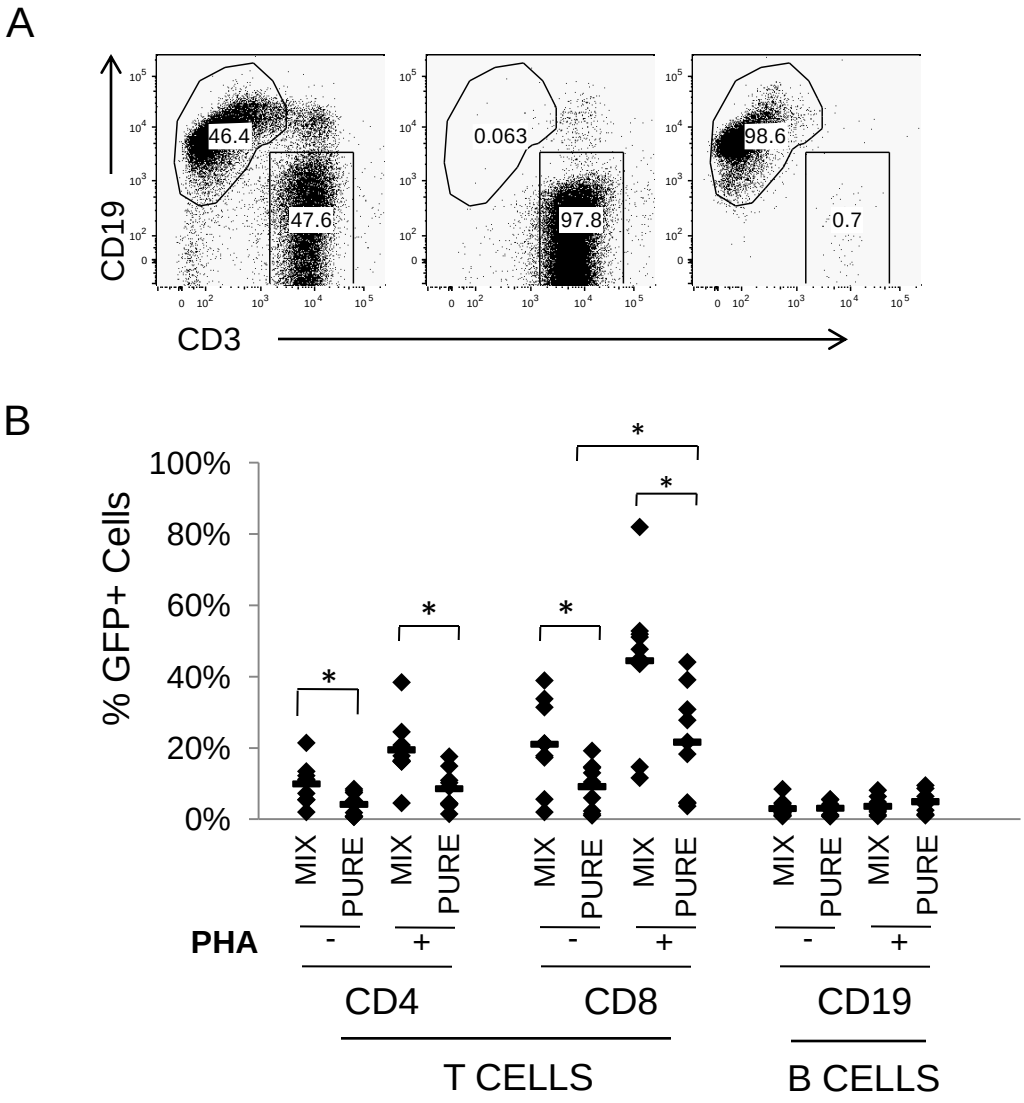
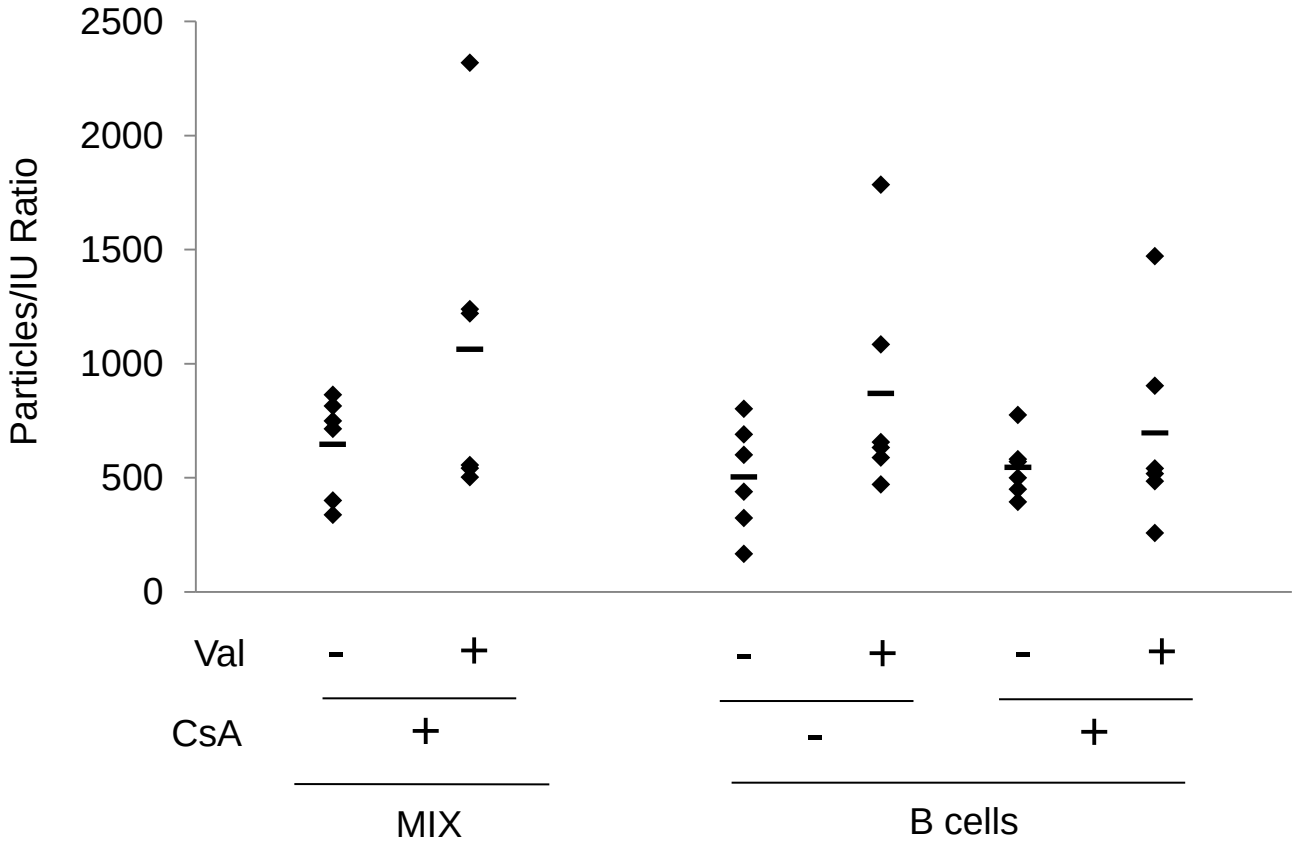
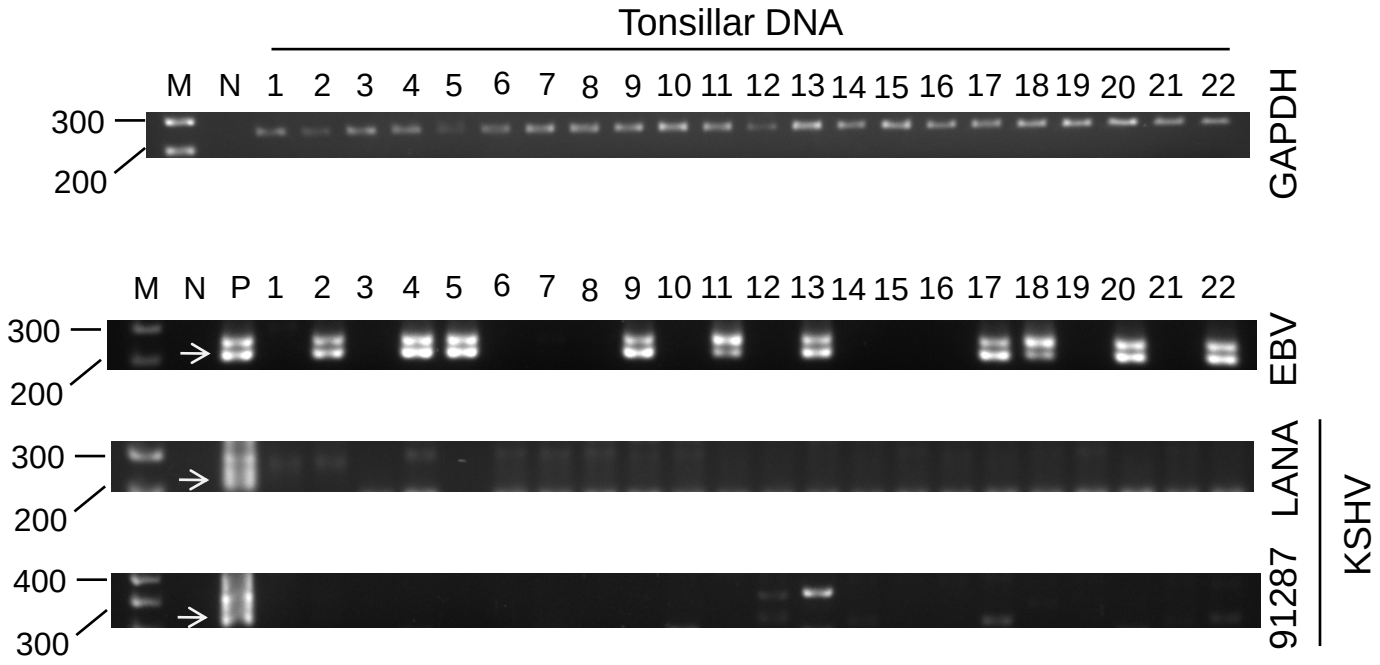


Supplementary Figure 1. Ex vivo KSHV infection in tonsillar cells.
(A) CD3+ T cells or CD19+ B cells were purified by magnetic beads. The purity of each cell preparation was examined by FACS. For better purity of T cells, untouched T cells were purified twice by negative selection while B cells were purified once. Only those cell preparations that demonstrated purity of each cell type higher than 98% were used for KSHV infection studies in (B). One representative FACS analysis on tonsillar cells is shown.
(B) KSHV infectivity, presented as the percent GFP+ cells in unfractionated (designated as "mix") or fractionated (designated as "pure") tonsillar B or T cells, was analyzed by flow cytometry. Where indicated, cells were activated by PHA (10 μg/ml) for 6 hr prior to virus infection. rKSHV.219 was infected in the absence of polybrene at MOI 