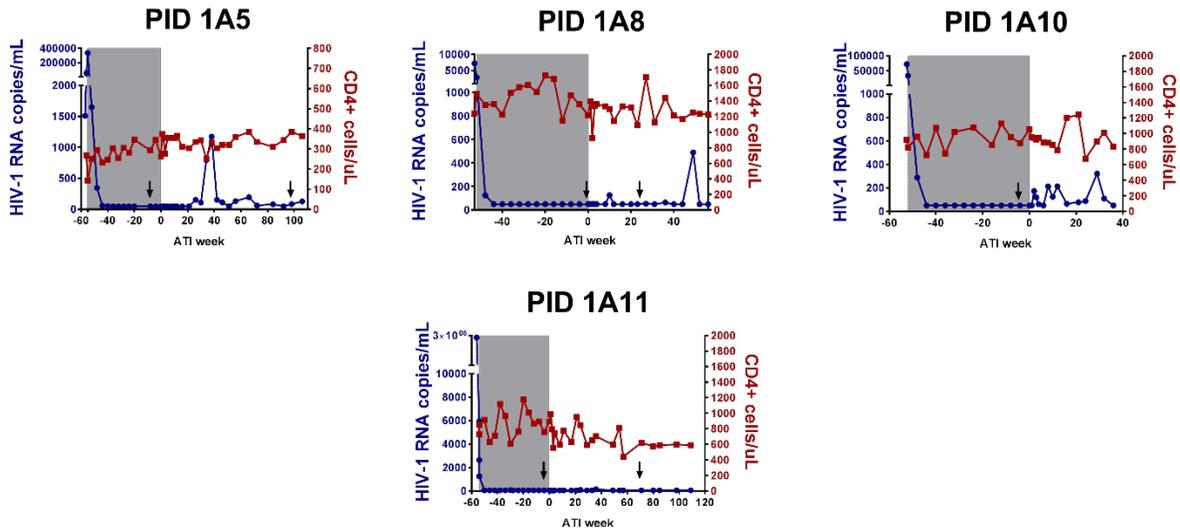
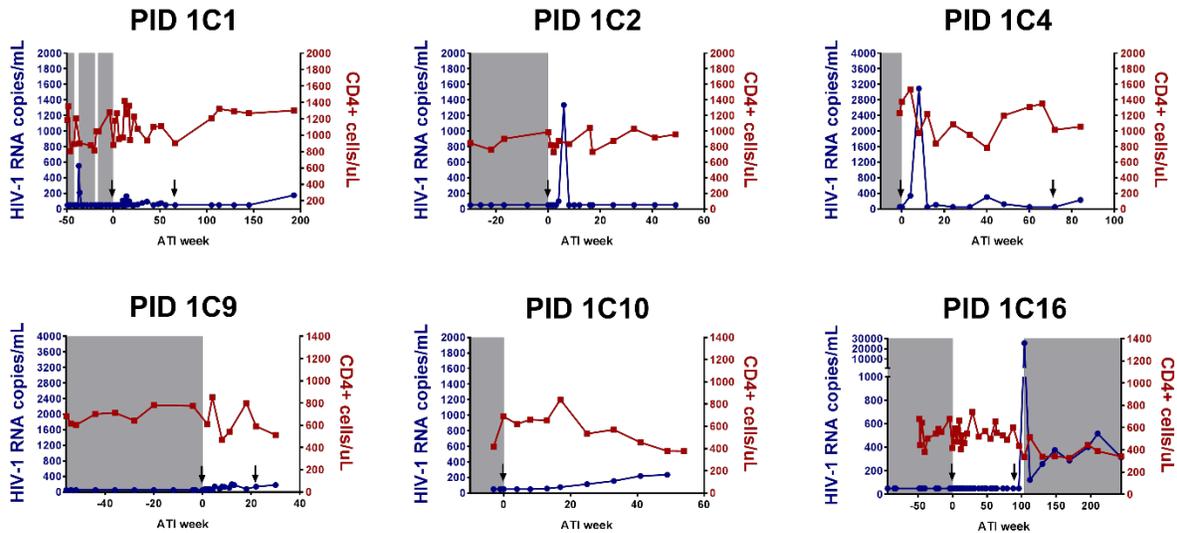


