**Supporting information**

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**Transcriptional identification of differentially expressed genes during the prepupal-pupal transition in the oriental armyworm, *Mythimna separata* (Walker) (Lepidoptera: Noctuidae)**

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**MATERIALS AND METHODS**

***Differential expression analysis of unigene***

FPKM is the number of fragments per kilobase length from a certain gene per million reads. FPKM considers the effect of sequencing depth and gene length on Reads count at the same time. The calculation formula is as follows: FPKM=106 C/ (NL/103). Suppose FPKM (A) represents the expression level of gene A, C is the number of fragments uniquely compared to gene A, N is the total number of fragments uniquely compared to the reference gene, and L is the number of bases of gene A.

The differential gene screening conditions are a multiple of 2 or greater and a Q-value or false discovery rate (FDR) of 0.01 or less. DESeq2 simulates the frequency of occurrence of the read counts in count matrix Kij following a negative binomial distribution, with a mean μij and a dispersion αi. The mean is calculated from a quantity qij and is proportional to the concentration of cDNA from the gene in the sample. Normalize them by a normalization factor sij to make them equal (μij = sijqij). In many cases, this constant sj can be shared by all genes in a sample, but sij will also be different when the sequencing depth between samples is different. DESeq2 uses a log-related generalized linear model log2qij = ΣRxjrβir, where xjr is the matrix element and βir is the regression coefficient. The simplest case is the comparison between the two components. The coefficients obtained by fitting the generalized linear model can infer the intensity of the overall gene expression and the log2fold value between the groups. When the generalized linear model fits all genes, the coefficients of the model need to be tested are significantly different from zero. DESeq2 uses a Wald test to obtain a Z statistic and compares it with the standard normal distribution. The *P*-value value obtained from the Wald test in the gene subset needs to be corrected by multiple tests.

***Quantitative real-time PCR analysis***

Amplifications were performed in 20 μL reaction systems containing 10 μL TB GreenTM Premix Ex TaqTM 2 (TliRNaseH Plus) (TaKaRa, Dalian, China), 7.2 μL nuclease-free water, 1 μL 10× diluted cDNA template, 0.8 μL of 10 μM sense primer and anti-sense primer under the following amplification protocol: 95℃ for 30 s, 40 cycles of 95℃ for 5 s and 60℃ for 30 s. A melting curve was conducted after amplification to ensure the specificity of the PCR products. Non-template controls (NTCs) with RNase-free water instead of cDNA templates and Non-reverse transcription controls (NRTs) using RNA without transcription, were included for each primer pair, to exclude the genomic DNA contamination. Each reaction was performed in triplicate and each test was repeated with three independent mRNA samples.

Table S1. The main gene families and number of DEGs in membrane and integral component of membrane sub-categories.

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| Sub-category | Gene family | ML-vs-W | W-vs-P1 | P1-vs-P5 | P5-vs-P10 |
| Membrane | Solute carrier family | 298 | 285 | 281 | 384 |
| MFS transporter | 181 | 162 | 133 | 181 |
| low-density lipoprotein receptor | 103 | 93 | 53 | 89 |
| Glucuronosyltransferase | 72 | 53 | 53 | 52 |
| ATP-binding cassette | 62 | 48 | 65 | 61 |
| P450 | 62 | 61 | 49 | 62 |
| Alcohol-forming fatty acyl-CoA reductase | 49 | 46 | 31 | 55 |
| ATPase | 38 | 29 | 30 | 90 |
| NADH dehydrogenase | 24 | 15 | 21 | 50 |
| stearoyl-CoA desaturase | 17 | 12 | 20 | 21 |
| chitin | 15 | 18 | 15 | 12 |
| fatty acids | 15 | 10 | 12 | 14 |
| E3 ubiquitin-protein | 13 | 19 | 17 | 17 |
| Integral component of membrane | Solute carrier family | 298 | 286 | 281 | 385 |
| MFS transporter | 181 | 162 | 133 | 181 |
| low-density lipoprotein receptor | 103 | 93 | 53 | 89 |
| Glucuronosyltransferase | 71 | 52 | 53 | 52 |
| ATP-binding cassette | 62 | 48 | 65 | 61 |
| P450 | 62 | 61 | 49 | 62 |
| Alcohol-forming fatty acyl-CoA reductase | 49 | 46 | 31 | 55 |
| ATPase | 38 | 29 | 30 | 87 |
| NADH dehydrogenase | 15 | 9 | 11 | 25 |
| stearoyl-CoA desaturase | 17 | 12 | 20 | 21 |
| chitin | 15 | 18 | 15 | 12 |
| fatty acids | 12 | 10 | 12 | 14 |
| E3 ubiquitin-protein | 11 | 18 | 15 | 16 |

Table S2. Number of DEGs in cuticular proteins, JH, and 20E identified in the membrane and integral component of membrane sub-categories.

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| sub-categories |  | ML-vs-W | W-vs-P1 | P1-vs-P5 | P5-vs-P10 |
| Membrane | CP | 9 | 8 | 7 | 10 |
| JH | 11 | 11 | 3 | 10 |
| 20E | 3 | 2 | 3 | 2 |
| Integral component of membrane | CP | 10 | 10 | 9 | 11 |
| JH | 11 | 11 | 3 | 10 |
| 20E | 3 | 2 | 3 | 2 |

Table S3. Number of cuticular proteins, JH, and 20E genes identified in the prepupal-pupal transition of *M. separata*

|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
| Families | Detected in total | Detected in ML (%) | Detected in W (%) | Detected in P1 (%) | Detected in P5 (%) | Detected in P10 (%) |
| Cuticular proteins | 33 | 33（100） | 33（100） | 33（100） | 32（97） | 32（97） |
| Juvenile hormone | 18 | 16（89） | 15（83） | 15（83） | 13（72） | 15（83） |
| 20-hydroxyecdysone | 7 | 7（100） | 7（100） | 7（100） | 7（100） | 7（100） |

