Pollara et al. Supplemental material

Table S1. Individual sample scRNA-seq results.

Table S2. Cell cluster computational inference of cell type.

Table S3. Genes upregulated in each cluster in scRNA-seq total PBMC.

Table S4. Genes differentially expressed between HIV-1-infected compared to seronegative.

Table S5. Genes differentially expressed between HIV-1-treated compared to seronegative.

Table S6. GSEA enrichment of untreated HIV-1 compared to control.

 Table S7. GSEA enrichment of ART-treated HIV-1 compared to control.

 Table S8. Genes upregulated in each cluster in scRNA-seq T and NK cells.

Table S9. Genes differentially expressed between HIV-1-infected compared to seronegative CD4+ T cells.

 Table S10. Genes differentially expressed between HIV-1-infected compared to seronegative CD8+ T cells.

Table S11. Genes differentially expressed between HIV-1-treated compared to seronegative CD4+ T cells.

Table S12. Genes differentially expressed between HIV-1-treated compared to seronegative CD8+ T cells.

 Table S13. Genes correlated or anti-correlated with HIV-1 gag transcript expression.

Figure S1. scRNA-seq individual cell QC data.

Figure S2. Determining cell types and genes in each cluster.

Figure S3. NK and T cell reclustering.

Table S1. Individual sample scRNA-seq results

Sample	Sample	Number of cells	Median UMI	Median Genes
U	Group			
0036	HIV-1	9274	2345	839.5
	seronegative			
1363	HIV-1	5392	3107.5	1023
	seronegative			
1628	HIV-1	10300	3928.5	1157
	seronegative			
0501	HIV-1	7424	2578	1012
	untreated			
0010	HIV-1	5329	2770	995
	untreated			
0468	HIV-1	5089	2575	912
	untreated			
0694	HIV-1	4163	2628	961
	untreated			
0782	HIV-1	6608	1725	705
	untreated			
0391	HIV-1	3929	3569	1284
	untreated			
0592	HIV-1 ART	7354	4146.5	1162
	treated			
0010	HIV-1 ART	10889	1807	723
	treated			
0694	HIV-1 ART	5484	2218	810
	treated			

Table S2.	Cell cluster	computational	inference of	of cell type
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seurat_clusters	DatabaseImmuneCellExpressionData	MonacolmmuneData		
0	T cells, CD4+	CD4+ T cells		
1	T cells, CD8+	CD4+ T cells		
2	NK cells	T cells		
3	NK cells	NK cells		
4	NK cells	T cells		
5	Monocytes	Monocytes		
6	T cells, CD4+	T cells		
7	B cells	B cells		
8	Monocytes	Monocytes		
9	Monocytes	Monocytes		
10	NK cells	T cells		
11	B cells	B cells		
12	NK cells	T cells		
13	NA	NA		
14	NK cells	T cells		
15	Monocytes	Monocytes		
16	Monocytes	Monocytes		
17	Monocytes	Dendritic cells		
18	B cells	B cells		
19	NK cells	NK cells		
20	NA	Dendritic cells		
21	NK cells	T cells		
22	NK cells	Progenitors		

NAME	SI Z	ES	NES	NOM p-val	FDR q-val	FWER p-val	RANK AT MAX	LEADING EDGE
HALLMARK_G2M_CHECK POINT	<u>Е</u> 83	0.525 24215	1.920 1477	0	0.001	0.002	734	tags=73%, list=37%, signal=111%
HALLMARK_MITOTIC_SPI NDLE	41	0.558 15804	1.808 7457	0	0.007	0.014	628	tags=71%, list=31%, signal=101%
HALLMARK_P53_PATHWA Y	41	0.525 4313	1.734 5463	0	0.01	0.048	397	tags=44%, list=20%, signal=54%
HALLMARK_INTERFERON _ALPHA_RESPONSE	26	0.565 7851	1.731 2152	0.001	0.012	0.048	640	tags=73%, list=32%, signal=106%
HALLMARK_COMPLEMEN T	59	0.497 2665	1.722 6	0	0.01	0.055	500	tags=56%, list=25%, signal=72%
HALLMARK_FATTY_ACID_ METABOLISM	23	0.573 2651	1.682 2027	0.009	0.016	0.094	326	tags=43%, list=16%, signal=51%
HALLMARK_CHOLESTER OL_HOMEOSTASIS	16	0.610 4012	1.663 567	0.004	0.017	0.116	482	tags=63%, list=24%, signal=82%
HALLMARK_XENOBIOTIC _METABOLISM	39	0.489 44244	1.610 2582	0.013	0.027	0.201	486	tags=51%, list=24%, signal=66%
HALLMARK_E2F_TARGET S	98	0.425 62306	1.573 0865	0	0.036	0.285	691	tags=55%, list=35%, signal=80%
HALLMARK_INFLAMMATO RY_RESPONSE	79	0.426 35623	1.535 1864	0.004	0.049	0.393	537	tags=44%, list=27%, signal=58%

