

Supplemental Figures:

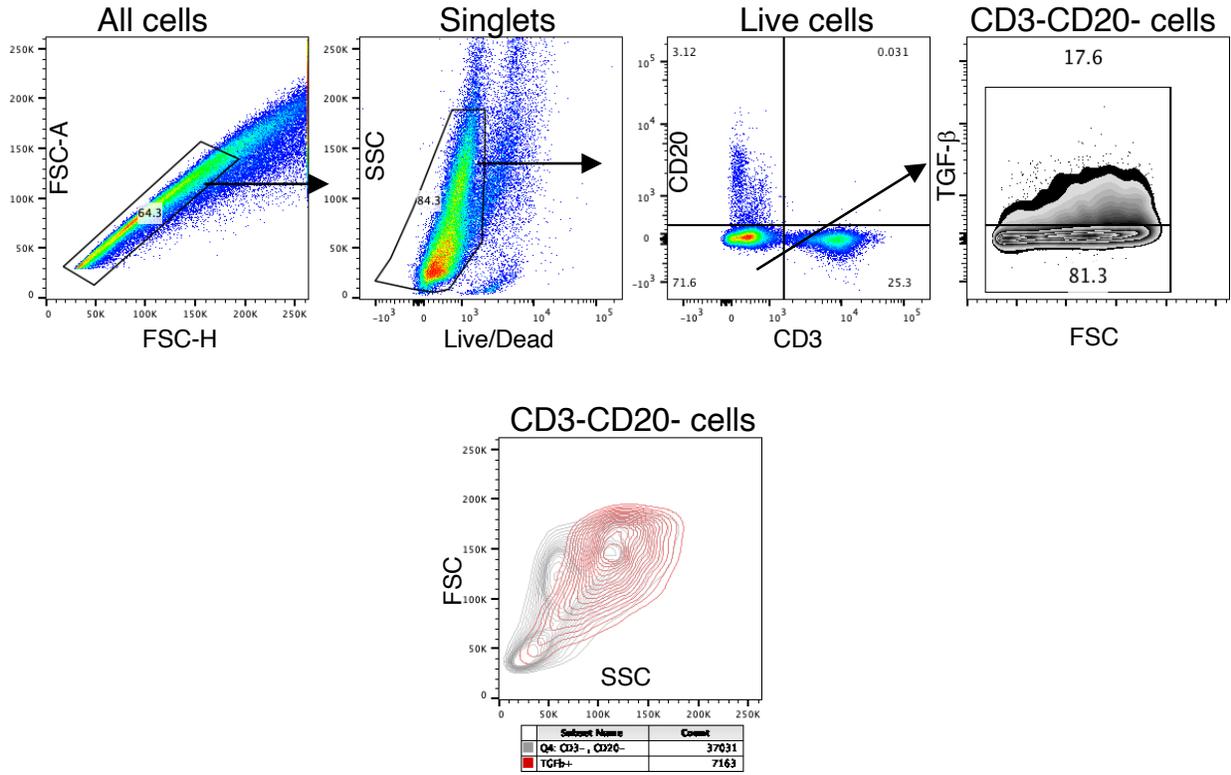
Supplemental Figure S1. Intracellular cytokine flow cytometry for TGF- β responses from a representative SIV infected RhM. Cells were gated first on singlets, live cells and then gated based as CD3⁺, CD20⁺ and CD3⁻CD20⁻ cells based on their surface CD3 and CD20 expression. Cell subsets were further gated as TGF- β ⁺ and TGF- β ⁻ cells based on the production of TGF- β as shown in the box. The frequency in each box and in quadrant represents the frequency of that subpopulation. The bottom contour plot shows the overlay distribution of TGF- β ⁺ cells gated from CD3⁻CD20⁻ cell population. Interestingly, the majority of the cells displayed high forward and side scatter, suggesting that TGF- β ⁺ cells are bigger in size and/or complexity or granularity like macrophages, NKs and/or dendritic cells.

Supplemental Figure S2. Mean values of the respective population positive of TGF- β ⁺ from CD3⁻CD20⁻ cells in SIV acutely infected macaques (21 dpi, n=3). Cells were gated first on singlets, live cells and then gated based as CD3⁺, CD20⁺ and CD3⁻CD20⁻ cells based on their surface CD3 and CD20 expression. The TGF- β ⁺ cells from CD3⁻CD20⁻ cells were further stained for different markers (NKG2A, CD163, CD14, CD45, CD68, CD8 and IL-10) and analyzed. Note, the majority of the TGF- β ⁺ cells from CD3⁻CD20⁻ cells were CD68 positive (mean \pm the standard errors, 96.3 ± 1.5).

