Supplementary Materials

Supplemental Table 1: Clinical details on individual study subjects. The pre-treatment CD4 count reflects the value closest to the initiation of ART. For all study subjects, this was the first start of therapy. Samples examined in the study were in the months surrounding therapy initiation, with a range of 8-24 months.

Subject	Year of enrollment	Pre-treatment CD4	Year of treatment	ART regimen
A1	2002	284	2009	EFV,FTC,TDF,RAL
A2	2007	185	2010	FTC,TDF,RAL
A3	2008	554	2008	EFV,FTC,TDF
A4	2010	593	2010	EFV,FTC,TDF
A5	2004	799	2004	EFV,FTC,TDF
A6	2004	293	2004	AZT/3TC/LOP/RTV
A7	2005	229	2006	EFV,AZT,3TC
A8	2004	338	2005	AZT/3TC/ABC/TDF/FUZ/TIP/RTV

Abbreviation list: EFV=efavirenz, FTC=emtricitabine, TDF=tenofovir, RAL=raltegravir, AZT=zidovudine, 3TC=lamivudine, LOP=lopinavir, RTV=ritonavir, ABC=abacavir, FUZ=enfuvirtide, TIP=tipranavir

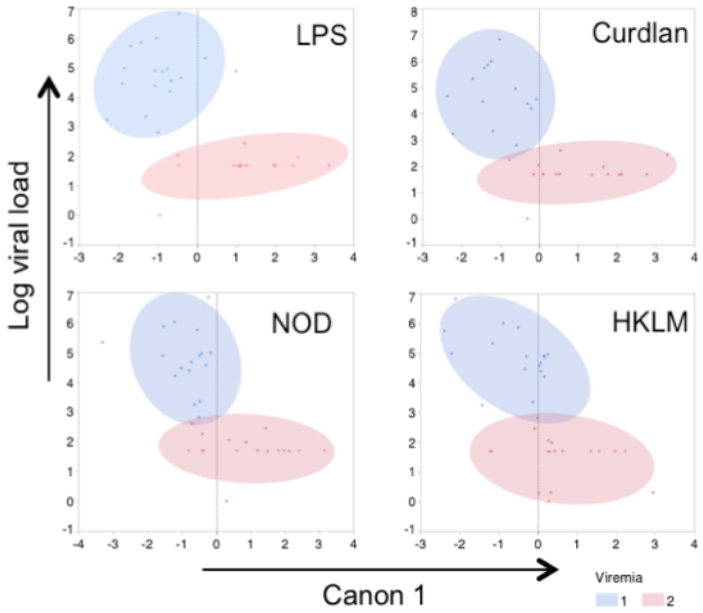
Supplemental Table S2. Antibody clones and volume of antibody used for staining in all panels including T cell activation, monocyte subsets, and intracellular cytokine staining as detailed in the Methods section. All staining done in a volume of ~100uL with cell count ranging between 0.5 to 1.5 x 10^6 cells depending on the experiment.

Antibody	Clone	Volume
HLA-DR PerCP	L243	6uL
HLA-DR PB	L243	1uL
TNF-α PE-Cy7	MAb11	3uL
IL-1β PE	CRM56	1uL
CD3 AF700	UCHT1	1uL
CD4 PB	RPA-T4	0.5uL
CD8 PE-Cy7	SK1	4uL
CD11c APC	V S143	6uL
CD14 APC-Cy7	MphiP9	1uL
CD19 AF700	HIB19	2uL
CD25 APC	M-A251	8uL
CD38 PE	HB7	8uL
CD56 AF700	B159	2uL
CD69 FITC	FN50	6uL
CD123 PE-Cy5	9F5	6uL

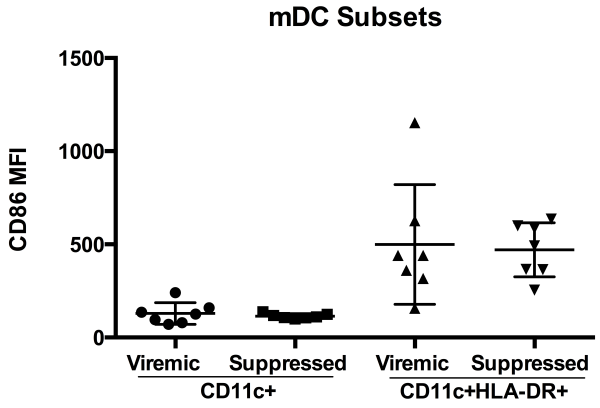
Supplemental Table S3. Antibody clones and commercial sources of CHIP grade antibodies used for chromatin immunoprecipitation experiments.

