24	.22
PDS score (t5-t0) ~ DNAm AR (b [female])	0.02	0.12	[-0.34, 0.05]	0.20	.85
DNAm AR ~ PCDD73 (a [female])	-0.09	0.08	[-0.27, 0.05]	-1.03	.30
PDS score (t5-t0) ~ PCDD73 (c [male])	0.05	0.04	[-0.05, 0.13]	1.15	.25
PDS score (t5-t0) ~ DNAm AR (b [male])	0.01	0.15	[-0.06, 0.40]	0.07	.94
DNAm AR ~ PCDD73 (a [male])	0.06	0.12	[-0.19, 0.28]	0.48	.63

Note. Coefficient = *Regressions* beta value, SE = standard error, CI = confidence interval, z = z -statistic, p = p -value, c = c-path, b = b-path, a = a-path.

Table A.159.ii. *Defined model parameters (effects)*

Effect	Coefficient	SE	95% CI	z	p
Indirect (female)	-2.04x10 ⁻⁰³	0.02	[-0.01, 0.05]	-0.14	.89
Total (female)	-0.05	0.04	[-0.14, 0.01]	-1.35	.18
Indirect (male)	6.24x10 ⁻⁰⁴	0.02	[-0.04, 0.05]	0.03	.98
Total (male)	0.05	0.05	[-0.05, 0.13]	1.09	.28
Difference in indirect (male - female)	-2.66x10 ⁻⁰³	0.03	[-0.05, 0.06]	-0.10	.92
Difference in total (male - female)	-0.10	0.06	[-0.22, 0.02]	-1.69	.09

Note. Coefficient = estimated model parameter, SE = standard error, CI = confidence interval, z = z -statistic, p = p -value.

Tables A.160.i & ii. Results of the mediation model with the predictor congener PCDD75, the mean DNA methylation of the CpGs in the promoter region of AR, and the predicted difference in PDS score between baseline (t0) & last follow-up (t5) as outcome, for the female and male subsample separately.

Table A.160.i. *Regressions*

	Coefficient	SE	95% CI	z	p
PDS score (t5-t0) ~ PCDD75 (c [female])	-0.02	0.04	[-0.11, 0.06]	-0.39	.70
PDS score (t5-t0) ~ DNAm AR (b [female])	0.02	0.12	[-0.33, 0.06]	0.20	.84
DNAm AR ~ PCDD75 (a [female])	-0.25	0.16	[-0.61, 0.02]	-1.56	.12
PDS score (t5-t0) ~ PCDD75 (c [male])	0.10	0.05	[-0.01, 0.20]	1.89	.06
PDS score (t5-t0) ~ DNAm AR (b [male])	8.86x10 ⁻⁰³	0.14	[-0.06, 0.39]	0.06	.95
DNAm AR ~ PCDD75 (a [male])	0.09	0.12	[-0.13, 0.32]	0.78	.44

Note. Coefficient = *Regressions* beta value, SE = standard error, CI = confidence interval, z = z -statistic, p = p -value, c = c-path, b = b-path, a = a-path.

Table A.160.ii. *Defined model parameters (effects)*

Effect	Coefficient	SE	95% CI	z	p
Indirect (female)	-5.90x10 ⁻⁰³	0.03	[-0.03, 0.07]	-0.23	.82
Total (female)	-0.02	0.04	[-0.10, 0.05]	-0.55	.58
Indirect (male)	7.95x10 ⁻⁰⁴	0.02	[-0.02, 0.07]	0.04	.97
Total (male)	0.10	0.05	[0.00, 0.21]	1.86	.06
Difference in indirect (male - female)	-6.70x10 ⁻⁰³	0.03	[-0.07, 0.08]	-0.20	.84
Difference in total (male - female)	-0.12	0.07	[-0.25, 0.01]	-1.84	.07

Note. Coefficient = estimated model parameter, *SE* = standard error, *CI* = confidence interval, *z* = *z*-statistic, *p* = *p*-value.

Tables A.161.i & ii. Results of the mediation model with the predictor congener PCDF114, the mean DNA methylation of the CpGs in the promoter region of *AR*, and the predicted difference in PDS score between baseline (t0) & last follow-up (t5) as outcome, for the female and male subsample separately.

Table A.161.i. *Regressions*

	Coefficient	<i>SE</i>	95% CI	<i>z</i>	<i>p</i>
PDS score (t5-t0) ~ PCDF114 (c [female])	-0.05	0.04	[-0.13, 0.02]	-1.30	.19
PDS score (t5-t0) ~ DNAm <i>AR</i> (b [female])	0.02	0.11	[-0.30, 0.05]	0.17	.87
DNAm <i>AR</i> ~ PCDF114 (a [female])	-0.22	0.15	[-0.56, 0.01]	-1.52	.13
PDS score (t5-t0) ~ PCDF114 (c [male])	0.11	0.06	[-0.04, 0.21]	1.73	.08
PDS score (t5-t0) ~ DNAm <i>AR</i> (b [male])	-8.21x10 ⁻⁰³	0.15	[-0.08, 0.37]	-0.06	.96
DNAm <i>AR</i> ~ PCDF114 (a [male])	0.05	0.20	[-0.37, 0.43]	0.26	.80

Note. Coefficient = *Regressions* beta value, *SE* = standard error, *CI* = confidence interval, *z* = *z*-statistic, *p* = *p*-value, c = c-path, b = b-path, a = a-path.

Table A.161.ii. *Defined model parameters (effects)*

Effect	Coefficient	<i>SE</i>	95% CI	<i>z</i>	<i>p</i>
Indirect (female)	-4.06x10 ⁻⁰³	0.02	[-0.02, 0.06]	-0.20	.84
Total (female)	-0.06	0.04	[-0.13, 0.03]	-1.42	.16
Indirect (male)	-4.27x10 ⁻⁰⁴	0.03	[-0.08, 0.06]	-0.01	.99
Total (male)	0.11	0.07	[-0.06, 0.22]	1.57	.12
Difference in indirect (male - female)	-3.63x10 ⁻⁰³	0.04	[-0.07, 0.10]	-0.10	.92
Difference in total (male - female)	-0.17	0.08	[-0.30, 0.03]	-2.05	.04

Note. Coefficient = *Regressions* beta value, *SE* = standard error, *CI* = confidence interval, *z* = *z*-statistic, *p* = *p*-value, c = c-path, b = b-path, a = a-path.

Tables A.162.i & ii. Results of the mediation model with the predictor congener PCDF118, the mean DNA methylation of the CpGs in the promoter region of *AR*, and the predicted difference in PDS score between baseline (t0) & last follow-up (t5) as outcome, for the female and male subsample separately.

Table A.162.i. *Regressions*

	Coefficient	<i>SE</i>	95% CI	<i>z</i>	<i>p</i>
PDS score (t5-t0) ~ PCDF118 (c [female])	-0.05	0.05	[-0.16, 0.04]	-0.96	.34
PDS score (t5-t0) ~ DNAm <i>AR</i> (b [female])	0.02	0.12	[-0.33, 0.06]	0.15	.88
DNAm <i>AR</i> ~ PCDF118 (a [female])	-0.31	0.19	[-0.73, -0.02]	-1.65	.10
PDS score (t5-t0) ~ PCDF118 (c [male])	0.11	0.06	[-0.03, 0.21]	1.83	.07
PDS score (t5-t0) ~ DNAm <i>AR</i> (b [male])	-7.62x10 ⁻⁰³	0.15	[-0.08, 0.38]	-0.05	.96
DNAm <i>AR</i> ~ PCDF118 (a [male])	0.03	0.23	[-0.47, 0.43]	0.13	.90

Note. Coefficient = *Regressions* beta value, *SE* = standard error, *CI* = confidence interval, *z* = *z*-statistic, *p* = *p*-value, c = c-path, b = b-path, a = a-path.

Table A.162.ii. *Defined model parameters (effects)*

Effect	Coefficient	<i>SE</i>	95% CI	<i>z</i>	<i>p</i>
Indirect (female)	-5.34x10 ⁻⁰³	0.02	[-0.03, 0.07]	-0.22	.83
Total (female)	-0.06	0.05	[-0.15, 0.04]	-1.14	.26
Indirect (male)	-2.32x10 ⁻⁰⁴	0.04	[-0.10, 0.07]	-6.34x10 ⁻⁰³	.995
Total (male)	0.11	0.07	[-0.07, 0.21]	1.57	.12
Difference in indirect (male - female)	-5.11x10 ⁻⁰³	0.04	[-0.07, 0.12]	-0.12	.91
Difference in total (male - female)	-0.17	0.09	[-0.31, 0.03]	-1.93	.05

Note. Coefficient = estimated model parameter, *SE* = standard error, *CI* = confidence interval, *z* = *z*-statistic, *p* = *p*-value.

Tables A.163.i & ii. Results of the mediation model with the predictor congener PCDF121, the mean DNA methylation of the CpGs in the promoter region of *AR*, and the predicted difference in PDS score between baseline (t0) & last follow-up (t5) as outcome, for the female and male subsample separately.

Table A.163.i. *Regressions*

	Coefficient	SE	95% CI	z	p
PDS score (t5-t0) ~ PCDF121 (c [female])	-0.03	0.05	[-0.14, 0.06]	-0.66	.51
PDS score (t5-t0) ~ DNAm <i>AR</i> (b [female])	0.02	0.12	[-0.32, 0.06]	0.18	.86
DNAm <i>AR</i> ~ PCDF121 (a [female])	-0.23	0.14	[-0.56, -0.01]	-1.59	.11
PDS score (t5-t0) ~ PCDF121 (c [male])	0.12	0.07	[-0.05, 0.22]	1.67	.09
PDS score (t5-t0) ~ DNAm <i>AR</i> (b [male])	-6.80x10 ⁻⁰³	0.15	[-0.08, 0.38]	-0.05	.96
DNAm <i>AR</i> ~ PCDF121 (a [male])	0.11	0.17	[-0.24, 0.42]	0.63	.53

Note. Coefficient = *Regressions* beta value, SE = standard error, CI = confidence interval, z = z-statistic, p = p-value, c = c-path, b = b-path, a = a-path.

Table A.163.ii. *Defined model parameters (effects)*

Effect	Coefficient	SE	95% CI	z	p
Indirect (female)	-4.84x10 ⁻⁰³	0.02	[-0.02, 0.05]	-0.28	.80
Total (female)	-0.04	0.04	[-0.12, 0.05]	-0.83	.41
Indirect (male)	-7.22x10 ⁻⁰⁴	0.03	[-0.05, 0.07]	-0.03	.98
Total (male)	0.11	0.07	[-0.06, 0.22]	1.62	.11
Difference in indirect (male - female)	-4.12x10 ⁻⁰³	0.03	[-0.07, 0.06]	-0.13	.90
Difference in total (male - female)	-0.15	0.08	[-0.29, 0.04]	-1.82	.07

Note. Coefficient = estimated model parameter, SE = standard error, CI = confidence interval, z = z-statistic, p = p-value.

Tables A.164.i & ii. Results of the mediation model with the predictor congener PCDF130, the mean DNA methylation of the CpGs in the promoter region of *AR*, and the predicted difference in PDS score between baseline (t0) & last follow-up (t5) as outcome, for the female and male subsample separately.

