



**Supplementary Figure S1.** Correlation between RNA sequencing and qRT-PCR gene expression data. The top differentially expressed transcripts found in RNA sequencing analysis (both up- and down-regulated genes) were selected. Tubulin  $\beta$  gene was used as a reference gene for the qRT-PCR expression analysis and the presented fold change was calculated relative to the expression at 1hpi. The correlation between the two data sets is presented as linear regression. The  $R^2$  value was calculated to be 0.9162 and the Pearson correlation coefficient 0.9572. P value <0.0001.