Table S4. Differentially expressed prepupal–pupal transition related genes in *M. separata*.

|  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- |
| **Gene ID** | **ML-vs-P1** | **ML-vs-P5** | **ML-vs-P10** | **PP-vs-P5** | **PP-vs-P10** | **P1-vs-P10** | **Blast nr** |
| **Cuticular proteins** | | | | | | | |
| CL9076.Contig3\_All | +1.7 | — | — | -1.5 | -1.1 | -1 | epidermal growth factor receptor isoform X1 |
| CL1027.Contig5\_All | +1.1 | -1.7 | -2.9 | -1.7 | -2.8 | -3.9 | 1-phosphatidylinositol 4,5-bisphosphate phosphodiesterase gamma-1 |
| CL12980.Contig3\_All | — | — | +2 | — | +1.9 | +2.2 | calcium/calmodulin-dependent protein kinase type II alpha chain |
| CL16856.Contig2\_All | +1.2 | — | — | — | — | — | nuclear migration protein nudC |
| Unigene15668\_All | — | — | — | — | — | — | nudC domain-containing protein 3 |
| CL1779.Contig9\_All | — | +1.2 | +2 | — | — | +1.3 | protein kinase C, brain isozyme isoform X1 |
| CL8545.Contig7\_All | — | — | +1.2 | — | +1.4 | +1.6 | protein kinase C, brain isozyme isoform X1 |
| CL13841.Contig4\_All | — | +1 | — | +1.3 | — | — | E3 ubiquitin-protein ligase CBL-B-B isoform X2 |
| CL1699.Contig11\_All | — | — | — | — | — | — | E3 ubiquitin-protein ligase CBL-B-B isoform X2 |
| CL3149.Contig3\_All | — | — | — | -2.8 | -2.1 | — | TBC1 domain family member 23 |
| CL1279.Contig108\_All | — | +1.6 | — | -1.8 | -2.5 | — | signal transducer and activator of transcription 5B isoform X2 |
| CL1337.Contig49\_All | +1.7 | +1.9 | — | — | -1.1 | — | tyrosine-protein kinase Src64B isoform X1 |
| CL2288.Contig92\_All | — | +1 | — | — | — | — | tyrosine-protein kinase Src64B isoform X3 |
| CL16647.Contig3\_All | +1.3 | — | — | -1.2 | -1.4 | -1.1 | focal adhesion kinase 1 isoform X1 |
| CL4698.Contig2\_All | — | +1.1 | — | — | — | — | serine/threonine-protein kinase PAK mbt |
| Unigene3483\_All | — | +1.5 | — | +2.5 | +1.8 | — | serine/threonine-protein kinase PAK mbt |
| CL7815.Contig1\_All | — | — | -2.1 | — | -1.8 | -1.9 | serine/threonine-protein kinase PAK 3 |
| CL1585.Contig16\_All | — | — | +1 | -1 | — | — | acid phosphatase type 7-like |
| CL9103.Contig5\_All | — | +1.7 | +1.7 | +1.6 | +1.6 | +2.1 | dual specificity mitogen-activated protein kinase kinase 4-like |
| CL4397.Contig3\_All | — | — | +1.2 | — | — | +1.3 | stress-activated protein kinase JNK isoform X1 |
| Unigene12087\_All | — | — | — | — | — | — | transcription factor jun-D |
| CL18975.Contig2\_All | — | -1.4 | -1.2 | -2 | -1.6 | -1.4 | SHC-transforming protein 1 |
| CL6698.Contig6\_All | — | — | — | -1.2 | -1.2 | — | protein son of sevenless |
| CL2596.Contig51\_All | — | — | — | -1.6 | -2.2 | — | GTPase HRas |
| CL6991.Contig6\_All | — | — | — | — | — | -1.2 | GTPase HRas |
| CL8021.Contig5\_All | — | +1.7 | +1.6 | — | — | — | raf homolog serine/threonine-protein kinase phl isoform X1 |
| Unigene8645\_All | — | — | — | — | -1.3 | -1 | dual specificity mitogen-activated protein kinase kinase dSOR1 isoform X1 |
| CL14604.Contig2\_All | -3.5 | — | -3.5 | -1.5 | -1.6 | — | gonadotropin-releasing hormone receptor isoform X1 |
| CL6175.Contig4\_All | -1.8 | -3.7 | -1.3 | -3.6 | -1.2 | — | gonadotropin-releasing hormone receptor |
| CL10689.Contig4\_All | — | — | — | — | — | — | guanine nucleotide-binding protein G(q) subunit alpha isoform X2 |
| CL9739.Contig5\_All | — | — | +1.8 | — | +2.2 | +1.9 | 1-phosphatidylinositol 4,5-bisphosphate phosphodiesterase isoform X2 |
| CL7899.Contig3\_All | — | -1.4 | -2.3 | +3.5 | +2.8 | -2.1 | putative protein kinase C delta type homolog isoform X4 |
| CL10379.Contig10\_All | +3.1 | — | -1.1 | -3.4 | -3.6 | -4 | matrix metalloproteinase-14 isoform X2 |
| **Juvenile hormone** | | | | | | | |
| CL3825.Contig60\_All | +2.4 | — | +1 | +1.1 | +2.5 | -1.3 | farnesol dehydrogenase-like |
| CL5146.Contig76\_All | — | -2.4 | — | — | +1.7 | -1.2 | odorant binding protein 23 |
| CL696.Contig45\_All | -4.7 | -8.3 | -2.7 | -4.3 | — | +2 | farnesol dehydrogenase-like |
| CL9391.Contig2\_All | -2.6 | -1.9 | -4.3 | -2 | -4.3 | -1.6 | juvenile hormone acid methyltransferase |
| Unigene19996\_All | — | — | +6 | — | +5.6 | +5.3 | juvenile hormone acid O-methyltransferase-like |
| CL16686.Contig3\_All | — | — | — | — | — | -1.5 | farnesoate epoxidase-like |
| CL15147.Contig1\_All | -1.3 | +1.7 | +3 | +3 | +4.3 | +4.3 | calexcitin-2 |
| CL17942.Contig2\_All | -6.5 | -7.7 | -5.8 | -1.2 | — | — | calexcitin-2-like |
| Unigene10260\_All | -6.9 | -7.2 | -7 | — | — | — | sarcoplasmic calcium-binding proteins I, III, and IV-like |
| CL1111.Contig45\_All | -7.5 | -7.9 | -7.6 | — | — | — | carboxylesterase |
| CL14984.Contig2\_All | -4 | -3.8 | -4.7 | — | -1 | — | carboxylesterase 12 |
| CL11190.Contig1\_All | — | -3.2 | -4.6 | -7.3 | -8.4 | -4.8 | juvenile hormone epoxide hydrolase-like |
| CL15275.Contig2\_All | -5.5 | -6.8 | -5.5 | -1.9 | — | — | juvenile hormone epoxide hydrolase-like |
| CL16665.Contig4\_All | — | +1.2 | — | +1.1 | — | — | juvenile hormone epoxide hydrolase-like |
| CL18477.Contig4\_All | — | -3.3 | — | -6.3 | -2.6 | +1.8 | juvenile hormone epoxide hydrolase-like |
| CL4540.Contig4\_All | -1.7 | -2.1 | -4.5 | — | -2 | -2.7 | juvenile hormone epoxide hydrolase-like |
| CL5616.Contig2\_All | — | +3.1 | — | +4.4 | +3.2 | — | juvenile hormone epoxide hydrolase-like |
| CL817.Contig4\_All | -4.6 | -6.3 | -4.7 | -3.9 | -2.2 | — | juvenile hormone epoxide hydrolase |
| **20-hydroxyecdysone** | | | | | | | |
| CL14010.Contig2\_All | — | -3.2 | -5.5 | -1.7 | — | -4.1 | cytochrome P450 307A1 |
| Unigene18829\_All | — | -1.3 | -1.9 | — | — | -1.4 | cytochrome P450 306A1 |
| CL8044.Contig1\_All | +1.1 | — | — | — | — | — | cytochrome P450 CYP339A1 |
| Unigene29505\_All | — | -2 | — | — | — | — | cytochrome P450 302A1 |
| Unigene4431\_All | -2 | -1.4 | -1.7 | — | — | — | cytochrome P450 315A1 |
| CL17221.Contig1\_All | -2.7 | — | -2 | — | — | — | cytochrome P450 314A1 |
| CL19241.Contig2\_All | — | — | -2.2 | — | — | — | cytochrome P450 CYP18A1 |