On-ART
 Off-ART
 Viral load
 CD4 count

Early-treated participants



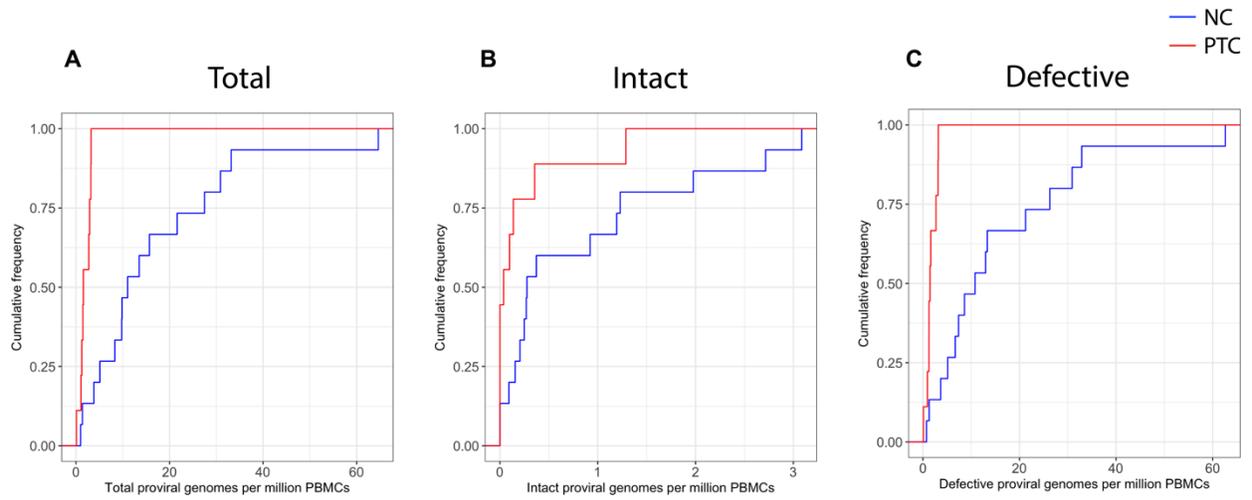
Chronic-treated participants



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 867
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 872

Figure S1. Viral loads and CD4 counts for PTCs.

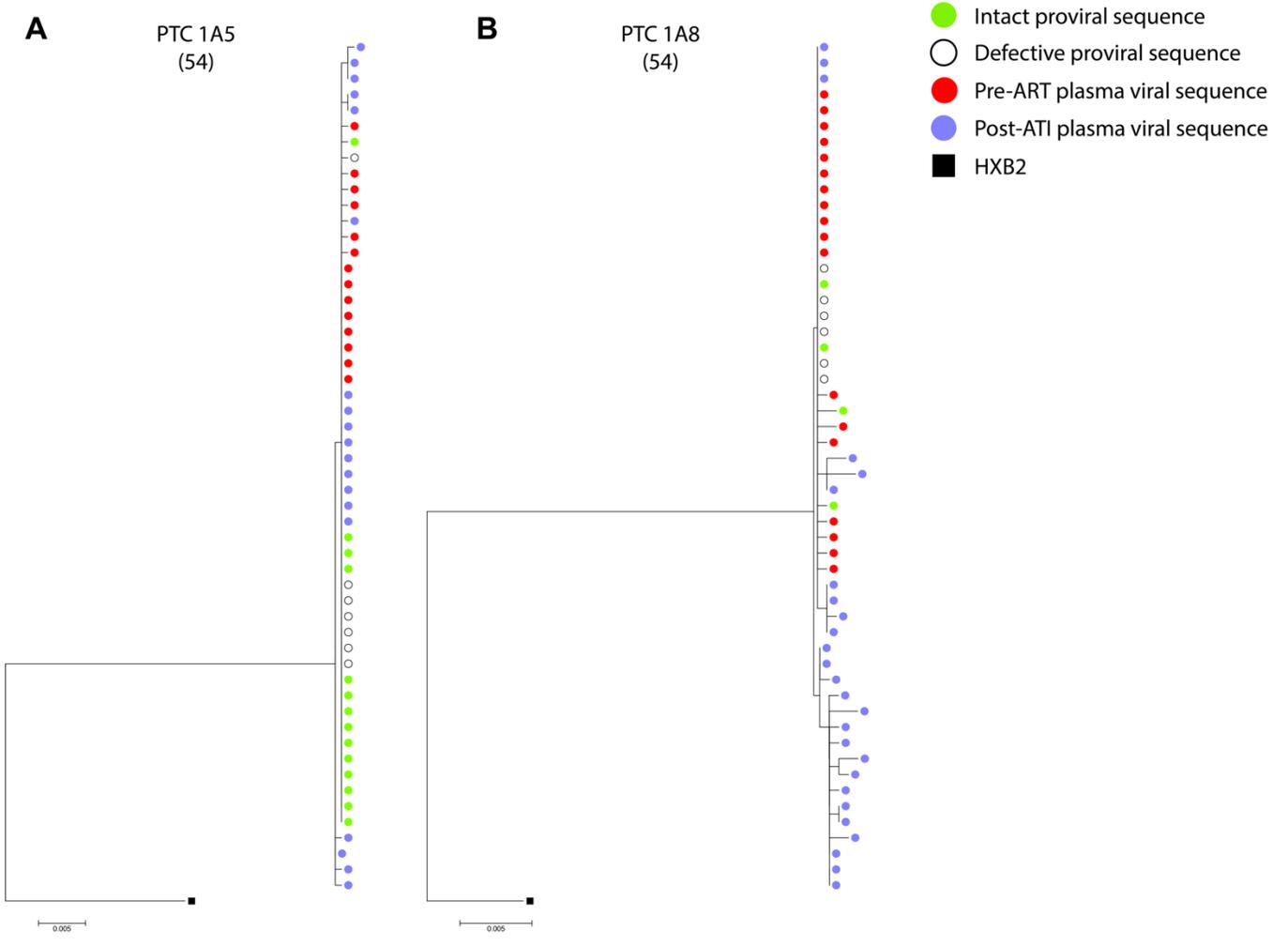
For each of the PTCs, viral loads are graphed in blue and CD4 counts in red. Black arrows represent time points used for proviral genome sequencing at either the pre-ATI or the post-ATI timepoint. On-ART period is shaded in grey and the off-ART period shown as white.



