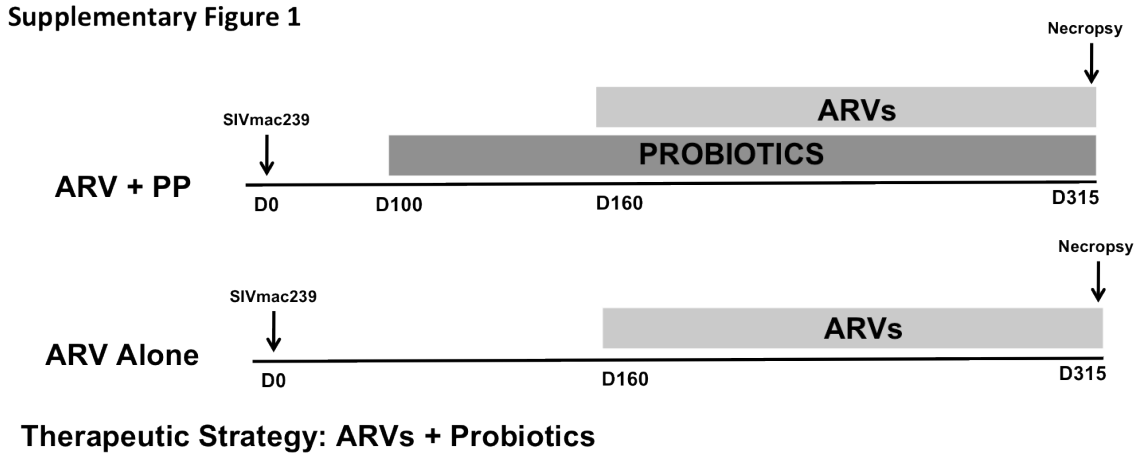
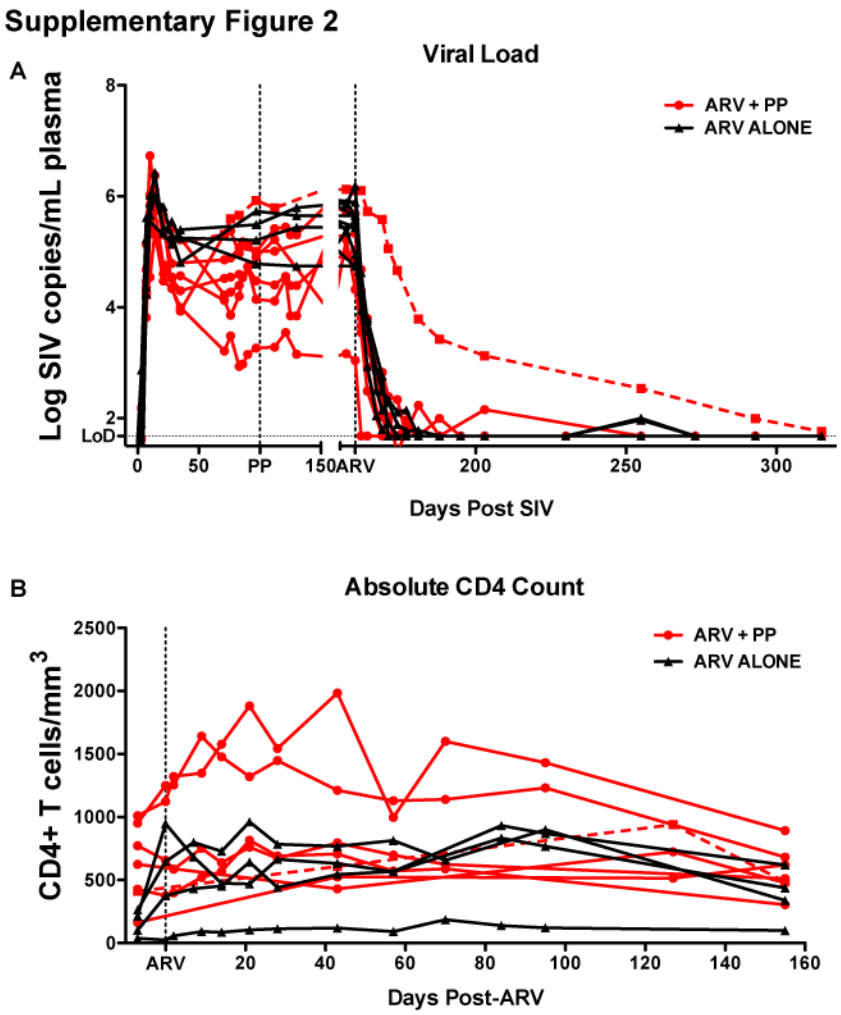
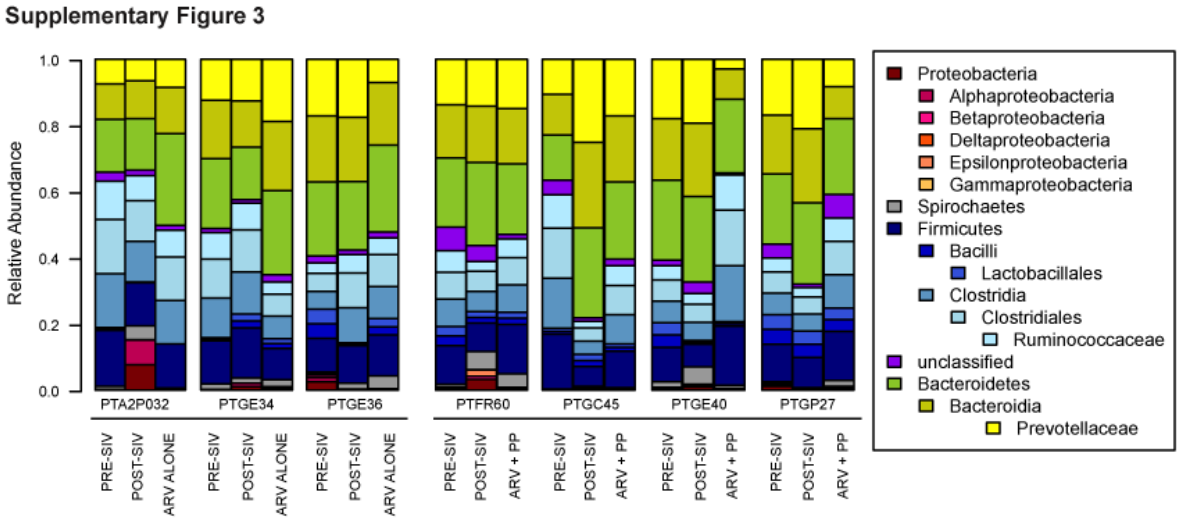
Supplementary Figures



