

S9 Table: Quantitation of reads spanning splice junctions in the latency region¹

Spliced intron ²	LEC-K1-3	BEC-K1-3	TIME-K2,3	TIME-K1	VERO-K	BCBL(K)
5'ORF72-DR6 (a)	1179±29%	1094±10%	612±8%	496	49	71
5'ORF73-5'ORF72 (b)	7±71%	6±82%	7±100%	0	0	0
5'ORF73-DR6 (c)	0	0	0	0	0	0
5'ORF72-5'ORF71 (d)	0	0	0	0	0	0
5'ORF73-ORF73 (long) (e)	2±41%	6±82%	4±100%	0	0	0
5'ORF73-ORF73 (short) (f)	0	1±141%	1±100%	0	0	0
DR6-ORF67A ³	98±19%	96±7%	44±20%	0	13	0
DR6-ORF66 ³	86±32%	94±8%	28±100%	0	0	4
K14-classical ³	19±16%	28±6%	30±22%	0	11	0
K15-7 intron average ³	187±15%	86±6%	108±1%	96	0	0

¹RNA-seq reads spanning splice junctions from triplicate independent infections of LEC, BEC, and TIME endothelial cells and single infections of Vero and BCBL-1 cells were quantitated using TopHat2. Average and standard deviation were determined for replicate infections.

²introns shown in Fig. 10C

³not shown in Fig. 10C. Transcripts containing the DR6-ORF67A and DR6-ORF66 splices would have alternate 3' ends and secondary distal ORFs. The K14 classical splice junction spans the intron between 12,9369 and 12,9516 bp, as indicated in the KSHV RefSeq NC_009333. The reads spanning the splice junctions in K15 were determined as an average of the split reads across all 7 K15 introns.