The second to fifth columns of numbers represent | log2Ratio |. + stands for up-regulated, - stands for down-regulated and — represents no DEGs. Differentially genes screening conditions are FDR≤0.01 and | log2Ratio | ≥1.

Table S5.Primers used in this study.

|  |  |  |
| --- | --- | --- |
| Gene ID | Primer sequence (5′ to 3′) | Length (bp) |
| CL17942.Contig2\_All | F:AGCCATCGCCAGAATCAC  R:TCGGACTTGCCTTTAGCC | 348 |
| CL4540.Contig4\_All | F:ACCTCCACCACTGCCTGAC  R:CCTTCGGCGTGACCCT | 338 |
| CL817.Contig4\_All | F:CTTGGGCGTGGCAGTATG  R:TGGCGTCTGTTTTGTGAGC | 481 |
| CL14010.Contig2\_All | F:TGGTCCAACCTTCAACTACG  R:TTTCCCTCTGCTCCACAAT | 427 |
| CL17221.Contig1\_All | F:TCAACGGGACTCTTACTATGGA  R:GCAAGGTCTTCGGCACTCA | 369 |
| CL19241.Contig2\_All | F:GAACCCCGAAGCAAAGAA  R:CGTGCCCTCCAGCGAC | 472 |
| Unigene12087\_All | F:GTGGGGCGGGGCATC  R:CGGTCCAGGTCGGCGTA | 302 |
| CL2596.Contig51\_All | F:GCGGGGCAAGAGGAGT  R:TCGGACGAGCGTGTAGAA | 309 |
| Unigene8645\_All | F:ACGGCGGCGTAGTAATGA  R:AATGCGTGCCTTGGAGTC | 486 |
| CL10379.Contig10\_All | F:ATGAGGAAACGACAAAAGTAATG  R:GAGCAGCGACCTGGAAAA | 439 |
| *β-actin* | F: AACTTCCCGACGGTCAAGTCAT  R: TGTTGGCGTACAAGTCCTTACG | 168 |

