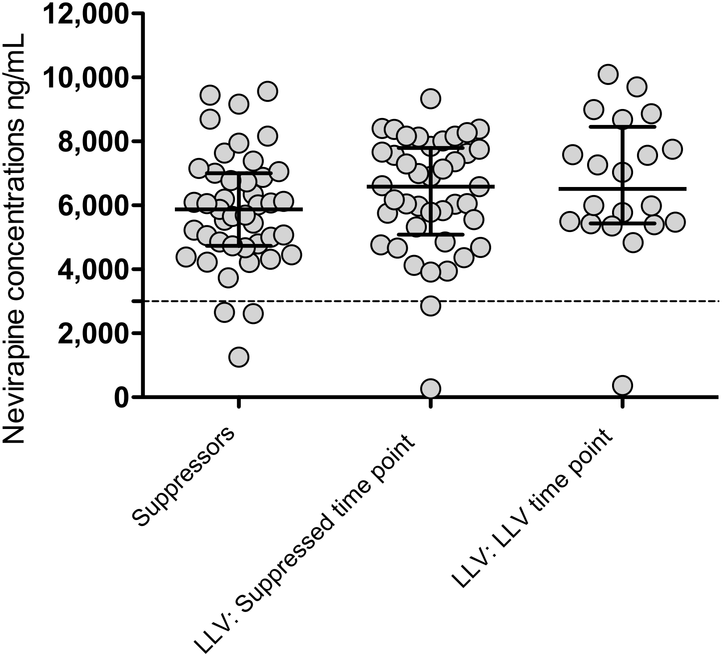
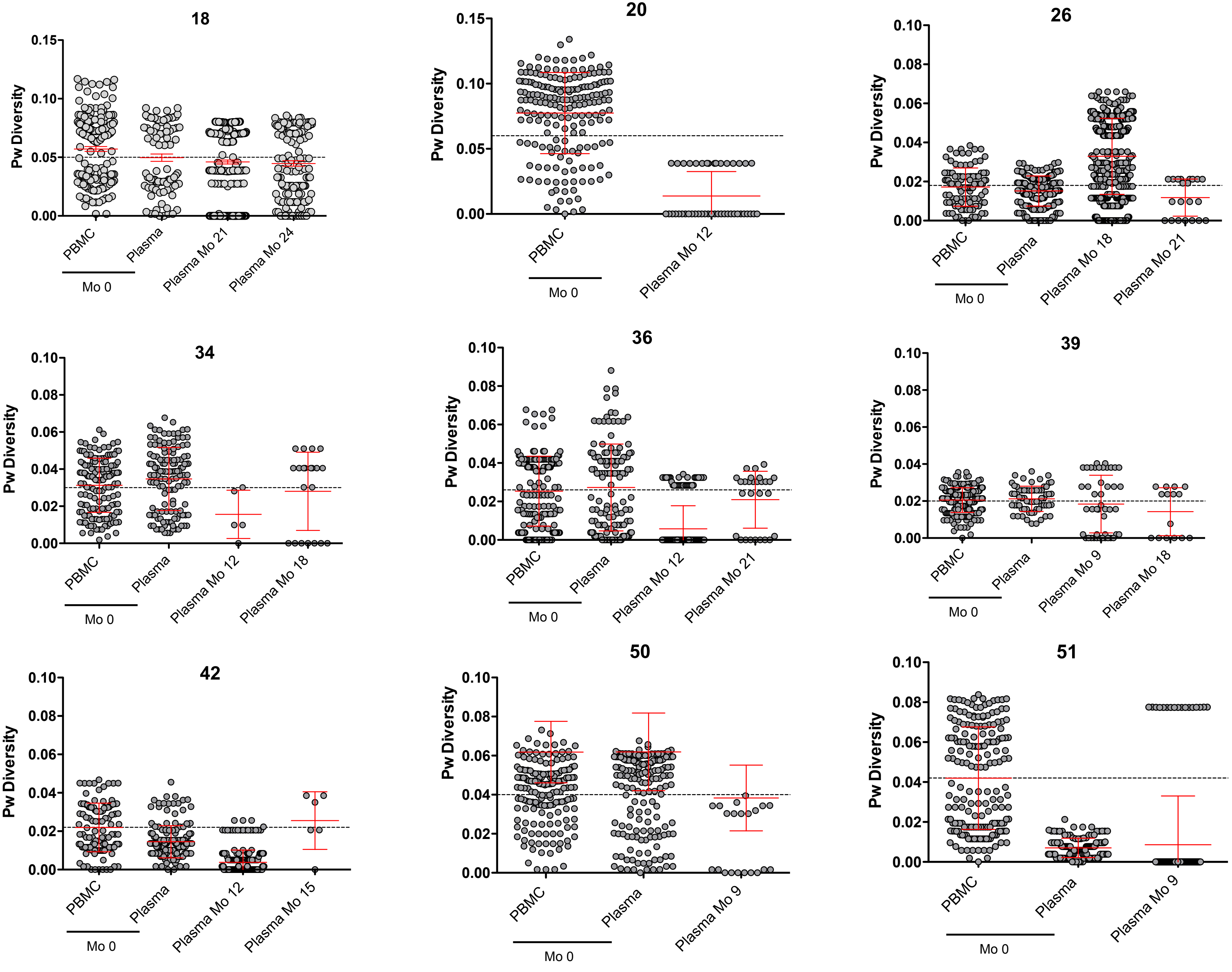
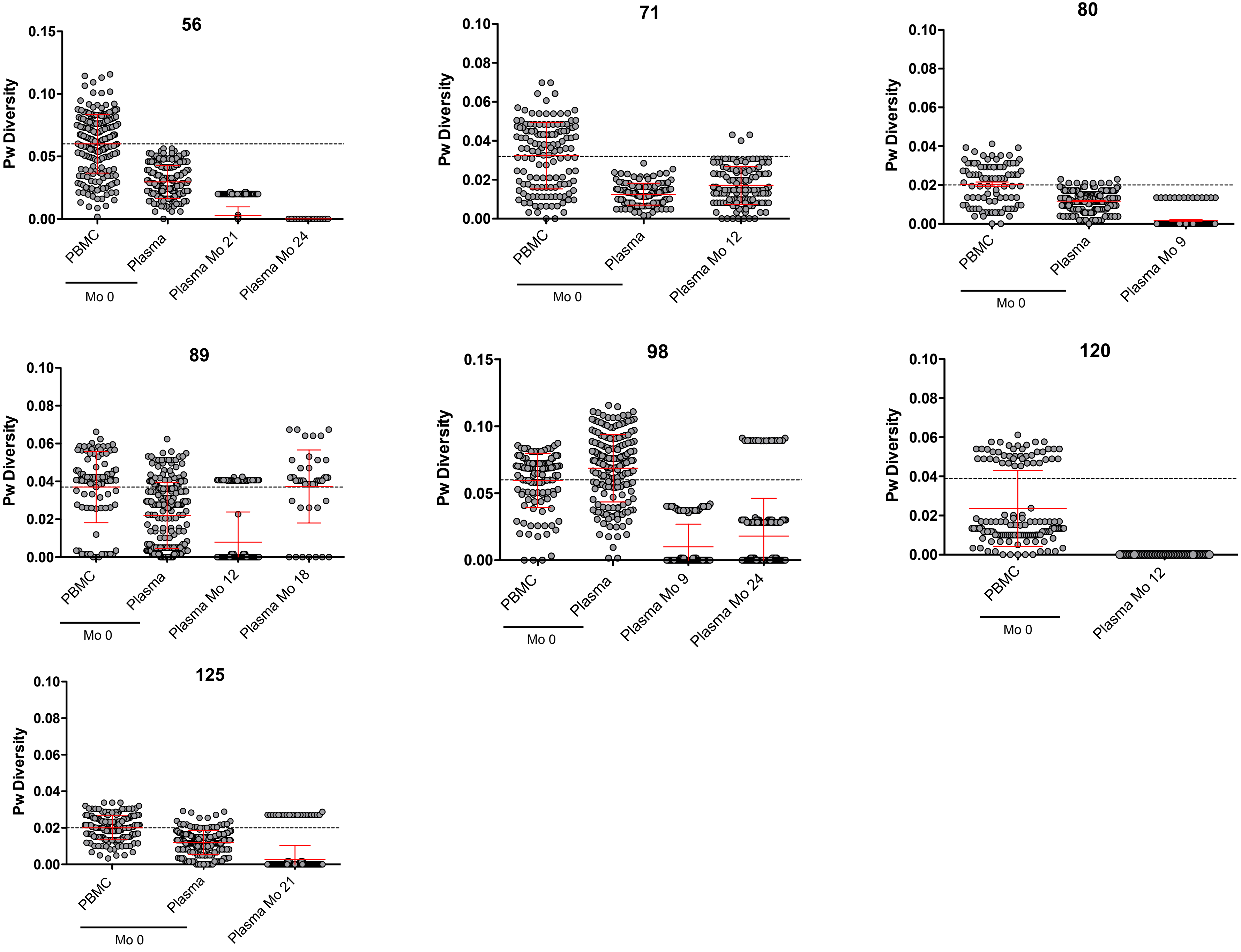
Bull et al., Supplemental Figure 1



