



Figure S1. Comparison of the reads mapping to the KSHV genome in the RNA-seq libraries from different infected cell types. RNA reads from the RNA-seq libraries prepared from KSHV-infected BCBL-1 cells, three independent replicate primary KSHV infections of TIME (K1-3), LEC (K1-3) and BEC (K1-3) cell cultures and a single primary infection of VERO cells were mapped to the KSHV reference genome (NC_009333) (A) and compared to the number of total RNA reads (B). Notably, the number of KSHV mapped reads from the TIME-K1 infection was 10 fold less than the other TIME cell infections, indicating a significant difference in the infection outcome. The KSHV reads from the TIME-K1 infection were subsequently analyzed separate from the TIME-K2, -K3 infections to characterize this difference.