Table A.164.i. *Regressions*

	Coefficient	SE	95% CI	z	p
PDS score (t5-t0) ~ PCDF130 (c [female])	-7.05x10 ⁻⁰³	0.03	[-0.09, 0.05]	-0.21	.84
PDS score (t5-t0) ~ DNAm <i>AR</i> (b [female])	0.03	0.10	[-0.28, 0.06]	0.26	.79
DNAm <i>AR</i> ~ PCDF130 (a [female])	-0.04	0.05	[-0.13, 0.05]	-0.77	.44
PDS score (t5-t0) ~ PCDF130 (c [male])	0.13	0.06	[0.00, 0.25]	2.04	.04
PDS score (t5-t0) ~ DNAm <i>AR</i> (b [male])	-0.02	0.14	[-0.11, 0.36]	-0.16	.87
DNAm <i>AR</i> ~ PCDF130 (a [male])	0.13	0.11	[-0.08, 0.34]	1.22	.22

Note. Coefficient = *Regressions* beta value, SE = standard error, CI = confidence interval, z = z-statistic, p = p-value, c = c-path, b = b-path, a = a-path.

Table A.164.ii. *Defined model parameters (effects)*

Effect	Coefficient	SE	95% CI	z	p
Indirect (female)	-9.51x10 ⁻⁰⁴	4.22x10 ⁻⁰³	[-0.01, 0.01]	-0.23	.82
Total (female)	-8.00x10 ⁻⁰³	0.03	[-0.09, 0.05]	-0.24	.81
Indirect (male)	-3.04x10 ⁻⁰³	0.02	[-0.03, 0.04]	-0.18	.86
Total (male)	0.12	0.06	[0.00, 0.24]	2.05	.04
Difference in indirect (male - female)	2.09x10 ⁻⁰³	0.02	[-0.04, 0.03]	0.12	.90
Difference in total (male - female)	-0.13	0.07	[-0.27, 0.00]	-1.91	.06

Note. Coefficient = estimated model parameter, SE = standard error, CI = confidence interval, z = z-statistic, p = p-value.

Tables A.165.i & ii. Results of the mediation model with the predictor congener PCDF131, the mean DNA methylation of the CpGs in the promoter region of *AR*, and the predicted difference in PDS score between baseline (t0) & last follow-up (t5) as outcome, for the female and male subsample separately.

Table A.165.i. *Regressions*

	Coefficient	SE	95% CI	z	p
PDS score (t5-t0) ~ PCDF131 (c [female])	0.03	0.03	[-0.03, 0.08]	0.93	.35
PDS score (t5-t0) ~ DNAm <i>AR</i> (b [female])	0.03	0.10	[-0.26, 0.06]	0.31	.76
DNAm <i>AR</i> ~ PCDF131 (a [female])	-0.04	0.07	[-0.23, 0.02]	-0.63	.53
PDS score (t5-t0) ~ PCDF131 (c [male])	0.05	0.04	[-0.03, 0.14]	1.08	.28
PDS score (t5-t0) ~ DNAm <i>AR</i> (b [male])	5.06x10 ⁻⁰³	0.14	[-0.06, 0.41]	0.03	.97
DNAm <i>AR</i> ~ PCDF131 (a [male])	0.05	0.07	[-0.09, 0.20]	0.71	.48

Note. Coefficient = *Regressions* beta value, SE = standard error, CI = confidence interval, z = z-statistic, p = p-value, c = c-path, b = b-path, a = a-path.

Table A.165.ii. *Defined model parameters (effects)*

Effect	Coefficient	SE	95% CI	z	p
Indirect (female)	-1.22x10 ⁻⁰³	8.93x10 ⁻⁰³	[-0.01, 0.03]	-0.14	.89
Total (female)	0.02	0.03	[-0.03, 0.08]	0.92	.36
Indirect (male)	2.58x10 ⁻⁰⁴	0.01	[-0.01, 0.04]	0.02	.97
Total (male)	0.05	0.04	[-0.03, 0.14]	1.11	.27
Difference in indirect (male - female)	-1.48x10 ⁻⁰³	0.02	[-0.04, 0.03]	-0.09	.93
Difference in total (male - female)	-0.02	0.05	[-0.13, 0.07]	-0.47	.64

Note. Coefficient = estimated model parameter, SE = standard error, CI = confidence interval, z = z-statistic, p = p-value.

Tables A.166.i & ii. Results of the mediation model with the predictor congener PCB126, the mean DNA methylation of the CpGs in the promoter region of *ESR1*, and the predicted difference in PDS score between baseline (t0) & last follow-up (t5) as outcome.

Table A.166.i. *Regressions*

	Coefficient	SE	95% CI	z	p
PDS score (t5-t0) ~ PCB126 (c)	8.81x10 ⁻⁰⁴	0.03	[-0.06, 0.04]	0.03	.97
PDS score (t5-t0) ~ Sex	-0.78	0.04	[-0.85, -0.70]	-20.73	< .001
PDS score (t5-t0) ~ PCB126:Sex (c:Sex)	0.04	0.07	[-0.12, 0.16]	0.51	.61
PDS score (t5-t0) ~ DNAm <i>ESR1</i> (b)	0.19	0.09	[0.00, 0.37]	2.00	.05
DNAm <i>ESR1</i> ~ PCB126 (a)	-0.02	0.03	[-0.10, 0.03]	-0.71	.48
DNAm <i>ESR1</i> ~ Sex	-0.03	0.06	[-0.15, 0.07]	-0.51	.61
DNAm <i>ESR1</i> ~ PCB126:Sex (a:Sex)	-0.21	0.14	[-0.52, 0.03]	-1.45	.15

Note. Coefficient = *Regressions* beta value, SE = standard error, CI = confidence interval, z = z-statistic, p = p-value, c = c-path, b = b-path, a = a-path.

Table A.166.ii. *Defined model parameters (effects)*

Effect	Coefficient	SE	95% CI	z	p
Indirect (female)	-4.47x10 ⁻⁰³	7.97x10 ⁻⁰³	[-0.03, 0.01]	-0.56	.58
Total (female)	-3.59x10 ⁻⁰³	0.03	[-0.08, 0.03]	-0.13	.89
Indirect (male)	-0.04	0.04	[-0.14, 0.00]	-1.12	.26
Total (male)	-4.44x10 ⁻⁰³	0.08	[-0.20, 0.12]	-0.05	.96
Difference in indirect (male - female)	0.04	0.04	[-0.01, 0.13]	1.04	.30
Difference in total (male - female)	8.57x10 ⁻⁰⁴	0.09	[-0.15, 0.20]	9.58x10 ⁻⁰³	.99

Note. Coefficient = estimated model parameter, *SE* = standard error, *CI* = confidence interval, *z* = *z*-statistic, *p* = *p*-value.

Tables A.167.i & ii. Results of the mediation model with the predictor congener PCB169, the mean DNA methylation of the CpGs in the promoter region of *ESR1*, and the predicted difference in PDS score between baseline (t0) & last follow-up (t5) as outcome.

Table A.167.i. *Regressions*

	Coefficient	<i>SE</i>	95% CI	<i>z</i>	<i>p</i>
PDS score (t5-t0) ~ PCB169 (c)	-0.04	0.04	[-0.11, 0.03]	-0.99	.32
PDS score (t5-t0) ~ Sex	-0.79	0.03	[-0.85, -0.72]	-22.74	< .001
PDS score (t5-t0) ~ PCB169:Sex (c:Sex)	0.15	0.07	[0.02, 0.27]	2.30	.02
PDS score (t5-t0) ~ DNAm <i>ESR1</i> (b)	0.16	0.09	[-0.02, 0.33]	1.74	.08
DNAm <i>ESR1</i> ~ PCB169 (a)	-0.04	0.03	[-0.11, 0.02]	-1.27	.21
DNAm <i>ESR1</i> ~ Sex	-0.03	0.06	[-0.17, 0.07]	-0.57	.57
DNAm <i>ESR1</i> ~ PCB169:Sex (a:Sex)	-0.05	0.09	[-0.25, 0.10]	-0.51	.61

Note. Coefficient = *Regressions* beta value, *SE* = standard error, *CI* = confidence interval, *z* = *z*-statistic, *p* = *p*-value, c = c-path, b = b-path, a = a-path.

Table A.167.ii. *Defined model parameters (effects)*

Effect	Coefficient	<i>SE</i>	95% CI	<i>z</i>	<i>p</i>
Indirect (female)	-6.93x10 ⁻⁰³	7.46x10 ⁻⁰³	[-0.03, 0.00]	-0.93	.35
Total (female)	-0.04	0.04	[-0.12, 0.02]	-1.20	.23
Indirect (male)	-0.01	0.02	[-0.06, 0.01]	-0.80	.43
Total (male)	0.10	0.06	[-0.03, 0.19]	1.78	.08
Difference in indirect (male - female)	7.23x10 ⁻⁰³	0.02	[-0.02, 0.05]	0.42	.68
Difference in total (male - female)	-0.14	0.07	[-0.27, 0.00]	-2.08	.04

Note. Coefficient = estimated model parameter, *SE* = standard error, *CI* = confidence interval, *z* = *z*-statistic, *p* = *p*-value.

Tables A.168.i & ii. Results of the mediation model with the predictor congener PCB77, the mean DNA methylation of the CpGs in the promoter region of *ESR1*, and the predicted difference in PDS score between baseline (t0) & last follow-up (t5) as outcome.

Table A.168.i. *Regressions*

	Coefficient	<i>SE</i>	95% CI	<i>z</i>	<i>p</i>
PDS score (t5-t0) ~ PCB77 (c)	-0.02	0.05	[-0.10, 0.09]	-0.33	.74
PDS score (t5-t0) ~ Sex	-0.78	0.03	[-0.85, -0.71]	-22.72	< .001
PDS score (t5-t0) ~ PCB77:Sex (c:Sex)	0.18	0.09	[0.00, 0.35]	2.04	.04
PDS score (t5-t0) ~ DNAm <i>ESR1</i> (b)	0.23	0.09	[0.05, 0.41]	2.61	.01
DNAm <i>ESR1</i> ~ PCB77 (a)	-0.05	0.07	[-0.16, 0.10]	-0.71	.48
DNAm <i>ESR1</i> ~ Sex	-0.03	0.06	[-0.16, 0.07]	-0.48	.63
DNAm <i>ESR1</i> ~ PCB77:Sex (a:Sex)	0.08	0.10	[-0.12, 0.28]	0.77	.44

Note. Coefficient = *Regressions* beta value, *SE* = standard error, *CI* = confidence interval, *z* = *z*-statistic, *p* = *p*-value, c = c-path, b = b-path, a = a-path.

Table A.168.ii. *Defined model parameters (effects)*

Effect	Coefficient	SE	95% CI	z	p
Indirect (female)	-0.01	0.02	[-0.04, 0.02]	-0.65	.52
Total (female)	-0.03	0.05	[-0.11, 0.09]	-0.51	.61
Indirect (male)	7.81x10 ⁻⁰³	0.02	[-0.03, 0.06]	0.39	.70
Total (male)	0.17	0.08	[0.04, 0.34]	2.23	.03
Difference in indirect (male - female)	-0.02	0.03	[-0.08, 0.03]	-0.70	.48
Difference in total (male - female)	-0.20	0.09	[-0.39, -0.01]	-2.09	.04

Note. Coefficient = estimated model parameter, SE = standard error, CI = confidence interval, z = z-statistic, p = p-value.