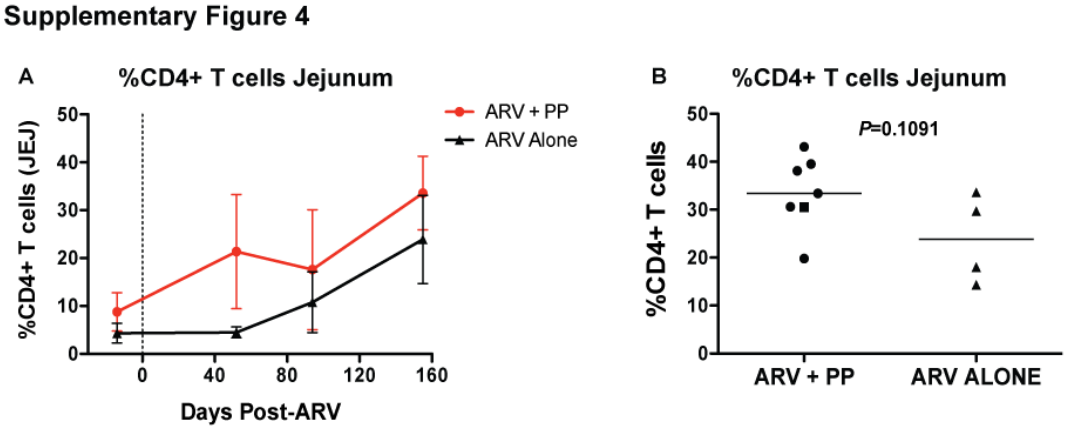
Supplementary Figure 1. Treatment schematic of SIV infection and ARV and PP therapies.