Table S6. Other Differentially expressed genes related to metamorphosis from WL to W

|  |  |  |  |
| --- | --- | --- | --- |
| **GeneID** | **log2Fold** | **Diff** | **Nr-annotation** |
| CL3145.Contig6\_All | -11.43 | Down | macrophage migration inhibitory factor-like protein [*Antheraea yamamai*] |
| Unigene8654\_All | -11.39 | Down | PREDICTED: dentin sialophosphoprotein [*Nomascus leucogenys*] |
| CL249.Contig15\_All | -10.58 | Down | PREDICTED: twitchin [*Amyelois transitella*] |
| CL8622.Contig1\_All | -10.53 | Down | PREDICTED: cell surface glycoprotein 1-like isoform X4 [*Amyelois transitella*] |
| Unigene12166\_All | -10.37 | Down | pancreatic lipase 3 [*Mamestra configurata*] |
| CL999.Contig2\_All | -10.37 | Down | rCG23821 [*Rattus norvegicus*] |
| CL4476.Contig9\_All | -10.31 | Down | PREDICTED: proteoglycan 4 isoform X1 [*Bombyx mori*] |
| CL10821.Contig9\_All | -10.20 | Down | Inducible metalloproteinase inhibitor protein [*Papilio xuthus*] |
| CL16463.Contig1\_All | -10.13 | Down | PREDICTED: sucrose-6-phosphate hydrolase-like [*Amyelois transitella*] |
| CL1427.Contig2\_All | -10.13 | Down | putative ecdysone oxidase [*Helicoverpa zea*] |
| CL1427.Contig1\_All | -10.01 | Down | putative ecdysone oxidase [*Helicoverpa zea*] |
| CL15279.Contig1\_All | 10.04 | Up | uncharacterized protein LOC106118712 precursor [*Papilio xuthus*] |
| CL19329.Contig2\_All | 10.06 | Up | x-tox [*Spodoptera exigua*] |
| CL518.Contig1\_All | 10.06 | Up | unknown secreted protein [*Papilio polytes*] |
| CL13027.Contig5\_All | 10.10 | Up | PREDICTED: uncharacterized protein LOC106130660 [*Amyelois transitella*] |
| CL2717.Contig8\_All | 10.12 | Up | PREDICTED: nucleolin-like isoform X1 [*Papilio machaon*] |
| CL696.Contig20\_All | 10.16 | Up | C-type lectin 2 [*Helicoverpa armigera*] |
| Unigene2739\_All | 10.26 | Up | PREDICTED: eisosome protein SEG2 [*Bombyx mori*] |
| CL15279.Contig3\_All | 10.26 | Up | uncharacterized protein LOC106118712 precursor [*Papilio xuthus*] |
| CL518.Contig5\_All | 10.29 | Up | unknown secreted protein [*Papilio polytes*] |
| CL10899.Contig4\_All | 10.35 | Up | PREDICTED: histidine-rich glycoprotein-like [*Plutella xylostella*] |
| CL1167.Contig10\_All | 10.42 | Up | immune related protein [*Spodoptera frugiperda*] |
| CL1698.Contig1\_All | 10.53 | Up | hypothetical protein [*Papilio polytes*] |
| CL1698.Contig4\_All | 10.63 | Up | hypothetical protein [*Papilio polytes*] |
| CL5501.Contig2\_All | 10.67 | Up | PREDICTED: 4-coumarate--CoA ligase 1-like [*Amyelois transitella*] |
| CL14869.Contig5\_All | 10.68 | Up | Catalase [*Papilio machaon*] |
| Unigene22799\_All | 10.69 | Up | osiris 18 precursor [*Bombyx mori*] |
| CL13027.Contig4\_All | 10.76 | Up | PREDICTED: uncharacterized protein LOC106130660 [*Amyelois transitella*] |
| Unigene32976\_All | 10.79 | Up | PREDICTED: uncharacterized protein LOC106130706 [*Amyelois transitella*] |
| CL2476.Contig8\_All | 10.82 | Up | 37-kDa protease precursor [*Bombyx mori*] |
| CL2717.Contig3\_All | 10.90 | Up | PREDICTED: nucleolin-like isoform X1 [*Papilio machaon*] |
| CL10899.Contig2\_All | 10.90 | Up | PREDICTED: histidine-rich glycoprotein-like [*Plutella xylostella*] |
| CL1167.Contig11\_All | 10.98 | Up | x-tox [*Spodoptera exigua*] |
| Unigene3493\_All | 10.98 | Up | PREDICTED: uncharacterized protein LOC106142643 [*Amyelois transitella*] |
| CL1285.Contig8\_All | 11.18 | Up | PREDICTED: muscle M-line assembly protein unc-89-like isoform X4 [*Papilio xuthus*] |
| CL1167.Contig3\_All | 11.21 | Up | Heli-5-tox protein [*Helicoverpa armigera*] |
| CL4907.Contig18\_Al | 11.33 | Up | PREDICTED: uncharacterized protein LOC101741030 [*Bombyx mori*] |
| Unigene33404\_All | 11.51 | Up | osiris 9 [*Danaus plexippus*] |
| CL14869.Contig3\_All | 11.73 | Up | Catalase [*Papilio machaon*] |

|  |
| --- |
|  |

Table S7. Other Differentially expressed genes related to metamorphosis from W to P1

