

Supplemental table and figure legends

Table S1. Primers used in qRT-PCR analysis.

Table S2. Pearson pairwise correlation between biological replicates.

Table S3. A list of 76 up-regulated proteins in baculovirus infected larval fat body.

Table S4. A list of 373 down-regulated proteins in baculovirus infected larval fat body.

Table S5. A whole list of proteins identified in *H. armigera* fat body proteomics analysis.

Fig. S1. Survival and morphological changes in cotton bollworm larvae infected by baculovirus. (A) Survival curves of cotton bollworm larvae after *per os* infection. Survival of larvae in the two groups was monitored until pupation or death. The survival curves of normal and infected larvae were significantly different, as determined by the Wilcoxon signed-rank test. P-values were reported. Survival analysis confirmed the virulence and lethality of the HearNPV strain employed in this study. (B) The photographs of larvae from the control and infected groups at four time points. Compared with the control group, the larvae in the infected group were significantly smaller in body size starting at 24 hpi.

Fig. S2. Schematic overview of transcriptomic data analysis. The fat body samples were collected from *H. armigera* larvae at 4 time points after infection by baculovirus. Sample preparation and data analysis were performed as described in the Experimental Procedures.

Fig. S3. Summary of *de novo* assembly by Trinity. (A) The summary of the transcriptome assembly. (B) Length distribution of the assembled transcript sequences. (C) Histogram representing the species distribution of the top BLAST hits.

Fig. S4. A global overview of the gene expression levels among all of the libraries and volcano plots for DEGs at four time points post infection. (A) PCA analysis of gene expression across the libraries at the four time points evaluated. The first three components, PC1, PC2 and PC3, define the x-, y- and z-axes of the three-dimensional space, respectively, so the distance between two points reflects the variance in gene expression between them. PC1, PC2 and PC3 accounted for 87.11%, 3.88% and 2.40%, respectively, of the contribution to the variance. The three-dimensional scatter plot of

the PCA of host genes is shown. **(B)** Volcano plots for DEGs between the mock and infected groups at four time points. As observed in the figure, each gene was marked as a dot; those genes that were significantly up-regulated were highlighted in red, the down-regulated genes were highlighted in green, and the non-significant genes were labeled as blue dots. In the figure, the gray lines indicate the marginal lines separating DEGs from non-DEGs, with the horizontal lines denoting the p value threshold ($p \leq 0.05$) and the vertical lines the fold change cutoff (≥ 1.5 or < 0.67).

Fig. S5. SDS-polyacrylamide gel electrophoresis (SDS-PAGE) protein separation and flowchart of the proteomic analysis. **(A)** Equal amounts of proteins were separated by SDS-PAGE. The arrow indicates the band with the strongest intensity, postulated to be the polyhedrin protein encoded by baculovirus. **(B)** Schematic of in-gel digestion and LC-MS/MS data analysis flowchart. Proteins were in-gel digested using trypsin and peptides were subjected to subsequent LC-MS/MS analysis. Mass spectrometry data were used for protein identification and relative quantification.

Fig. S6. Overview of proteins identified in the fat body by LC-MS/MS analysis. **(A)** COG functional classes were assigned to proteins identified in the larval fat body of control and infected larvae. 'J', 'O' and 'R' represented the top three largest clusters. COG designations are as follows: A, RNA processing and modification; B, chromatin structure and dynamics; C, energy production and conversion; D, cell cycle control, cell division, chromosome partitioning; E, amino acid transport and metabolism; F, nucleotide transport and metabolism; G, carbohydrate transport and metabolism; H, coenzyme transport and metabolism; I, lipid transport and metabolism; J, translation, ribosomal structure and biogenesis; K, transcription; L, replication, recombination and repair; M, cell wall/membrane/envelope biogenesis; N, cell motility; O, posttranslational modification, protein turnover, chaperones; P, inorganic ion transport and metabolism; Q, secondary metabolites biosynthesis, transport and catabolism; R, general function prediction; S, function unknown; T, signal transduction mechanisms; U, intracellular trafficking, secretion, and vesicular transport; V, defense mechanisms; W, extracellular structures; X, mobilome: prophages, transposons; Z, cytoskeleton. **(B)** Gene ontology biological processes assigned to proteins identified in the larval fat body 72 h after immune challenge with baculovirus. Most of the proteins were associated with metabolic functions.

