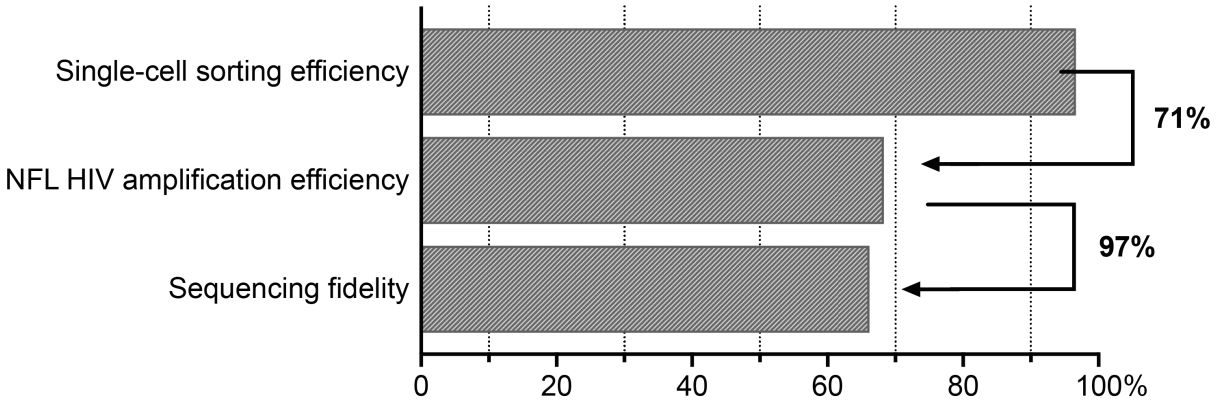
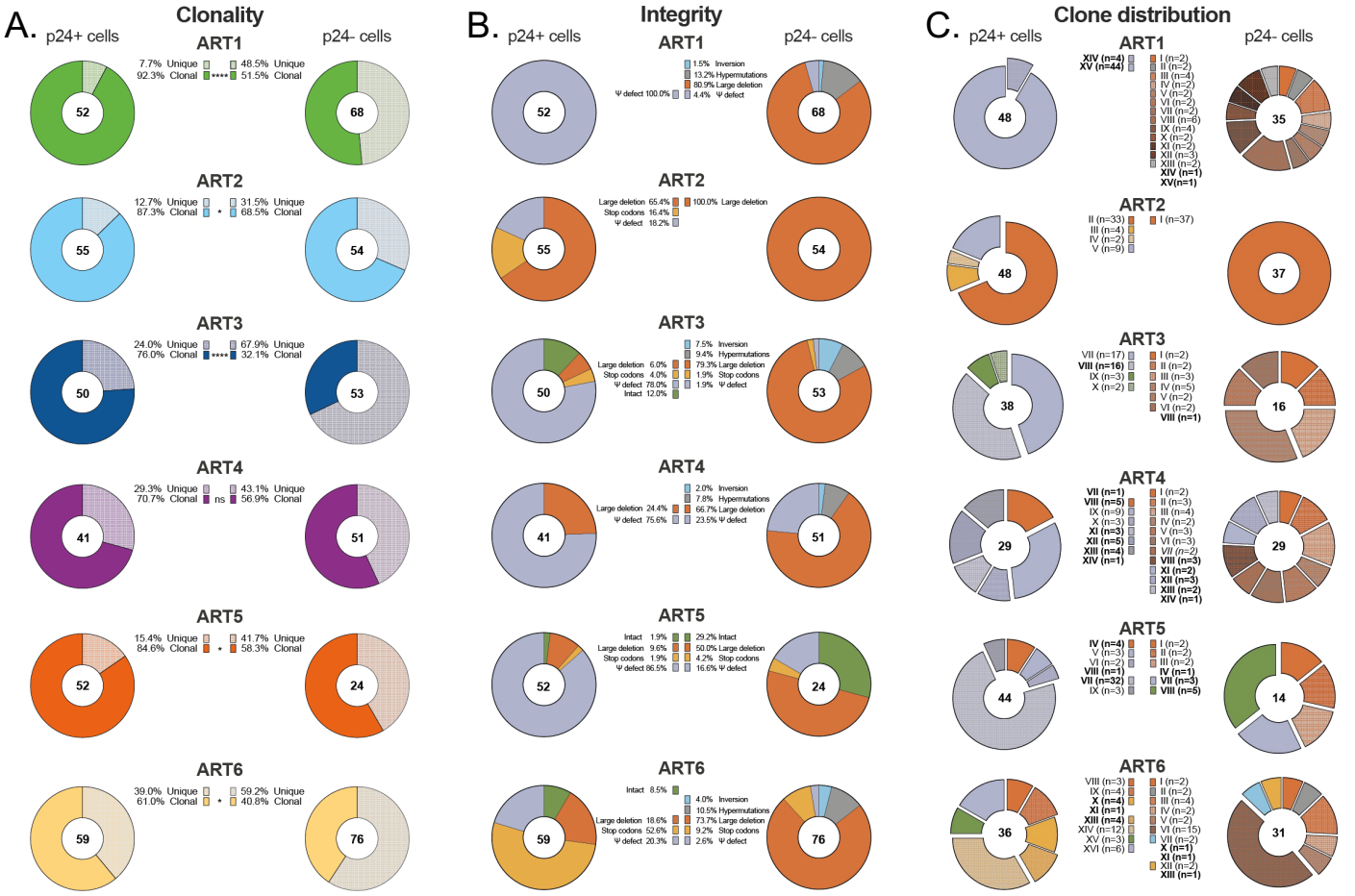
Supplementary figure 1



