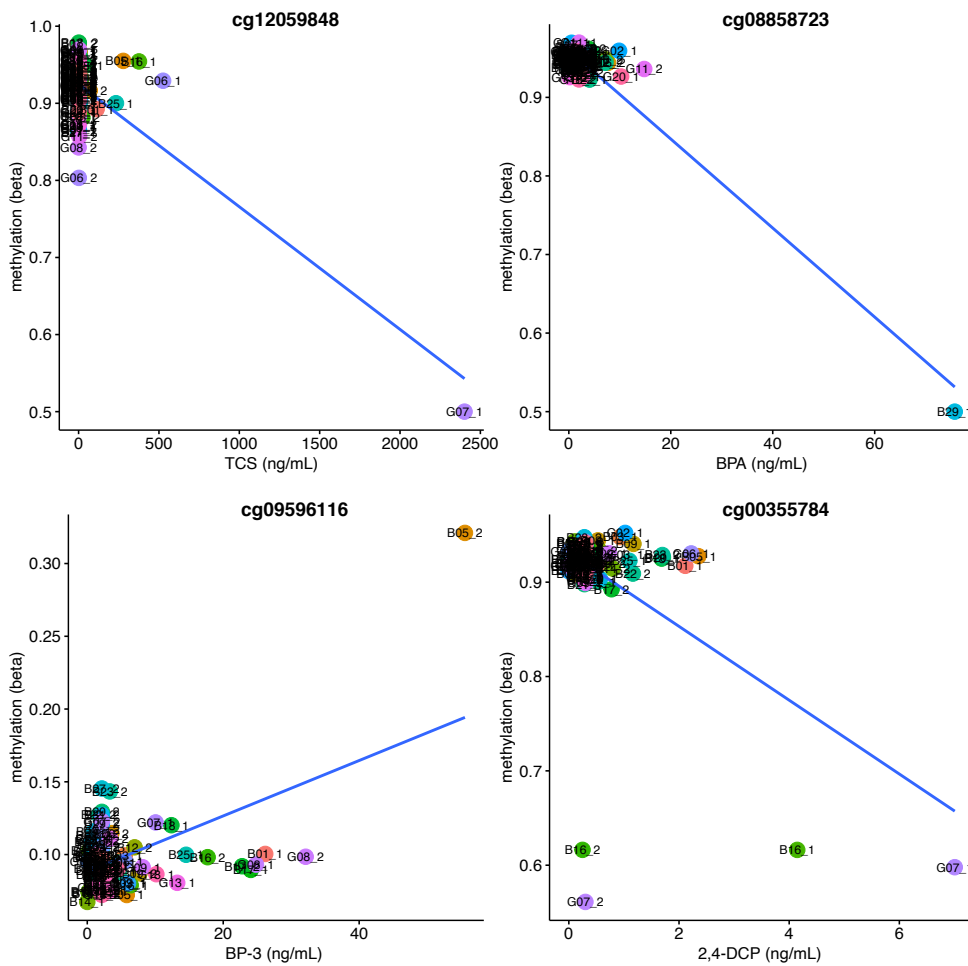


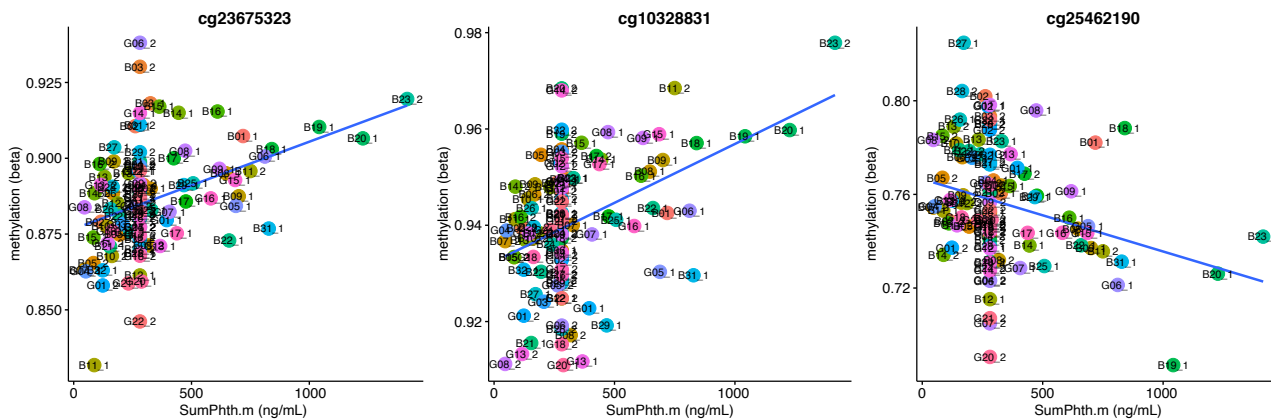
Levels of endocrine disrupting chemicals associated with the peri-pubertal epigenome

Supplementary file 1

Examples of single-CpGs associated with TCS, BPA, 2,4-DCP, and BP-3 at FDR<0.05, respectively, that appears to be driven by single EDC measurements. Single extreme values are found both among girls (G) and boys (B) and both pre- (\_1) and post-pubertal (\_2).