Table S7. GSEA enrichment of ART-treated HIV-1 compared to control

$ \begin{array}{ c c c c c c c c c c c c c c c c c c c$	NAME	SI	FS	NES			FWE	RANK	
$\begin{array}{ c c c c c c c c c c c c c c c c c c c$		7		INLO			R n-		
HALLMARK TNFA_SIGNALIN Lo Lo Value MAL Mark Mark <td></td> <td></td> <td></td> <td></td> <td>p-vai</td> <td>q-vai</td> <td>val</td> <td>ΜΔΥ</td> <td></td>					p-vai	q-vai	val	ΜΔΥ	
HALLMARK_INFLAMMATORY 99 0.573 5.16 0 0 0 0 12 lage-19%, signal=93%, signal=93%, signal=93%, signal=95%, s	HALLMARK THEA SIGNALIN		0 727	2 1 9	0	0		202	toge=70%
S_UM_NRB IS-20%, signal=53% HALLMARK INFLAMMATORY _RESPONSE 79 0.552 2.29 0 0 0 570 tags=71%, isgnal=95% HALLMARK_IVPOXIA 43 0.579 2.11 0 7.44E 0.001 320 tags=44%, isgnal=95% HALLMARK_ESTROGEN_RE SPONSE_LATE 50 0.524 2.01 0 0.001 0.004 331 tags=38%, isgnal=51% HALLMARK_UV_RESPONSE 33 0.557 1.91 0 0.004 0.012 320 tags=48%, isgnal=57%, signal=57% HALLMARK_KRAS_SIGNALIN 51 0.482 1.84 0.004 0.007 0.024 488 tags=53%, isgnal=57%, signal=68% HALLMARK_KRAS_SIGNALIN 51 0.482 1.83 0.002 0.004 signal=68% HALLMARK_SOPOPTOSIS 48 0.489 1.83 0.002 0.024 488 tags=53%, ist=16%, ist=16%, signal=66% HALLMARK_COMPLEMENT 59 0.445 1.74 0.007 0.013 0.062 436 tags=55%, istgnal=66%	C VIA NEKR	99	0.737	0007	0	0	0	592	lays=1970,
HALLMARK_INFLAMMATORY 79 0.552 2.29 0 0 570 tags=71%, ist=29%, signal=95% HALLMARK_HYPOXIA 43 0.579 2.11 0 7.44E 0.001 320 tags=44%, ist=16%, signal=51% HALLMARK_ESTROGEN_RE SPONSE_LATE 50 0.524 2.01 0 0.001 0.004 393 tags=38%, ist=16%, signal=61% HALLMARK_VU_RESPONSE 33 0.557 1.91 0 0.004 0.012 320 tags=48%, ist=16%, signal=67% HALLMARK_VU_RESPONSE 33 0.557 1.91 0 0.004 0.012 320 tags=48%, istr=16%, signal=67% HALLMARK_KRAS_SIGNALIN G_UP 51 0.482 1.84 0.004 0.007 0.024 489 tags=53%, istr=16%, signal=66% HALLMARK_APOPTOSIS 48 0.489 1.83 0.002 0.006 0.025 320 tags=53%, istr=16%, signal=66% HALLMARK_ODPLEMENT 59 0.445 1.74 0.007 0.013 0.062 436 tags=53%, istr=2%, signal=56%, iste=2%, signal=56			09977	0007					1151-20%
HALLMARK_INFERFERONSE 75 0.352 2.25 0 0 0 0 10 13/0 13/2 <		70	0 5 5 0	0	0	0	<u> </u>	570	
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$\begin{array}{c c c c c c c c c c c c c c c c c c c $	HALLMARK_UV_RESPONSE	33	0.557	1.91	0	0.004	0.012	320	tags=48%,
$\begin{array}{ c c c c c c c c c c c c c c c c c c c$	_UP		4774	0361		56023			list=16%,
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$\begin{array}{ c c c c c c c c c c c c c c c c c c c$	G_UP		9574	7277	88998	79019			list=24%,
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Image: marking the state of the st			05066	9892	22892	5565			list=22%,
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				4					signal=47%



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Α

Figure S1. scRNA-seq individual cell QC data. (A-B) Plots of each cell in the **(A)** PBMC samples or **(B)** the primary CD4 T cell model samples for the number of genes detected, number of unique molecular identifiers (UMI) for each RNA molecule and the percentage of genes that are of mitochondrial origin. Each point represents an individual cell.



Figure S2. Determining cell types and genes in each cluster. (A) Expression of immune cell transcripts that are associated with cell identity used to identify clusters of cells. **(B)** Heatmap of the top 3 upregulated transcripts in each identified cluster. **(C)** Bar graph showing the fraction of total single cells in each transcriptional cluster by group.



Figure S3. NK and T cell reclustering. (A) Heatmap of top 3 upregulated genes in each of the 17 clusters identified. **(B)** Heatmap of the top 5 upregulated transcripts in each identified cluster. **(C)** Expression of immune cell transcripts that are associated with cell identity used to identify clusters of cells.