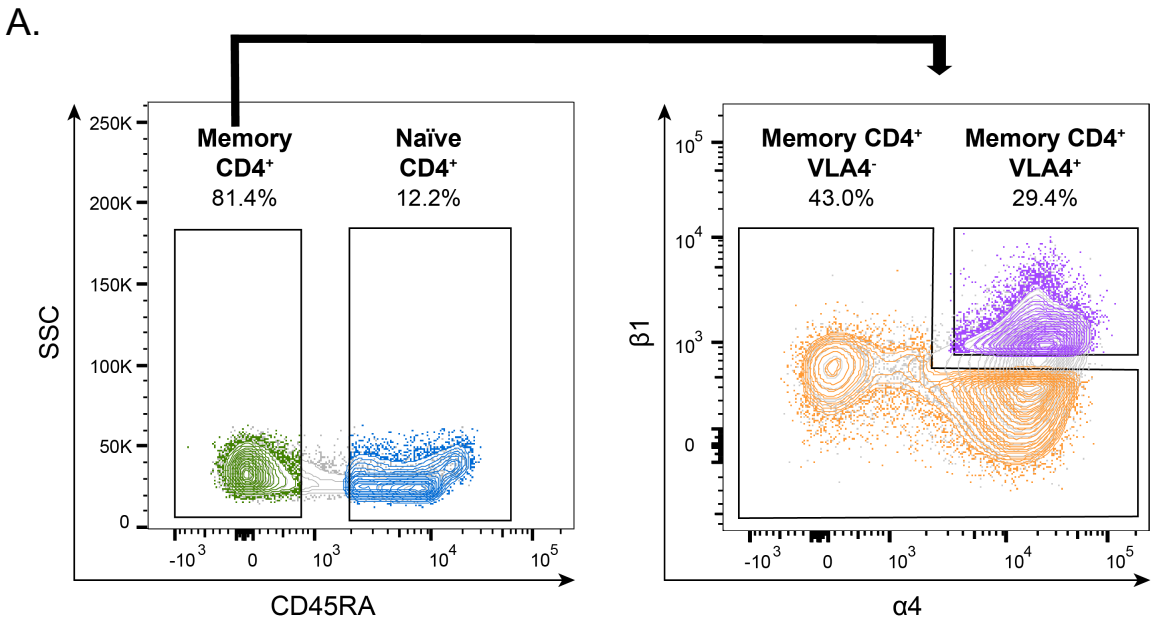
Supplementary figure 1: Efficiency of the approach. ACH-2 cells were single sorted and subjected to near full-length HIV genome amplification. Amplified products were barcoded and sent for PacBio next-generation sequencing. Single sorted ACH2 cells were retrieved from 96.7% of the wells (detectable CD3 gene by qPCR) and 70.1% of the genomes were successfully amplified. Proviral sequences from 93.0% of the amplified near full-length genomes were identical to each other and matched the MN691959.1 HIV-1 isolate ACH-2 reference (https://www.ncbi.nlm.nih.gov/nuccore/MN691959). The proportion of single-cell sorting efficiency, NFL HIV amplification efficiency, and sequencing fidelity are indicated.