Tables A.169.i & ii. Results of the mediation model with the predictor congener PCB81, the mean DNA methylation of the CpGs in the promoter region of *ESR1*, and the predicted difference in PDS score between baseline (t0) & last follow-up (t5) as outcome

Table A.169.i. *Regressions*

	Coefficient	SE	95% CI	z	p
PDS score (t5-t0) ~ PCB81	-0.02	0.03	[-0.06, 0.05]	-0.57	.57
(c)					
PDS score (t5-t0) ~ Sex	-0.78	0.04	[-0.85, -0.69]	-19.80	< .001
PDS score (t5-t0) ~ PCB81:Sex	0.03	0.07	[-0.12, 0.15]	0.36	.72
(c:Sex)					
PDS score (t5-t0) ~ DNAm <i>ESR1</i>	0.19	0.09	[0.01, 0.38]	2.02	.04
(b)					
DNAm <i>ESR1</i> ~ PCB81	-0.04	0.03	[-0.10, 0.02]	-1.40	.16
(a)					
DNAm <i>ESR1</i> ~ Sex	-0.02	0.06	[-0.14, 0.08]	-0.34	.74
DNAm <i>ESR1</i> ~ PCB81:Sex	-0.07	0.08	[-0.23, 0.07]	-0.90	.37
(a:Sex)					

Note. Coefficient = *Regressions* beta value, SE = standard error, CI = confidence interval, z = z-statistic, p = p-value, c = c-path, b = b-path, a = a-path.

Table A.169.ii. *Defined model parameters (effects)*

Effect	Coefficient	SE	95% CI	z	p
Indirect (female)	-8.04x10 ⁻⁰³	7.81x10 ⁻⁰³	[-0.03, 0.00]	-1.03	.30
Total (female)	-0.02	0.03	[-0.07, 0.05]	-0.83	.41
Indirect (male)	-0.02	0.02	[-0.06, 0.00]	-1.17	.24
Total (male)	-0.01	0.06	[-0.14, 0.11]	-0.19	.85
Difference in indirect (male - female)	0.01	0.02	[-0.02, 0.05]	0.75	.45
Difference in total (male - female)	-0.01	0.07	[-0.15, 0.13]	-0.17	.86

Note. Coefficient = estimated model parameter, SE = standard error, CI = confidence interval, z = z-statistic, p = p-value.

Tables A.170.i & ii. Results of the mediation model with the predictor congener PCDD48, the mean DNA methylation of the CpGs in the promoter region of *ESR1*, and the predicted difference in PDS score between baseline (t0) & last follow-up (t5) as outcome.

Table A.170.i. *Regressions*

	Coefficient	SE	95% CI	z	p
PDS score (t5-t0) ~ PCDD48	-0.04	0.03	[-0.11, 0.01]	-1.40	.16
(c)					
PDS score (t5-t0) ~ Sex	-0.77	0.04	[-0.85, -0.70]	-21.62	< .001
PDS score (t5-t0) ~ PCDD48:Sex	0.06	0.06	[-0.08, 0.18]	0.97	.33
(c:Sex)					
PDS score (t5-t0) ~ DNAm <i>ESR1</i>	0.19	0.09	[0.00, 0.37]	1.99	.05
(b)					

DNAm <i>ESR1</i> ~ PCDD48 (a)	-0.03	0.03	[-0.09, 0.04]	-0.95	.34
DNAm <i>ESR1</i> ~ Sex	-0.03	0.06	[-0.16, 0.07]	-0.56	.58
DNAm <i>ESR1</i> ~ PCDD48:Sex (a:Sex)	-0.07	0.10	[-0.29, 0.08]	-0.77	.44

Note. Coefficient = *Regressions* beta value, *SE* = standard error, *CI* = confidence interval, *z* = *z*-statistic, *p* = *p*-value, *c* = *c*-path, *b* = *b*-path, *a* = *a*-path.

Table A.170.ii. *Defined model parameters (effects)*

Effect	Coefficient	<i>SE</i>	95% CI	<i>z</i>	<i>p</i>
Indirect (female)	-5.99x10 ⁻⁰³	7.61x10 ⁻⁰³	[-0.02, 0.01]	-0.79	.43
Total (female)	-0.05	0.03	[-0.11, 0.00]	-1.69	.09
Indirect (male)	-0.02	0.02	[-0.08, 0.01]	-0.90	.37
Total (male)	-6.81x10 ⁻⁰⁴	0.06	[-0.14, 0.10]	-0.01	.99
Difference in indirect (male - female)	0.01	0.02	[-0.02, 0.07]	0.62	.54
Difference in total (male - female)	-0.05	0.07	[-0.17, 0.11]	-0.69	.49

Note. Coefficient = estimated model parameter, *SE* = standard error, *CI* = confidence interval, *z* = *z*-statistic, *p* = *p*-value.

Tables A.171.i & ii. Results of the mediation model with the predictor congener PCDD54, the mean DNA methylation of the CpGs in the promoter region of *ESR1*, and the predicted difference in PDS score between baseline (t0) & last follow-up (t5) as outcome.

Table A.171.i. *Regressions*

	Coefficient	<i>SE</i>	95% CI	<i>z</i>	<i>p</i>
PDS score (t5-t0) ~ PCDD54 (c)	-0.03	0.04	[-0.12, 0.05]	-0.68	.49
PDS score (t5-t0) ~ Sex	-0.78	0.04	[-0.84, -0.70]	-21.61	< .001
PDS score (t5-t0) ~ PCDD54:Sex (c:Sex)	0.08	0.08	[-0.08, 0.24]	1.07	.29
PDS score (t5-t0) ~ DNAm <i>ESR1</i> (b)	0.18	0.09	[0.00, 0.36]	2.02	.04
DNAm <i>ESR1</i> ~ PCDD54 (a)	-0.02	0.05	[-0.11, 0.07]	-0.42	.68
DNAm <i>ESR1</i> ~ Sex	-0.04	0.06	[-0.18, 0.07]	-0.58	.56
DNAm <i>ESR1</i> ~ PCDD54:Sex (a:Sex)	-0.09	0.12	[-0.36, 0.09]	-0.79	.43

Note. Coefficient = *Regressions* beta value, *SE* = standard error, *CI* = confidence interval, *z* = *z*-statistic, *p* = *p*-value, *c* = *c*-path, *b* = *b*-path, *a* = *a*-path.

Table A.171.ii. *Defined model parameters (effects)*

Effect	Coefficient	<i>SE</i>	95% CI	<i>z</i>	<i>p</i>
Indirect (female)	-3.59x10 ⁻⁰³	9.69x10 ⁻⁰³	[-0.03, 0.02]	-0.37	.71
Total (female)	-0.03	0.04	[-0.12, 0.05]	-0.76	.45
Indirect (male)	-0.02	0.02	[-0.09, 0.01]	-0.82	.41
Total (male)	0.03	0.07	[-0.13, 0.16]	0.47	.64
Difference in indirect (male - female)	0.02	0.03	[-0.02, 0.08]	0.64	.52
Difference in total (male - female)	-0.07	0.09	[-0.22, 0.12]	-0.80	.43

Note. Coefficient = estimated model parameter, *SE* = standard error, *CI* = confidence interval, *z* = *z*-statistic, *p* = *p*-value.

Tables A.172.i & ii. Results of the mediation model with the predictor congener PCDD66, the mean DNA methylation of the CpGs in the promoter region of *ESR1*, and the predicted difference in PDS score between baseline (t0) & last follow-up (t5) as outcome.

Table A.172.i. *Regressions*

	Coefficient	SE	95% CI	z	p
PDS score (t5-t0) ~ PCDD66 (c)	-0.04	0.04	[-0.13, 0.04]	-0.93	.35
PDS score (t5-t0) ~ Sex	-0.78	0.04	[-0.85, -0.71]	-21.10	< .001
PDS score (t5-t0) ~ PCDD66:Sex (c:Sex)	0.08	0.08	[-0.07, 0.24]	1.07	.28
PDS score (t5-t0) ~ DNAm <i>ESR1</i> (b)	0.18	0.10	[-0.02, 0.36]	1.85	.06
DNAm <i>ESR1</i> ~ PCDD66 (a)	-0.06	0.05	[-0.15, 0.04]	-1.27	.21
DNAm <i>ESR1</i> ~ Sex	-0.04	0.06	[-0.16, 0.07]	-0.61	.54
DNAm <i>ESR1</i> ~ PCDD66:Sex (a:Sex)	-0.08	0.11	[-0.33, 0.10]	-0.75	.45

Note. Coefficient = *Regressions* beta value, SE = standard error, CI = confidence interval, z = z-statistic, p = p-value, c = c-path, b = b-path, a = a-path.

Table A.172.ii. *Defined model parameters (effects)*

Effect	Coefficient	SE	95% CI	z	p
Indirect (female)	-0.01	0.01	[-0.04, 0.01]	-0.99	.32
Total (female)	-0.05	0.04	[-0.14, 0.03]	-1.19	.24
Indirect (male)	-0.03	0.02	[-0.09, 0.01]	-1.03	.30
Total (male)	0.02	0.07	[-0.14, 0.15]	0.25	.80
Difference in indirect (male - female)	0.01	0.02	[-0.02, 0.08]	0.61	.54
Difference in total (male - female)	-0.07	0.09	[-0.23, 0.11]	-0.80	.42

Note. Coefficient = estimated model parameter, SE = standard error, CI = confidence interval, z = z-statistic, p = p-value.

Tables A.173.i & ii. Results of the mediation model with the predictor congener PCDD67, the mean DNA methylation of the CpGs in the promoter region of *ESR1*, and the predicted difference in PDS score between baseline (t0) & last follow-up (t5) as outcome.

Table A.173.i. *Regressions*

	Coefficient	SE	95% CI	z	p
PDS score (t5-t0) ~ PCDD67 (c)	-0.03	0.04	[-0.13, 0.05]	-0.77	.44
PDS score (t5-t0) ~ Sex	-0.78	0.04	[-0.85, -0.71]	-21.11	< .001
PDS score (t5-t0) ~ PCDD67:Sex (c:Sex)	0.10	0.08	[-0.08, 0.24]	1.20	.23
PDS score (t5-t0) ~ DNAm <i>ESR1</i> (b)	0.18	0.09	[-0.01, 0.36]	1.95	.05
DNAm <i>ESR1</i> ~ PCDD67 (a)	-0.05	0.05	[-0.14, 0.04]	-1.04	.30
DNAm <i>ESR1</i> ~ Sex	-0.04	0.06	[-0.17, 0.07]	-0.62	.54
DNAm <i>ESR1</i> ~ PCDD67:Sex (a:Sex)	-0.06	0.09	[-0.28, 0.09]	-0.68	.50

Note. Coefficient = *Regressions* beta value, SE = standard error, CI = confidence interval, z = z-statistic, p = p-value, c = c-path, b = b-path, a = a-path.

Table A.173.ii. *Defined model parameters (effects)*

Effect	Coefficient	SE	95% CI	z	p
Indirect (female)	-8.62x10 ⁻⁰³	0.01	[-0.03, 0.01]	-0.86	.39
Total (female)	-0.04	0.04	[-0.13, 0.04]	-0.98	.33
Indirect (male)	-0.02	0.02	[-0.07, 0.00]	-1.01	.31
Total (male)	0.04	0.07	[-0.13, 0.16]	0.57	.57
Difference in indirect (male - female)	0.01	0.02	[-0.02, 0.06]	0.57	.57

Difference in total (male - female)	-0.08	0.09	[-0.23, 0.10]	-0.99	.32
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Note. Coefficient = estimated model parameter, SE = standard error, CI = confidence interval, z = z -statistic, p = p -value.

Tables A.174.i & ii. Results of the mediation model with the predictor congener PCDD70, the mean DNA methylation of the CpGs in the promoter region of *ESR1*, and the predicted difference in PDS score between baseline (t0) & last follow-up (t5) as outcome.