Supplementary Figure 2. SIV replication and $CD4^+$ T cell count. (**A**) Log SIVmac239 copies/mL plasma after SIV infection (day 0). Dotted vertical line at day 100 post-SIV represents initiation of probiotics/prebiotics alone in ARV+PP animals (ARV alone not treated). Dotted vertical line at day 155 post-SIV represents initiation of antiretroviral therapy in all animals. (**B**) Absolute $CD4^+$ T cell count/mm^3 blood. Frequency of $CD4^+$ T cells and lymphocyte complete blood cell count used for analysis. Dotted verticle line represents initiation of ARV therapy at 155 days post-SIV. (**A-B**) Solid red lines, animals treated with ARVs and PP with suppressed viremia PTM; dotted red line, slow responder PTM treated with ARVs and PP; Black lines, animals treated with ARVs alone.

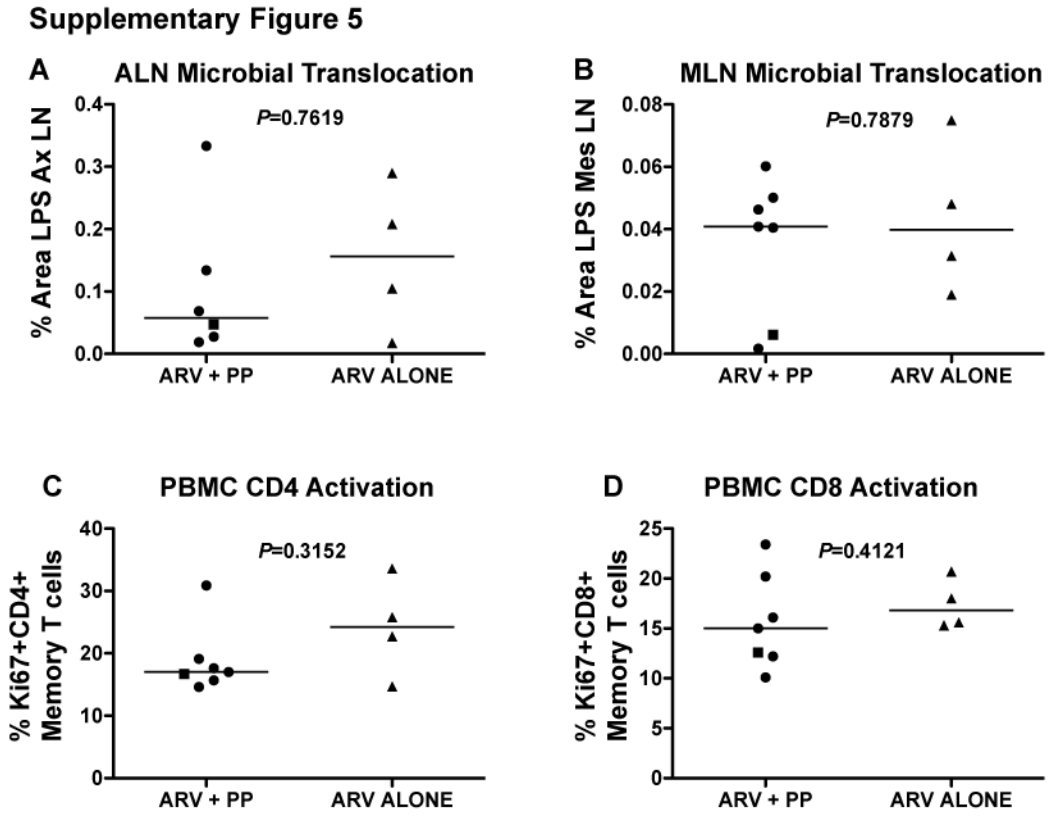


Supplementary Figure 3. Fecal microbiome analysis. Pyrosequencing of 16s rRNA was performed on fecal samples. (**a**) Ribosomal Database Project (RDP) classification was used for taxonomical assignments. Left, ARV alone PTM, right, ARV + PP PTM, separated left to right in order of: pre-infection, post-infection (D90), after treatment with 5 months ARVs alone or ARVs + PP. Animal names denoted under bars.



