**Supplemental Table S1. Estimation of cord blood cell composition based on 450K methylation array profiles and correlation with PFAS levels**

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| 　 | 　 | 　 | log10(PFOS) | 　 | log10(PFOA) |
|  | Mean ± SD |  | Spearman's correlation test (ρ) | *P*-Value |  | Spearman's correlation test (ρ) | *P*-Value |
|  |  |  |
| 　 | 　 | 　 |
| CD8T | 0.12 ± 0.04 |  | 0.030 |  | 0.681 |  | –0.002 |  | 0.975 |
| CD4T | 0.15 ± 0.06 |  | –0.023 |  | 0.755 |  | –0.016 |  | 0.831 |
| NK cells | 0.01 ± 0.02 |  | –0.079 |  | 0.280 |  | –0.057 |  | 0.436 |
| B cells | 0.09 ± 0.02 |  | –0.078 |  | 0.284 |  | –0.044 |  | 0.544 |
| Monocytes | 0.07 ± 0.02 |  | –0.125 |  | 0.087 |  | –0.009 |  | 0.904 |
| Granulocytes | 0.53 ± 0.10 |  | 0.002 |  | 0.978 |  | 0.061 |  | 0.403 |
| nRBCs | 0.07 ± 0.05 | 　 | 0.115 | 　 | 0.116 | 　 | 0.013 | 　 | 0.860 |

**Supplemental Table S2.** Characteristics of study population of the replication cohort (*n* = 37)

|  |  |  |
| --- | --- | --- |
| **Concentration in maternal blood** | **n** | **Median (25th, 75th)** |
|  PFOS (ng/mL) |  | 37 | 12.2 (9.2, 15.3) |
|  PFOA (ng/mL) |  | 1.8 (1.1, 2.6) |
|  |  | **n** | **Mean ±SD or (%)** |
| **Maternal characteristics** |  |  |  |
|  Maternal age (year) |  | 37 | 28.6 ±5.2 |
|  Pre-pregnancy BMI (kg/m2) |  | 37 | 20.3 ±2.5 |
|  Parity (times) | 0 | 20 | 54.1 |
|  | ≥ 1 | 15 | 40.5 |
|  | missing | 2 | 5.4 |
|  Blood sampling period | < 28 weeks | 0 | 0 |
|  | 28–36 weeks | 37 | 100 |
|  | ≧36 weeks | 0 | 0 |
|  Educational level (year) | ≤ 12 | 14 | 37.8 |
|  | > 12 | 23 | 62.2 |
|  Smoking during pregnancy | No | 37 | 100 |
|  | Yes | 0 | 0 |
|  Alcohol consumption during pregnancy |  |  |
|  | No | 33 | 89.2 |
|  | Yesa | 1 | 2.7 |
|  | missing | 3 | 8.1 |
| **Infant characteristics** |  |  |  |
|  Sex | Male | 23 | 62.2 |
|  | Female | 14 | 37.8 |
|  Gestational age (week) |  | 37 | 38.7 ±1.3 |
|  Birth weight (g) | 　 | 37 | 3117 ±355 |

**Supplemental Table S5**. Top 20 CpGs ranked by the absolute value of the coefficient out of 854 CpGs (PFOS) and 600 CpGs (PFOA) with *P* < 0.001.

