



Fig. S2: Enrichment of hyper- and hypomethylated CpG sites in iPSC-derived HPCs.

Changes in DNA methylation (Δ mean β -value >0.5 or <-0.5) in comparison **(a)** between iHPCs d20 and iPSCs (GSE37066) or **(b)** between iHPCs d20 and primary CD34⁺ cells from human cord blood (GSE40799). The differentially methylated CpGs were classified according to gene regions and in relation to CpG islands. Hypergeometric distribution: * = $P < 0.05$; # = $P < 0.01$; \$ = $P < 0.001$; § = $P < 0.0001$; ♦ = $P < 0.00001$.