**Table S1.**

Primer information for the qRT-PCR.

|  |  |  |
| --- | --- | --- |
| Primer ID | Forward（5’-3’） | Reverse（5’-3’） |
| PER | GTGTACGGCTCCGACGAGA | GCCAGCAAGGAAGCATTTAG |
| CBA | TGTGGAAGGTATGGTGCTCTG | CAGCATTTGTGTTACTTTTGGGT |
| HSP | CCCAGGAGGAGTATGGAGAGT | AAAGAGGTCAAAGGGAGCACG |
| PDS | GGCTATCTCTCGCTCCATTG | CTTCGCCCTCCACTCCTTG |
| PK | GTAGACTGTTTGGTGATGCTTGG | CATTAGCCAACCACACCCATT |
| RPL18 | GCACTGTCACCGATGACCTC | CCTTGCACCAGCAGAGTGTT |

**Table S2.**

The stability of RPL-18 during the development of *P. trituberculatus* larvae*.*

|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
| Development stage | Z1 | Z2 | Z3 | Z4 | M | C |
| 60S ribosomal protein L18(RPL-18) | 17.57±0.05 | 17.62±0.06 | 17.65±0.09 | 17.68±0.06 | 17.62±0.11 | 17.55±0.05 |

Values represent the standard expressions measured by Microarray sequencing

**Table S3.**

The information of the 16 DEGs during the development of *P. trituberculatus* larvae in Figure 2C*.*

|  |  |  |
| --- | --- | --- |
| Probe ID | Target ID | Description |
| CUST\_35029\_PI429384579 | IE2IK4G02IVGGZ | unknown |
| CUST\_38305\_PI429384491 | contig07634 | solute carrier family 15 member 1-like (LOC123504113), transcript variant X2, mRNA |
| CUST\_25862\_PI429384588 | GT558198.1 | UDP-glucosyltransferase 2-like (LOC123506105), transcript variant X3, misc\_RNA |
| CUST\_44350\_PI429384574 | IE2IK4G02GFPBL | Uncultured bacterium clone Ovdat62b10 16S ribosomal RNA gene, partial sequence |
| CUST\_30589\_PI429384588 | GT558198.1 | UDP-glucosyltransferase 2-like (LOC123506105), transcript variant X3, misc\_RNA |
| CUST\_33556\_PI429384588 | GT559851.1 | solute carrier family 15 member 1-like (LOC123504113), transcript variant X2, mRNA |
| CUST\_15235\_PI429384588 | GW400403.1 | uncharacterized LOC123516137 (LOC123516137), mRNA |
| CUST\_30060\_PI429384588 | GT558413.1 | uncharacterized LOC123512209 (LOC123512209), mRNA |
| CUST\_34415\_PI429384584 | IE2IK4G01BU1N8 | Piscicola geometra genome assembly, chromosome: 15 |
| CUST\_39877\_PI429384588 | GT558717.1 | uncharacterized LOC123508727 (LOC123508727), ncRNA |
| CUST\_22178\_PI429384588 | GW401973.1 | haplotype BE D-loop, partial sequence; mitochondrial |
| CUST\_37098\_PI429384570 | IE2IK4G02JLPLF | uncharacterized LOC123502626 (LOC123502626), mRNA |
| CUST\_95292\_PI429384491 | contig14968 | unknown |
| CUST\_26125\_PI429384579 | IE2IK4G01BGDFS | unknown |
| CUST\_31800\_PI429384588 | GT555861.1 | protein obstructor-E-like (LOC123511490), transcript variant X1, mRNA |

All of the above differential genes can encode protein

**Table S4.**

Differentially expressed genes in“AMPK signaling pathway”term between the forth zoeae (Z4) and the magalopae (M) of *P. trituberculatus.*

|  |  |  |  |
| --- | --- | --- | --- |
| Comparison | Gene name | Unigene ID | Fold Change |
| Z4\_vs\_M | glucose-6-phosphatase(G6PC)\* | contig20533 | 13.9 |
|  | phosphoenolpyruvate carboxykinase （PCK)\* | contig03971 | 7.7 |
|  | macrophage-stimulating protein receptor-like isoform X1 | IE2IK4G02FTLZL | 6.4 |
|  | transforming growth factor beta-activated kinase 1（TGF-β-activated kinase 1） | IE2IK4G01CH56N | 4.6 |
|  | sterol regulatory element-binding protein 1 | contig10222 | 3.0 |
|  | 6-phosphofructo-2-kinase/fructose-2,6-bisphosphatase 2\* | IE2IK4G01CCC1G | 2.4 |
|  | 6-phosphofructo-2-kinase/fructose-2,6-bisphosphatase 1 isoform X1 | IE2IK4G02GLIGI | 2.0 |