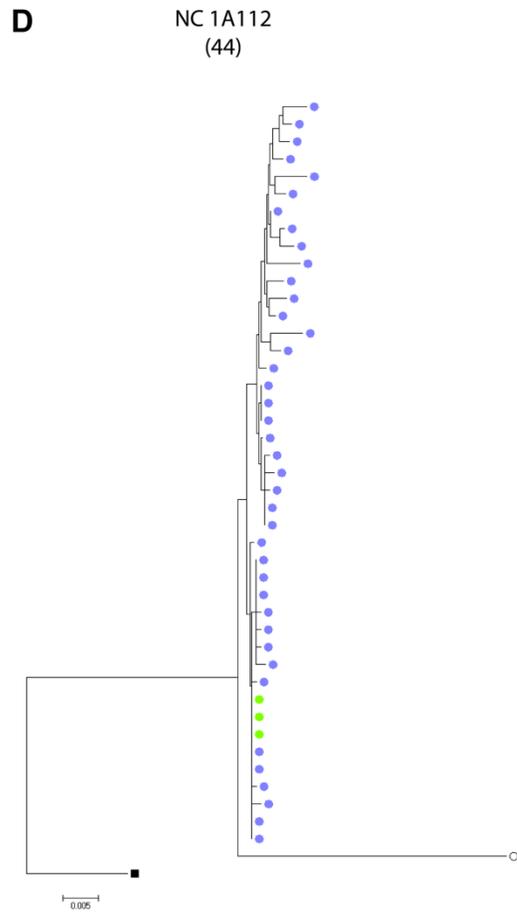
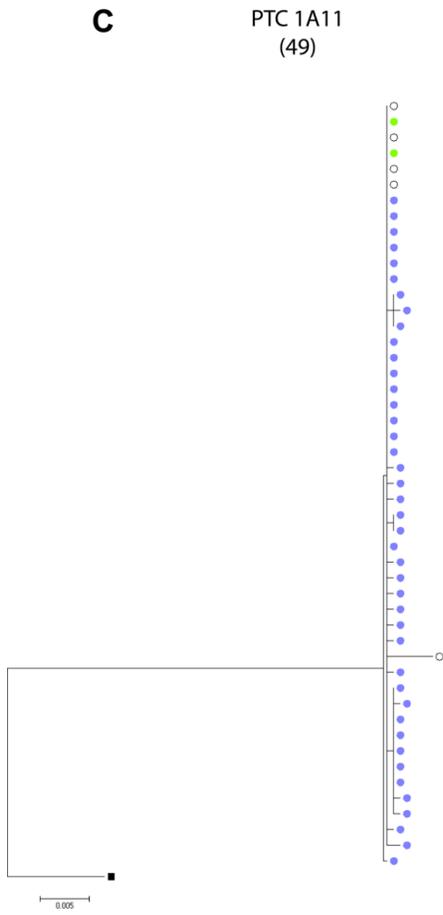
873
874

875 **Figure S2. Cumulative frequency plots.** Cumulative plots of the copy numbers of total (A),
876 intact (B) and defective (C) proviruses are shown.
877

