Supplementary Material

Table S1. List of primers used in RT-qPCR experiments.

Use	Primers	Sequences	Size (pb)	Reference
Housekeeping	GAPDH-Fw	5′-AGGTCGGAGTCAACGGATTT-3′	112	[1]
	GAPDH-Rv	5′-TAGTTGAGGTCAATGAAGGG-3′	112	
ER stress	BIP-Fw	5′-ACCGCTGAGGCTTATTGGG-3′	147	[1]
	BIP-Rv	5′-TGCCGTAGGCTCGTTGATG-3′	147	
PERK	ATF4-Fw	5′-CCAACAACAGCAAGGAGGAT-3′	143	[2]
	ATF4-Rv	5′-GTGTCATCCAACGTGGTCAG-3′	143	
ATF6	ATF6-Fw	5′-CGAATAGCCCAGTGAA-3′	180	[3]
	ATF6-Rv	5′-ATCTCGCCTCTAACCC-3′	180	
MAPK	p38α-Fw	5′-GCCCAAGCCCTTGCACAT-3′	156	[4]
	p38α-Rv	5′-TGGTGGCACAAAGCTGATGAC-3′	156	
Apoptosis	Casp12-Fw	5′-CCAGGAACGTTCTAGATGGCA-3′	113	This study
	Casp12-Rv	5′-TCCAGCGTTGTTCACCATGA-3′	113	
Apoptosis	CHOP-Fw	5′-ACCAAGGGAGAACCAGGAAACG-3′	201	[5]
	CHOP-Rv	5′-TCACCATTCGGTCAATCAGAGC-3′	201	
EAV Bucyrus	N-Fw	5′- GGGGATCCAGCTTGTCGATGGCGTC-3′	333	[6]
	N-Rv	5′- TTGAGCTCAATATCCACGTCTTACGG-3	333	

The Caspase-12 primers were designed using the Primer-BLAST tool of the *National Center of Biotechnology Information* database, based on the predicted *Chlorocebus sabaeus* caspase-12 mRNA sequence (accession number XM_038005267.1).

Table S2. List of primers used in RT-PCR experiments for the detection of both XBP1u/XBP1s form.

Use	Primers	Sequences	Size (pb)	Reference
IRE1α	XBP1-Fw	5′- CCTTGTAGTTGAGAACCAGG -3′	440/414	[1]
	XBP1-Rv	5′- GGGGCTTGGTATATATGTGG -3′	440/414	

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Supplementary Figure S1

4μ8c influence in the replicative EAV cycle

In order to examine the impact of IRE1α pathway suppression on the EAV replication process, a time-addition experiment was conducted in which the inhibitor was added at different times point following the infection. Following 8 hpi, the cells were harvested, and reverse transcription–quantitative PCR (RT-qPCR) was performed using primers specific to NSP1 and N genes (Figure S1).

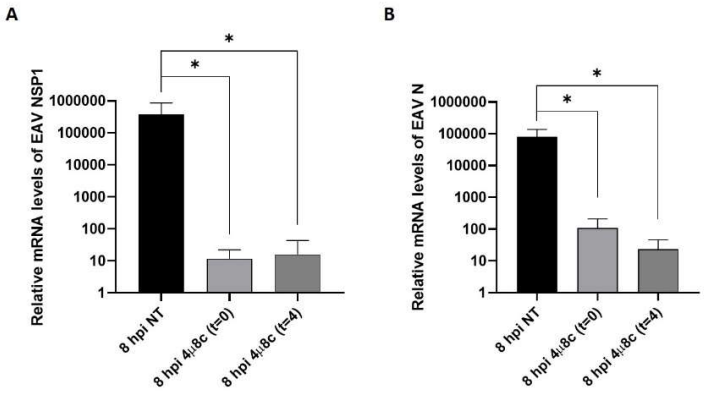


Figure S1. Quantification of specific viral EAV transcript after the inhibition of the IRE1α pathway. Vero cells were treated with 50 μM of IRE1α inhibitor, 4μ8c. The inhibitor was added prior to the infection experiment, at time equal zero (t=0) or 4 hours post-infection, at time equal 4 (t=4). GAPDH gene and the MOCK infected wells were used to normalized and relativized the values, respectively. **A.** Levels of EAV NSP1 transcript at different conditions. The primers were as follows: PFw: 5′-TATAAGCTTGCGACCATGGCAACCTTCTCCG-3′ and PRv: 5′-TATACTCGAGGCCGTAGTTGCCAGCAGG-3′. **B.** Levels of EAV N transcript at different conditions. The primers used are described in Table 1 of the Supplementary Materials. The bars represent the mean ± SD after three independent experiments and the statistical analysis was obtained after comparation with the not treated (NT) group. *$p < 0,05$.