Table A.174.i. *Regressions*

	Coefficient	SE	95% CI	z	p
PDS score (t5-t0) ~ PCDD70 (c)	-0.04	0.04	[-0.12, 0.05]	-0.87	.39
PDS score (t5-t0) ~ Sex	-0.78	0.04	[-0.84, -0.71]	-21.96	< .001
PDS score (t5-t0) ~ PCDD70:Sex (c:Sex)	0.08	0.07	[-0.08, 0.21]	1.04	.30
PDS score (t5-t0) ~ DNAm <i>ESR1</i> (b)	0.18	0.09	[0.00, 0.35]	1.97	.05
DNAm <i>ESR1</i> ~ PCDD70 (a)	-0.04	0.04	[-0.13, 0.05]	-0.93	.35
DNAm <i>ESR1</i> ~ Sex	-0.04	0.06	[-0.17, 0.07]	-0.61	.54
DNAm <i>ESR1</i> ~ PCDD70:Sex (a:Sex)	-0.12	0.13	[-0.40, 0.09]	-0.94	.35

Note. Coefficient = *Regressions* beta value, SE = standard error, CI = confidence interval, z = z -statistic, p = p -value, c = c-path, b = b-path, a = a-path.

Table A.174.ii. *Defined model parameters (effects)*

Effect	Coefficient	SE	95% CI	z	p
Indirect (female)	-7.49x10 ⁻⁰³	1.00x10 ⁻⁰²	[-0.03, 0.01]	-0.75	.45
Total (female)	-0.04	0.04	[-0.12, 0.04]	-1.07	.28
Indirect (male)	-0.03	0.03	[-0.10, 0.01]	-0.99	.32
Total (male)	0.01	0.07	[-0.15, 0.13]	0.16	.87
Difference in indirect (male - female)	0.02	0.03	[-0.02, 0.10]	0.74	.46
Difference in total (male - female)	-0.05	0.08	[-0.20, 0.13]	-0.67	.51

Note. Coefficient = estimated model parameter, SE = standard error, CI = confidence interval, z = z -statistic, p = p -value.

Tables A.175.i & ii. Results of the mediation model with the predictor congener PCDD73, the mean DNA methylation of the CpGs in the promoter region of *ESR1*, and the predicted difference in PDS score between baseline (t0) & last follow-up (t5) as outcome.

Table A.175.i. *Regressions*

	Coefficient	SE	95% CI	z	p
PDS score (t5-t0) ~ PCDD73 (c)	-0.04	0.04	[-0.12, 0.02]	-1.13	.26
PDS score (t5-t0) ~ Sex	-0.78	0.04	[-0.85, -0.71]	-21.50	< .001
PDS score (t5-t0) ~ PCDD73:Sex (c:Sex)	0.08	0.06	[-0.03, 0.20]	1.42	.15
PDS score (t5-t0) ~ DNAm <i>ESR1</i> (b)	0.18	0.09	[0.00, 0.35]	1.94	.05
DNAm <i>ESR1</i> ~ PCDD73 (a)	-0.07	0.04	[-0.14, 0.01]	-1.81	.07
DNAm <i>ESR1</i> ~ Sex	-0.04	0.06	[-0.17, 0.07]	-0.66	.51
DNAm <i>ESR1</i> ~ PCDD73:Sex (a:Sex)	-0.12	0.12	[-0.38, 0.08]	-1.02	.31

Note. Coefficient = *Regressions* beta value, *SE* = standard error, *CI* = confidence interval, *z* = *z*-statistic, *p* = *p*-value, *c* = *c*-path, *b* = *b*-path, *a* = *a*-path.

Table A.175.ii. *Defined model parameters (effects)*

Effect	Coefficient	<i>SE</i>	95% <i>CI</i>	<i>z</i>	<i>p</i>
Indirect (female)	-0.01	0.01	[-0.04, 0.00]	-1.21	.23
Total (female)	-0.05	0.03	[-0.13, 0.01]	-1.50	.13
Indirect (male)	-0.03	0.03	[-0.11, 0.00]	-1.17	.24
Total (male)	8.89x10 ⁻⁰³	0.05	[-0.11, 0.11]	0.16	.87
Difference in indirect (male - female)	0.02	0.03	[-0.02, 0.09]	0.82	.41
Difference in total (male - female)	-0.06	0.07	[-0.19, 0.07]	-0.92	.36

Note. Coefficient = estimated model parameter, *SE* = standard error, *CI* = confidence interval, *z* = *z*-statistic, *p* = *p*-value.

Tables A.176.i & ii. Results of the mediation model with the predictor congener PCDD75, the mean DNA methylation of the CpGs in the promoter region of *ESR1*, and the predicted difference in PDS score between baseline (t0) & last follow-up (t5) as outcome.

Table A.176.i. *Regressions*

	Coefficient	<i>SE</i>	95% <i>CI</i>	<i>z</i>	<i>p</i>
PDS score (t5-t0) ~ PCDD75 (c)	-0.02	0.04	[-0.10, 0.05]	-0.50	.62
PDS score (t5-t0) ~ Sex	-0.78	0.04	[-0.85, -0.71]	-21.72	< .001
PDS score (t5-t0) ~ PCDD75:Sex (c:Sex)	0.11	0.06	[-0.01, 0.24]	1.76	.08
PDS score (t5-t0) ~ DNAm <i>ESR1</i> (b)	0.19	0.09	[0.01, 0.35]	2.15	.03
DNAm <i>ESR1</i> ~ PCDD75 (a)	-0.08	0.04	[-0.17, -0.01]	-1.99	.05
DNAm <i>ESR1</i> ~ Sex	-0.03	0.06	[-0.15, 0.07]	-0.55	.58
DNAm <i>ESR1</i> ~ PCDD75:Sex (a:Sex)	-0.09	0.13	[-0.39, 0.11]	-0.73	.47

Note. Coefficient = *Regressions* beta value, *SE* = standard error, *CI* = confidence interval, *z* = *z*-statistic, *p* = *p*-value, *c* = *c*-path, *b* = *b*-path, *a* = *a*-path.

Table A.176.ii. *Defined model parameters (effects)*

Effect	Coefficient	<i>SE</i>	95% <i>CI</i>	<i>z</i>	<i>p</i>
Indirect (female)	-0.02	0.01	[-0.04, 0.00]	-1.34	.18
Total (female)	-0.03	0.04	[-0.11, 0.03]	-0.91	.36
Indirect (male)	-0.03	0.03	[-0.11, 0.00]	-1.13	.26
Total (male)	0.06	0.06	[-0.07, 0.18]	1.00	.32
Difference in indirect (male - female)	0.02	0.03	[-0.02, 0.08]	0.64	.52
Difference in total (male - female)	-0.10	0.07	[-0.24, 0.05]	-1.33	.18

Note. Coefficient = estimated model parameter, *SE* = standard error, *CI* = confidence interval, *z* = *z*-statistic, *p* = *p*-value.

Tables A.177.i & ii. Results of the mediation model with the predictor congener PCDF114, the mean DNA methylation of the CpGs in the promoter region of *ESR1*, and the predicted difference in PDS score between baseline (t0) & last follow-up (t5) as outcome.

Table A.177.i. *Regressions*

	Coefficient	<i>SE</i>	95% <i>CI</i>	<i>z</i>	<i>p</i>
PDS score (t5-t0) ~ PCDF114 (c)	-0.05	0.04	[-0.13, 0.03]	-1.19	.23
PDS score (t5-t0) ~ Sex	-0.78	0.04	[-0.85, -0.71]	-21.93	< .001

PDS score (t5-t0) ~ PCDF114:Sex (c:Sex)	0.14	0.08	[-0.04, 0.28]	1.78	.07
PDS score (t5-t0) ~ DNAm <i>ESR1</i> (b)	0.17	0.09	[-0.01, 0.35]	1.80	.07
DNAm <i>ESR1</i> ~ PCDF114 (a)	-0.06	0.05	[-0.15, 0.03]	-1.37	.17
DNAm <i>ESR1</i> ~ Sex	-0.04	0.06	[-0.17, 0.07]	-0.62	.53
DNAm <i>ESR1</i> ~ PCDF114:Sex (a:Sex)	-0.08	0.13	[-0.37, 0.11]	-0.65	.51

Note. Coefficient = *Regressions* beta value, *SE* = standard error, CI = confidence interval, *z* = *z*-statistic, *p* = *p*-value, c = c-path, b = b-path, a = a-path.

Table A.177.ii. *Defined model parameters (effects)*

Effect	Coefficient	<i>SE</i>	95% CI	<i>z</i>	<i>p</i>
Indirect (female)	-0.01	0.01	[-0.04, 0.01]	-0.97	.33
Total (female)	-0.06	0.04	[-0.13, 0.02]	-1.53	.13
Indirect (male)	-0.02	0.03	[-0.10, 0.01]	-0.89	.38
Total (male)	0.07	0.08	[-0.11, 0.19]	0.94	.35
Difference in indirect (male - female)	0.01	0.03	[-0.02, 0.08]	0.52	.60
Difference in total (male - female)	-0.13	0.09	[-0.27, 0.07]	-1.48	.14

Note. Coefficient = estimated model parameter, *SE* = standard error, CI = confidence interval, *z* = *z*-statistic, *p* = *p*-value.

Tables A.178.i & ii. Results of the mediation model with the predictor congener PCDF118, the mean DNA methylation of the CpGs in the promoter region of *ESR1*, and the predicted difference in PDS score between baseline (t0) & last follow-up (t5) as outcome.

Table A.178.i. *Regressions*

	Coefficient	<i>SE</i>	95% CI	<i>z</i>	<i>p</i>
PDS score (t5-t0) ~ PCDF118 (c)	-0.05	0.05	[-0.15, 0.04]	-1.02	.31
PDS score (t5-t0) ~ Sex	-0.78	0.04	[-0.84, -0.71]	-22.16	< .001
PDS score (t5-t0) ~ PCDF118:Sex (c:Sex)	0.14	0.08	[-0.02, 0.29]	1.81	.07
PDS score (t5-t0) ~ DNAm <i>ESR1</i> (b)	0.17	0.09	[-0.01, 0.35]	1.90	.06
DNAm <i>ESR1</i> ~ PCDF118 (a)	-0.07	0.06	[-0.18, 0.04]	-1.32	.19
DNAm <i>ESR1</i> ~ Sex	-0.04	0.06	[-0.18, 0.07]	-0.63	.53
DNAm <i>ESR1</i> ~ PCDF118:Sex (a:Sex)	-0.12	0.14	[-0.45, 0.11]	-0.82	.41

Note. Coefficient = *Regressions* beta value, *SE* = standard error, CI = confidence interval, *z* = *z*-statistic, *p* = *p*-value, c = c-path, b = b-path, a = a-path.

Table A.178.ii. *Defined model parameters (effects)*

Effect	Coefficient	<i>SE</i>	95% CI	<i>z</i>	<i>p</i>
Indirect (female)	-0.01	0.01	[-0.04, 0.01]	-0.99	.32
Total (female)	-0.06	0.05	[-0.16, 0.02]	-1.30	.19
Indirect (male)	-0.03	0.03	[-0.12, 0.01]	-1.00	.32
Total (male)	0.06	0.07	[-0.11, 0.18]	0.84	.40
Difference in indirect (male - female)	0.02	0.03	[-0.02, 0.10]	0.65	.52
Difference in total (male - female)	-0.12	0.09	[-0.28, 0.07]	-1.39	.17

Note. Coefficient = estimated model parameter, *SE* = standard error, CI = confidence interval, *z* = *z*-statistic, *p* = *p*-value.

Tables A.179.i & ii. Results of the mediation model with the predictor congener PCDF121, the mean DNA methylation of the CpGs in the promoter region of *ESR1*, and the predicted difference in PDS score between baseline (t0) & last follow-up (t5) as outcome.

