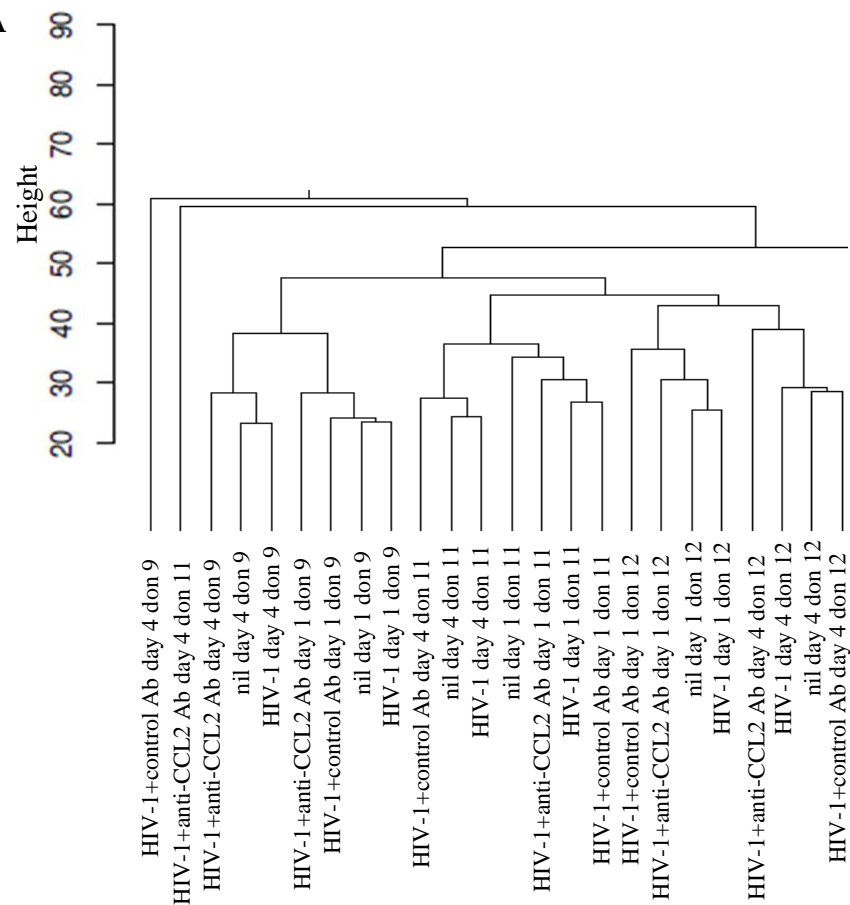
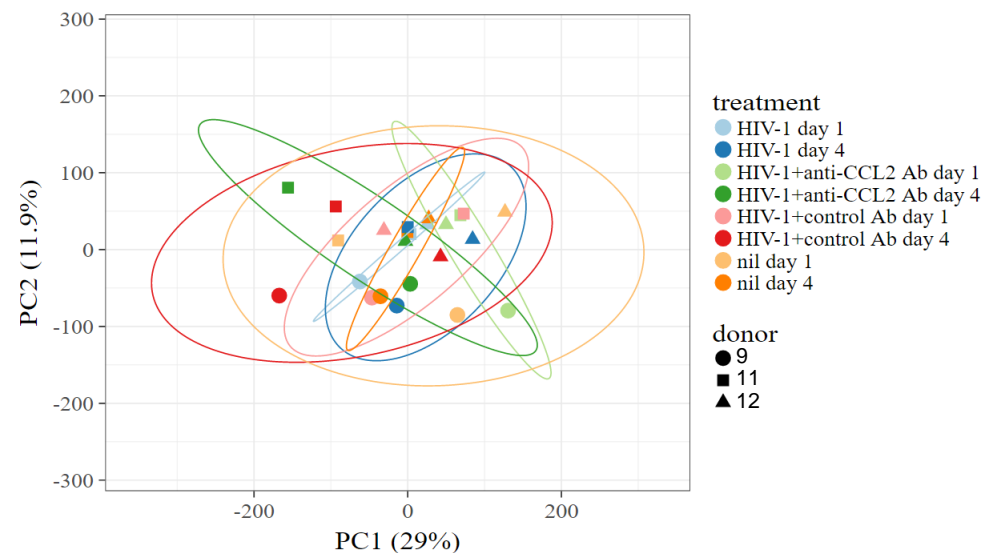


A**B**

Supplementary Figure 7. Clustering of RNA-seq dataset 3. MDMs obtained from 3 different donors were treated or not with anti-CCL2 or control Ab (2.5 $\mu\text{g/ml}$) for 4 h and then infected with HIV-1. Total RNA was extracted at day 1 and 4 p.i., subjected to poly(A) selection followed by reverse transcription, generation of cDNA libraries, and sequencing. (A) Hierarchical clustering of RNA-seq data. (B) Principal component analysis of RNA-seq data. Unit variance scaling was applied to rows; SVD with imputation was used to calculate principal components; $n = 24$ data points. Prediction ellipses are such that with probability 0.95, a new observation from the same group will fall inside the ellipse.