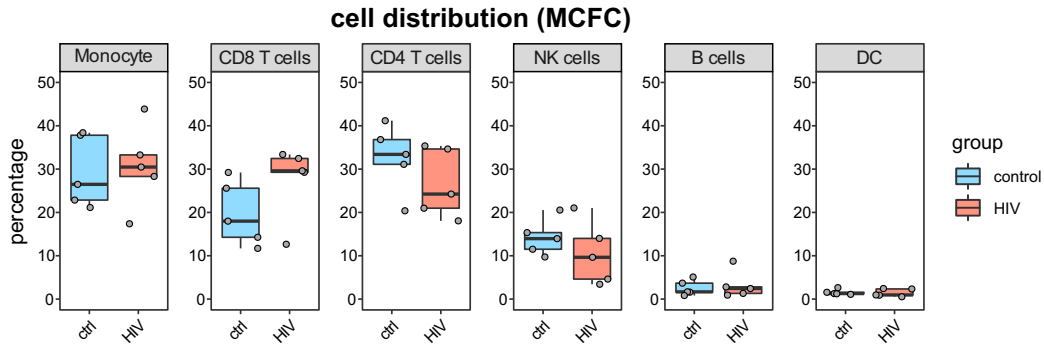


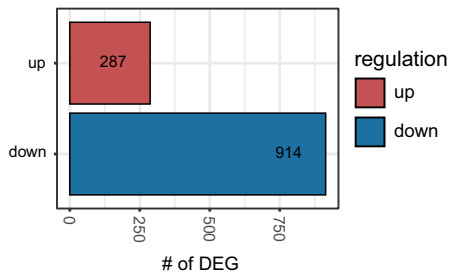
# Figure S1

## A



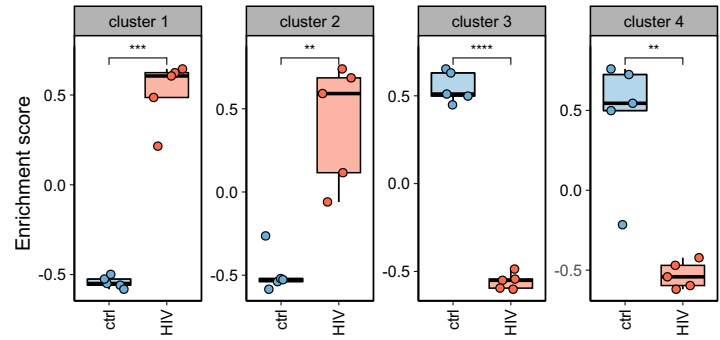
## B

**DEG HIV vs. Ctrl (bulk RNA PBMC)**



## C

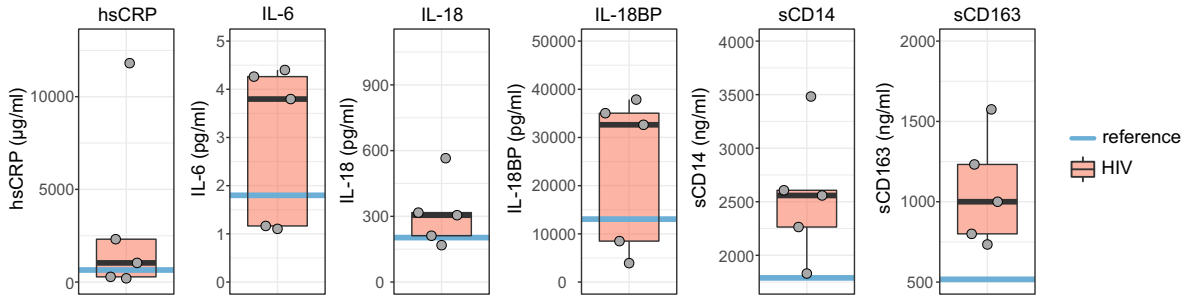
**gene enrichment (GSVA) of DE heatmap clusters**