|  |  |  |  |
| --- | --- | --- | --- |
| **GeneID** | **log2Fold** | **Diff** | **Nr-annotation** |
| CL263.Contig6\_All | -10.60 | Down | PREDICTED: alpha-protein kinase 1 [*Bombyx mori*] |
| CL1111.Contig183\_All | -10.48 | Down | neutral lipase [*Danaus plexippus*] |
| CL14688.Contig2\_All | -10.28 | Down | PREDICTED: putative uncharacterized protein DDB\_G0282133 isoform X1 [*Cricetulus griseus*] |
| CL159.Contig5\_All | -10.27 | Down | PREDICTED: protein alan shepard [*Amyelois transitella*] |
| CL12407.Contig3\_All | 10.03 | Up | RecName: Full=Pupal cuticle protein 36 [*Manduca sexta*] |
| CL13796.Contig1\_All | 10.04 | Up | putative cuticle protein [*Operophtera brumata*] |
| CL4476.Contig9\_All | 10.08 | Up | PREDICTED: proteoglycan 4 isoform X1 [*Bombyx mori*] |
| CL2398.Contig4\_All | 10.09 | Up | hypothetical protein KGM\_14032 [*Danaus plexippus*] |
| CL7082.Contig3\_All | 10.14 | Up | hypothetical protein [*Ixodes ricinus*] |
| CL4049.Contig1\_All | 10.19 | Up | PREDICTED: uncharacterized protein LOC105386674 isoform X1 [*Plutella xylostella*] |
| CL479.Contig1\_All | 10.32 | Up | odorant binding protein 33 [*Spodoptera litura*] |
| CL1865.Contig3\_All | 10.79 | Up | Chymotrypsin-2 [*Papilio xuthus*] |
| CL7380.Contig2\_All | 11.05 | Up | PREDICTED: larval/pupal rigid cuticle protein 66-like [*Amyelois transitella*] |
| CL169.Contig67\_All | 11.06 | Up | PREDICTED: transmembrane protease serine 9-like [*Papilio xuthus*] |
| CL16577.Contig3\_All | 11.11 | Up | PREDICTED: cuticular protein RR-1 motif 9 isoform X1, partial [*Bombyx mori*] |
| CL601.Contig8\_All | 11.21 | Up | lebocin [*Helicoverpa armigera*] |
| CL3199.Contig3\_All | 11.27 | Up | Uncharacterized protein OBRU01\_04074 [*Operophtera brumata*] |
| CL3199.Contig2\_All | 12.00 | Up | Uncharacterized protein OBRU01\_04074 [*Operophtera brumata*] |

Table S8. Other Differentially expressed genes related to metamorphosis from P1 to P5

|  |  |  |  |
| --- | --- | --- | --- |
| **GeneID** | **log2Fold** | **Diff** | **Nr-annotation** |
| CL3199.Contig2\_All | -12.37 | Down | Uncharacterized protein OBRU01\_04074 [*Operophtera brumata*] |
| CL329.Contig1\_All | -12.15 | Down | PREDICTED: carbonic anhydrase 2-like [*Amyelois transitella*] |
| CL5904.Contig7\_All | -11.77 | Down | PREDICTED: transmembrane protease serine 9-like [*Papilio xuthus*] |
| CL13796.Contig2\_All | -11.22 | Down | putative cuticle protein [*Operophtera brumata*] |
| CL1673.Contig24\_All | -11.09 | Down | PREDICTED: monocarboxylate transporter 5 [*Amyelois transitella*] |
| CL10019.Contig2\_All | -10.86 | Down | PREDICTED: phosphatidate phosphatase LPIN2 isoform X3 [*Bombyx mori*] |
| CL4096.Contig6\_All | -10.65 | Down | PREDICTED: uncharacterized protein LOC106136206 [*Amyelois transitella*] |
| CL8444.Contig7\_All | -10.63 | Down | PREDICTED: proteasome subunit alpha type-5 isoform X1 [*Papilio machaon*] |
| CL11993.Contig9\_All | -10.56 | Down | PREDICTED: probable malate dehydrogenase, mitochondrial [*Papilio machaon*] |
| CL17652.Contig1\_All | -10.43 | Down | PREDICTED: glucose dehydrogenase [FAD, quinone] [*Bombyx mori*] |
| CL10298.Contig1\_All | -10.42 | Down | hypothetical protein AND\_005598 [*Anopheles darlingi*] |
| CL2288.Contig69\_All | -10.33 | Down | PREDICTED: uncharacterized protein LOC106114729 [*Papilio xuthus*] |
| CL5591.Contig6\_All | -10.30 | Down | pumilio, partial [*Cydia pomonella*] |
| CL2027.Contig3\_All | -10.30 | Down | scavenger receptor class B member 1-like [*Bombyx mori*] |
| CL169.Contig97\_All | -10.06 | Down | PREDICTED: transmembrane protease serine 9-like [*Papilio xuthus*] |
| CL10358.Contig16\_All | -10.06 | Down | PREDICTED: calcium-activated potassium channel slowpoke isoform X2 [*Papilio xuthus*] |
| CL9505.Contig2\_All | -10.01 | Down | Nose resistant to fluoxetine protein 6 [*Papilio xuthus*] |
| CL182.Contig33\_All | -10.01 | Down | PREDICTED: elongation of very long chain fatty acids protein 4 [*Bombyx mori*] |
| CL8967.Contig3\_All | 10.21 | Up | Drosophila cueball like protein, partial [*Mythimna separata*] |
| CL6231.Contig7\_All | 10.21 | Up | PREDICTED: espin [*Amyelois transitella*] |
| Unigene5295\_All | 10.23 | Up | PREDICTED: uncharacterized protein LOC101740242 [*Bombyx mori*] |
| CL2029.Contig1\_All | 10.25 | Up | lipophorin receptor [*Galleria mellonella*] |
| CL3248.Contig3\_All | 10.31 | Up | PREDICTED: serine proteinase stubble isoform X3 [*Papilio machaon*] |
| CL10861.Contig2\_All | 10.36 | Up | hypothetical protein KGM\_13045 [*Danaus plexippus*] |
| CL12069.Contig6\_All | 10.37 | Up | Uncharacterized protein OBRU01\_05878 [*Operophtera brumata*] |
| CL9874.Contig2\_All | 11.08 | Up | PREDICTED: protein grainyhead isoform X1 [*Papilio machaon*] |
| CL4265.Contig3\_All | 11.39 | Up | PREDICTED: uncharacterized protein LOC101741662 [*Bombyx mori*] |
| CL2986.Contig1\_All | 11.95 | Up | PR domain zinc finger protein 1 [*Papilio xuthus*] |
| CL518.Contig6\_All | 11.95 | Up | unknown secreted protein [*Papilio polytes*] |
| CL263.Contig6\_All | 12.09 | Up | PREDICTED: alpha-protein kinase 1 [*Bombyx mori*] |