Table A.179.i. *Regressions*

	Coefficient	SE	95% CI	z	p
PDS score (t5-t0) ~ PCDF121 (c)	-0.03	0.04	[-0.12, 0.05]	-0.78	.434
PDS score (t5-t0) ~ Sex	-0.78	0.04	[-0.84, -0.71]	-21.95	< .001
PDS score (t5-t0) ~ PCDF121:Sex (c:Sex)	0.13	0.08	[-0.05, 0.27]	1.55	.12
PDS score (t5-t0) ~ DNAm <i>ESR1</i> (b)	0.17	0.09	[0.00, 0.35]	1.95	.05
DNAm <i>ESR1</i> ~ PCDF121 (a)	-0.06	0.05	[-0.15, 0.05]	-1.18	.24
DNAm <i>ESR1</i> ~ Sex	-0.04	0.06	[-0.18, 0.07]	-0.65	.52
DNAm <i>ESR1</i> ~ PCDF121:Sex (a:Sex)	-0.12	0.14	[-0.44, 0.11]	-0.84	.40

Note. Coefficient = *Regressions* beta value, SE = standard error, CI = confidence interval, z = z-statistic, p = p-value, c = c-path, b = b-path, a = a-path.

Table A.179.ii. *Defined model parameters (effects)*

Effect	Coefficient	SE	95% CI	z	p
Indirect (female)	-0.01	0.01	[-0.04, 0.01]	-0.91	.36
Total (female)	-0.04	0.04	[-0.13, 0.04]	-1.05	.29
Indirect (male)	-0.03	0.03	[-0.12, 0.01]	-0.95	.34
Total (male)	0.06	0.08	[-0.12, 0.18]	0.82	.41
Difference in indirect (male - female)	0.02	0.03	[-0.02, 0.10]	0.65	.52
Difference in total (male - female)	-0.11	0.09	[-0.26, 0.10]	-1.20	.23

Note. Coefficient = estimated model parameter, SE = standard error, CI = confidence interval, z = z-statistic, p = p-value.

Tables A.180.i & ii. Results of the mediation model with the predictor congener PCDF130, the mean DNA methylation of the CpGs in the promoter region of *ESR1*, and the predicted difference in PDS score between baseline (t0) & last follow-up (t5) as outcome.

Table A.180.i. *Regressions*

	Coefficient	SE	95% CI	z	p
PDS score (t5-t0) ~ PCDF130 (c)	-0.01	0.03	[-0.08, 0.04]	-0.49	.62
PDS score (t5-t0) ~ Sex	-0.79	0.04	[-0.86, -0.72]	-21.74	< .001
PDS score (t5-t0) ~ PCDF130:Sex (c:Sex)	0.12	0.07	[-0.01, 0.26]	1.69	.09
PDS score (t5-t0) ~ DNAm <i>ESR1</i> (b)	0.17	0.09	[-0.02, 0.34]	1.88	.06
DNAm <i>ESR1</i> ~ PCDF130 (a)	0.01	0.04	[-0.07, 0.09]	0.33	.74
DNAm <i>ESR1</i> ~ Sex	-0.03	0.06	[-0.16, 0.07]	-0.51	.61
DNAm <i>ESR1</i> ~ PCDF130:Sex (a:Sex)	-0.15	0.10	[-0.37, 0.01]	-1.59	.11

Note. Coefficient = *Regressions* beta value, SE = standard error, CI = confidence interval, z = z-statistic, p = p-value, c = c-path, b = b-path, a = a-path.

Table A.180.ii. *Defined model parameters (effects)*

Effect	Coefficient	SE	95% CI	z	p
Indirect (female)	2.23x10 ⁻⁰³	7.53x10 ⁻⁰³	[-0.01, 0.02]	0.30	.77

Total (female)	-0.01	0.03	[-0.08, 0.04]	-0.39	.70
Indirect (male)	-0.02	0.02	[-0.08, 0.00]	-1.06	.29
Total (male)	0.08	0.06	[-0.06, 0.20]	1.20	.23
Difference in indirect (male - female)	0.03	0.02	[0.00, 0.09]	1.08	.28
Difference in total (male - female)	-0.09	0.07	[-0.23, 0.05]	-1.24	.22

Note. Coefficient = estimated model parameter, *SE* = standard error, CI = confidence interval, *z* = *z*-statistic, *p* = *p*-value.

Tables A.181.i & ii. Results of the mediation model with the predictor congener PCDF131, the mean DNA methylation of the CpGs in the promoter region of *ESR1*, and the predicted difference in PDS score between baseline (t0) & last follow-up (t5) as outcome.

Table A.181.i. *Regressions*

	Coefficient	<i>SE</i>	95% CI	<i>z</i>	<i>p</i>
PDS score (t5-t0) ~ PCDF131 (c)	0.02	0.02	[-0.02, 0.08]	0.90	.37
PDS score (t5-t0) ~ Sex	-0.78	0.04	[-0.85, -0.70]	-21.37	< .001
PDS score (t5-t0) ~ PCDF131:Sex (c:Sex)	0.02	0.05	[-0.07, 0.12]	0.43	.67
PDS score (t5-t0) ~ DNAm <i>ESR1</i> (b)	0.18	0.09	[0.00, 0.35]	2.03	.04
DNAm <i>ESR1</i> ~ PCDF131 (a)	-0.03	0.03	[-0.09, 0.04]	-1.04	.30
DNAm <i>ESR1</i> ~ Sex	-0.03	0.06	[-0.14, 0.07]	-0.47	.64
DNAm <i>ESR1</i> ~ PCDF131:Sex (a:Sex)	-0.13	0.14	[-0.42, 0.08]	-0.90	.37

Note. Coefficient = *Regressions* beta value, *SE* = standard error, CI = confidence interval, *z* = *z*-statistic, *p* = *p*-value, c = c-path, b = b-path, a = a-path.

Table A.181.ii. *Defined model parameters (effects)*

Effect	Coefficient	<i>SE</i>	95% CI	<i>z</i>	<i>p</i>
Indirect (female)	-6.38x10 ⁻⁰³	7.41x10 ⁻⁰³	[-0.02, 0.01]	-0.86	.39
Total (female)	0.02	0.03	[-0.03, 0.08]	0.60	.55
Indirect (male)	-0.03	0.03	[-0.10, 0.01]	-0.97	.33
Total (male)	0.01	0.05	[-0.09, 0.12]	0.25	.80
Difference in indirect (male - female)	0.02	0.03	[-0.02, 0.10]	0.78	.44
Difference in total (male - female)	2.49x10 ⁻⁰³	0.06	[-0.11, 0.12]	0.04	.97

Note. Coefficient = estimated model parameter, *SE* = standard error, CI = confidence interval, *z* = *z*-statistic, *p* = *p*-value.

Tables A.182.i & ii. Results of the mediation model with the predictor congener PCB126, the mean DNA methylation of the CpGs in the promoter region of *ESR2*, and the predicted difference in PDS score between baseline (t0) & last follow-up (t5) as outcome.

Table A.182.i. *Regressions*

	Coefficient	<i>SE</i>	95% CI	<i>z</i>	<i>p</i>
PDS score (t5-t0) ~ PCB126 (c)	3.67x10 ⁻⁰³	0.03	[-0.07, 0.04]	0.14	.89
PDS score (t5-t0) ~ Sex	-0.76	0.04	[-0.84, -0.69]	-19.60	< .001
PDS score (t5-t0) ~ PCB126:Sex (c:Sex)	0.06	0.07	[-0.10, 0.18]	0.82	.42
PDS score (t5-t0) ~ DNAm <i>ESR2</i> (b)	0.16	0.08	[0.02, 0.33]	1.97	.05
DNAm <i>ESR2</i> ~ PCB126 (a)	-7.01x10 ⁻⁰³	0.03	[-0.06, 0.05]	-0.25	.81
DNAm <i>ESR2</i> ~ Sex	-0.05	0.04	[-0.12, 0.02]	-1.30	.19

DNAm <i>ESR2</i> ~ PCB126:Sex (a:Sex)	-0.03	0.07	[-0.18, 0.10]	-0.47	.64
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Note. Coefficient = *Regressions* beta value, *SE* = standard error, CI = confidence interval, *z* = *z*-statistic, *p* = *p*-value, c = c-path, b = b-path, a = a-path.

Table A.182.ii. *Defined model parameters (effects)*

Effect	Coefficient	<i>SE</i>	95% CI	<i>z</i>	<i>p</i>
Indirect (female)	-1.09x10 ⁻⁰³	5.23x10 ⁻⁰³	[-0.01, 0.01]	-0.21	.84
Total (female)	2.58x10 ⁻⁰³	0.03	[-0.07, 0.04]	0.10	.92
Indirect (male)	-6.33x10 ⁻⁰³	0.01	[-0.03, 0.02]	-0.54	.59
Total (male)	0.05	0.06	[-0.09, 0.15]	0.86	.39
Difference in indirect (male - female)	5.24x10 ⁻⁰³	0.01	[-0.02, 0.03]	0.41	.68
Difference in total (male - female)	-0.05	0.07	[-0.17, 0.10]	-0.75	.45

Note. Coefficient = estimated model parameter, *SE* = standard error, CI = confidence interval, *z* = *z*-statistic, *p* = *p*-value.

Tables A.183.i & ii. Results of the mediation model with the predictor congener PCB169, the mean DNA methylation of the CpGs in the promoter region of *ESR2*, and the predicted difference in PDS score between baseline (t0) & last follow-up (t5) as outcome.

Table A.183.i. *Regressions*

	Coefficient	<i>SE</i>	95% CI	<i>z</i>	<i>p</i>
PDS score (t5-t0) ~ PCB169 (c)	-0.03	0.04	[-0.10, 0.04]	-0.80	.42
PDS score (t5-t0) ~ Sex	-0.77	0.04	[-0.85, -0.69]	-20.32	< .001
PDS score (t5-t0) ~ PCB169:Sex (c:Sex)	0.15	0.06	[0.02, 0.27]	2.41	.02
PDS score (t5-t0) ~ DNAm <i>ESR2</i> (b)	0.13	0.08	[-0.02, 0.30]	1.75	.08
DNAm <i>ESR2</i> ~ PCB169 (a)	-0.05	0.03	[-0.12, 0.01]	-1.56	.12
DNAm <i>ESR2</i> ~ Sex	-0.05	0.04	[-0.12, 0.02]	-1.32	.19
DNAm <i>ESR2</i> ~ PCB169:Sex (a:Sex)	0.07	0.06	[-0.04, 0.18]	1.25	.21

Note. Coefficient = *Regressions* beta value, *SE* = standard error, CI = confidence interval, *z* = *z*-statistic, *p* = *p*-value, c = c-path, b = b-path, a = a-path.

Table A.183.ii. *Defined model parameters (effects)*

Effect	Coefficient	<i>SE</i>	95% CI	<i>z</i>	<i>p</i>
Indirect (female)	-6.91x10 ⁻⁰³	6.67x10 ⁻⁰³	[-0.02, 0.00]	-1.04	.30
Total (female)	-0.04	0.04	[-0.11, 0.03]	-1.00	.32
Indirect (male)	2.38x10 ⁻⁰³	7.05x10 ⁻⁰³	[-0.01, 0.02]	0.34	.74
Total (male)	0.13	0.05	[0.02, 0.22]	2.51	.01
Difference in indirect (male - female)	-9.30x10 ⁻⁰³	0.01	[-0.03, 0.01]	-0.89	.38
Difference in total (male - female)	-0.16	0.06	[-0.28, -0.03]	-2.61	.01

Note. Coefficient = estimated model parameter, *SE* = standard error, CI = confidence interval, *z* = *z*-statistic, *p* = *p*-value.

