

Table 2S. Spearman's correlation coefficients between placental DNA methylation and metabolic variables of newborns in E-21 and Gen3G cohorts

DNA methylation levels ^a	E-21 cohort		Gen3G cohort	
	Leptin level n=105	Glucose level n=74	Leptin level n=167	Glucose level n=168
<i>PRDM16</i> -CpG1	r=-0.02 NS	r=-0.14 NS	r<-0.01 NS	r=-0.05 NS
<i>PRDM16</i> -CpG2	r=-0.22 p=0.02	<i>r=-0.19</i> <i>p=0.09</i>	r<-0.01 NS	r=0.11 NS
<i>PRDM16</i> -CpG3	r=-0.14 p=0.14	r=-0.13 NS	- -	- -
<i>PRDM16</i> -CpG4	r=-0.20 p=0.04	r=0.20 p=0.04	- -	- -
Mean <i>BMP7</i>	r=-0.11 NS	r=-0.06 NS	r<-0.01 NS	r=-0.04 NS
Mean <i>CTBP2</i>	r=-0.16 NS	r=-0.11 NS	- -	- -
Mean <i>PPARGC1α</i> -CpG1,2	r=-0.12 NS	r=0.25 p=0.04	- -	- -
<i>PPARGC1α</i> -CpG3	r=0.20 p=0.04	<i>r=0.21</i> <i>p=0.06</i>	r=-0.06 NS	r=0.12 p=0.12
<i>PPARGC1α</i> -CpG4	<i>r=0.18</i> <i>p=0.07</i>	r=-0.02 NS	- -	- -

^aResidual scores of DNA methylation levels were used in the statistical models. They were obtained by using unstandardized analysis of residuals computed by linear regressions which included: gestational age, newborn's sex and weight, smoking during pregnancy, weight gain between 1st and 2nd trimester and maternal BMI at 1st trimester. Statistically significant results ($p \leq 0.05$) are shown in bold, whereas statistical trends ($p \leq 0.10$) are shown in italics. NS = $p > 0.15$