

**S2 Table: Comparison of total and primary transcripts encoding ORFs in the PAN region<sup>1</sup>**

UCDS Feature <sup>2</sup>	LEC-K1-3 (TPM) <sup>3</sup>	BEC-K1-3 (TPM)	TIME-K2,K3 (TPM)	TIME-K1 (TPM)	BCBL(K) (TPM)	VERO-K (TPM)
K3	4331±5%	4220±10%	3446±0%	6100	5094	10844
ORF70	3407±6%	3261±13%	2751±0%	5084	2582	8239
K4	20088±4%	22877±2%	16272±1%	20912	26916	63647
K4.1 <sup>4</sup>	555±78% <sup>5</sup>	781±44%	877±34%	1098	15	1483
K4.2A <sup>6</sup>	6372±10%	7896±12%	6922±16%	3128	1189	2534
K4.2 <sup>7</sup>	149±16%	163±6%	102±22%	169	88	271
LIR1	117±32%	87±13%	59±28%	114	76	73
DR1	3032±40%	1890±16%	837±8%	722	6053	6150
DR2	1229±38%	737±10%	396±5%	190	4463	2435
OLAP	3108±35%	1884±8%	884±7%	608	14789	7759
K5	9145±21%	6549±13%	4463±11%	10723	7833	11963
K6	4537±23%	3848±10%	2271±4%	3322	13459	7630
K7 <sup>8</sup>	2567±26%	1968±7%	1075±2%	622	2798	5694
PAN	429503±5%	435022±3%	465811±1%	327965	650560	540860
ORF16	586±13%	549±9%	506±10%	310	471	732
ORF17.5 <sup>9</sup>	11554±2%	12777±5%	12659±2%	6274	7724	6473

<sup>1</sup>Primary RNA transcripts were quantitated using HTSEQ from RNA isolated from triplicate Independent infections of LEC, BEC and TIME endothelial cells and single infections of VERO and BCBL-1 cells, as described in Table 3. The initial TIME cell infection (TIME-K1) is analyzed separately, as discussed in the text.

<sup>2</sup>UCDS features used by HTSEQ to quantitate RNAseq reads; see Table 3

<sup>3</sup>TPM=transcripts per million mapped KSHV reads

<sup>4</sup>K4.1 primary transcript quantitation= K4.1 UCDS TPM (total) - K4.2A UCDS TPM (total) (see Table 3)

<sup>5</sup>TPM values with standard deviations above 15% are highlighted in yellow

<sup>6</sup>K4.2A = C-terminal region of K4.2 ORF common to short K4.2A and long K4.2 transcripts;

K4.2A primary transcript quantitation=K4.2A UCDS TPM (total) – K4.2 UCDS TPM (total) (see Table 3)

<sup>7</sup>K4.2 = N-terminal region of K4.2 ORF only in long K4.2 transcript

<sup>8</sup>The K7 UCDS feature corresponds to the 5' untranslated region of the K7 transcript upstream of the PAN RNA.

<sup>9</sup>ORF17.5 = C-terminal region of ORF17 common to short ORF17.5 and long ORF17 transcripts;

ORF17.5 primary transcript quantitation = ORF17.5 UCDS TPM (total) - ORF17 UCDS TPM (total)(see Table 3)