# Figure S2

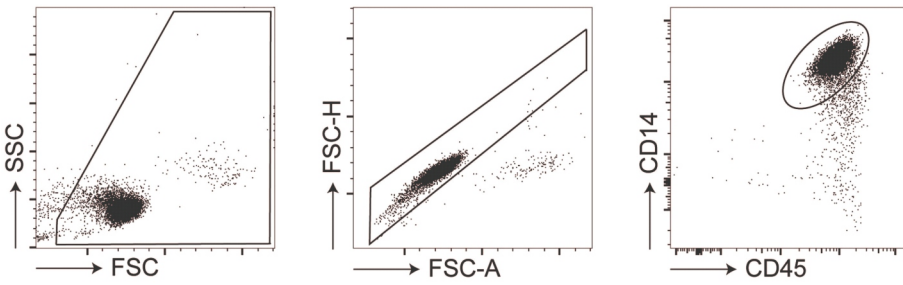
**A**

## clinical marker (serum measurement)



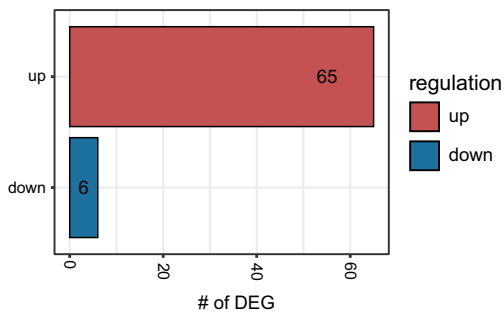
**B**

## CD14 MACS positive selection



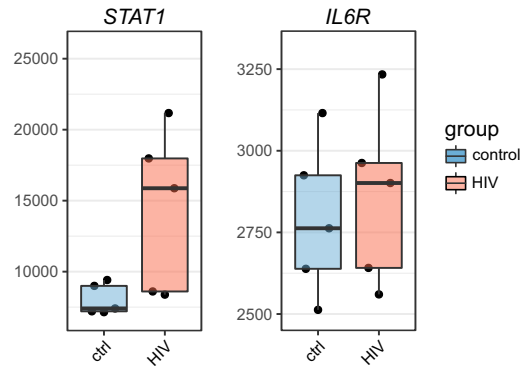
**C**

## DEG HIV vs. Ctrl (bulk RNA CD14)



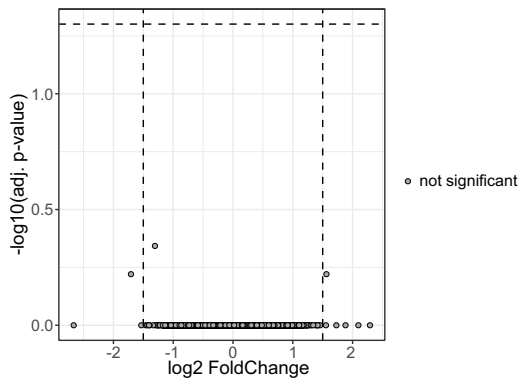
**D**

## selected genes (bulk RNA CD14)



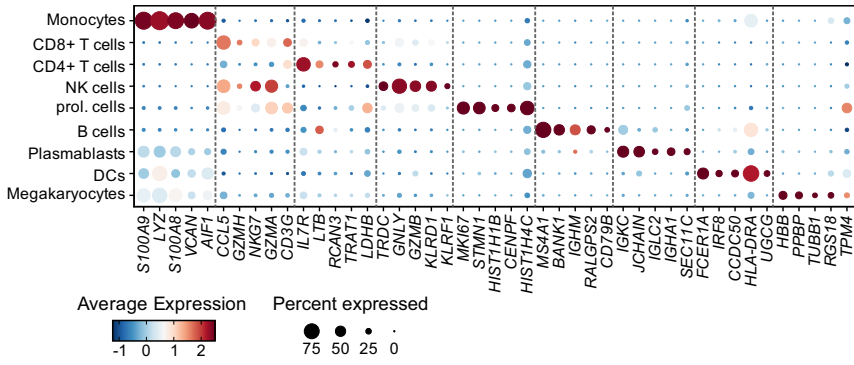