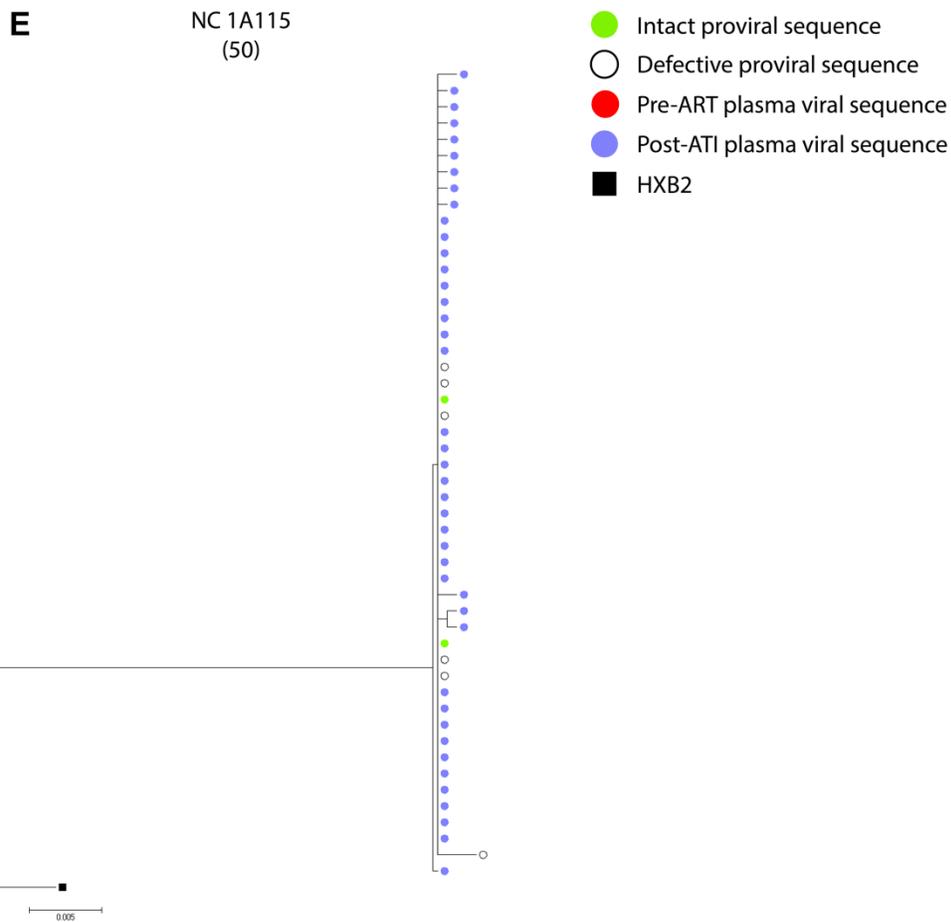
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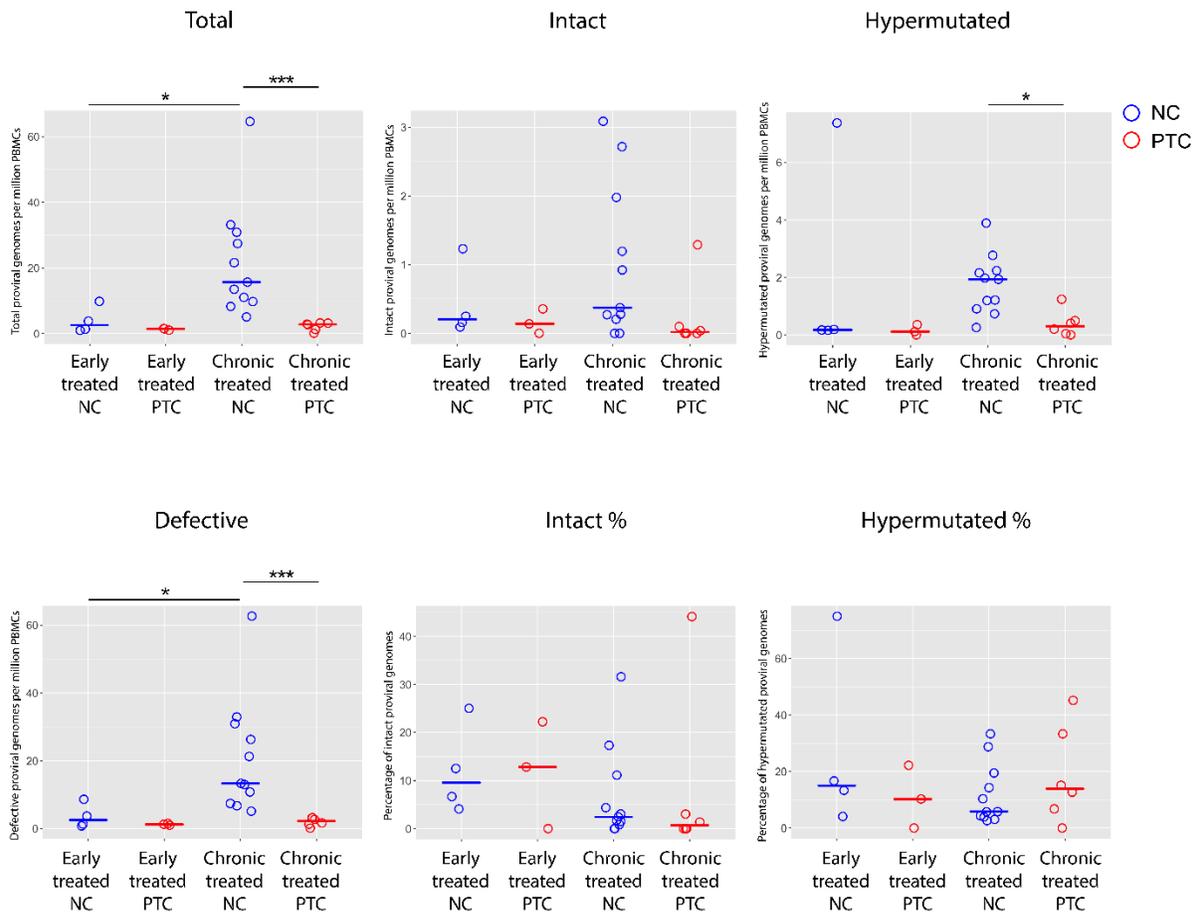
- Intact proviral sequence
- Defective proviral sequence
- Pre-ART plasma viral sequence
- Post-ATI plasma viral sequence
- HXB2