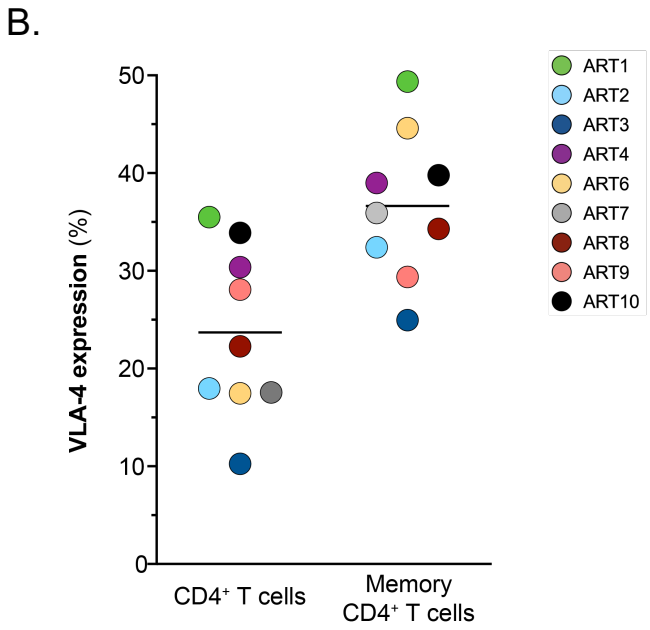
Supplementary figure 2



Supplementary figure 2: Integrity and clonality of HIV genomes retrieved from p24+ and p24- cells for each participant. A. Pie charts representing the proportions of unique (dotted color) and clonal (solid color) proviral sequences retrieved from p24+ and p24- cells. Percentages are indicated. The number of proviral sequences analyzed is indicated in each pie chart. For each participant, Fisher's exact test was used to determine differences in clonality between the two populations (*: $p<0.05$; ****: $p<0.0001$). **B.** Pie charts representing the proportions of genomes with different types of genetic defects in p24+ and p24- cells. Genetic defects are color-coded and their percentages are indicated. The total number of proviral sequences analyzed is indicated in each pie chart. **C.** Distribution and genetic integrity of the clonally expanded clones. Each fraction of the pie chart represents a clonal expansion and is color-coded according to the type of defect as in B. The number of individual cells belonging to each clone is indicated. The total number of clonally expanded proviral sequences analyzed is indicated in each pie chart. Clones in bold are shared between p24+ and p24- cells. **D.** Proportions of Ψ defective proviruses with major splicing donor site point mutation (dark purple), stem loop 2 deletion (purple) and larger psi deletion (light purple) in p24+ and p24- cells. The number of proviral sequences analyzed is indicated in each pie chart. Differences in the contribution of each defect to the total population was performed using the Fisher's exact test.

Supplementary figure 3





Supplementary figure 3: α4β1 cell-sorting strategy. A. Dot Plots showing the expression of CD45RA, α4 and β1 in isolated CD4+ T cells from a representative participant. Memory CD4+ T cells expressing VLA-4 (VLA-4+: CD45RA-α4high β1high; purple contour plot) or not (VLA-4-: CD45RA-α4low/- β1low/-; orange contour plot) were sorted by flow cytometry. **B.** Frequencies of CD4+ T cells and memory CD4+ T cells expressing VLA-4 in the blood of 9 ART-suppressed participants.