Figure 1S. CD4⁺ T-cell counts and viral loads in PLWH on ART. Associated with Table 1. (A) CD4⁺ T-cell counts and (B) viral loads at intervals between 0 (baseline) and 24 weeks of ART.

Figure 2S. Per sample amplicon sequence variants. Associated with Figure 1. Number of amplicon sequence variants (ASV) in baseline and week 24 samples. Dashed line indicates y-intersection of 50 ASV. Single sample below the dashed line was removed from all analysis.

Figure 3S. Paired analysis of bacterial alpha diversity in the salivary microbiome of PLWH on ART. Associated with Figure 2. Paired (A) bacterial richness and (B) Shannon diversity in the salivary microbiome of samples collected at baseline or following 24 weeks of ART. Differences between groups were considered statistically significant if p < 0.05 using the Wilcoxon matched-pairs signed rank test. n.s. indicates not significant.

Figure 4S. Alpha diversity of the salivary microbiome in VL high and VL low groups. Associated with Figure 6. (A&B) Bacterial richness and (C&D) Shannon diversity in VL high and low samples at in baseline samples and samples collected following 24 weeks of ART. Differences between groups were considered statistically significant if p < 0.05 using the nonparametric Mann-Whitney test. The median for each group is indicated with a horizontal line, and error bars indicate the interquartile range. n.s. indicates not significant.

Figure 5S. Alpha diversity of the salivary microbiome in samples taken prior to or following 24 weeks of ART in VL low samples. (A) Bacterial richness and (B) Shannon diversity in viral load low (<100,000 cp/ml) samples at baseline and week 24. Differences between groups were considered statistically significant if p < 0.05 using the Wilcoxon matched-pairs signed rank test. n.s. indicates not significant.

Figure 6S. Alpha diversity of the salivary microbiome in samples taken prior to or following 24 weeks of ART grouped by CD4 category. Bacterial richness in (A) baseline and (B) week 24 samples. Shannon diversity in (C) baseline and (D) week 24 samples. Differences between groups were considered statistically significant if p < 0.05 using the nonparametric Mann-Whitney test. The median for each group is indicated with a horizontal line, and error bars indicate the interquartile range. n.s. indicates not significant.

Figure 7S. Inflammatory biomarkers at baseline or following 24 weeks of ART. Associated with Figure 4. Paired values for (A) sCD14, (B) sTNF-r1, (C) sTNF-r2, and (D) IL-6.
Figure S1. CD4⁺ T-cell counts and viral loads in PLWH on ART.
Figure S2. Per sample amplicon sequence variants.
Figure S3. Paired analysis of bacterial alpha diversity in the salivary microbiome of PLWH on ART.
Figure S4. Alpha diversity of the salivary microbiome in VL high and VL low groups.
Figure S5. Alpha diversity of the salivary microbiome in samples taken prior to or following 24 weeks of ART in VL low samples.

Figure 6. Alpha diversity of the salivary microbiome in samples taken prior to or following 24 weeks of ART in VL low samples.
Figure S6. Alpha diversity of the salivary microbiome in samples taken prior to or following 24 weeks of ART grouped by CD4 category.
Figure S7. Inflammatory biomarkers at baseline or following 24 weeks of ART

A) sCD14

B) sTNFr-1

C) sTNFr-2

D) IL-6