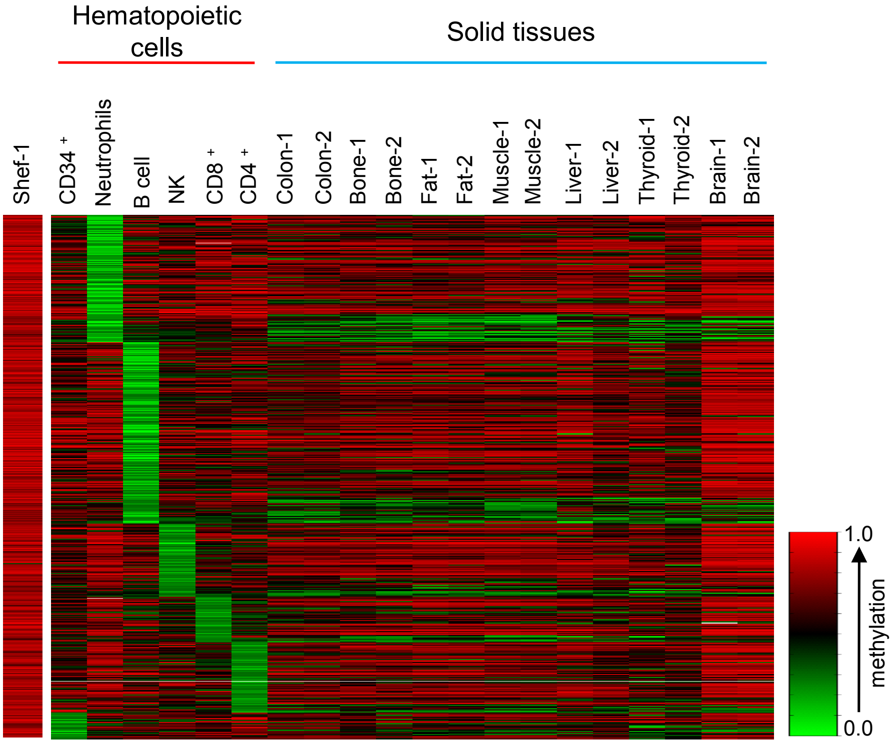
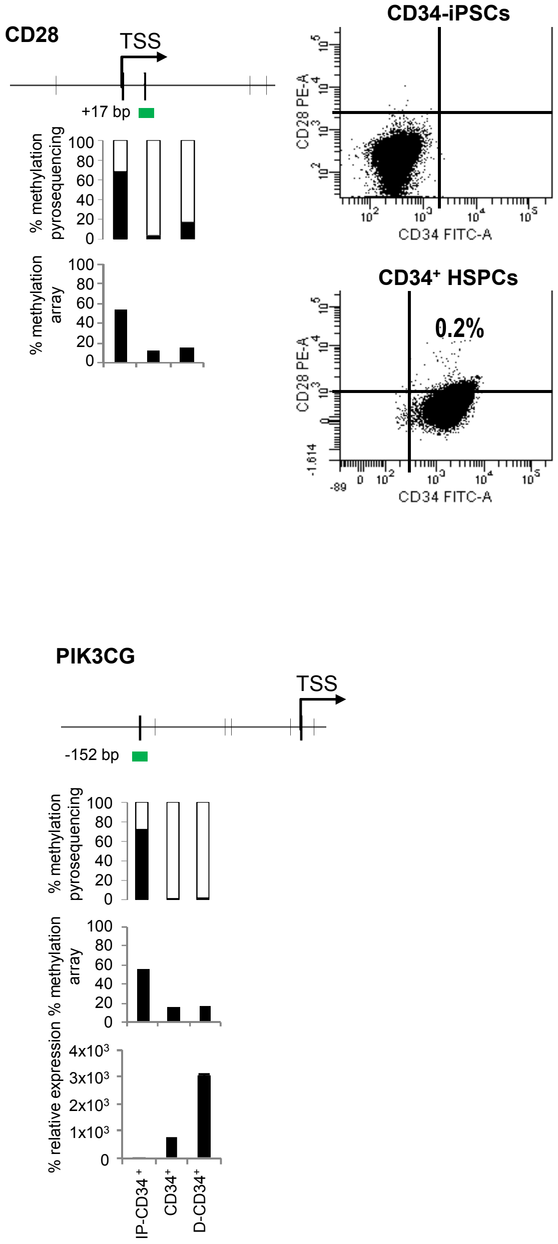
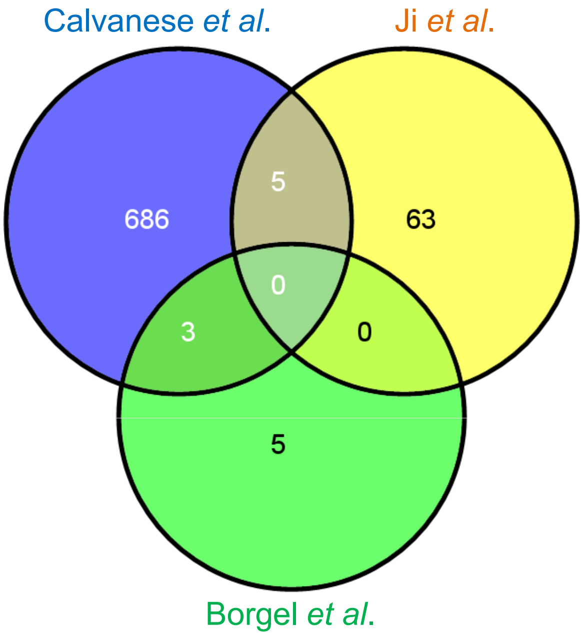
Supplementary Figure 1. Heatmap showing the methylation status of cell type-specifically demethylated genes (461 genes/490 CpG sites) in various blood cell types and in non-hematopoietic tissues.



