

Pollara et al. Supplemental material

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Figure S1. scRNA-seq individual cell QC data.

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Figure S3. NK and T cell reclustering.

Table S1. Individual sample scRNA-seq results

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

Table S2. Cell cluster computational inference of cell type

seurat_clusters	DatabasImmuneCellExpressionData	MonacolImmuneData
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

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

NAME	SI Z E	ES	NES	NOM p-val	FDR q-val	FWER p-val	RANK AT MAX	LEADING EDGE
HALLMARK_G2M_CHECK POINT	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

NAME	SI Z E	ES	NES	NOM p-val	FDR q-val	FWE R p- val	RANK AT MAX	LEADING EDGE
HALLMARK_TNFA_SIGNALING_VIA_NFKB	99	0.737 09977	3.18 8007 6	0	0	0	392	tags=79%, list=20%, signal=93%
HALLMARK_INFLAMMATORY_RESPONSE	79	0.552 49864	2.29 6178 8	0	0	0	570	tags=71%, list=29%, signal=95%
HALLMARK_HYPOXIA	43	0.579 9632	2.11 8108	0	7.44E -04	0.001	320	tags=44%, list=16%, signal=51%
HALLMARK_ESTROGEN_RESPONSE_LATE	50	0.524 76484	2.01 8298 9	0	0.001 68096	0.004	393	tags=38%, list=20%, signal=46%
HALLMARK_UV_RESPONSE_UP	33	0.557 4774	1.91 0361 8	0	0.004 56023	0.012	320	tags=48%, list=16%, signal=57%
HALLMARK_KRAS_SIGNALING_UP	51	0.482 9574	1.84 7277 6	0.004 88998	0.007 79019	0.024	489	tags=53%, list=24%, signal=68%
HALLMARK_APOPTOSIS	48	0.489 9276	1.83 6889	0.002 24215	0.006 93623	0.025	320	tags=48%, list=16%, signal=56%
HALLMARK_INTERFERON_GAMMA_RESPONSE	68	0.447 20253	1.79 2968 5	0	0.010 59651	0.044	528	tags=53%, list=26%, signal=69%
HALLMARK_P53_PATHWAY	41	0.482 05066	1.74 9892 7	0.007 22892	0.013 5565	0.062	436	tags=51%, list=22%, signal=64%
HALLMARK_COMPLEMENT	59	0.445 15666	1.74 2876 8	0.002 48139	0.013 3448	0.068	493	tags=49%, list=25%, signal=63%
HALLMARK_ESTROGEN_RESPONSE_EARLY	31	0.508 3145	1.72 8501 4	0.004 51467	0.013 36376	0.075	381	tags=45%, list=19%, signal=55%
HALLMARK_EPITHELIAL_MESENCHYMAL_TRANSITION	52	0.446 02725	1.72 7738 9	0.006 68151	0.012 25011	0.075	320	tags=31%, list=16%, signal=36%
HALLMARK_COAGULATION	36	0.456 8763	1.62 5861 4	0.011 46789	0.028 01298	0.174	386	tags=36%, list=19%, signal=44%
HALLMARK_MITOTIC_SPINDLE	41	0.448 85015	1.62 2089 6	0.006 92841	0.026 53278	0.176	171	tags=17%, list=9%, signal=18%
HALLMARK_XENOBIOTIC_METABOLISM	39	0.435 73573	1.57 6376 4	0.025 05695	0.035 18377	0.239	386	tags=38%, list=19%, signal=47%

