Table S4. Associations between placental DNA methylation levels in significant CpG sites and anthropometric and metabolic profile of mothers from the Gen3G birth cohort.

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| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| probe ID | BMI at 1st trimester of pregnancy | Fasting glucose at 2nd trimester of pregnancy | 2h-post 75g-OGTT | Matsuda index | HOMA-IR at 2nd trimester of pregnancy | Gestational weight gain throughout pregnancy | HDL-C at 2nd trimester of pregnancy | LDL-C at 2nd trimester of pregnancy | TG at 2nd trimester of pregnancy | Total Cholesterol at 2nd trimester of pregnancy |
| cg22593959 | β=-0.001 p=0.490 | β=0.003 p=0.881 | β=0,003 p=0.609 | β=0.001 p=0.737 | β=0.001 p=0.930 | β=-0.001 p=0.436 | β=-0.039 p=0.724 | β=-0.054 p=0.633 | β=-0.018 p=0.726 | β=0.058 p=0.609 |
| cg22436429 | β=-0.001 p=0.853 | β=0.011 p=0.356 | β=0,003 p=0.373 | β=-0.001 p=0.132 | β=0.001 p=0.001 | β=-0.001 p=0.806 | β=0.117 p=0.066 | **β=0.142 p=0.029** | β=0.044 p=0.140 | **β=-0.128 p=0.048** |

Associations between maternal profile and DNA methylation levels at significant epimutations were assessed using linear regression models with gestational age at delivery, sex of the offspring, maternal age and placental cellular heterogeneity (5 PCs) as covariates.