880

881 **Figure S3. Neighbor-joining trees of the *pro-rt* region in both proviral and plasma-derived**
 882 **sequences.** Each figure subplot depicts a phylogenetic tree of sequences obtained from one
 883 participant rooted to HXB2. Proviral sequences were obtained from PBMCs pre-treatment
 884 interruption and plasma viral sequences were obtained either pre-ART or post-ATI as indicated
 885 in the legend. Numbers in parentheses indicate absolute frequency of analyzed sequences per
 886 participant. (A-C) are PTCs and (D-E) are NCs. ART, antiretroviral therapy; ATI, analytic
 887 treatment interruption.

888

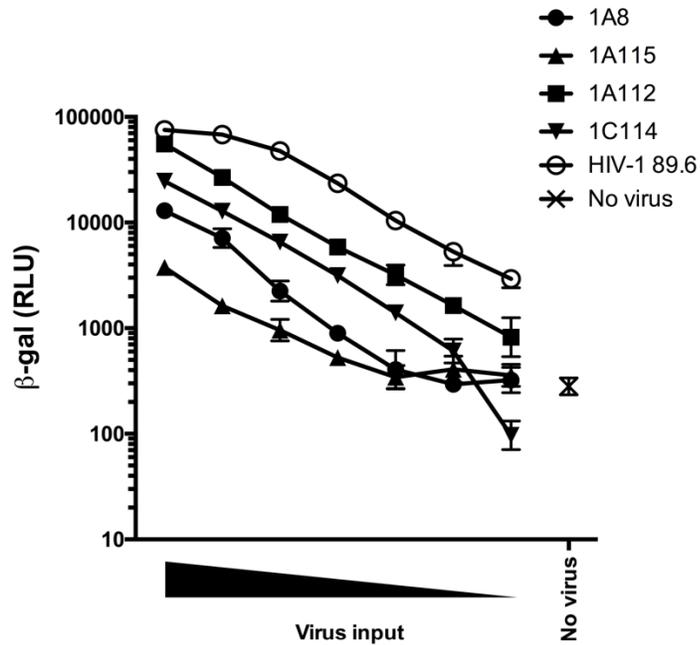


889

890 **Figure S4. Comparison of reservoir measures between early and chronic-treated participants.**

891 $P < 0.05$ was considered significant and denoted as * and $P < 0.001$ as ***.