Fig. S7. Gene ontology enrichment analysis for DEPs identified in the fat body. **(A)**

Biological process GO enrichment analysis. **(B)** Molecular function GO enrichment analysis. The GO term abbreviations: MTA, molecular transducer activity; TLRA, translation regulator activity; TCRA, transcription regulator activity; ERA, enzyme regulator activity; AOA, antioxidant activity; ECA, electron carrier activity; BIND, binding; TA, transporter activity; SMA, structural molecule activity; CA, catalytic activity; BR, biological regulation; EOL, establishment of localization; LOC, localization; RTS, response to stimulus; CCB, cellular component biogenesis; PIG, pigmentation; DP, developmental process; MOP, multicellular organismal process; RP, reproductive process; CCO, cellular component organization; ASF, anatomical structure formation; CP, cellular process; MP, metabolic process; ISP, immune system process; RPD, reproduction.

Fig. S8. The relative abundance of CM-related enzymes at the protein level in the fat body of mock and infected larvae. As shown in the figure, a large proportion of CM-related enzymes, such as glucose-6-phosphate isomerase (*GPI*), aldolase, triose-phosphate isomerase (*TPI*), enolase, succinyl-CoA synthetase (*STK*), fumarase, fructose-1, 6-bisphosphatase (*FBP*), trehalose-6-phosphate synthase (*TPS*) and transaldolase, was down-regulated at the protein level after challenge with baculovirus. Student's t test was used for statistical analysis. * $p \leq 0.05$, ** $p \leq 0.01$, *** $p \leq 0.001$.

Supplemental figures

Figure S1.

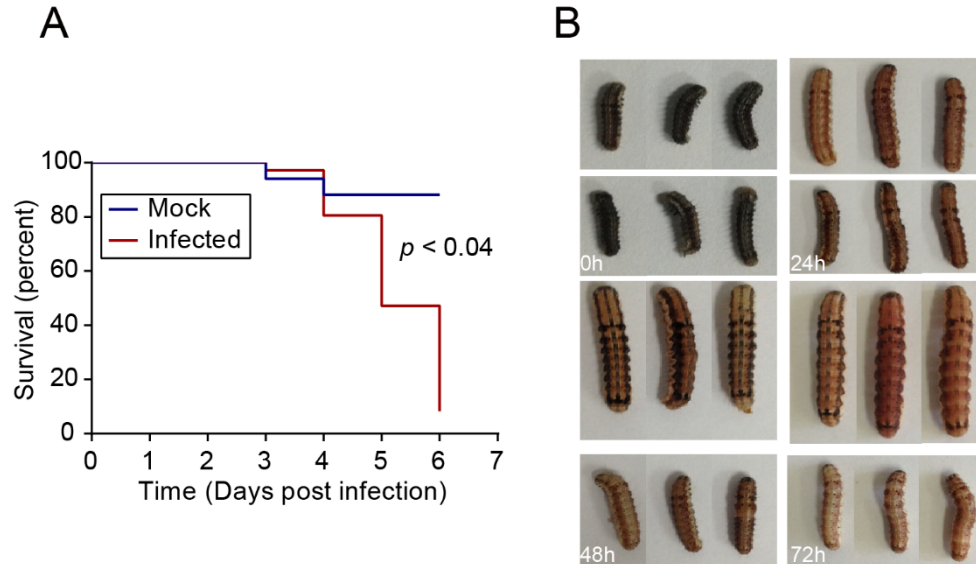


Figure S2.

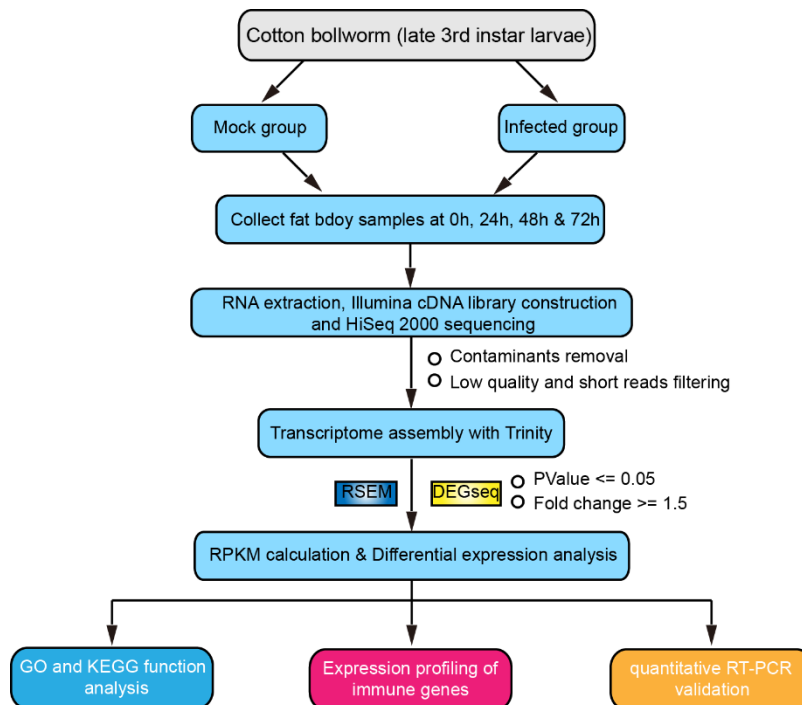
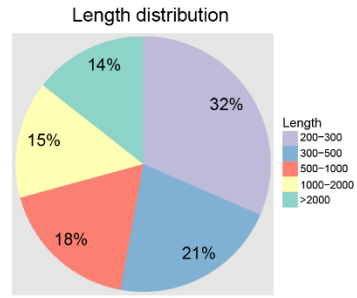


Figure S3.