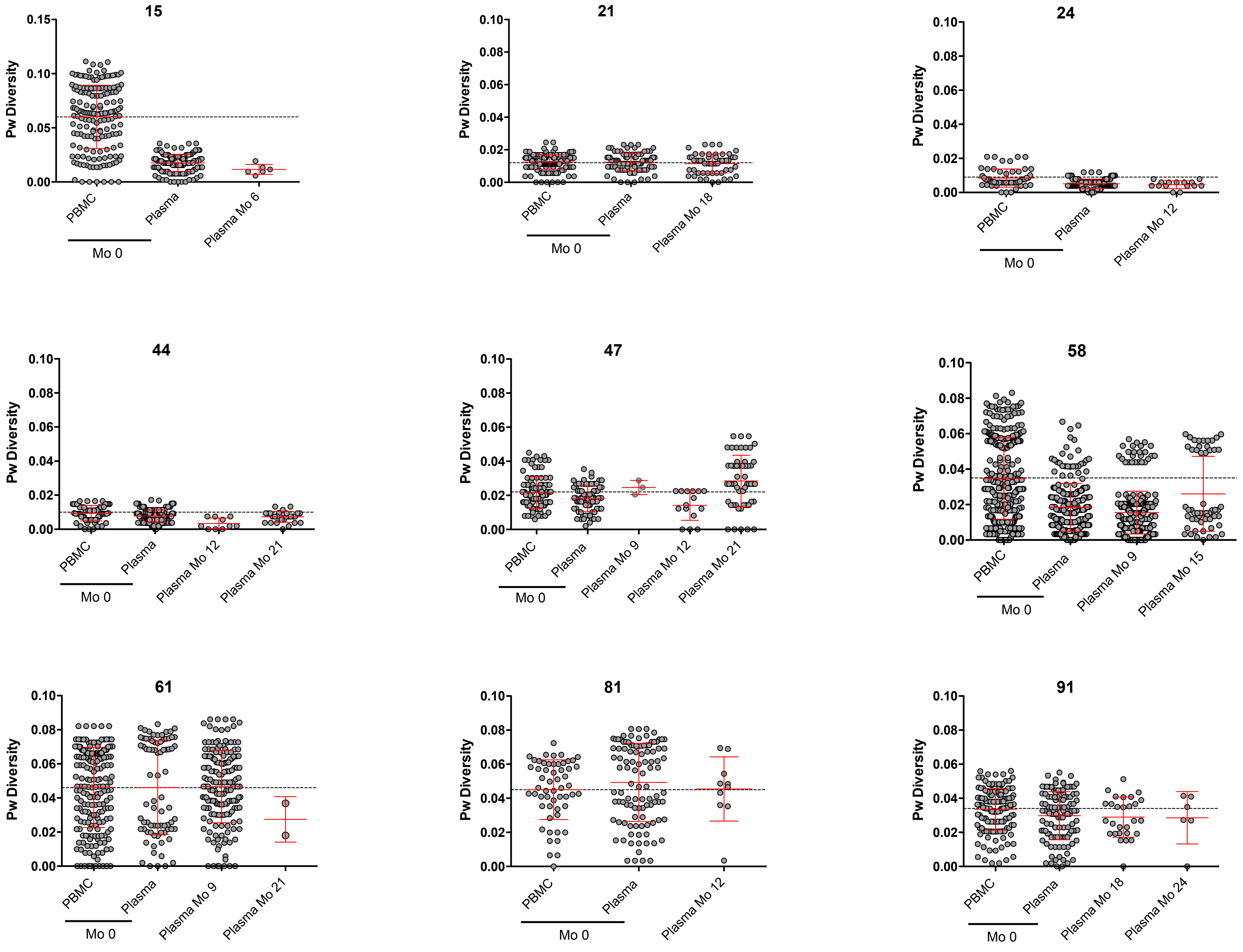
Bull et al. Supplemental Figure 2, Panel A