\* *P* value＜0.001. For genes without asterisks, *P* value ＜0.05

**Table S5.**

Differentially expressed genes in“retinol metabolism”term between the forth zoeae (Z4) and the magalopae (M) of *P. trituberculatu*s.

|  |  |  |  |
| --- | --- | --- | --- |
| Comparison | Gene name | Unigene ID | Fold Change |
| M\_vs\_Z4 | cytochrome P450 enzyme\* | contig08218 | 52.5 |
|  | retinol dehydrogenase 12 isoform X3(RDH12)\* | contig20898 | 47.2 |
|  | retinoid isomerohydrolase\* | IE2IK4G02IKWNO | 34.9 |
|  | hypothetical protein C0J52\_16171\* | IE2IK4G02HSPNX | 25.4 |
|  | UDP-glucuronosyltransferase\* | IE2IK4G01EARN0 | 25.3 |
|  | UDP-glucuronosyltransferase- isoform X3\* | contig08276 | 22.0 |
|  | retinol dehydrogenase 13-like isoform X6\* | IE2IK4G01ALEJA | 19.6 |
|  | beta,beta-carotene 9',10'-oxygenase-like isoform X1(CMO2)\* | IE2IK4G02GNM4G | 17.2 |
|  | Epidermal retinal dehydrogenase 2\* | contig12808 | 9.8 |
|  | cytochrome P450 6k1\* | IE2IK4G01AZBUZ | 7.9 |
|  | beta,beta-carotene 9',10'-oxygenase(CMO2) | IE2IK4G01CYQ4A | 7.6 |
|  | cytochrome P450 9E1 | IE2IK4G01DGL7U | 5.6 |
|  | UDP-glucuronosyltransferase 2C1\* | IE2IK4G01CP94Z | 5.6 |
|  | alcohol dehydrogenase class-3 | IE2IK4G01DHEKE | 5.3 |
|  | Retinol dehydrogenase 13(RDH13) | contig14383 | 5.0 |
|  | alcohol dehydrogenase class -3, partial\* | contig18148 | 3.9 |
|  | cytochrome P450 3A24 | contig11426 | 2.9 |
|  | short-chain dehydrogenase/reductase family 16C member 6-like | IE2IK4G01CIQ4C | 2.5 |
|  | Retinol dehydrogenase 14(RDH14) | contig12426 | 2.3 |
|  | retinol dehydrogenase 11(RDH11) | contig12804 | 2.3 |

\* *P* value＜0.001. For genes without asterisks, *P* value ＜0.05

**Table S6.**

Differentially expressed genes in“Insect hormone biosynthesis” term and IAG gene between the forth zoeae (Z4) and the magalopae (M) of *P. trituberculatu*s.

|  |  |  |  |
| --- | --- | --- | --- |
| Comparison | Gene name | Unigene ID | Fold Change |
| M\_vs\_Z4 | cytochrome P450(CYP15)\* | IE2IK4G02HI3HE | 65.5 |
|  | CYP2\* | contig15890 | 30.1 |
|  | cytochrome P450 302a1, mitochondrial\* | IE2IK4G01AU1I1 | 27.9 |
|  | CYP2\* | contig06017 | 19.7 |
|  | juvenile hormone epoxide hydrolase(JHEH)\* | contig21677 | 15.6 |
|  | cytochrome P450 epoxidase\* | contig19499 | 7.9 |
|  | probable cytochrome P450 49a1\* | IE2IK4G02GQT1N | 3.3 |
|  | CYP307, partial | IE2IK4G01EPD0Z | 3.0 |
|  | cytochrome P450 CYP2 | IE2IK4G02GXSUT | 2.2 |
| M\_vs\_Z4 | insulin-like androgenic gland hormone\* | contig11412 | 3.2 |

\* *P* value＜0.001. For genes without asterisks, *P* value ＜0.05