Bull et al., Supplemental Figure 1

Nevirapine concentrations ng/mL

Suppressors

LLV: Suppressed time point

LLV: LLV time point
Bull et al. Supplemental Figure 2, Panel B

The figure shows scatter plots comparing Pw Diversity across different time points and conditions. The x-axis represents different time points (Mo 0, Plasma, Plasma Mo 12, Plasma Mo 18, Plasma Mo 9, Plasma Mo 24, Plasma Mo 21). The y-axis represents the Pw Diversity values ranging from 0.00 to 0.15. Each plot includes data points and error bars indicating variability. The plots are labeled with specific time points and conditions.
Supplemental Figure 1: Quantification of plasma nevirapine (NVP) concentrations in participants with and without LLV. NVP concentrations were compared in specimens within participants when ART-suppressed and at LLV, and across participants at time-points with and without LLV. The NVP concentrations were similar in participants with and without LLV detected during the study; and in the former, both at LLV time-points and time-points when their plasma HIV RNA was <30c/mL.

Supplemental Figure 2: Phylogenetic HIV pairwise env diversity from participants evaluated for low-level viremias (LLV) grouped by phylogenetic pattern into those with (A) monotypic pattern #1 and with (B) a diverse pattern #2. Single genome amplicons (SGA) were generated as described in methods and sequences aligned using the MUSCLE algorithm in Geneious (BioMatters, Newark, NJ) and employed PhyML in DIVEIN [18] to generate maximum likelihood trees and pair-wise diversity (pwDiversity).