



Supplementary Figure 1. Methylation level of differentially methylated CpG sites.

After adjustment over all umbilical cord cell types, 12 CpGs yielded experiment-wide level of significance when combining the effects of all cell types (A-L). Data are presented as box plots of the methylation levels determined as the tensor() function in TCA for Unexposed and Exposed groups (See text for additional methods). Ten sites were hypomethylated, and two were hypermethylated. Sites in A-I were detected in B cells and sites in J-L in CD4+ T cells.