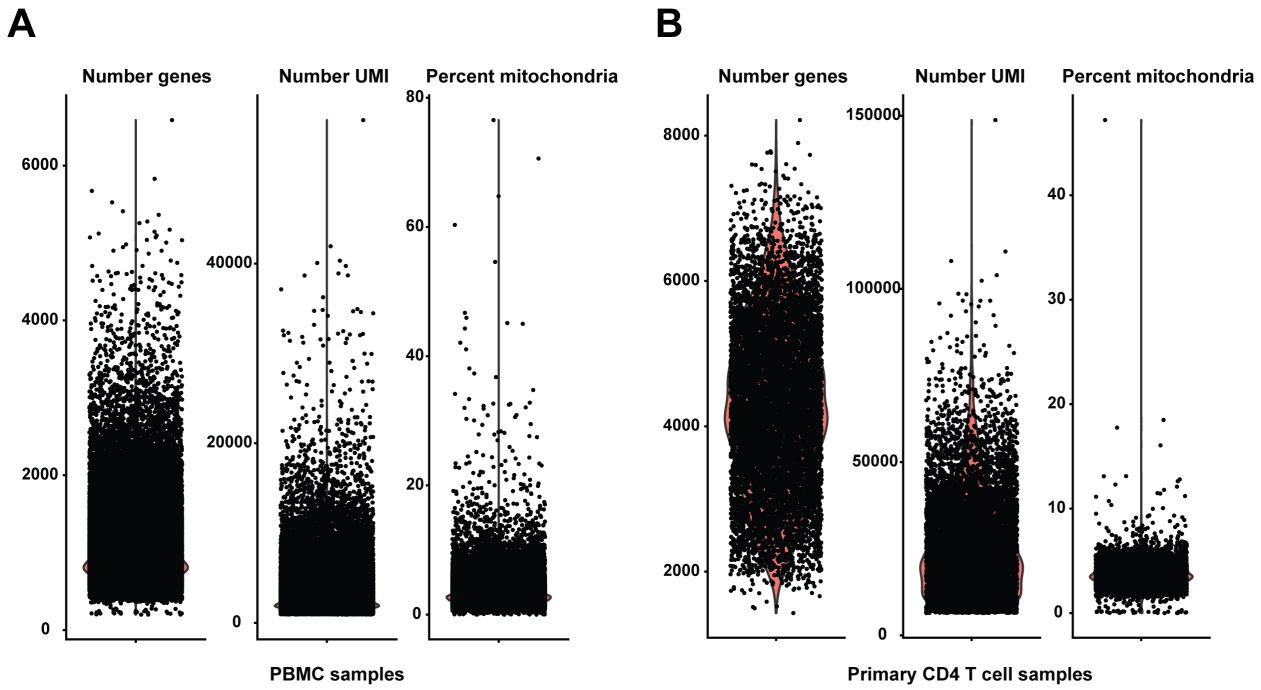


Figure S1. scRNA-seq individual cell QC data. (A-B) Plots of each cell in the (A) PBMC samples or (B) the primary CD4 T cell model samples for the number of genes detected, number of unique molecular identifiers (UMI) for each RNA molecule and the percentage of genes that are of mitochondrial origin.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