1 for 2 days. CD4+ or CD8+ T cells and CD19+ B cells were gated for GFP expression in fractionated and unfractionated tonsillar cells. Each dot represents rKSHV.219 infectivity of each individual tonsillar cells. The mean of data from 7 different tonsils is indicated by the horizontal bar. *, $p<0.05$ by Student *t*-test.



Supplemental Figure 2. Infectivity of viruses is comparable from unfractionated (mixed) and B cells cultures in response to various induction stimuli. Viral genome was extracted from culture supernatants from cells (the same cells used in Figure 1) after Dnase I treatment (for details, see Methods). The number of KSHV episomes in a given sample was determined by real-time PCR using probe targeting viral poly-adenylated nuclear (PAN) RNA promoter. The number of particles was divided by infectious unite (IU) to calculate the ratio (Y axis). Horizontal bar indicates average of each experimental group.



Supplemental Figure 3. KSHV DNA was not detected by nested PCR in 22 tonsillar samples while ca. 45% of samples displayed EBV infection. To detect KSHV viral DNA (vDNA), total DNA was extracted from 22 tonsils and as a positive control, total DNA was extracted from EBV+ Akata cells or stable SLK cells, harboring rKSHV.219. 3 different sets of nested PCR primers, targeting 2 different regions of KSHV vDNA as indicated, were employed for nested PCR (for details, see Methods) while EBV nested PCR primers target LMP-1 gene. To analyze the quality of DNA, amplification of human GAPDH (regular PCR, 25 cycles) and EBV vDNA (nested PCR) was performed on the same samples. N and P denotes negative control (water) and postive control, respectively. Size makers on the left lane are indicated in base pairs (bp). The expected band of 2nd PCR reaction is indicated by arrow. Note that 2 different regions of KSHV were amplified and the number on the right denotes the first base of the first PCR target in the viral genome.