|  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- |
| Probe ID | Gene | Chr | Featurea | Discovery cohort | 　 | Replication cohort | Replicatedd |
| Coefb | 　 | P-Value | 　 | Coefb | 　 | P-Value |
| log10(PFOS)  |  |  |  |  |  |  |  |  |  |  |
| cg25623271c | *GREM2* | 1 | 3'UTR | 0.087 |  | 5.66E-05 |  | 0.023 |  | 0.637 |  |
| cg20846728c | *MYT1L* | 2 | Body | 0.226 |  | 1.12E-04 |  | 0.037 |  | 0.709 |  |
| cg18396357 | *NRXN1* | 2 | Body | 0.127 |  | 1.36E-04 |  | -0.119 |  | 0.083 |  |
| cg05782966 | *GULP1* | 2 | IGR | 0.088 |  | 1.58E-04 |  | -0.064 |  | 0.366 |  |
| cg02841482c | *VEPH1* | 3 | 5'UTR | 0.102 |  | 3.71E-05 |  | 0.030 |  | 0.074 |  |
| cg19668234c | *PRSS50* | 3 | TSS200 | 0.101 |  | 9.73E-04 |  | 0.080 |  | 0.192 |  |
| cg03251918c | *MAP9* | 4 | TSS1500 | 0.113 |  | 6.80E-04 |  | 0.004 |  | 0.896 |  |
| cg24405174c | *PL-5283* | 7 | TSS1500 | 0.177 |  | 8.08E-04 |  | 0.087 |  | 0.162 |  |
| cg00795791c | *PL-5283* | 7 | TSS1500 | 0.116 |  | 2.49E-05 |  | 0.030 |  | 0.381 |  |
| cg20528787 | *PTPRN2* | 7 | Body | 0.116 |  | 9.09E-04 |  | -0.045 |  | 0.309 |  |
| cg01788773c | *LOC286083* | 8 | IGR | 0.131 |  | 2.79E-04 |  | 0.172 |  | 0.002 | ✓ |
| cg08599792c | *ODF1* | 8 | IGR | 0.105 |  | 9.69E-05 |  | 0.024 |  | 0.599 |  |
| cg17165241c | *PKP3* | 11 | Body | 0.148 |  | 1.04E-04 |  | 0.082 |  | 0.546 |  |
| cg01794156c | *PKP3* | 11 | Body | 0.115 |  | 1.33E-05 |  | 0.019 |  | 0.782 |  |
| cg17840408c | *PKP3* | 11 | Body | 0.100 |  | 2.37E-04 |  | 0.009 |  | 0.888 |  |
| cg25258098c | *PKP3* | 11 | Body | 0.096 |  | 8.71E-04 |  | 0.015 |  | 0.756 |  |
| cg03673989c | *B4GALNT4* | 11 | Body | 0.118 |  | 6.97E-04 |  | 0.045 |  | 0.235 |  |
| cg23625390c | *SCAPER* | 15 | TSS200 | 0.089 |  | 3.61E-04 |  | 0.014 |  | 0.039 | ✓ |
| cg21293934c | *ANKRD30B* | 18 | TSS200 | 0.107 |  | 2.09E-04 |  | 0.048 |  | 0.369 |  |
| cg09920172 | *ATCAY* | 19 | IGR | 0.108 | 　 | 2.14E-04 | 　 | -0.133 | 　 | 0.089 | 　 |
| log10(PFOA)  |  |  |  |  |  |  |  |  |  |  |
| cg17476910c | *MIR5087* | 1 | IGR | -0.109 |  | 9.52E-04 |  | -0.022 |  | 0.280 |  |
| cg19172429 | *MIR4786* | 2 | IGR | 0.112 |  | 3.71E-04 |  | -0.030 |  | 0.591 |  |
| cg06471380 | *MIR4786* | 2 | IGR | 0.109 |  | 5.30E-05 |  | -0.042 |  | 0.404 |  |
| cg26376241 | *SPRED2* | 2 | TSS200 | 0.064 |  | 3.17E-04 |  | -0.058 |  | 0.008 |  |
| cg22795891 | *OBFC2A* | 2 | Body | 0.063 |  | 1.94E-04 |  | -0.018 |  | 0.393 |  |
| cg23202468 | *ZBTB47* | 3 | Body | 0.067 |  | 6.87E-04 |  | -0.039 |  | 0.021 |  |
| cg22219379c | *SLC25A36* | 3 | IGR | -0.057 |  | 9.65E-04 |  | -0.011 |  | 0.670 |  |
| cg02546416c | *RP5-1086L22.1* | 6 | IGR | 0.096 |  | 2.28E-04 |  | 0.098 |  | 0.007 | ✓ |
| cg14036627 | *PSORS1C3* | 6 | IGR | 0.077 |  | 6.43E-04 |  | -0.007 |  | 0.868 |  |
| cg09179646 | *PSORS1C3* | 6 | IGR | 0.068 |  | 3.86E-04 |  | -0.006 |  | 0.815 |  |
| cg24427850 | *PSORS1C3* | 6 | IGR | 0.062 |  | 2.11E-04 |  | -0.008 |  | 0.780 |  |
| cg03078486 | *PSORS1C3* | 6 | IGR | 0.057 |  | 6.98E-04 |  | -0.011 |  | 0.699 |  |
| cg09756125c | *PTPRN2* | 7 | Body | 0.167 |  | 2.41E-04 |  | 0.013 |  | 0.855 |  |
| cg03454775 | *MYOM2* | 8 | Body | 0.069 |  | 9.09E-04 |  | -0.018 |  | 0.497 |  |
| cg07745373c | *DTX4* | 11 | Body | -0.068 |  | 4.59E-04 |  | -0.009 |  | 0.746 |  |
| cg13837679 | *ALX4* | 11 | Body | -0.058 |  | 3.86E-05 |  | 0.023 |  | 0.334 |  |
| cg10665891c | *MAP1LC3B2* | 12 | IGR | 0.086 |  | 4.83E-04 |  | 0.002 |  | 0.955 |  |
| cg05974580c | *FRS2* | 12 | TSS1500 | 0.071 |  | 8.43E-04 |  | 0.013 |  | 0.670 |  |
| cg04063936 | *FAM38A* | 16 | Body | -0.059 |  | 3.48E-04 |  | 0.015 |  | 0.335 |  |
| cg26772386 | *PDE9A* | 21 | Body | 0.088 | 　 | 8.31E-04 | 　 | -0.055 | 　 | 0.222 | 　 |

Abbreviations: Chr, chromosome; body, gene body; TSS, transcription start site; TSS200, 200 bases from TSS; TSS1500, 1500 bases from TSS; IGR, intergenic region; UTR, untranslated region.

aGene feature category of the methylation locus.

bPartial regression coefficient; the magnitude of the effect on DNA methylation.

cCpG that showed the same direction of effect in both the discovery and replication cohorts.

dSuccessful replication defined as having the same direction of effect and *P*-value < 0.05 in the discovery cohort.