

Supplementary Figure S4. Validation of RNASeq results by RT-qPCR representing fold change of *cul3*, *psmb5*, *keap1*, *sec13*, *ikbkb*, *rab7* and *traf6* genes in the transcriptomic analysis of VHSV-exposed RBCs at 4 and 72 hpe. Gene expression values were calculated with normalization to unexposed RBCs. Data represent the mean \pm SD (n=4). A Mann-Whitney test was used to test statistical significances between VHSV-exposed and unexposed RBCs.