A

Transcripts	94,813
Unigene	71,033
Annotated	40,359
Longest	29,520
Median	457
Mean	1,010
Shortest	201
N50	2,047

B



C

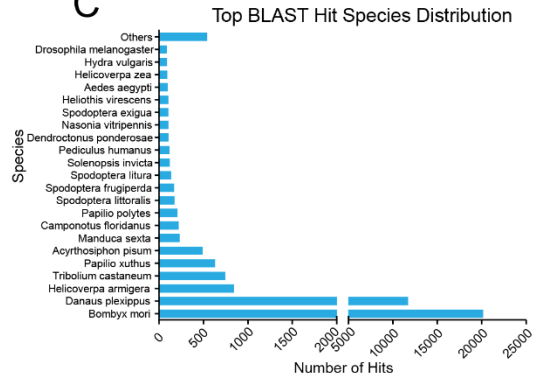
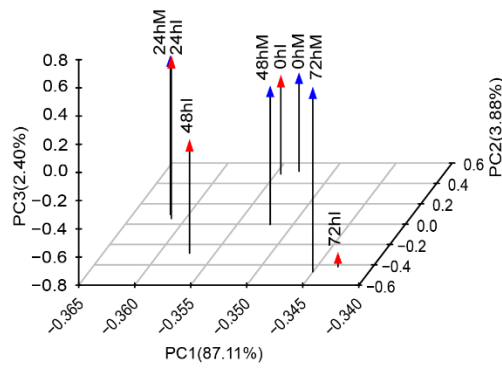


Figure S4.

A



B

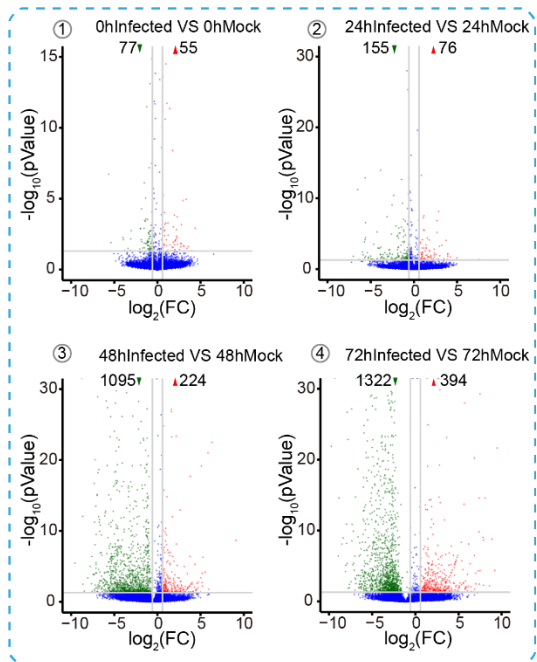


Figure S5.

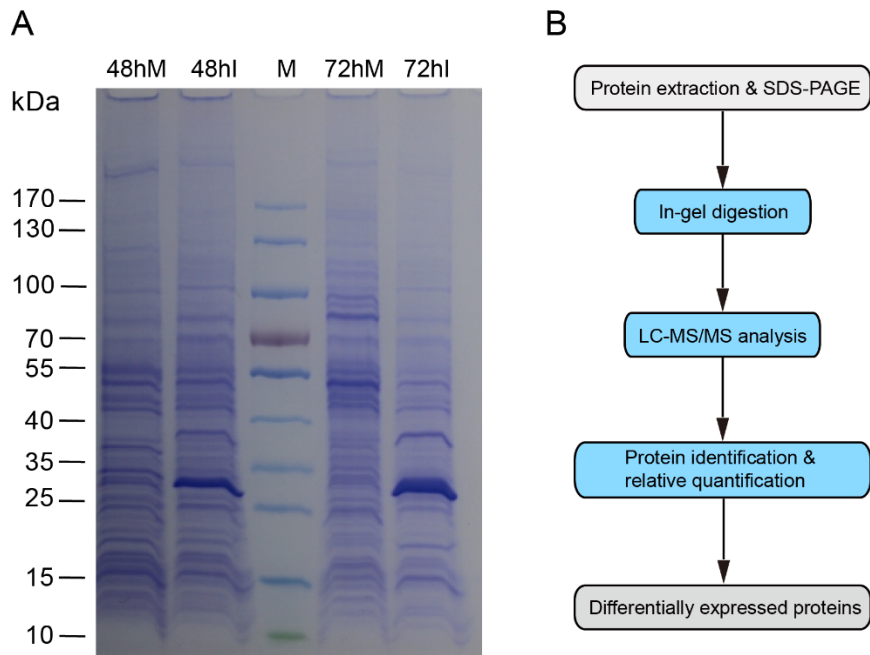


Figure S6.

