





#### S4. Quantitative measurement of methylation at individual CpGs of analysed DMRs

A: DIRAS3. B: PLAGL1. C: IGF2 DMR0. D: H19 ICR. E: KvDMR. F: MEG3

Promoter. G: SNRPN. H: MCTS2. I: NESP Promoter J: Non DMR. To quantify DMR methylation we analysed 10 DMRs by pyrosequencing in 12 PBL samples, and compared them to fetal brain. Pyrosequencing allowed analysis of between three and 11 CpGs per region, with methylation levels shown as individual box plots for the PBL samples, and a black cross for the fetal brain sample. Average methylation between the 12 PBL samples is shown as a box plot. Each of the DMRs analysed revealed the expected methylation level for a DMR in PBL and in brain. The non DMR region in (J) was hypomethylated in PBL compared to brain.