892



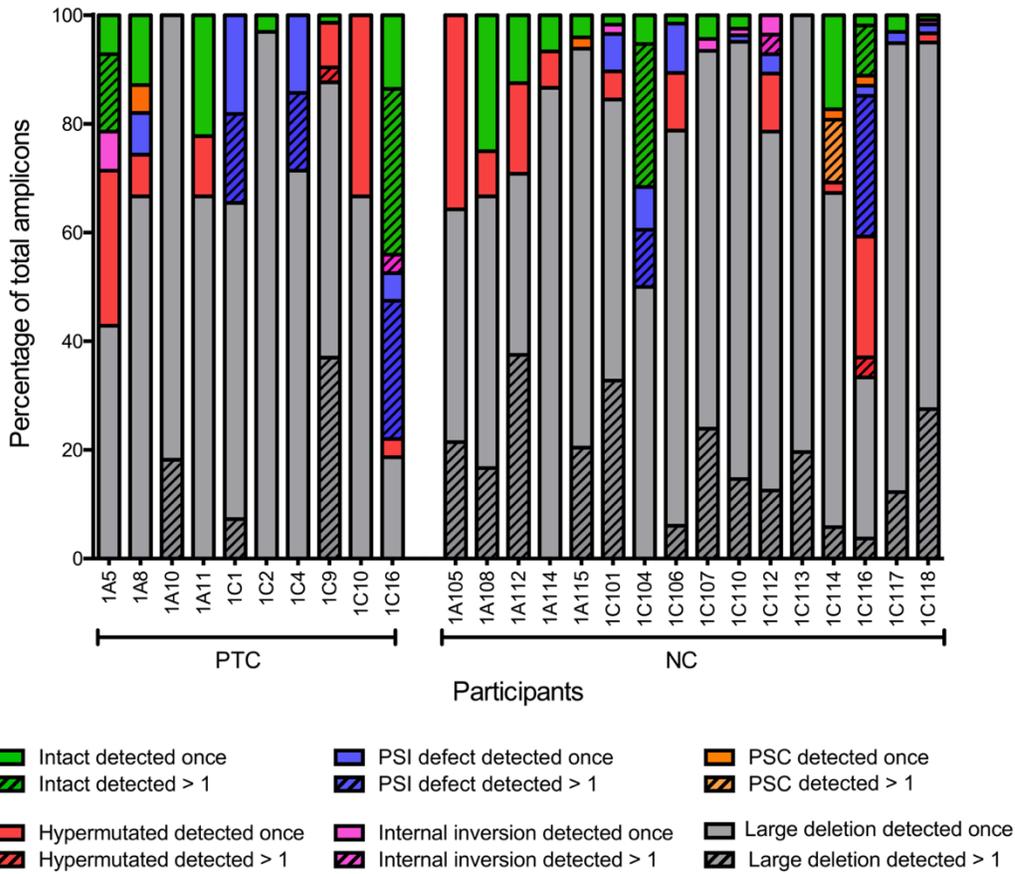
893

894

895 **Figure S5. Infectivity assay on TZM-bl cells.** Infectivity of recombinant virions generated using
 896 *env* PCR fragments from intact proviral genomes was tested in a TZM-bl assay. RLU, relative
 897 luminescence units.

898

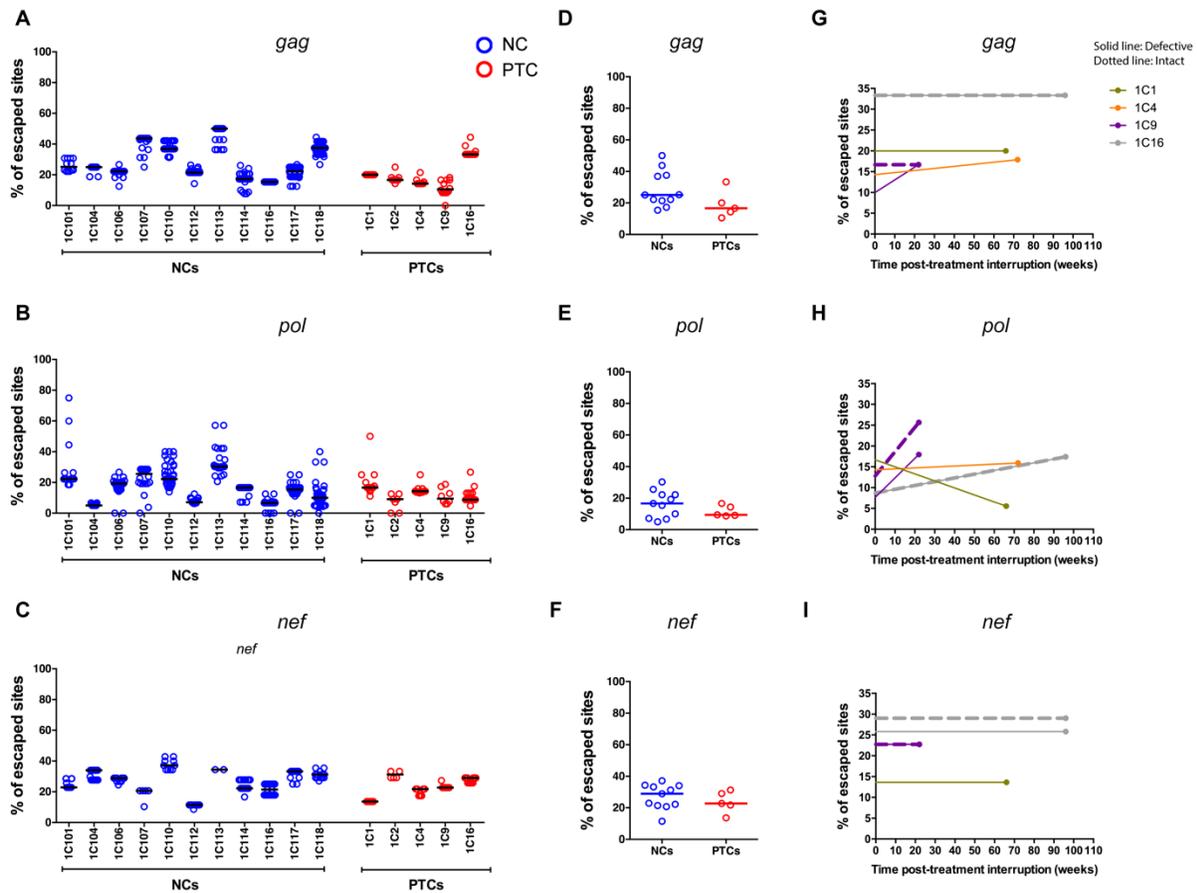
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902

903 **Figure S6. Percentage of each proviral species per participant.** Solid colors represent
904 sequences identified only once and striped bars represent identical sequences detected more
905 than once. PSI, packaging signal; PSC, premature stop codon; PTC, post-treatment controllers;
906 NC, post-treatment non-controllers.