Tables A.184.i & ii. Results of the mediation model with the predictor congener PCB77, the mean DNA methylation of the CpGs in the promoter region of *ESR2*, and the predicted difference in PDS score between baseline (t0) & last follow-up (t5) as outcome.

Table A.184.i. *Regressions*

	Coefficient	<i>SE</i>	95% CI	<i>z</i>	<i>p</i>
PDS score (t5-t0) ~ PCB77 (c)	2.47x10 ⁻⁰⁴	0.05	[-0.08, 0.11]	4.95x10 ⁻⁰³	.996

PDS score (t5-t0) ~ Sex	-0.76	0.04	[-0.83, -0.69]	-21.07	< .001
PDS score (t5-t0) ~ PCB77:Sex (c:Sex)	0.14	0.09	[-0.04, 0.32]	1.57	.12
PDS score (t5-t0) ~ DNAm <i>ESR2</i> (b)	0.15	0.08	[0.02, 0.33]	1.91	.06
DNAm <i>ESR2</i> ~ PCB77 (a)	-0.02	0.04	[-0.09, 0.08]	-0.42	.68
DNAm <i>ESR2</i> ~ Sex	-0.05	0.04	[-0.12, 0.02]	-1.33	.18
DNAm <i>ESR2</i> ~ PCB77:Sex (a:Sex)	0.10	0.11	[-0.09, 0.33]	0.96	.34

Note. Coefficient = *Regressions* beta value, *SE* = standard error, *CI* = confidence interval, *z* = *z*-statistic, *p* = *p*-value, c = c-path, b = b-path, a = a-path.

Table A.184.ii. *Defined model parameters (effects)*

Effect	Coefficient	<i>SE</i>	95% <i>CI</i>	<i>z</i>	<i>p</i>
Indirect (female)	-2.74x10 ⁻⁰³	7.74x10 ⁻⁰³	[-0.02, 0.01]	-0.35	.72
Total (female)	-2.49x10 ⁻⁰³	0.05	[-0.09, 0.11]	-0.05	.96
Indirect (male)	0.01	0.02	[-0.01, 0.06]	0.70	.48
Total (male)	0.16	0.08	[0.02, 0.33]	2.05	.04
Difference in indirect (male - female)	-0.02	0.02	[-0.07, 0.02]	-0.77	.44
Difference in total (male - female)	-0.16	0.09	[-0.35, 0.02]	-1.71	.09

Note. Coefficient = estimated model parameter, *SE* = standard error, *CI* = confidence interval, *z* = *z*-statistic, *p* = *p*-value.

Tables A.185.i & ii. Results of the mediation model with the predictor congener PCB81, the mean DNA methylation of the CpGs in the promoter region of *ESR2*, and the predicted difference in PDS score between baseline (t0) & last follow-up (t5) as outcome.

Table A.185.i. *Regressions*

	Coefficient	<i>SE</i>	95% <i>CI</i>	<i>z</i>	<i>p</i>
PDS score (t5-t0) ~ PCB81 (c)	-0.03	0.03	[-0.07, 0.04]	-0.97	.33
PDS score (t5-t0) ~ Sex	-0.76	0.04	[-0.84, -0.68]	-18.68	< .001
PDS score (t5-t0) ~ PCB81:Sex (c:Sex)	0.05	0.07	[-0.09, 0.19]	0.76	.45
PDS score (t5-t0) ~ DNAm <i>ESR2</i> (b)	0.15	0.08	[0.00, 0.33]	1.88	.06
DNAm <i>ESR2</i> ~ PCB81 (a)	3.25x10 ⁻⁰⁴	0.03	[-0.06, 0.06]	0.01	.99
DNAm <i>ESR2</i> ~ Sex	-0.04	0.03	[-0.11, 0.02]	-1.23	.22
DNAm <i>ESR2</i> ~ PCB81:Sex (a:Sex)	-0.05	0.07	[-0.18, 0.08]	-0.82	.41

Note. Coefficient = *Regressions* beta value, *SE* = standard error, *CI* = confidence interval, *z* = *z*-statistic, *p* = *p*-value, c = c-path, b = b-path, a = a-path.

Table A.185.ii. *Defined model parameters (effects)*

Effect	Coefficient	<i>SE</i>	95% <i>CI</i>	<i>z</i>	<i>p</i>
Indirect (female)	4.96x10 ⁻⁰⁵	5.28x10 ⁻⁰³	[-0.01, 0.01]	9.39x10 ⁻⁰³	.99
Total (female)	-0.03	0.03	[-0.08, 0.04]	-0.93	.35
Indirect (male)	-8.27x10 ⁻⁰³	0.01	[-0.03, 0.01]	-0.79	.43
Total (male)	0.02	0.07	[-0.11, 0.15]	0.28	.78
Difference in indirect (male - female)	8.32x10 ⁻⁰³	0.01	[-0.02, 0.03]	0.71	.48
Difference in total (male - female)	-0.05	0.07	[-0.18, 0.09]	-0.65	.52

Note. Coefficient = estimated model parameter, *SE* = standard error, *CI* = confidence interval, *z* = *z*-statistic, *p* = *p*-value.

Tables A.186.i & ii. Results of the mediation model with the predictor congener PCDD48, the mean DNA methylation of the CpGs in the promoter region of *ESR2*, and the predicted difference in PDS score between baseline (t0) & last follow-up (t5) as outcome.

Table A.186.i. *Regressions*

	Coefficient	SE	95% CI	z	p
PDS score (t5-t0) ~ PCDD48 (c)	-0.04	0.03	[-0.09, 0.02]	-1.42	.16
PDS score (t5-t0) ~ Sex	-0.76	0.04	[-0.83, -0.69]	-20.19	< .001
PDS score (t5-t0) ~ PCDD48:Sex (c:Sex)	0.07	0.06	[-0.06, 0.18]	1.19	.24
PDS score (t5-t0) ~ DNAm <i>ESR2</i> (b)	0.14	0.08	[0.00, 0.32]	1.83	.07
DNAm <i>ESR2</i> ~ PCDD48 (a)	-0.05	0.03	[-0.11, 0.00]	-2.00	.05
DNAm <i>ESR2</i> ~ Sex	-0.05	0.04	[-0.12, 0.02]	-1.34	.18
DNAm <i>ESR2</i> ~ PCDD48:Sex (a:Sex)	0.05	0.05	[-0.05, 0.15]	0.99	.32

Note. Coefficient = *Regressions* beta value, SE = standard error, CI = confidence interval, z = z-statistic, p = p-value, c = c-path, b = b-path, a = a-path.

Table A.186.ii. *Defined model parameters (effects)*

Effect	Coefficient	SE	95% CI	z	p
Indirect (female)	-7.76x10 ⁻⁰³	6.25x10 ⁻⁰³	[-0.02, 0.00]	-1.24	.22
Total (female)	-0.05	0.03	[-0.10, 0.01]	-1.67	.10
Indirect (male)	-4.73x10 ⁻⁰⁴	6.81x10 ⁻⁰³	[-0.01, 0.01]	-0.07	.95
Total (male)	0.03	0.05	[-0.09, 0.12]	0.58	.56
Difference in indirect (male - female)	-7.28x10 ⁻⁰³	9.64x10 ⁻⁰³	[-0.03, 0.01]	-0.76	.45
Difference in total (male - female)	-0.08	0.06	[-0.19, 0.05]	-1.30	.19

Note. Coefficient = estimated model parameter, SE = standard error, CI = confidence interval, z = z-statistic, p = p-value.

Tables A.187.i & ii. Results of the mediation model with the predictor congener PCDD54, the mean DNA methylation of the CpGs in the promoter region of *ESR2*, and the predicted difference in PDS score between baseline (t0) & last follow-up (t5) as outcome.

Table A.187.i. *Regressions*

	Coefficient	SE	95% CI	z	p
PDS score (t5-t0) ~ PCDD54 (c)	-0.02	0.05	[-0.11, 0.07]	-0.44	.66
PDS score (t5-t0) ~ Sex	-0.76	0.04	[-0.83, -0.68]	-20.01	< .001
PDS score (t5-t0) ~ PCDD54:Sex (c:Sex)	0.10	0.08	[-0.07, 0.25]	1.18	.24
PDS score (t5-t0) ~ DNAm <i>ESR2</i> (b)	0.16	0.08	[0.02, 0.33]	2.01	.04
DNAm <i>ESR2</i> ~ PCDD54 (a)	-0.04	0.04	[-0.13, 0.04]	-0.81	.42
DNAm <i>ESR2</i> ~ Sex	-0.05	0.04	[-0.12, 0.02]	-1.33	.18
DNAm <i>ESR2</i> ~ PCDD54:Sex (a:Sex)	0.02	0.08	[-0.14, 0.17]	0.27	.79

Note. Coefficient = *Regressions* beta value, SE = standard error, CI = confidence interval, z = z-statistic, p = p-value, c = c-path, b = b-path, a = a-path.

Table A.187.ii. *Defined model parameters (effects)*

Effect	Coefficient	SE	95% CI	z	p
Indirect (female)	-5.55x10 ⁻⁰³	8.37x10 ⁻⁰³	[-0.03, 0.01]	-0.66	.51

Total (female)	-0.03	0.05	[-0.11, 0.07]	-0.56	.58
Indirect (male)	-2.25x10 ⁻⁰³	0.01	[-0.03, 0.02]	-0.19	.85
Total (male)	0.07	0.06	[-0.06, 0.20]	1.13	.26
Difference in indirect (male - female)	-3.30x10 ⁻⁰³	0.01	[-0.04, 0.02]	-0.23	.82
Difference in total (male - female)	-0.10	0.08	[-0.25, 0.06]	-1.24	.22

Note. Coefficient = estimated model parameter, SE = standard error, CI = confidence interval, z = z -statistic, p = p -value.

Tables A.188.i & ii. Results of the mediation model with the predictor congener PCDD66, the mean DNA methylation of the CpGs in the promoter region of *ESR2*, and the predicted difference in PDS score between baseline (t0) & last follow-up (t5) as outcome.

Table A.188.i. *Regressions*

	Coefficient	SE	95% CI	z	p
PDS score (t5-t0) ~ PCDD66 (c)	-0.04	0.04	[-0.13, 0.05]	-0.90	.37
PDS score (t5-t0) ~ Sex	-0.77	0.04	[-0.85, -0.69]	-19.32	< .001
PDS score (t5-t0) ~ PCDD66:Sex (c:Sex)	0.11	0.07	[-0.05, 0.25]	1.45	.15
PDS score (t5-t0) ~ DNAm <i>ESR2</i> (b)	0.15	0.08	[0.00, 0.32]	1.91	.06
DNAm <i>ESR2</i> ~ PCDD66 (a)	-0.04	0.04	[-0.12, 0.04]	-0.88	.38
DNAm <i>ESR2</i> ~ Sex	-0.05	0.04	[-0.12, 0.02]	-1.35	.18
DNAm <i>ESR2</i> ~ PCDD66:Sex (a:Sex)	0.01	0.08	[-0.14, 0.15]	0.18	.86

Note. Coefficient = *Regressions* beta value, SE = standard error, CI = confidence interval, z = z -statistic, p = p -value, c = c-path, b = b-path, a = a-path.