**E**

## DAR HIV vs. Ctrl (bulk ATAC CD14)

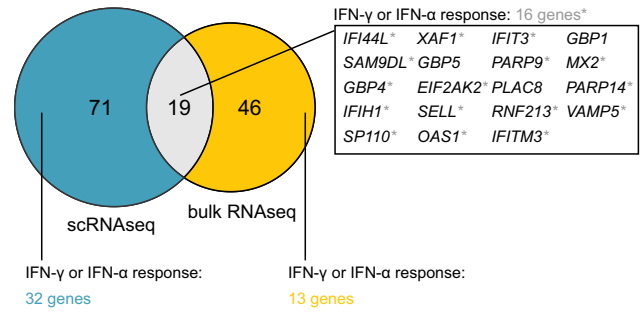


# Figure S3

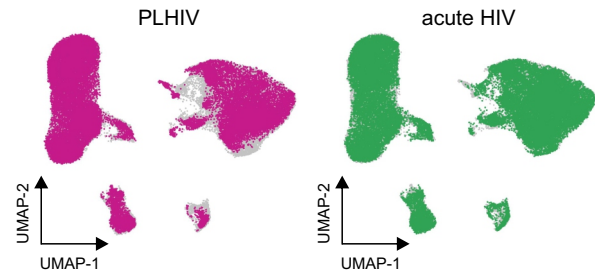
## A cell type marker PLHIV (scRNAseq PBMC)



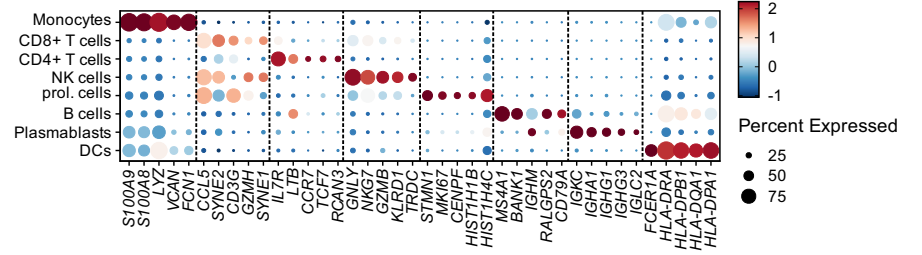
## B up-regulated DEG comparison monocytes (HIV vs ctrl.)



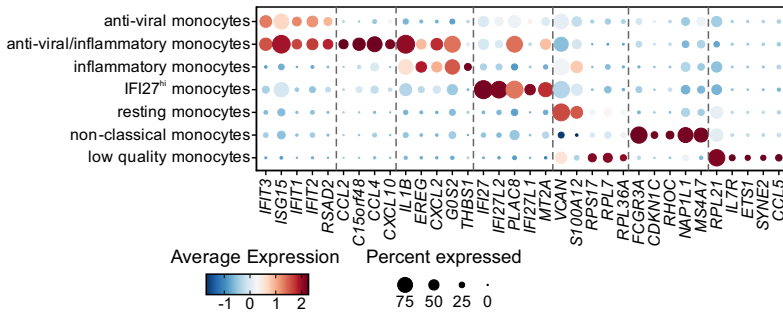
## C integrated PBMC by dataset



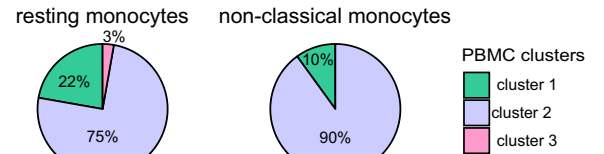
## D cell type marker integrated PBMC (PLHIV+acute HIV)