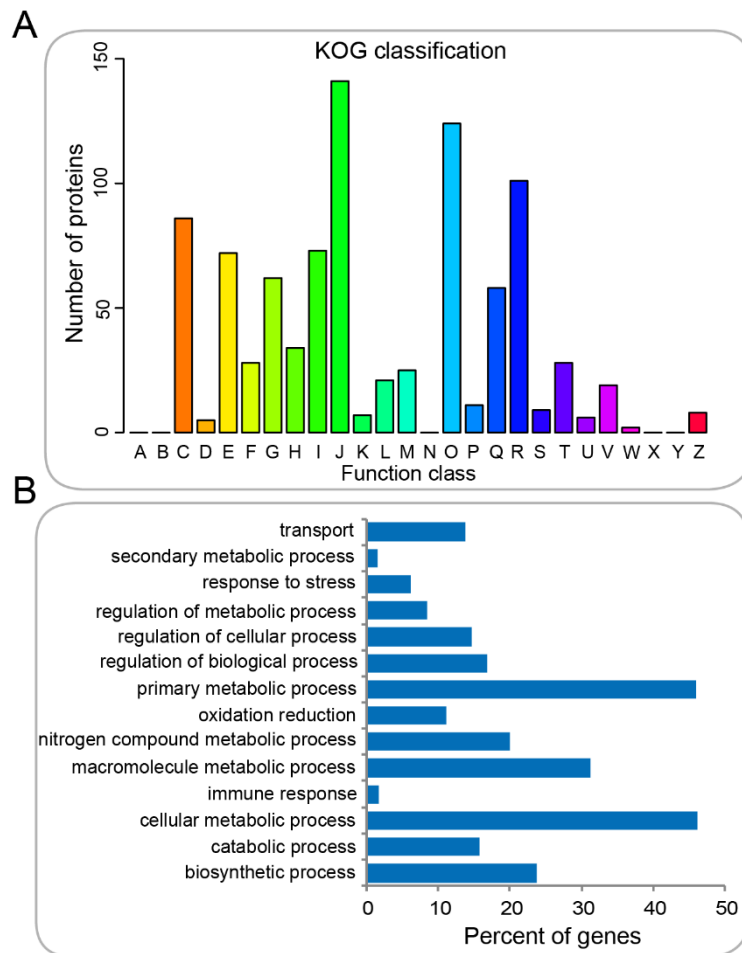


Figure S7.

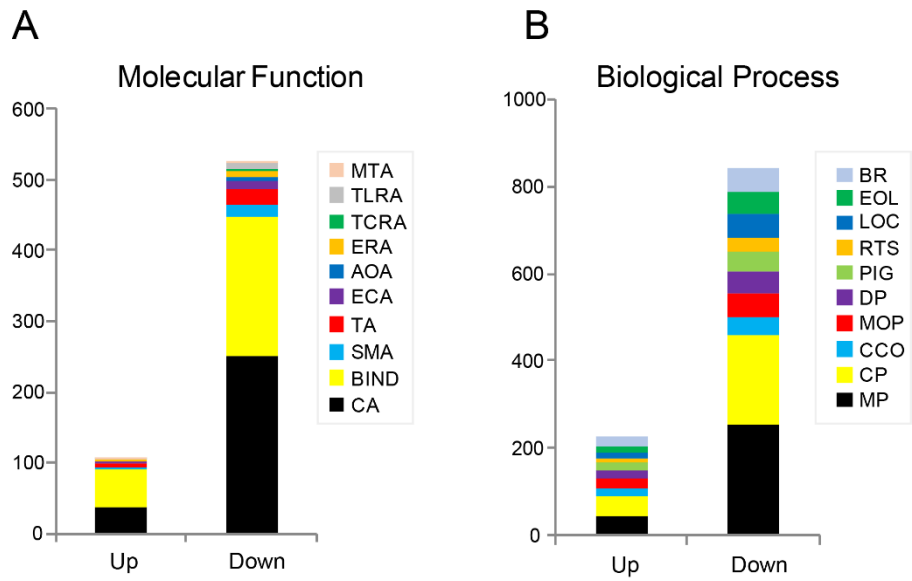


Figure S8.