Table A.188.ii. *Defined model parameters (effects)*

Effect	Coefficient	SE	95% CI	z	p
Indirect (female)	-5.44x10 ⁻⁰³	7.56x10 ⁻⁰³	[-0.02, 0.01]	-0.72	.47
Total (female)	-0.05	0.04	[-0.13, 0.04]	-1.02	.31
Indirect (male)	-3.38x10 ⁻⁰³	0.01	[-0.03, 0.02]	-0.31	.76
Total (male)	0.06	0.06	[-0.07, 0.17]	1.09	.27
Difference in indirect (male - female)	-2.05x10 ⁻⁰³	0.01	[-0.03, 0.02]	-0.16	.88
Difference in total (male - female)	-0.11	0.07	[-0.25, 0.05]	-1.49	.14

Note. Coefficient = estimated model parameter, SE = standard error, CI = confidence interval, z = z -statistic, p = p -value.

Tables A.189.i & ii. Results of the mediation model with the predictor congener PCDD67, the mean DNA methylation of the CpGs in the promoter region of *ESR2*, and the predicted difference in PDS score between baseline (t0) & last follow-up (t5) as outcome.

Table A.189.i. *Regressions*

	Coefficient	SE	95% CI	z	p
PDS score (t5-t0) ~ PCDD67 (c)	-0.03	0.05	[-0.12, 0.06]	-0.73	.46
PDS score (t5-t0) ~ Sex	-0.77	0.04	[-0.84, -0.69]	-19.42	< .001
PDS score (t5-t0) ~ PCDD67:Sex (c:Sex)	0.11	0.08	[-0.06, 0.25]	1.43	.15
PDS score (t5-t0) ~ DNAm <i>ESR2</i> (b)	0.15	0.08	[0.01, 0.32]	1.95	.05
DNAm <i>ESR2</i> ~ PCDD67 (a)	-0.05	0.05	[-0.16, 0.03]	-1.01	.31
DNAm <i>ESR2</i> ~ Sex	-0.05	0.04	[-0.12, 0.02]	-1.32	.19

DNAm <i>ESR2</i> ~ PCDD67:Sex (a:Sex)	0.04	0.07	[-0.10, 0.18]	0.61	.54
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Note. Coefficient = *Regressions* beta value, *SE* = standard error, CI = confidence interval, *z* = *z*-statistic, *p* = *p*-value, c = c-path, b = b-path, a = a-path.

Table A.189.ii. *Defined model parameters (effects)*

Effect	Coefficient	<i>SE</i>	95% CI	<i>z</i>	<i>p</i>
Indirect (female)	-7.45x10 ⁻⁰³	9.40x10 ⁻⁰³	[-0.03, 0.00]	-0.79	.43
Total (female)	-0.04	0.05	[-0.13, 0.05]	-0.89	.37
Indirect (male)	-8.70x10 ⁻⁰⁴	8.82x10 ⁻⁰³	[-0.02, 0.02]	-0.10	.92
Total (male)	0.08	0.06	[-0.08, 0.18]	1.23	.22
Difference in indirect (male - female)	-6.58x10 ⁻⁰³	0.01	[-0.04, 0.02]	-0.51	.61
Difference in total (male - female)	-0.12	0.08	[-0.26, 0.05]	-1.52	.13

Note. Coefficient = estimated model parameter, *SE* = standard error, CI = confidence interval, *z* = *z*-statistic, *p* = *p*-value.

Tables A.190.i & ii. Results of the mediation model with the predictor congener PCDD70, the mean DNA methylation of the CpGs in the promoter region of *ESR2*, and the predicted difference in PDS score between baseline (t0) & last follow-up (t5) as outcome.

Table A.190.i. *Regressions*

	Coefficient	<i>SE</i>	95% CI	<i>z</i>	<i>p</i>
PDS score (t5-t0) ~ PCDD70 (c)	-0.04	0.04	[-0.12, 0.04]	-0.95	.34
PDS score (t5-t0) ~ Sex	-0.76	0.04	[-0.83, -0.69]	-20.24	< .001
PDS score (t5-t0) ~ PCDD70:Sex (c:Sex)	0.10	0.07	[-0.05, 0.23]	1.45	.15
PDS score (t5-t0) ~ DNAm <i>ESR2</i> (b)	0.15	0.08	[0.01, 0.32]	1.92	.06
DNAm <i>ESR2</i> ~ PCDD70 (a)	-0.01	0.04	[-0.09, 0.06]	-0.36	.72
DNAm <i>ESR2</i> ~ Sex	-0.05	0.04	[-0.12, 0.02]	-1.27	.20
DNAm <i>ESR2</i> ~ PCDD70:Sex (a:Sex)	0.02	0.08	[-0.16, 0.17]	0.20	.84

Note. Coefficient = *Regressions* beta value, *SE* = standard error, CI = confidence interval, *z* = *z*-statistic, *p* = *p*-value, c = c-path, b = b-path, a = a-path.

Table A.190.ii. *Defined model parameters (effects)*

Effect	Coefficient	<i>SE</i>	95% CI	<i>z</i>	<i>p</i>
Indirect (female)	-2.12x10 ⁻⁰³	6.98x10 ⁻⁰³	[-0.02, 0.01]	-0.30	.76
Total (female)	-0.04	0.04	[-0.12, 0.04]	-0.99	.32
Indirect (male)	4.44x10 ⁻⁰⁴	0.01	[-0.03, 0.03]	0.03	.97
Total (male)	0.06	0.06	[-0.06, 0.16]	1.12	.26
Difference in indirect (male - female)	-2.57x10 ⁻⁰³	0.02	[-0.04, 0.03]	-0.17	.86
Difference in total (male - female)	-0.10	0.07	[-0.23, 0.04]	-1.50	.13

Note. Coefficient = estimated model parameter, *SE* = standard error, CI = confidence interval, *z* = *z*-statistic, *p* = *p*-value.

Tables A.191.i & ii. Results of the mediation model with the predictor congener PCDD73, the mean DNA methylation of the CpGs in the promoter region of *ESR2*, and the predicted difference in PDS score between baseline (t0) & last follow-up (t5) as outcome.

Table A.191.i. *Regressions*

	Coefficient	<i>SE</i>	95% CI	<i>z</i>	<i>p</i>
PDS score (t5-t0) ~ PCDD73 (c)	-0.04	0.03	[-0.12, 0.01]	-1.30	.19

PDS score (t5-t0) ~ Sex	-0.77	0.04	[-0.84, -0.69]	-20.23	< .001
PDS score (t5-t0) ~ PCDD73:Sex (c:Sex)	0.10	0.06	[-0.01, 0.21]	1.82	.07
PDS score (t5-t0) ~ DNAm <i>ESR2</i> (b)	0.15	0.08	[0.02, 0.32]	1.98	.05
DNAm <i>ESR2</i> ~ PCDD73 (a)	-0.04	0.03	[-0.11, 0.02]	-1.21	.23
DNAm <i>ESR2</i> ~ Sex	-0.05	0.04	[-0.12, 0.02]	-1.36	.17
DNAm <i>ESR2</i> ~ PCDD73:Sex (a:Sex)	0.02	0.06	[-0.10, 0.12]	0.34	.74

Note. Coefficient = *Regressions* beta value, *SE* = standard error, *CI* = confidence interval, *z* = *z*-statistic, *p* = *p*-value, c = c-path, b = b-path, a = a-path.

Table A.191.ii. *Defined model parameters (effects)*

Effect	Coefficient	<i>SE</i>	95% <i>CI</i>	<i>z</i>	<i>p</i>
Indirect (female)	-6.09x10 ⁻⁰³	6.48x10 ⁻⁰³	[-0.02, 0.00]	-0.94	.35
Total (female)	-0.05	0.04	[-0.13, 0.01]	-1.42	.16
Indirect (male)	-3.24x10 ⁻⁰³	7.60x10 ⁻⁰³	[-0.02, 0.01]	-0.43	.67
Total (male)	0.05	0.04	[-0.04, 0.13]	1.23	.22
Difference in indirect (male - female)	-2.85x10 ⁻⁰³	9.73x10 ⁻⁰³	[-0.02, 0.02]	-0.29	.77
Difference in total (male - female)	-0.10	0.06	[-0.22, 0.01]	-1.85	.06

Note. Coefficient = estimated model parameter, *SE* = standard error, *CI* = confidence interval, *z* = *z*-statistic, *p* = *p*-value.

Tables A.192.i & ii. Results of the mediation model with the predictor congener PCDD75, the mean DNA methylation of the CpGs in the promoter region of *ESR2*, and the predicted difference in PDS score between baseline (t0) & last follow-up (t5) as outcome

Table A.192.i. *Regressions.*

	Coefficient	<i>SE</i>	95% <i>CI</i>	<i>z</i>	<i>p</i>
PDS score (t5-t0) ~ PCDD75 (c)	-0.02	0.03	[-0.09, 0.05]	-0.49	.63
PDS score (t5-t0) ~ Sex	-0.77	0.04	[-0.84, -0.69]	-20.03	< .001
PDS score (t5-t0) ~ PCDD75:Sex (c:Sex)	0.12	0.06	[0.00, 0.25]	1.86	.06
PDS score (t5-t0) ~ DNAm <i>ESR2</i> (b)	0.15	0.07	[0.02, 0.32]	2.08	.04
DNAm <i>ESR2</i> ~ PCDD75 (a)	-0.05	0.04	[-0.13, 0.02]	-1.33	.18
DNAm <i>ESR2</i> ~ Sex	-0.05	0.04	[-0.12, 0.02]	-1.30	.19
DNAm <i>ESR2</i> ~ PCDD75:Sex (a:Sex)	0.04	0.06	[-0.09, 0.16]	0.74	.46

Note. Coefficient = *Regressions* beta value, *SE* = standard error, *CI* = confidence interval, *z* = *z*-statistic, *p* = *p*-value, c = c-path, b = b-path, a = a-path.

Table A.192.ii. *Defined model parameters (effects)*

Effect	Coefficient	<i>SE</i>	95% <i>CI</i>	<i>z</i>	<i>p</i>
Indirect (female)	-7.73x10 ⁻⁰³	7.44x10 ⁻⁰³	[-0.03, 0.00]	-1.04	.30
Total (female)	-0.02	0.04	[-0.10, 0.04]	-0.67	.51
Indirect (male)	-7.83x10 ⁻⁰⁴	8.37x10 ⁻⁰³	[-0.02, 0.02]	-0.09	.93
Total (male)	0.10	0.05	[0.00, 0.21]	1.91	.06
Difference in indirect (male - female)	-6.94x10 ⁻⁰³	0.01	[-0.03, 0.01]	-0.60	.55
Difference in total (male - female)	-0.13	0.06	[-0.26, -0.01]	-1.97	.05

Note. Coefficient = estimated model parameter, *SE* = standard error, *CI* = confidence interval, *z* = *z*-statistic, *p* = *p*-value.

Tables A.193.i & ii. Results of the mediation model with the predictor congener PCDF114, the mean DNA methylation of the CpGs in the promoter region of *ESR2*, and the predicted difference in PDS score between baseline (t0) & last follow-up (t5) as outcome.

