**Supplemental figures**

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**Figure S1: Cloning and validation of the HIV-1 molecular clone pBR43IeG-BaL (BaL-GFP). A)** The cloning strategy to generate the pBR43IeG-BaL HIV-1 molecular clone used in this study. The vector, pBR43IeG, is a pNL4-3-based, full-length HIV-1 molecular clone which expresses GFP from an IRES inserted downstream of the Nef ORF. The insert, p81A-4, is also a full-length HIV-1 molecular clone that expresses the V1-V3 loops of the BaL envelope. In order to generate the pBR43IeG plasmid, the *AgeI-BsaBI* fragment of pBR43IeG was replaced with the *AgeI-BsaBI* fragment of p81A-4. **B)** The resulting plasmid map of pBR43IeG is shown. **C)**Predicted HindIII diagnostic digests of pBR43IeG-BaL (lane 1) and pNL4-3 WT (lane 2) simulated relative to a 1kb Plus DNA ladder on a TAE gel. Figure created using SnapGene.

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**Figure S2**: **Characteristics of cell isolation and infection.** Ficoll density purification of PBMCs from whole blood collected on the day of tissue resection was used to isolate CD4+ T-cells using positive selection. CD4-depleted PBMCs containing monocytes were also reserved. **A)** Isolate purity was determined by live/dead, and antibody staining of ~1x105 cells from each population with Zombie Yellow, CD3+, and CD4+ antibodies. Data shown indicate the % live cells that are CD3+ and CD4+ in each population as determined by flow cytometry. Data shown are means ± SDs of independent cases (N=13). **B)** Infected CD4+ T-cells and MDMs were collected on DIV 5, Day 2 post-infection and ~1x105 cells were reserved to determine the percent infected producer cells by live/dead staining and GFP fluorescence as determined by flow cytometry. Data shown are means ± SDs of independent cases (T-cells, N=9; MDMs, N=10). **C)** On DIV 5, Day 2 post-infection, infected CD4+ T-cells or MDMs were used to inoculate slices. The number of CD4+ T-cells or MDMs added per slice are indicated. Data shown are means and SDs of independent cases (T-cells, N=9; MDMs, N=10). **D)** The number of infected cells added per slice were calculated by the percent GFP+ cells (**B**) multiplied by the # of cells added per slice (**C**) (T-cells,N=9 and MDMs,N=10). Individual data points per case indicated by unique symbols. Data analyzed by unpaired, two-tailed Student’s t-test; \*\*\*\* p<0.0001.