



Figure S7. Quantitation of reads mapping to the primary transcripts of ORFs 58-62. The total number of reads mapping to the UCDS feature for each ORF were quantitated by HTSEQ and normalized (TPM) with the average and standard deviation for the replicate infections (open bars). The number of reads mapping only to the primary transcript, in which the designated ORF is 5' proximal were quantitated by subtraction of the number of reads attributed to transcripts in which the designated ORF is distal in a polycistronic transcript (black bars; see Table 3 and Table S7). Negative values for ORF58 indicate the absence of an ORF58 primary transcript and the presence of an uncharacterized ORF59 monocistronic transcript, which terminates before ORF58. A) BEC-K1-3; B) LEC-K1-3; C) TIME-K2,3; D) VERO-K; E) BCBL(K). The proposed pattern of transcription is indicated at the bottom.