Table A.193.i. *Regressions*

	Coefficient	SE	95% CI	z	p
PDS score (t5-t0) ~ PCDF114 (c)	-0.04	0.04	[-0.12, 0.03]	-1.16	.25
PDS score (t5-t0) ~ Sex	-0.77	0.04	[-0.84, -0.69]	-20.18	< .001
PDS score (t5-t0) ~ PCDF114:Sex (c:Sex)	0.15	0.08	[-0.02, 0.28]	2.00	.05
PDS score (t5-t0) ~ DNAm <i>ESR2</i> (b)	0.14	0.08	[0.00, 0.31]	1.79	.07
DNAm <i>ESR2</i> ~ PCDF114 (a)	-0.07	0.04	[-0.14, 0.00]	-1.78	.08
DNAm <i>ESR2</i> ~ Sex	-0.05	0.04	[-0.12, 0.02]	-1.38	.17
DNAm <i>ESR2</i> ~ PCDF114:Sex (a:Sex)	0.06	0.07	[-0.08, 0.19]	0.89	.37

Note. Coefficient = *Regressions* beta value, SE = standard error, CI = confidence interval, z = z-statistic, p = p-value, c = c-path, b = b-path, a = a-path.

Table A.193.ii. *Defined model parameters (effects)*

Effect	Coefficient	SE	95% CI	z	p
Indirect (female)	-9.23x10 ⁻⁰³	8.31x10 ⁻⁰³	[-0.03, 0.00]	-1.11	.27
Total (female)	-0.05	0.04	[-0.13, 0.02]	-1.41	.16
Indirect (male)	-7.30x10 ⁻⁰⁴	9.37x10 ⁻⁰³	[-0.02, 0.02]	-0.08	.94
Total (male)	0.11	0.06	[-0.05, 0.21]	1.66	.10
Difference in indirect (male - female)	-8.49x10 ⁻⁰³	0.01	[-0.04, 0.01]	-0.67	.50
Difference in total (male - female)	-0.16	0.08	[-0.29, 0.01]	-2.15	.03

Note. Coefficient = estimated model parameter, SE = standard error, CI = confidence interval, z = z-statistic, p = p-value.

Tables A.194.i & ii. Results of the mediation model with the predictor congener PCDF118, the mean DNA methylation of the CpGs in the promoter region of *ESR2*, and the predicted difference in PDS score between baseline (t0) & last follow-up (t5) as outcome.

Table A.194.i. *Regressions*

	Coefficient	SE	95% CI	z	p
PDS score (t5-t0) ~ PCDF118 (c)	-0.05	0.05	[-0.15, 0.04]	-1.08	.28
PDS score (t5-t0) ~ Sex	-0.76	0.04	[-0.83, -0.69]	-20.23	< .001
PDS score (t5-t0) ~ PCDF118:Sex (c:Sex)	0.16	0.08	[0.00, 0.30]	2.09	.04
PDS score (t5-t0) ~ DNAm <i>ESR2</i> (b)	0.15	0.08	[0.01, 0.31]	1.89	.06
DNAm <i>ESR2</i> ~ PCDF118 (a)	-0.06	0.05	[-0.15, 0.03]	-1.30	.19
DNAm <i>ESR2</i> ~ Sex	-0.05	0.04	[-0.12, 0.02]	-1.31	.19
DNAm <i>ESR2</i> ~ PCDF118:Sex (a:Sex)	0.07	0.08	[-0.11, 0.22]	0.80	.43

Note. Coefficient = *Regressions* beta value, SE = standard error, CI = confidence interval, z = z-statistic, p = p-value, c = c-path, b = b-path, a = a-path.

Table A.194.ii. *Defined model parameters (effects)*

Effect	Coefficient	SE	95% CI	z	p
Indirect (female)	-8.66x10 ⁻⁰³	9.08x10 ⁻⁰³	[-0.03, 0.00]	-0.95	.34

Total (female)	-0.06	0.05	[-0.16, 0.03]	-1.25	.21
Indirect (male)	1.15×10^{-03}	0.01	[-0.02, 0.03]	0.10	.92
Total (male)	0.11	0.06	[-0.02, 0.21]	1.85	.06
Difference in indirect (male - female)	-9.81×10^{-03}	0.02	[-0.05, 0.02]	-0.62	.54
Difference in total (male - female)	-0.17	0.07	[-0.31, -0.01]	-2.24	.03

Note. Coefficient = estimated model parameter, *SE* = standard error, CI = confidence interval, *z* = *z*-statistic, *p* = *p*-value.

Tables A.195.i & ii. Results of the mediation model with the predictor congener PCDF121, the mean DNA methylation of the CpGs in the promoter region of *ESR2*, and the predicted difference in PDS score between baseline (t0) & last follow-up (t5) as outcome.

Table A.195.i. *Regressions*

	Coefficient	<i>SE</i>	95% CI	<i>z</i>	<i>p</i>
PDS score (t5-t0) ~ PCDF121	-0.03	0.04	[-0.11, 0.05]	-0.85	.40
(c)					
PDS score (t5-t0) ~ Sex	-0.76	0.04	[-0.83, -0.68]	-20.06	< .001
PDS score (t5-t0) ~ PCDF121:Sex	0.14	0.08	[-0.05, 0.27]	1.67	.09
(c:Sex)					
PDS score (t5-t0) ~ DNAm <i>ESR2</i>	0.14	0.08	[0.00, 0.31]	1.73	.08
(b)					
DNAm <i>ESR2</i> ~ PCDF121	-0.04	0.04	[-0.13, 0.04]	-0.99	.32
(a)					
DNAm <i>ESR2</i> ~ Sex	-0.05	0.04	[-0.12, 0.02]	-1.25	.21
DNAm <i>ESR2</i> ~ PCDF121:Sex	0.08	0.08	[-0.08, 0.23]	1.03	.31
(a:Sex)					

Note. Coefficient = *Regressions* beta value, *SE* = standard error, CI = confidence interval, *z* = *z*-statistic, *p* = *p*-value, c = c-path, b = b-path, a = a-path.

Table A.195.ii. *Defined model parameters (effects)*

Effect	Coefficient	<i>SE</i>	95% CI	<i>z</i>	<i>p</i>
Indirect (female)	-5.75×10^{-03}	7.86×10^{-03}	[-0.03, 0.01]	-0.73	.64
Total (female)	-0.04	0.04	[-0.12, 0.04]	-0.96	.34
Indirect (male)	5.43×10^{-03}	0.01	[-0.02, 0.03]	0.46	.65
Total (male)	0.11	0.07	[-0.05, 0.21]	1.60	.11
Difference in indirect (male - female)	-0.01	0.02	[-0.05, 0.01]	-0.72	.47
Difference in total (male - female)	-0.15	0.08	[-0.28, 0.03]	-1.87	.06

Note. Coefficient = estimated model parameter, *SE* = standard error, CI = confidence interval, *z* = *z*-statistic, *p* = *p*-value.

Tables A.196.i & ii. Results of the mediation model with the predictor congener PCDF130, the mean DNA methylation of the CpGs in the promoter region of *ESR2*, and the predicted difference in PDS score between baseline (t0) & last follow-up (t5) as outcome.

Table A.196.i. *Regressions*

	Coefficient	<i>SE</i>	95% CI	<i>z</i>	<i>p</i>
PDS score (t5-t0) ~ PCDF130	-9.14×10^{-03}	0.03	[-0.08, 0.04]	-0.28	.78
(c)					
PDS score (t5-t0) ~ Sex	-0.78	0.04	[-0.85, -0.70]	-19.99	< .001
PDS score (t5-t0) ~ PCDF130:Sex	0.12	0.07	[-0.01, 0.26]	1.70	.09
(c:Sex)					
PDS score (t5-t0) ~ DNAm <i>ESR2</i>	0.14	0.08	[0.00, 0.31]	1.76	.08
(b)					
DNAm <i>ESR2</i> ~ PCDF130	-1.77×10^{-03}	0.03	[-0.06, 0.05]	-0.06	.95
(a)					
DNAm <i>ESR2</i> ~ Sex	-0.05	0.04	[-0.12, 0.02]	-1.26	.21

DNAm <i>ESR2</i> ~ PCDF130:Sex (a:Sex)	0.01	0.06	[-0.11, 0.12]	0.21	.84
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Note. Coefficient = *Regressions* beta value, *SE* = standard error, *CI* = confidence interval, *z* = *z*-statistic, *p* = *p*-value, *c* = *c*-path, *b* = *b*-path, *a* = *a*-path.

Table A.196.ii. *Defined model parameters (effects)*

Effect	Coefficient	<i>SE</i>	95% CI	<i>z</i>	<i>p</i>
Indirect (female)	-2.43x10 ⁻⁰⁴	4.67x10 ⁻⁰³	[-0.01, 0.01]	-0.05	.96
Total (female)	-9.38x10 ⁻⁰³	0.03	[-0.08, 0.04]	-0.28	.78
Indirect (male)	1.39x10 ⁻⁰³	8.43x10 ⁻⁰³	[-0.02, 0.02]	0.16	.87
Total (male)	0.11	0.06	[-0.01, 0.23]	1.81	.07
Difference in indirect (male - female)	-1.63x10 ⁻⁰³	9.78x10 ⁻⁰³	[-0.02, 0.02]	-0.17	.87
Difference in total (male - female)	-0.12	0.07	[-0.26, 0.01]	-1.75	.08

Note. Coefficient = estimated model parameter, *SE* = standard error, *CI* = confidence interval, *z* = *z*-statistic, *p* = *p*-value.

Tables A.197.i & ii. Results of the mediation model with the predictor congener PCDF131, the mean DNA methylation of the CpGs in the promoter region of *ESR2*, and the predicted difference in PDS score between baseline (t0) & last follow-up (t5) as outcome.

Table A.197.i. *Regressions*

	Coefficient	<i>SE</i>	95% CI	<i>z</i>	<i>p</i>
PDS score (t5-t0) ~ PCDF131 (c)	0.02	0.02	[-0.02, 0.08]	0.83	.41
PDS score (t5-t0) ~ Sex	-0.76	0.04	[-0.83, -0.68]	-20.19	< .001
PDS score (t5-t0) ~ PCDF131:Sex (c:Sex)	0.02	0.05	[-0.07, 0.12]	0.37	.71
PDS score (t5-t0) ~ DNAm <i>ESR2</i> (b)	0.13	0.08	[-0.01, 0.31]	1.65	.10
DNAm <i>ESR2</i> ~ PCDF131 (a)	-0.01	0.03	[-0.07, 0.05]	-0.38	.70
DNAm <i>ESR2</i> ~ Sex	-0.05	0.03	[-0.11, 0.02]	-1.32	.19
DNAm <i>ESR2</i> ~ PCDF131:Sex (a:Sex)	0.06	0.05	[-0.03, 0.15]	1.24	.21

Note. Coefficient = *Regressions* beta value, *SE* = standard error, *CI* = confidence interval, *z* = *z*-statistic, *p* = *p*-value, *c* = *c*-path, *b* = *b*-path, *a* = *a*-path.

Table A.197.ii. *Defined model parameters (effects)*

Effect	Coefficient	<i>SE</i>	95% CI	<i>z</i>	<i>p</i>
Indirect (female)	-1.48x10 ⁻⁰³	4.71x10 ⁻⁰³	[-0.01, 0.01]	-0.32	.75
Total (female)	0.02	0.02	[-0.03, 0.08]	0.73	.46
Indirect (male)	5.88x10 ⁻⁰³	6.70x10 ⁻⁰³	[0.00, 0.02]	0.88	.38
Total (male)	0.04	0.04	[-0.03, 0.14]	1.03	.31
Difference in indirect (male - female)	-7.36x10 ⁻⁰³	8.71x10 ⁻⁰³	[-0.03, 0.00]	-0.85	.40
Difference in total (male - female)	-0.03	0.05	[-0.13, 0.06]	-0.52	.60

Note. Coefficient = estimated model parameter, *SE* = standard error, *CI* = confidence interval, *z* = *z*-statistic, *p* = *p*-value.

References

Bayley, N. (1993). *Bayley Scales of Infant Development*. Psychological Corporation.