Table S9. Other Differentially expressed genes related to metamorphosis from P5 to P10

|  |  |  |  |
| --- | --- | --- | --- |
| **GeneID** | **log2Fold** | **Diff** | **Nr-annotation** |
| CL2722.Contig2\_All | -15.79 | Down | PREDICTED: uncharacterized protein LOC105385700 isoform X1 [*Plutella xylostella*] |
| Unigene13046\_All | -14.86 | Down | PREDICTED: uncharacterized protein LOC106130657 [*Amyelois transitella*] |
| CL17277.Contig2\_All | -14.83 | Down | PREDICTED: uncharacterized protein LOC106708361 isoform X2 [*Papilio machaon*] |
| CL18515.Contig2\_All | -14.82 | Down | PREDICTED: uncharacterized protein LOC105391587 isoform X1 [*Plutella xylostella*] |
| Unigene16002\_All | -14.16 | Down | PREDICTED: uncharacterized protein LOC106130655 [*Amyelois transitella*] |
| CL18515.Contig1\_All | -13.96 | Down | PREDICTED: uncharacterized protein LOC105391587 isoform X1 [*Plutella xylostella*] |
| CL2722.Contig1\_All | -13.82 | Down | PREDICTED: uncharacterized protein LOC101740498 isoform X2 [*Bombyx mori*] |
| CL18515.Contig3\_All | -13.34 | Down | PREDICTED: uncharacterized protein LOC105391587 isoform X1 [*Plutella xylostella*] |
| CL11267.Contig1\_All | -12.59 | Down | Osiris 21 [*Operophtera brumata*] |
| Unigene34787\_All | -12.59 | Down | PREDICTED: uncharacterized protein LOC106142223 isoform X3 [*Amyelois transitella*] |
| CL10049.Contig1\_All | -12.08 | Down | PREDICTED: proline-rich protein 4-like isoform X2 [*Bombyx mori*] |
| CL518.Contig6\_All | -11.74 | Down | unknown secreted protein [*Papilio polytes*] |
| CL3626.Contig1\_All | -11.54 | Down | chemosensory protein [*Mamestra brassicae*] |
| CL17277.Contig1\_All | -11.53 | Down | hypothetical protein RR46\_04252 [*Papilio xuthus*] |
| CL4535.Contig1\_All | -11.43 | Down | Uncharacterized protein OBRU01\_18039 [*Operophtera brumata*] |
| CL8437.Contig5\_All | -11.20 | Down | PREDICTED: uncharacterized protein LOC106714105 [*Papilio machaon*] |
| CL4265.Contig3\_All | -11.19 | Down | PREDICTED: uncharacterized protein LOC101741662 [*Bombyx mori*] |
| CL3387.Contig8\_All | -11.04 | Down | chemosensory protein 10 [*Spodoptera exigua*] |
| Unigene5238\_All | -10.88 | Down | cuticular protein RR-2 motif 133 precursor [*Bombyx mor*i] |
| CL11267.Contig2\_All | -10.84 | Down | Osiris 21 [*Operophtera brumata*] |
| CL4907.Contig18\_All | -10.83 | Down | PREDICTED: uncharacterized protein LOC101741030 [*Bombyx mori*] |
| Unigene29988\_All | -10.83 | Down | Uncharacterized protein OBRU01\_11895 [*Operophtera brumata*] |
| CL18179.Contig12\_All | -10.77 | Down | trypsinogen [*Helicoverpa punctigera*] |
| CL6957.Contig2\_All | -10.68 | Down | hypothetical protein RR46\_00551 [*Papilio xuthus*] |
| CL999.Contig1\_All | -10.67 | Down | rCG23821 [*Rattus norvegicus*] |
| CL15078.Contig2\_All | -10.63 | Down | Estrogen sulfotransferase [*Papilio xuthus*] |
| CL3327.Contig1\_All | -10.60 | Down | PREDICTED: hemicentin-1 [*Papilio xuthus*] |
| CL8437.Contig7\_All | -10.55 | Down | PREDICTED: uncharacterized protein LOC106714105 [*Papilio machaon*] |
| CL6957.Contig1\_All | -10.52 | Down | hypothetical protein RR46\_00551 [*Papilio xuthus*] |
| Unigene14906\_All | -10.49 | Down | PREDICTED: glycine-rich cell wall structural protein 1 [*Bombyx mori*] |
| CL10049.Contig2\_All | -10.47 | Down | PREDICTED: titin-like isoform X1 [*Bombyx mori*] |
| Unigene8507\_All | -10.35 | Down | PREDICTED: myb-like protein P [*Amyelois transitella*] |
| CL14881.Contig1\_All | -10.34 | Down | PREDICTED: uncharacterized protein LOC101741477 [*Bombyx mori*] |
| CL4265.Contig1\_All | -10.33 | Down | PREDICTED: uncharacterized protein LOC106130656 [*Amyelois transitella*] |
| CL12069.Contig6\_All | -10.33 | Down | Uncharacterized protein OBRU01\_05878 [*Operophtera brumata*] |
| Unigene26684\_All | -10.27 | Down | PREDICTED: plasma kallikrein-like [*Papilio xuthus*] |
| CL12410.Contig3\_All | -10.18 | Down | PREDICTED: uncharacterized protein LOC106138566 [*Amyelois transitella*] |
| Unigene19435\_All | -10.10 | Down | hypothetical protein OCBIM\_22009985mg, partial [*Octopus bimaculoides*] |
| CL11097.Contig6\_All | -10.09 | Down | endonuclease-reverse transcriptase [*Danaus plexippus*] |
