

	<i>IGF2DMR</i> methylation			<i>H19</i> methylation		
	β^1	95% CI	P-value	β^1	95% CI	P-value
MODEL 1: adjusted for correlations between CpG sites, bisulphite batch, gestational age at birth						
<i>Maternal tobacco smoking</i>						
No (n=277)		reference			reference	
First trimester only (n=37)	-0.82	-1.94; 0.31	0.154	0.48	-0.37; 1.33	0.265
Continued smoking, all (n=104)	-1.13	-1.87; -0.39	0.003	-0.43	-0.99; 0.13	0.135
<5 cigarettes per day (n=34)	-1.25	-2.43; -0.08	0.037	-0.92	-1.80; -0.04	0.041
≥ 5 cigarettes per day (n=51)	-0.93	-1.94; 0.07	0.068	-0.18	-0.91; 0.56	0.637
P for trend		0.021			0.300	
<i>Paternal tobacco smoking</i>						
No (n=176)		reference			reference	
Yes (n=100)	-0.19	-0.98; 0.60	0.639	0.17	-0.39; 0.73	0.550
<5 cigarettes per day (n=48)	-0.26	-1.30; 0.78	0.621	0.16	-0.58; 0.89	0.679
≥ 5 cigarettes per day (n=51)	-0.05	-1.06; 0.96	0.922	0.16	-0.56; 0.89	0.658
P for trend		0.819			0.603	
MODEL 2: model 1 + maternal characteristics (age, educational level, parity, BMI, periconceptional folic acid supplement use) and fetal gender						
<i>Maternal tobacco smoking</i>						
No (n=277)		reference			reference	
First trimester only (n=37)	-0.89	-2.04; 0.25	0.127	0.40	-0.46; 1.25	0.366
Continued smoking, all (n=104)	-1.18	-1.98; -0.37	0.004	-0.62	-1.24; -0.00	0.049
<5 cigarettes per day (n=34)	-1.30	-2.50; -0.10	0.033	-0.93	-1.82; -0.03	0.043
≥ 5 cigarettes per day (n=51)	-0.81	-1.88; 0.26	0.136	-0.32	-1.11; 0.46	0.420
P for trend		0.044			0.184	
<i>Paternal tobacco smoking</i>						
No (n=176)		reference			reference	
Yes (n=100)	-0.19	-1.01; 0.63	0.646	0.05	-0.51; 0.62	0.860
<5 cigarettes per day (n=48)	-0.23	-1.29; 0.83	0.670	0.14	-0.59; 0.86	0.712
≥ 5 cigarettes per day (n=51)	-0.07	-1.14; 1.00	0.895	-0.07	-0.82; 0.67	0.849
P for trend		0.803			0.958	

Table S3: Parental tobacco smoking habits and DNA methylation, with exclusion of ADHD cases

Results from linear mixed model analyses with maternal or paternal tobacco smoking as independent variable and DNA methylation as dependent variable. ¹Analyses were performed with square-root transformed methylation data and values are presented as regression coefficients (95% confidence interval). Analyses on paternal smoking were restricted to non-smoking mothers.