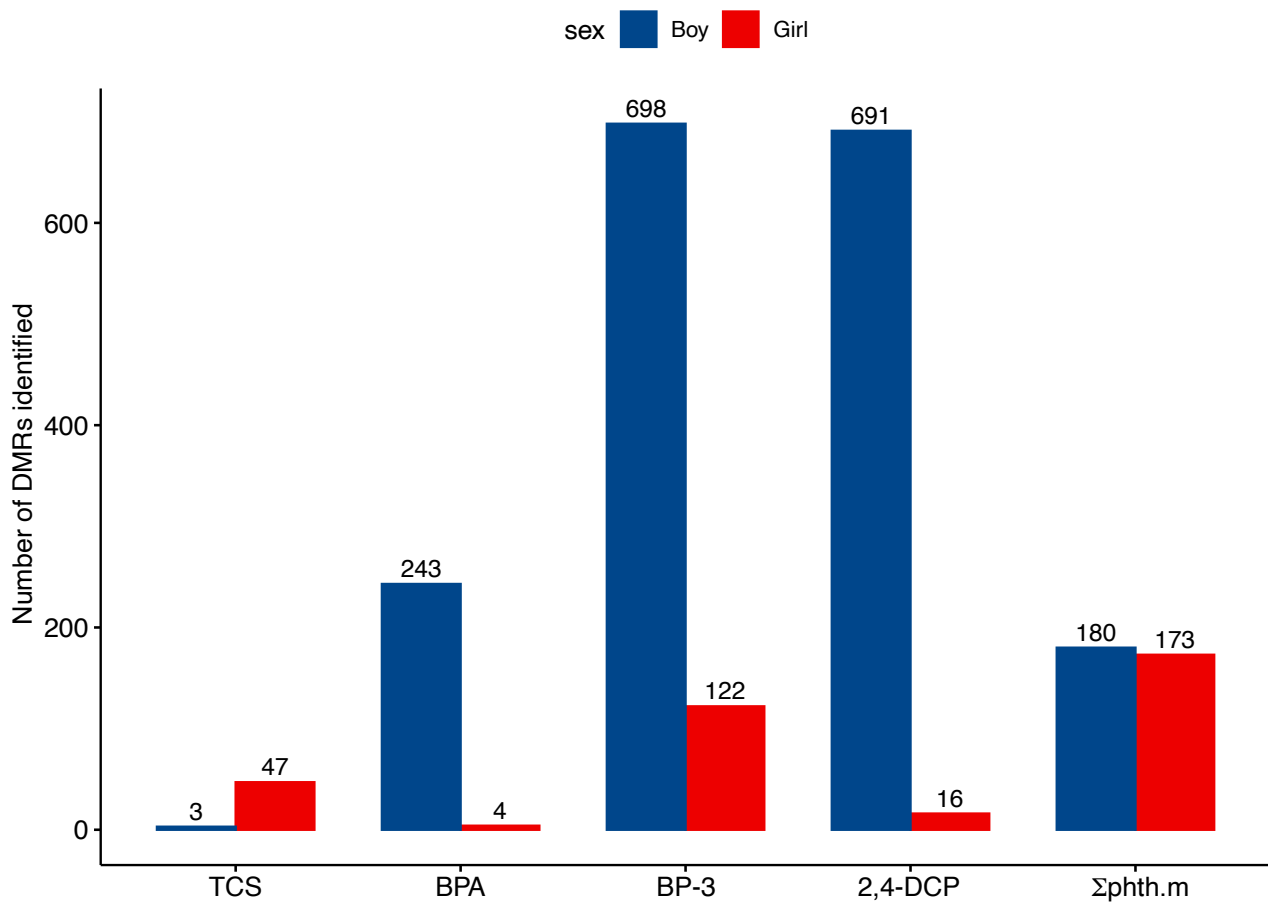


Single-CpGs associated to  $\Sigma$ phth.m at FDR<0.05 when urinary levels are log-transformed and raw DNA methylation values are corrected for bias with SVA.



cpG	FDR	position (chr, base)	symbol	site
cg23675323	0.0117	13, 114889227	RASA3	intron (NM_007368, intron 1 of 23)
cg10328831	0.0229	8, 10650046	MIR1322	intron (NM_017884, intron 6 of 6)
cg25462190	0.0304	5, 177547067	N4BP3	intron (NM_015111, intron 2 of 4)

Number of genomic regions identified to be associated with the mean of yearly dichotomized values when analysis was performed on either boys or girls alone.



Association between TRIP6 promoter methylation levels and circulating TRIP6 levels.

