

Supplementary figure legends

Figure S1. Functional domains predicted for the coding regions of the putative *Guachaca virus* (GUAV). (a) ORF1: The Methyltransferase, Peptidase, Helicase, and RNA-dependent RNA Polymerase domains were predicted from the primary sequence. (b) Coat: A signal cleave region was predicted near the amino-terminal region of the protein, followed by several antigenic domains through the soluble portion of the protein.

Figure S2. Growth curve of the putative GUAV in C6/36 cells through RT-qPCR. CT values \pm standard deviations were estimated for triplicates every experimental point during the time course.

Figure S3. Growth curve of the putative GUAV in human cells through RT-qPCR. CT values \pm standard deviations were estimated for every experimental point during the time course of 5 to 13 days post-infection in HEK 293, HeLa, A549, and U937 cells. Undetermined CT values representing absence of specific genome detection were arbitrarily assigned a value of zero.