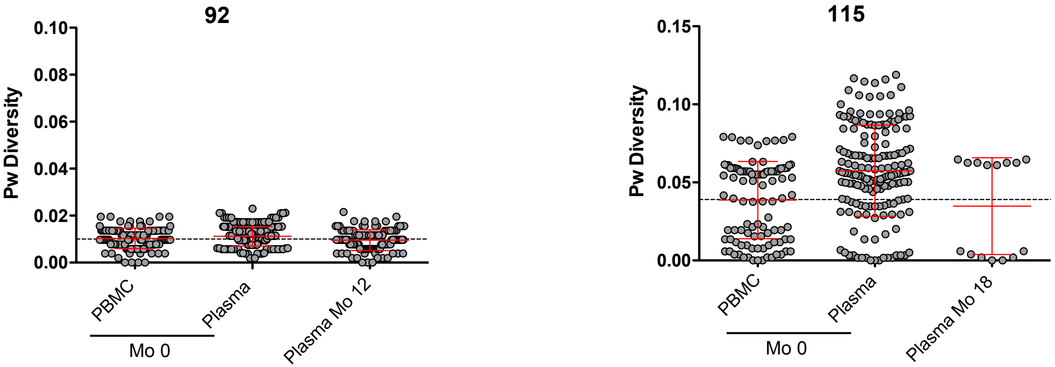
Bull et al. Supplemental Figure 2, Panel B



Bull et al. Supplemental Figure 2, Panel C



Bull et al. Supplemental Figure 2, Panel D



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).