| CL6171.Contig5\_All | -10.08 | Down | Serine protease inhibitor 28, partial [*Operophtera brumata*] |
| CL1111.Contig23\_All | -10.03 | Down | hypothetical protein KGM\_04229 [*Danaus plexippus*] |
| CL15746.Contig3\_All | -10.02 | Down | cryptopsoridial mucin, large thr stretch, signal peptide sequence [*Cryptosporidium parvum Iowa* II] |
| Unigene24478\_All | 10.01 | Up | Peptidyl-prolyl cis-trans isomerase 3 [*Toxocara canis*] |
| Unigene13934\_All | 10.02 | Up | chlorophyll a/b-binding protein II 1 [*Bigelowiella natans*] |
| CL19228.Contig1\_All | 10.03 | Up | PREDICTED: peroxidase-like [*Amyelois transitella*] |
| CL5586.Contig1\_All | 10.04 | Up | PREDICTED: suppressor protein SRP40-like [*Papilio polytes*] |
| CL398.Contig77\_All | 10.04 | Up | PREDICTED: transient-receptor-potential-like protein [*Bombyx mori*] |
| Unigene24660\_All | 10.07 | Up | unnamed protein product [*Vitrella brassicaformis* CCMP3155] |
| CL5226.Contig1\_All | 10.07 | Up | PREDICTED: FUN14 domain-containing protein 1 [*Amyelois transitella*] |
| CL16954.Contig2\_All | 10.08 | Up | PREDICTED: fibrohexamerin-like [*Bombyx mori*] |
| CL12917.Contig1\_All | 10.08 | Up | PREDICTED: cuticle protein 16.5, isoform A [*Bombyx mori*] |
| CL1877.Contig31\_All | 10.09 | Up | PREDICTED: proline-, glutamic acid- and leucine-rich protein 1 isoform X1 [*Amyelois transitella*] |
| Unigene23497\_All | 10.10 | Up | PREDICTED: uncharacterized protein LOC101740982 [*Bombyx mori*] |
| CL16954.Contig1\_All | 10.12 | Up | PREDICTED: fibrohexamerin-like [*Bombyx mori*] |
| CL17028.Contig7\_All | 10.12 | Up | PREDICTED: calphotin-like [*Amyelois transitella*] |
| CL4347.Contig5\_All | 10.13 | Up | PREDICTED: heterogeneous nuclear ribonucleoprotein R isoform X4 [*Amyelois transitella*] |
| CL7578.Contig3\_All | 10.13 | Up | PREDICTED: alpha-(1,3)-fucosyltransferase C-like [*Papilio polytes*] |
| CL920.Contig2\_All | 10.15 | Up | PREDICTED: shematrin-like protein 2 [*Bombyx mori*] |
| CL1473.Contig2\_All | 10.15 | Up | putative fatty acyl reductase FAR5, partial [*Spodoptera litura*] |
| Unigene24539\_All | 10.15 | Up | chlorophyll a/b binding protein CP29 [*Gymnochlora stellata*] |
| CL18581.Contig2\_All | 10.15 | Up | PREDICTED: mucin-5AC, partial [*Chlorocebus sabaeus*] |
| Unigene8640\_All | 10.16 | Up | PREDICTED: carbohydrate sulfotransferase 4-like [*Papilio xuthus*] |
| Unigene35167\_All | 10.17 | Up | photosystem II oxygen evolving enhancer protein 1 [*Gymnochlora stellata*] |
| CL2452.Contig3\_All | 10.17 | Up | PREDICTED: troponin I isoform X2 [*Papilio polytes*] |
| CL9784.Contig1\_All | 10.17 | Up | alcohol dehydrogenase 11, partial [*Helicoverpa assulta*] |
| CL515.Contig9\_All | 10.18 | Up | lysozyme-like protein 1 [*Spodoptera exigua*] |
| Unigene24743\_All | 10.19 | Up | Photosystem II 10 kDa polypeptide, chloroplast [*Salmo salar*] |
| CL16748.Contig2\_All | 10.22 | Up | PREDICTED: probable 4-coumarate--CoA ligase 1 [*Bombyx mori*] |
| CL3486.Contig3\_All | 10.23 | Up | peritrophin type-A domain protein 2 [*Danaus plexippus*] |
| CL583.Contig10\_All | 10.25 | Up | hypothetical protein KGM\_17086 [*Danaus plexippus*] |
| CL7350.Contig1\_All | 10.25 | Up | hypothetical protein RR46\_06980 [*Papilio xuthus*] |
| Unigene28152\_All | 10.26 | Up | Chlorophyll a-b binding protein, chloroplastic [*Trichinella nelsoni*] |
| CL1473.Contig3\_All | 10.27 | Up | putative fatty acyl reductase FAR5, partial [*Spodoptera litura*] |
| CL12767.Contig7\_All | 10.28 | Up | hypothetical protein RR48\_13663 [*Papilio machaon*] |
| CL469.Contig12\_All | 10.30 | Up | c-Cbl-associated protein isoform A [*Bombyx mori*] |
| CL5661.Contig2\_All | 10.31 | Up | hypothetical protein Y032\_0118g744 [*Ancylostoma ceylanicum*] |
| CL407.Contig4\_All | 10.34 | Up | PREDICTED: serine/threonine-protein kinase MARK2 [*Amyelois transitella*] |
| Unigene28201\_All | 10.36 | Up | fibrohexamerin homolog2 [*Samia ricini*] |
| CL19014.Contig2\_All | 10.40 | Up | hypothetical protein L798\_15423 [*Zootermopsis nevadensis*] |
| CL920.Contig1\_All | 10.45 | Up | PREDICTED: shematrin-like protein 2 [*Bombyx mori*] |
| CL5659.Contig1\_All | 10.47 | Up | PREDICTED: nose resistant to fluoxetine protein 6-like [*Amyelois transitella*] |