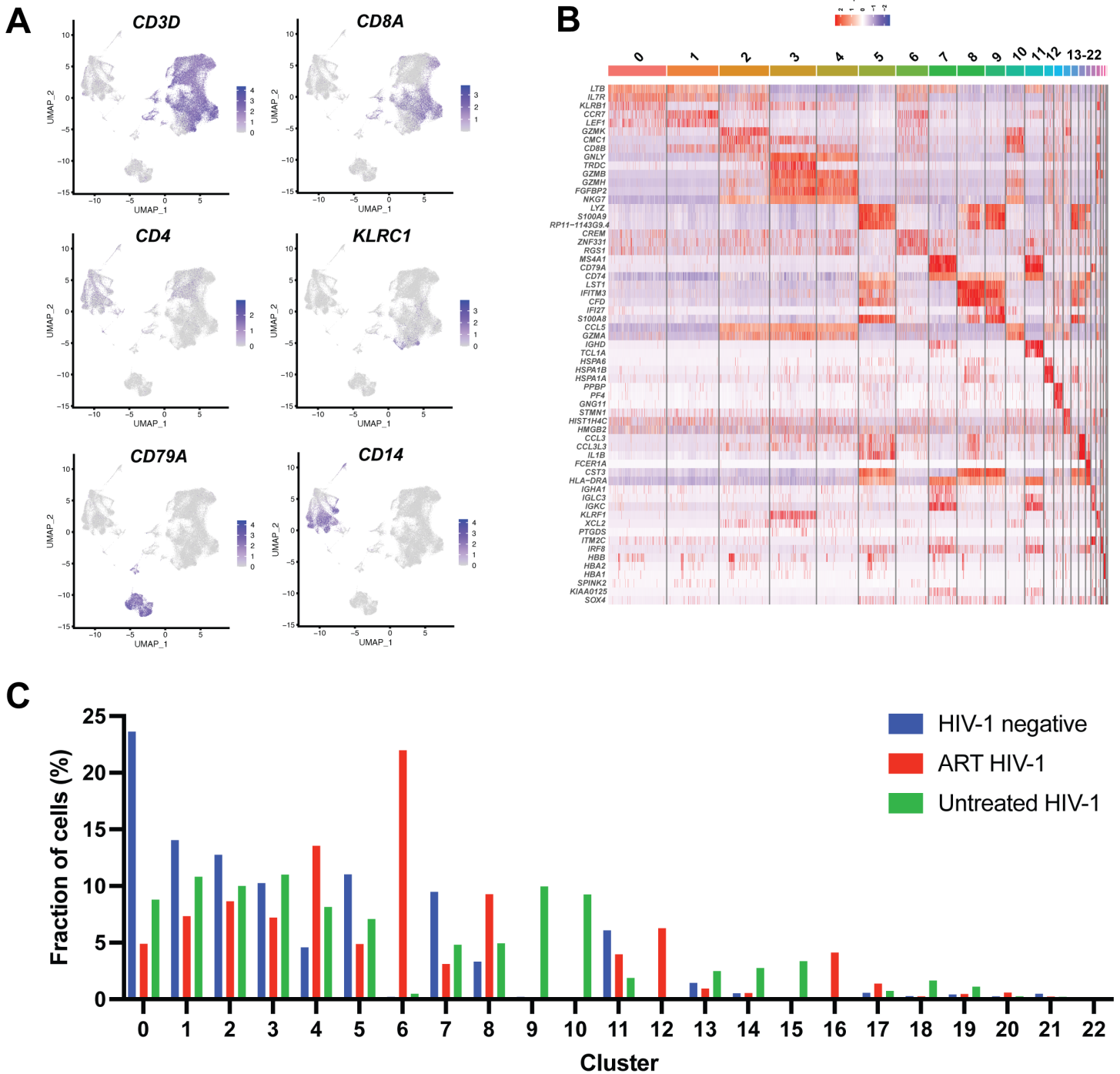


Figure S2. Determining cell types and genes in each cluster. (A) Expression of immune cell transcripts that are associated with cell identity used to identify clusters of cells. **(B)** Heatmap of the top 3 upregulated transcripts in each identified cluster. **(C)** Bar graph showing the fraction of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

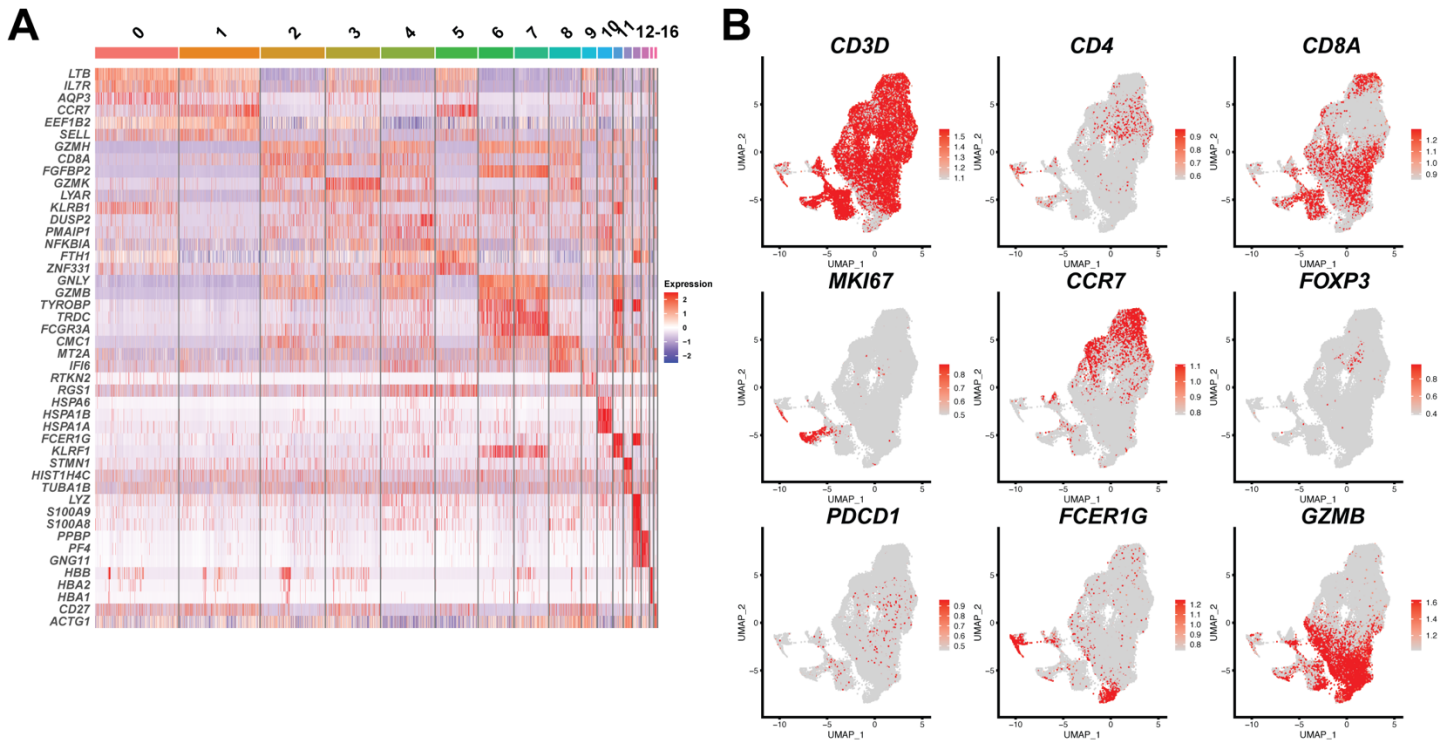


Figure S3. NK and T cell reclustering. (A) Heatmap of top 3 upregulated genes in each of the 17 clusters identified. **(B)** Heatmap of the top 5 upregulated transcripts in each identified cluster. **(C)** Expression of immune cell transcripts that are associated with cell identity used to identify clusters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