Antibody	**Millipore Reference number**
Anti-acetylated Histone 4	06-866
Anti-trimethyl Histone 3 (lysine 4)	17-164
Anti-monomethyl Histone 3 (lysine 9)	17-680
Anti-trimethyl Histone 3 (lysine 27)	07-449

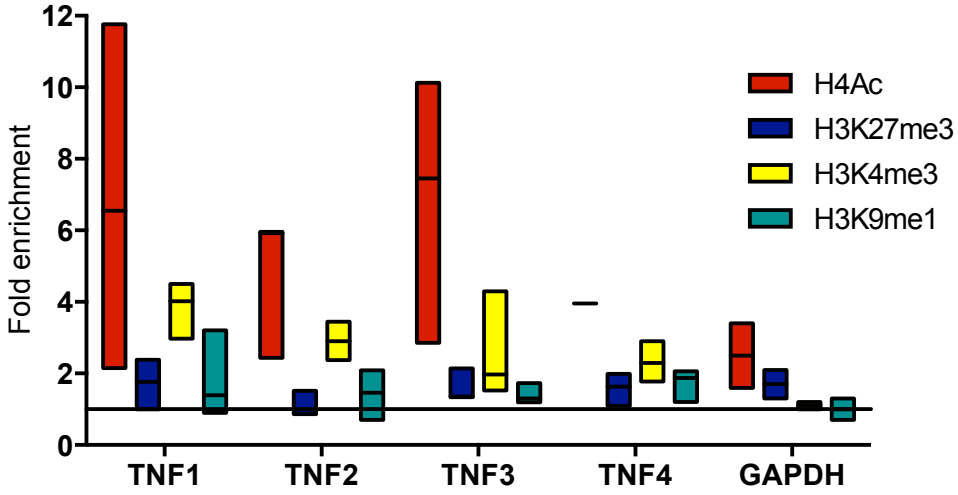
Supplemental Figure S1. **Multivariate analysis of culture supernatants can discriminate between samples from viremic and suppressed timepoints.** PLSDA was used to discriminate between samples derived from high viremia (1, blue) and viral suppression to <400 copies/mL (2, pink). Models were able to classify the samples with a single canonical value (Canon-1, on the x-axis, unique for each stimulant). Model performance estimates predicted classification accuracy of 84% (LPS), 86%(Curdlan), and 85%(NOD) with lower performance for HKLM (71%). Iterative exclusion of random subsets of the data was used to test model predictions. Over 10 iterations of the model, average predictive accuracy values were 87% (LPS), 88%(Curdlan), and 84% (NOD). HKLM had less consistent model performance, with 74% accuracy



Supplemental Figure S2. mDC subset distribution at viremic and suppressed timepoints. Median fluorescence intensity (MFI) of CD86, a costimulatory molecule, on total mDCs (CD3/19/56 negative, CD14 negative and CD11c positive) and on the portion of mDCs co-expressing HLA-DR was compared between viremic and suppressed timepoints. There was no significant difference between these timepoints (mean and standard deviation of MFI values shown, n=7, $p>0.05$, Mann-Whitney U).



Supplemental Figure S3. Histone modifications at the TNFα promoter. Summary data from two independent sample preparations and three immunoprecipitations documenting the fold change in histone modifications across the promoter site. Of note, median data for H4 acetylation at the TNF4 locus site was limited to only a single experiment. Data represented are the median (line) and range (min to max).



Supplemental Figure S4. Gating strategy for intracellular cytokine staining. All sample timepoints from any individual study participant were thawed, cultured and analyzed on the same day.