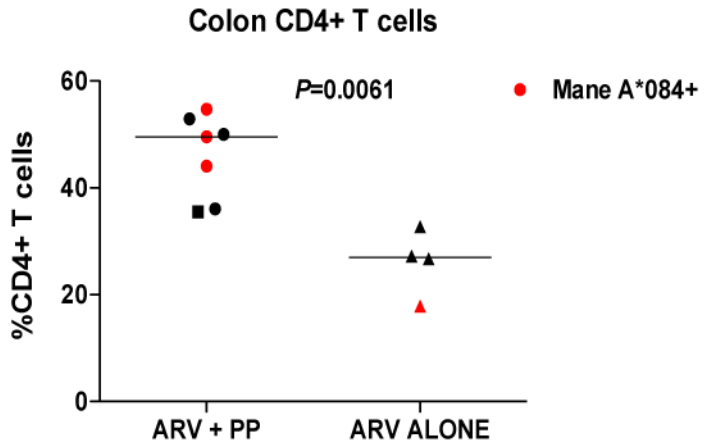
Supplementary Figure 4. $CD4^+$ T cells in jejunum and without Mane-A1*084+. (**A**) Longitudinal frequencies of $CD4^+$ T cells in jejunal biopsy samples. Red line, PTM treated with ARVs and probiotics (both suppressed and viremic animals), black line, PTM treated with ARV alone. Verticle dotted line, initiation of ARV at day 155 post-SIV infection. Points represent mean, vertical lines represent standard deviation. (**B**) Frequency of $CD4^+$ T cells from jejunum tissues at necropsy. Circles, ARVs and PP

treated PTM with suppressed viremia; square, ARVs and PP treated slow responder PTM; Triangles, PTMs treated with ARVs.



Supplementary Figure 5. Microbial translocation and immune activation. (**A-B**) Microbial translocation measured by the fraction of area stained for lipopolysaccharide (LPS) by immunohistochemistry in (**A**) axillary LN or (**B**) mesenteric LN taken at necropsy. (**C-D**) Peripheral immune activation measured by the fraction of (**C**) $CD4^+$ T cells or (**D**) $CD8^+$ T cells that expressed Ki67 in peripheral blood at necropsy. *P* value from Mann-Whitney T test. Circles, ARVs and PP treated PTM with suppressed viremia; square, ARVs and PP treated slow responder PTM; Triangles, PTMs treated with ARVs.

Supplementary Figure 6



Supplementary Figure 6. The fraction of CD4+ T cells in the colon, with PTM that expressed Mane-A1*084 in red. *P* values from Mann Whitney T test. Circles, ARVs and PP treated PTM with suppressed viremia; square, ARVs and PP treated slow responder PTM; Triangles, PTMs treated with ARVs.

Supplemental Methods

Microbiome Analysis

DNA from one gram of feces (collected and immediately stored at -80oC) was obtained using the QIAmp protocol for larger volumes of stool. This protocol was modified as follows: We performed initial lysis of bacterial cells for 5 minutes at 95oC (rather than 70oC) as recommended for gram negative bacteria and incubated Proteinase K for 20 minutes at 70oC (rather than 10 minutes). For quantitative analysis of 16S rDNA, real time PCR was performed using primers BacF (5'-CGGCAACGAGCGCAACCC-3') and BacR (5'-CCATTGTAGCACGTGTGTAGCC-3') (**2**). For sequencing of 16S rDNA amplicon libraries were prepared from sample DNA using Accuprime High Fidelity Taq polymerase (Invitrogen) and universal primers flanking variable regions V1 (primer 27F; 5'-AGAGTTTGATCCTGGCTCAG-3') and V3 (primer 534R; 5' ATTACCGCGGCTGCTGG-3'). For each sample, the universal primers were tagged with unique sequences ("barcodes") to allow for multiplexing/demultiplexing (**3**) PCR products were then purified using the Agencourt Ampure XP Kit (Beckman Counter Genomics) and quantitated using the QuantIT dsDNA High-Sensitivity Assay Kit (Invitrogen). Approximately equivalent amounts of each PCR product were then pooled and purified with a Qiagen minElute column (Qiagen) into 30 µl TE buffer prior to sequencing at the NIH Intramural Sequencing Center. Amplicon libraries were sequenced on a 454 FLX instrument using Titanium chemistry. Flowgrams were processed using the 454 Basecalling pipeline (v2.5.3). Sequence pre-processing, alignment and chimera removal: mothur (version 1.25.0) (*4*) was used for all 16S rRNA gene sequence analysis steps. Prior to analysis, sequences were trimmed of low quality ends and filtered to retain sequences with a minimum length of 200 bp. After alignment to a bacterial reference alignment (SILVA), chimeras were removed using the chimera slayer implementation in the mothur package. Taxonomic classification of reads was done using the RDP Classifier included in mothur.