907



908

909 **Figure S7. Frequency of HLA-associated escape mutations.**

910 (A-C) Percentages of HLA-associated escaped sites within (A) *gag*, (B) *pol* and (C) *nef* are

911 depicted for each study participant. Each data point represents one sequence. (D-F) The median

912 percentage of escaped sites in each study participant within (D) *gag*, (E) *pol* and (F) *nef* is

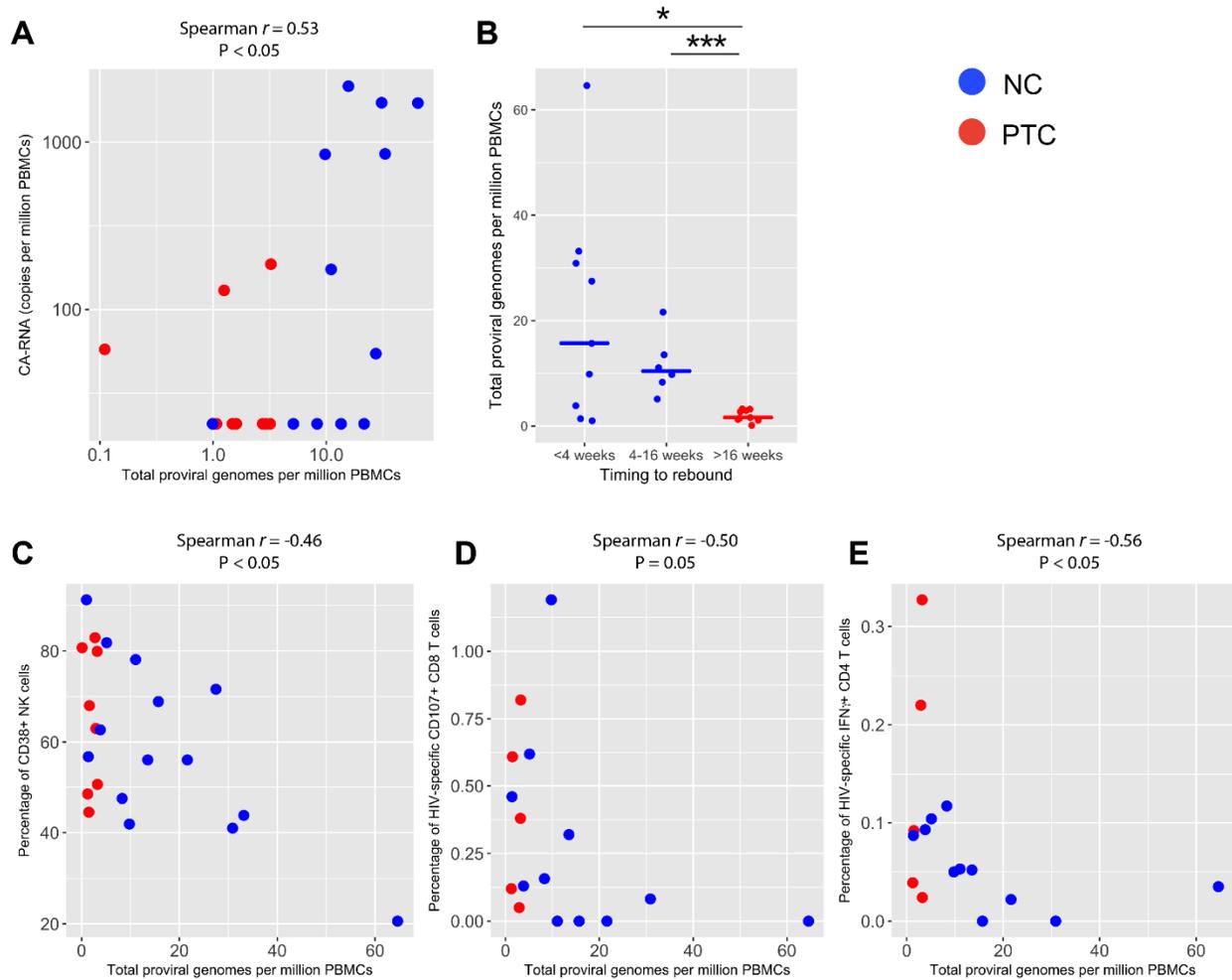
913 depicted. Each data point represents one study participant. (G-I) Longitudinal changes in the

914 percent of HLA-escaped sites from PTCs in (G) *gag*, (H) *pol* and (I) *nef* categorized by defective

915 (solid line) or intact (dotted line) proviruses. PTCs, post-treatment controllers; NCs, post-

916 treatment non-controllers.