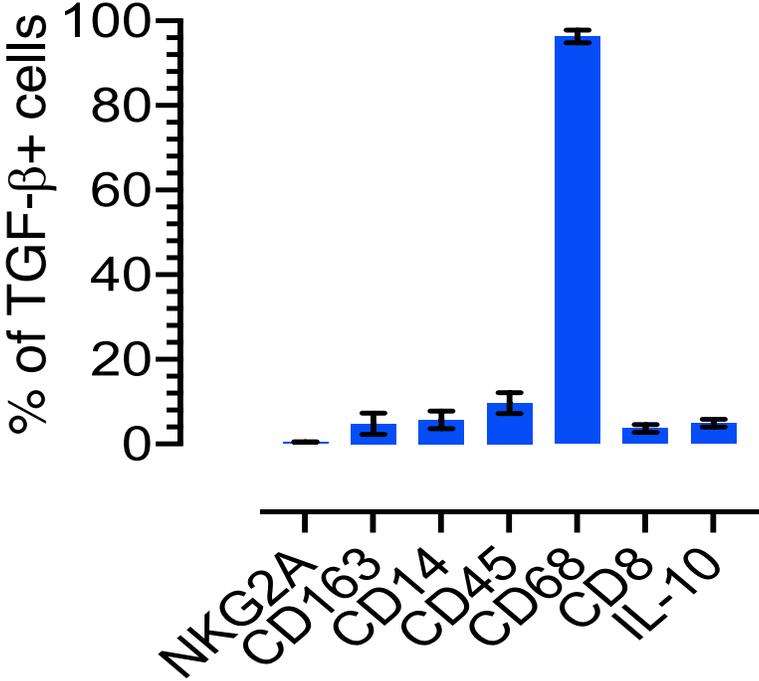
Supplemental Figure S3. Representative expression of TGF- β RII in SIV-uninfected (FK25), control as well as acute (CF65, 21 dpi), and chronic (EB09, 250 dpi) SIV infected RhMs by multi-label confocal microscopy. The labels in each image are indicated on the Y-axis. Epithelial cells (cytokeratin⁺) cells were positive for TGF- β RII as represented by yellow arrows. Of note, we did not see any upregulation of TGF- β RII expression in epithelial cells among SIV-infected and uninfected control RhMs.

Supplemental Figure S4. Relative fold changes (mean \pm the standard errors) of TGF- β , SMAD3, and SMAD7 gene expression are shown in jejunum tissues from female RhMs (n=3). All samples were normalized against 18S rRNA expression, and fold changes are relative to mean expression levels in male RhMs (n=3). The values above the bar represent mean fold change value for that specific gene.

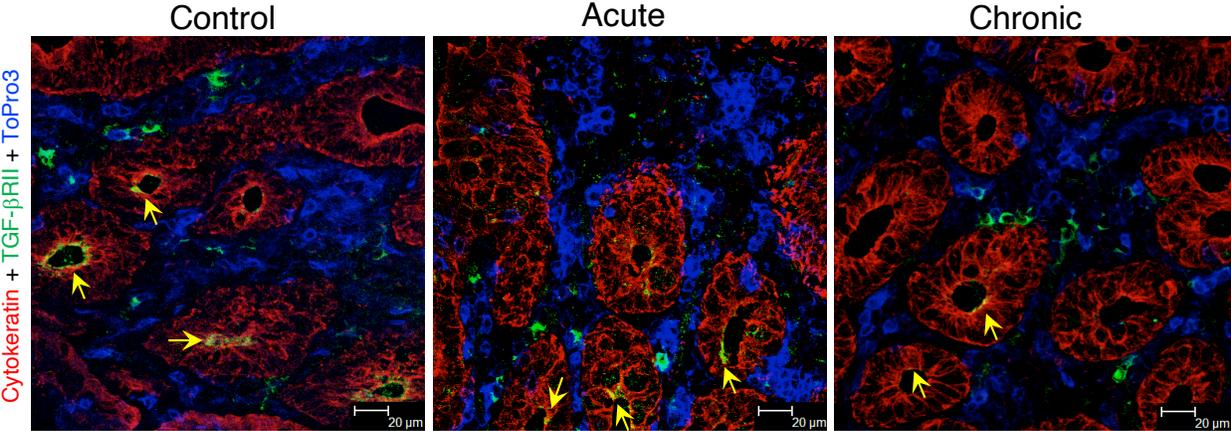
Supplemental Figure S1



Supplemental Figure S2



Supplemental Figure S3



Supplemental Figure S4

