

List of Supplemental Materials

Tables S1-S20.

- Table S1. Summary of Illumina RNA-seq reads generated from the AcMNPV-infected Tnms42 cells and the number of reads used for de novo assembly.
- Table S2. Annotation of *T. ni* unigenes
- Table S3. Read counts of *T. ni* unigenes at various times post infection
- Table S4. Average RPKM values of *T. ni* unigenes at various times post infection (≥ 5 RPKM are shown)
- Table S5. GO term results: Numbers of unigenes with ≥ 10 fold up-regulation at various times post infection (Biological Process)
- Table S6. GO term results: Numbers of unigenes with ≥ -10 fold down-regulation at various times post infection (Biological Process)
- Table S7. Unigenes >2 fold up- or down- regulated in response to infection at 6 h p.i.
- Table S8. Unigene clusters generated from normalized RPKM values.
- Tables S9-S20. Analysis of functional gene groups associated with specific pathways and processes. (S9, Endocytosis; S10, ESCRT and Vacuolar Protein Sorting; S11, PI3K; S12, MAP kinase; S13, Nuclear pore complex; S14, Transcript export; S15, small RNA; S16, apoptosis and stress; S17, Reactive oxygen species; S18, NF kappa B and I kappa B; S19, Immunity; S20, Histone deacetylase and Sirtuins).

Figures S1-S10.

Transcript profiles of *T. ni* homologs associated with various cellular pathways and gene groups. Gene names are those of either *D. melanogaster*, *B. mori*, *S. frugiperda*, *S. exigua*, *S. cerevisiae*, or *Homo sapiens*. The corresponding gene names are listed with *T. ni* unigene numbers and the calculated RPKM data for each unigene at all time points post infection in Tables S9-S20. Note: Some genes are not shown on graphs S1-S10 as RPKM values were below the cutoff threshold of 5. For example, although we identified homologs of Dicer 1 (UN008847) and Pasha (UN010331) (see Table S15), RPKM values were below 5 and data were therefore not included on the graph Fig. S6. Because caspase gene names are not consistent between species, the caspase gene names (Fig. S7A) also indicate the species from which the homolog was identified, in parenthesis.