

Supplementary Figure 1

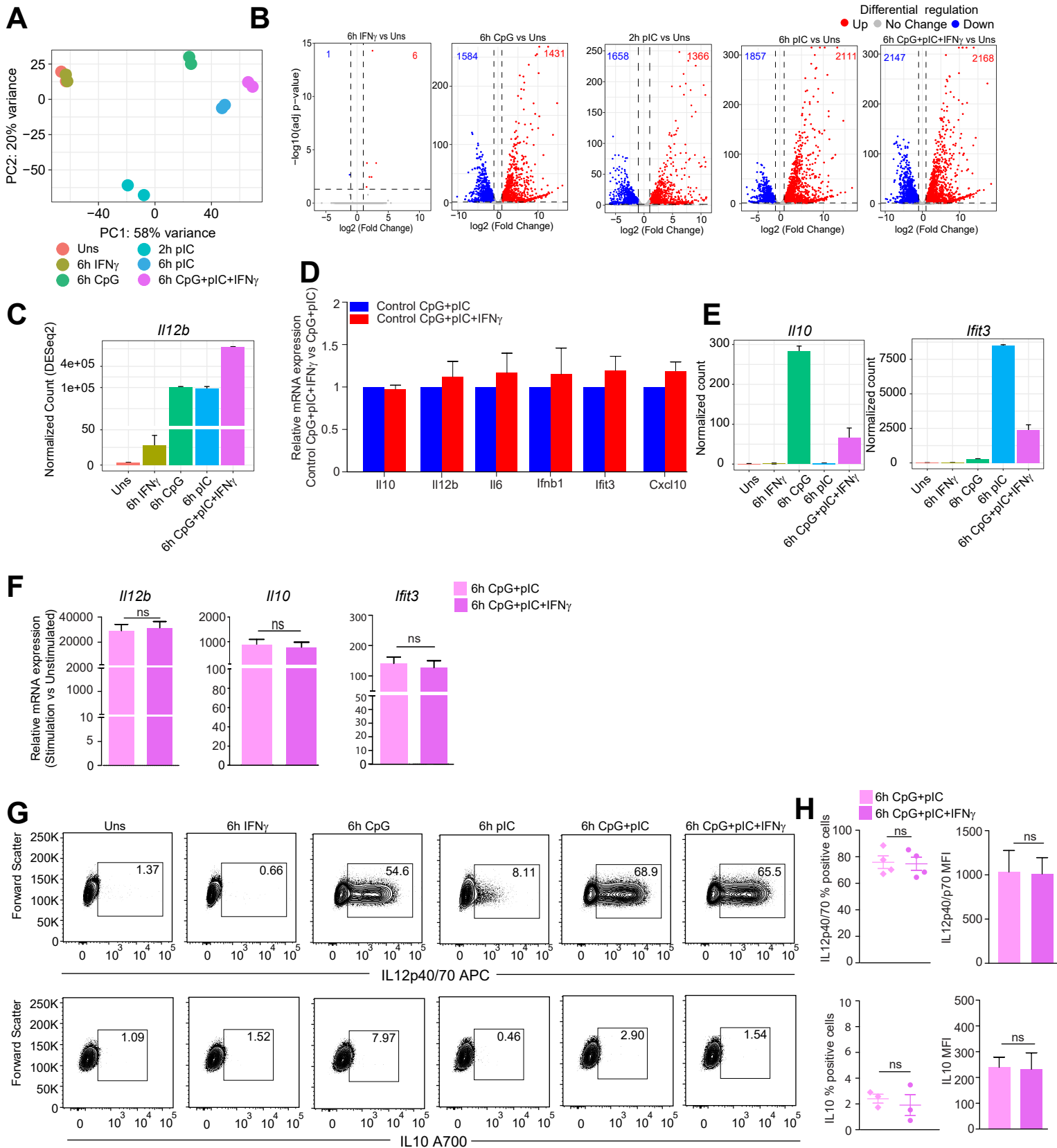


Figure S1. RNA-seq analysis of unstimulated and TLR activated cDC1

(A). PCA plot showing percent of variance explained by principal component 1 and 2 among unstimulated, IFN γ , CpG, pIC and CpG+pIC+IFN γ stimulation conditions in cDC1. (B). Volcano plot showing total number of differentially upregulated and downregulated genes at IFN γ , CpG, pIC and CpG+pIC+IFN γ activated DCs compared to unstimulated. (C). Bar plot showing DESeq2 normalized count of *Il12b* in TLR/IFN γ activated cDC1. (D). RT-qPCR showing relative mRNA expression of TLR response genes in 6h CpG+pIC+IFN γ vs 6h CpG+pIC stimulation condition in control cDC1 (n=3). (E). Bar plot showing DESeq2 normalized count of exemplary DC response genes showing antagonistic expression behavior after combined 6h CpG+pIC+IFN γ stimulation. (F). RT-qPCR showing relative mRNA expression of exemplary TLR response genes showing no significant difference between 6h CpG+pIC and CpG+pIC+IFN γ stimulation conditions in control cDC1 (n=6). (G). Contour plot from flow cytometry analysis depicting the intracellular cytokine expression of IL-12p40/70, IL-10, in control cDC1 before and after 6h TLR/IFN γ stimulation. (H). Scatter dot plot and bar-plot representing percent positive cells and MFI respectively for IL-12b (n=4) and IL-10 (n=3).