

Supplementary Figure 2

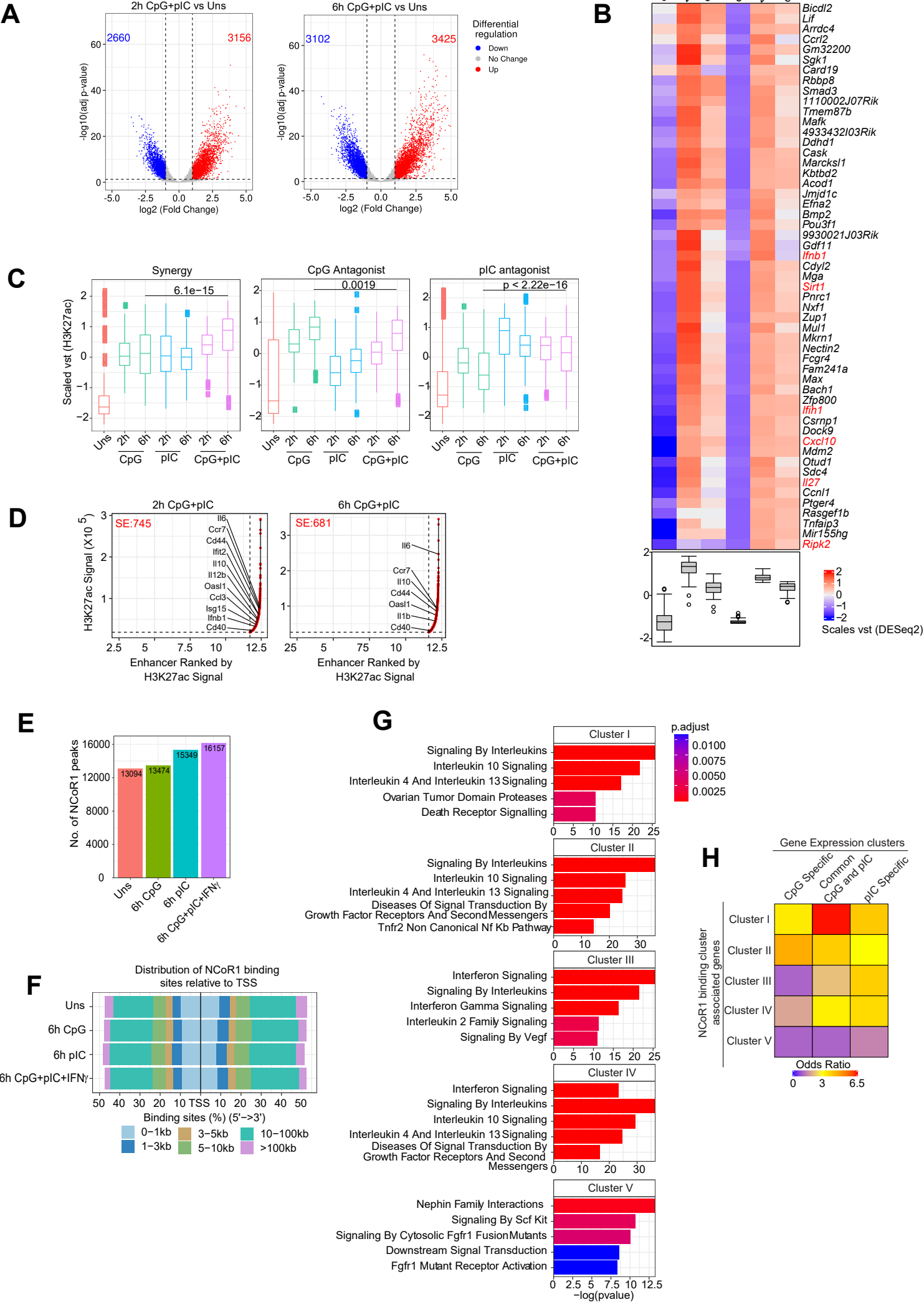


Figure S2. H3K27ac enrichment density and NCoR1 binding analysis.

(A). Volcano plot showing total number of differentially acetylated regions at 2h and 6h CpG+plC activated DCs compared to Unstimulated. **(B).** Heatmap showing scaled vst of H3K27ac enrichment from ChIP-seq and gene expression from RNA-seq data of plC specific genes in unstimulated, 2h and 6h stimulated condition **(C).** Boxplot showing distribution of scaled vst H3K27ac enrichment on synergistic, CpG and plC antagonized genes. **(D).** Scatter plots showing the Super Enhancers (SE) identified at 2hr, and 6hr CpG+plC stimulated cDC1. The CpG/plC specific genes annotated to the SE regions have been marked for each condition. **(E).** Bar plot showing total number of NCoR1 binding sites identified in unstimulated, 6h CpG, plC and CpG+plC+IFN γ stimulation conditions in cDC1. **(F).** Percent stacked bar plot showing percent of distribution of NCoR1 binding sites distance relative to TSS in unstimulated, 6h CpG, plC and CpG+plC+IFN γ stimulation conditions in cDC1. **(G).** Bar plot showing significantly enriched Reactome term from MSigDB for each NCoR1 binding cluster. **(H).** Heatmap showing odds ratio of overlap of genes associated to each NCoR1 binding cluster and genes classified based on expression as CpG, plC specific and common CpG-plC.