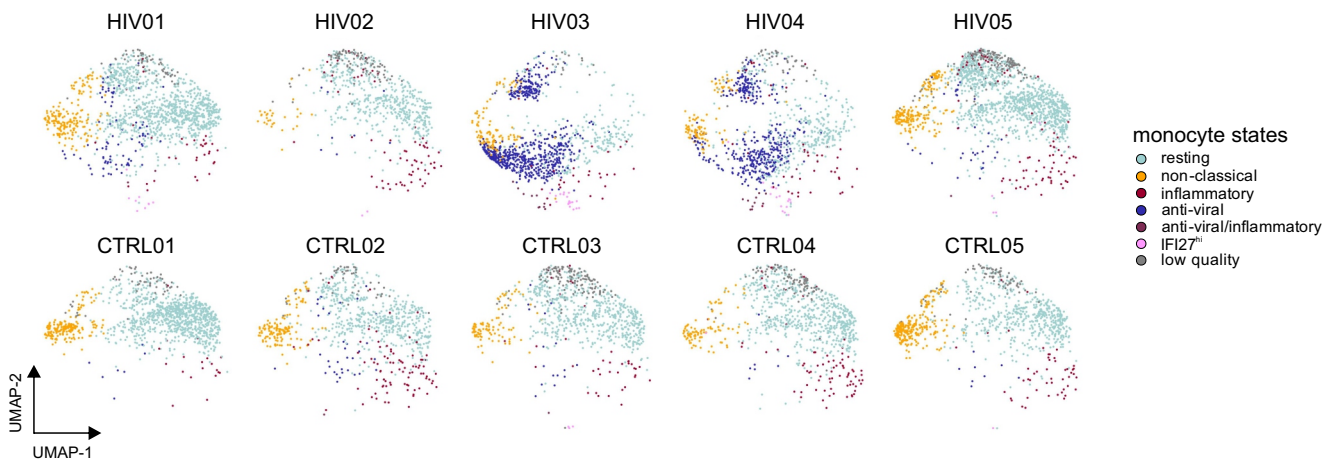
## E monocyte state marker (PLHIV+acute HIV)



## F mapping up DEG to PBMC clusters



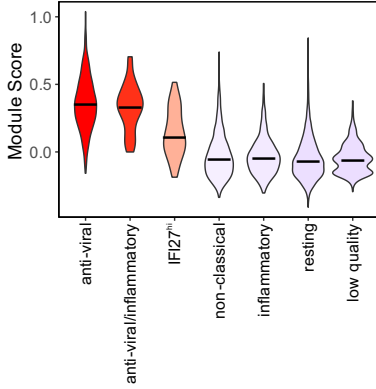
## G monocyte UMAP by PLHIV dataset donors



# Figure S4

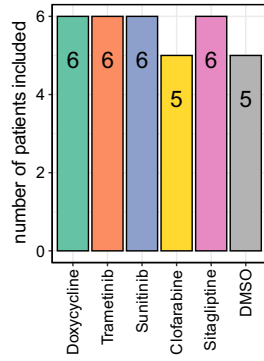
A

cluster 43 reurring target genes in monocyte states (scRNAseq)



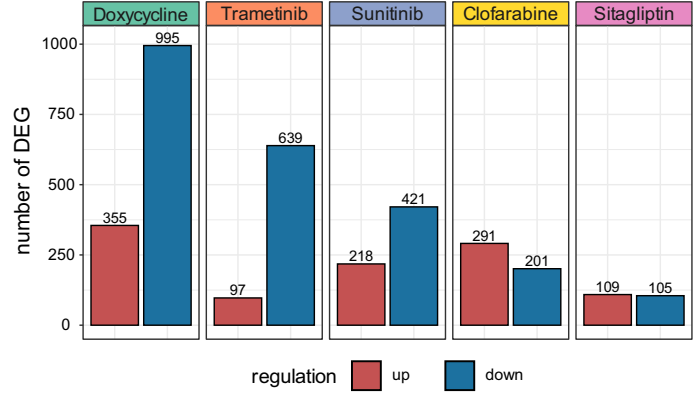
B

samples passing QC



C

number of DEG for treatment vs DMSO



D

leading edge of gene signatures by treatment