917



919

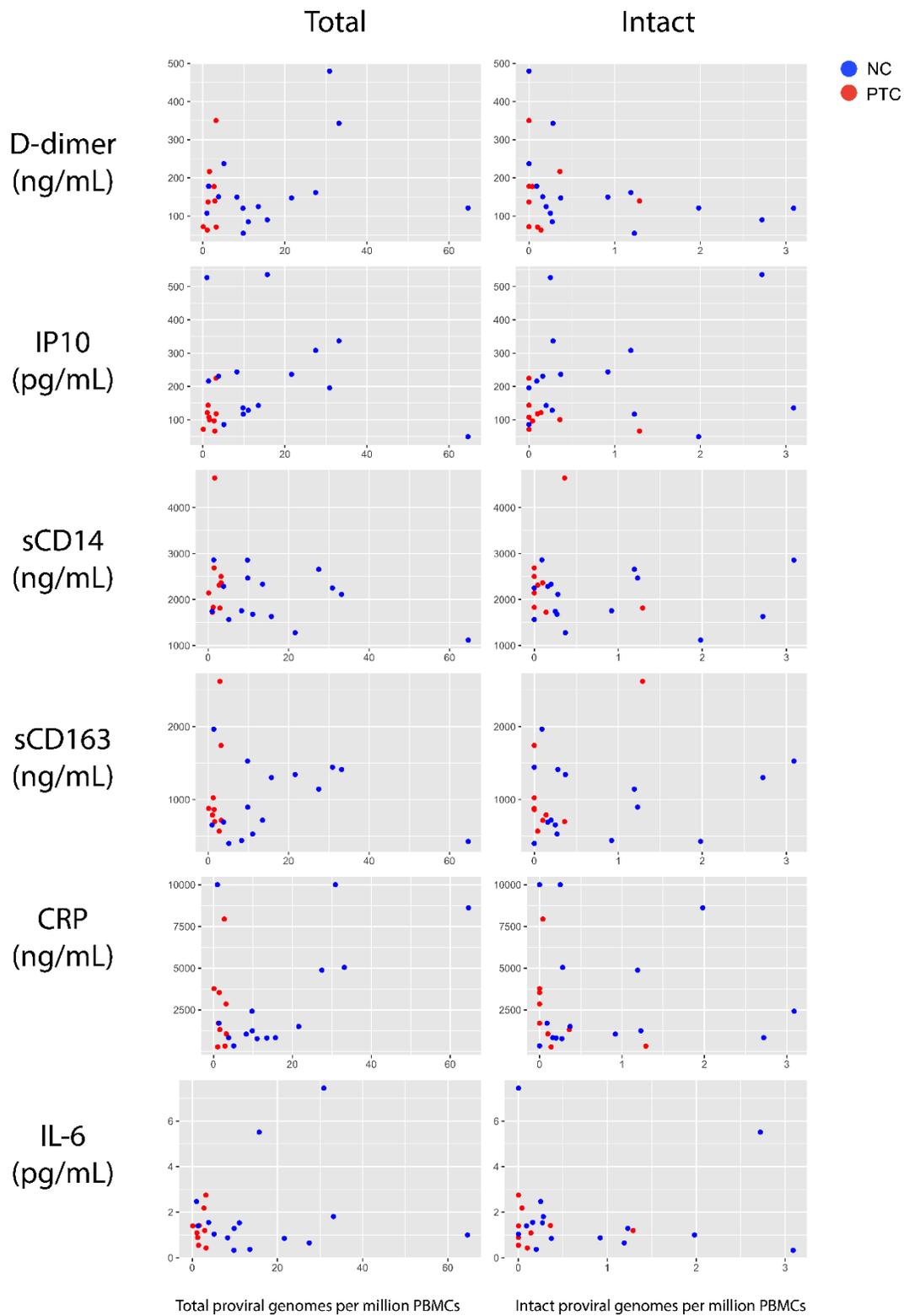
920 **Figure S8. Relationship between total proviral genome copy numbers and viral as well as**
 921 **immune markers.**

922 (A) Correlation between levels of cell-associated HIV RNA and copy numbers of total proviral
 923 genomes. (B) Individuals with delayed viral rebound had lower levels of total proviral genomes.
 924 Significance was calculated using a Wilcoxon rank-sum test; $P < 0.05$ was considered significant
 925 and denoted as * and $P < 0.001$ as ***. (C) Correlation between percentage of CD38+ NK cells
 926 and copy numbers of total proviral genomes. (D) Correlation between percentage of HIV-
 927 specific CD107+ CD8 T cells and copy numbers of total proviral genomes. (E) Correlation
 928 between percentage of HIV-specific IFN γ + CD4 T cells and copy numbers of total proviral
 929 genomes. NCs are depicted in blue and PTCs in red. Correlations between reservoir measures

930 were estimated with non-parametric Spearman correlation coefficients. PTC, post-treatment
931 controllers; NC, non-controllers.

932

933



934

935 **Figure S9. No significant correlation between levels of inflammatory markers and reservoir**

936 **measures.**