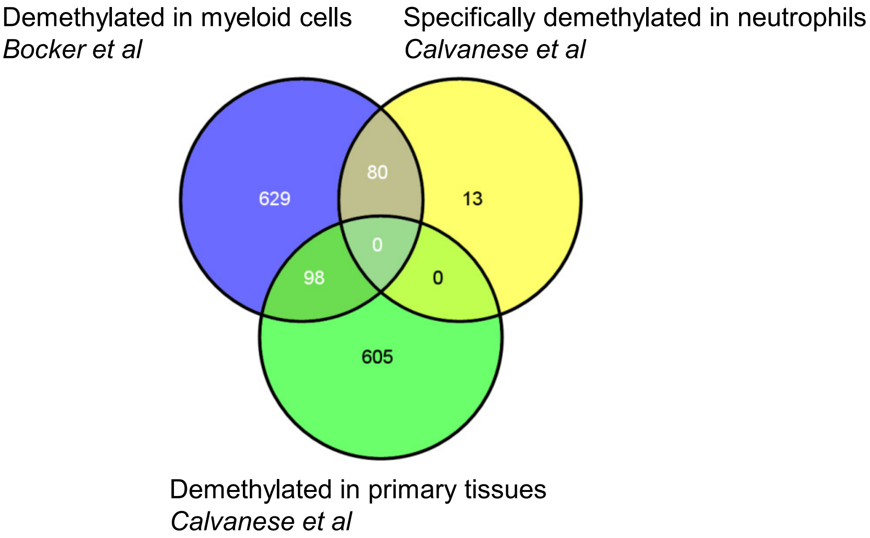
Supplementary Figure 2. Methylation and expression values for CD28 and PIK3CG (see Fig. 3). Expression by flow cytometry of CD28 in CD34-iPSC (top panel) and CD34$^+$ HSPCs (bottom panel).



Supplementary Figure 3. Venn diagram showing genes demethylated during hematopoietic differentiation commonly identified in three independent studies: Ji et al., Nature 2010; Borgel et al., Nature Genetics 2011 Calvanese et al., this study.



Supplementary Figure 4. Venn diagram showing CpG sites demethylated in myeloid cells (Bocker *et al, 2011*), neutrophils and primary tissues (our study).



Supplementary Figure 5. Heatmaps showing the methylation profile of adult CD34$^+$ cells (Bocker *et al.*) and our CD34$^+$ together with the terminally differentiated hematologic cells.