| CL7418.Contig1\_All | 10.48 | Up | PREDICTED: peroxidase-like isoform X1 [*Bombyx mori*] |
| CL12767.Contig8\_All | 10.49 | Up | hypothetical protein RR48\_13663 [*Papilio machaon*] |
| Unigene28331\_All | 10.50 | Up | Chlorophyll a-b binding protein, chloroplastic [*Trichinella nelsoni*] |
| CL9610.Contig4\_All | 10.50 | Up | larval cuticle protein A1A-like precursor [*Papilio polytes*] |
| CL10340.Contig4\_All | 10.55 | Up | PREDICTED: cuticle protein 70, isoforms A and B-like [*Amyelois transitella*] |
| CL10202.Contig3\_All | 10.55 | Up | PREDICTED: uncharacterized protein LOC106134414 [*Amyelois transitella*] |
| CL8444.Contig7\_All | 10.58 | Up | PREDICTED: proteasome subunit alpha type-5 isoform X1 [*Papilio machaon*] |
| Unigene8221\_All | 10.60 | Up | hypothetical protein EPH\_0019170 [*Eimeria praecox*] |
| CL647.Contig1\_All | 10.62 | Up | ribulose bisphosphate carboxylase/oxygenase small subunit 1 [*Gymnochlora stellata*] |
| Unigene20999\_All | 10.66 | Up | hypothetical protein KGM\_12987 [*Danaus plexippus*] |
| CL1959.Contig8\_All | 10.69 | Up | PREDICTED: low density lipoprotein receptor adapter protein 1-like [*Amyelois transitella*] |
| Unigene4824\_All | 10.69 | Up | neuropeptide-like precursor 4C [*Bombyx mori*] |
| CL7184.Contig45\_All | 10.71 | Up | PREDICTED: uncharacterized protein LOC105442198 [*Strongylocentrotus purpuratus*] |
| Unigene23819\_All | 10.71 | Up | PREDICTED: fibrohexamerin-like [*Bombyx mori*] |
| Unigene14119\_All | 10.71 | Up | Light-regulated protein, partial [*Trichinella nelsoni*] |
| CL923.Contig14\_All | 10.72 | Up | beta-N-acetylglucosaminidase [*Mamestra brassicae*] |
| Unigene13906\_All | 10.73 | Up | putative thiazole biosynthetic enzyme, partial [*Hirudo medicinalis*] |
| Unigene26899\_All | 10.73 | Up | PREDICTED: indole-3-acetaldehyde oxidase-like [*Bombyx mori*] |
| CL5904.Contig7\_All | 10.74 | Up | PREDICTED: transmembrane protease serine 9-like [*Papilio xuthus*] |
| CL8069.Contig1\_All | 10.75 | Up | PREDICTED: ejaculatory bulb-specific protein 3-like [*Plutella xylostella*] |
| CL150.Contig22\_All | 10.80 | Up | peptidoglycan recognition protein C [*Helicoverpa armigera*] |
| CL12767.Contig4\_All | 10.80 | Up | hypothetical protein RR48\_13663 [*Papilio machaon*] |
| CL12822.Contig1\_All | 10.86 | Up | Unknown (protein for IMAGE:5194336), partial [*Homo sapiens*] |
| CL13445.Contig1\_All | 10.86 | Up | cytochrome CYP340K4 [*Spodoptera littoralis*] |
| CL923.Contig2\_All | 10.88 | Up | beta-N-acetylglucosaminidase [*Mamestra brassicae*] |
| CL647.Contig2\_All | 10.88 | Up | ribulose bisphosphate carboxylase/oxygenase small subunit 1 [*Gymnochlora stellata*] |
| CL3899.Contig5\_All | 10.92 | Up | PREDICTED: fatty acid synthase [*Papilio xuthus*] |
| CL1643.Contig134\_All | 10.92 | Up | PREDICTED: trypsin-1-like [*Bombyx mori*] |
| CL19014.Contig1\_All | 10.93 | Up | PREDICTED: flocculation protein FLO11-like isoform X1 [*Lingula anatina*] |
| CL4011.Contig13\_All | 10.93 | Up | PREDICTED: angiomotin-like [*Bombyx mori*] |
| CL17028.Contig8\_All | 10.94 | Up | cuticle protein 19.8-like precursor [*Papilio polytes*] |
| CL12767.Contig3\_All | 10.95 | Up | hypothetical protein RR48\_13663 [*Papilio machaon*] |
| CL17028.Contig2\_All | 10.98 | Up | PREDICTED: calphotin-like [*Amyelois transitella*] |
| Unigene24511\_All | 11.00 | Up | PREDICTED: cuticle protein 8-like [*Amyelois transitella*] |
| CL469.Contig10\_All | 11.04 | Up | c-Cbl-associated protein isoform A [*Bombyx mori*] |
| CL17028.Contig3\_All | 11.05 | Up | cuticular protein RR-2 motif 68 precursor [*Bombyx mori*] |
| CL11036.Contig3\_All | 11.07 | Up | PREDICTED: transmembrane protease serine 9-like [*Bombyx mori*] |
| CL9452.Contig2\_All | 11.09 | Up | PREDICTED: extensin-like [*Bombyx mori*] |
| CL632.Contig9\_All | 11.12 | Up | PREDICTED: PDZ and LIM domain protein 3 isoform X6 [*Bombyx mori*] |
| Unigene19421\_All | 11.15 | Up | PREDICTED: endocuticle structural glycoprotein SgAbd-8-like [*Plutella xylostella*] |
| Unigene22410\_All | 11.16 | Up | Uncharacterized protein OBRU01\_12140, partial [*Operophtera brumata*] |
| CL407.Contig25\_All | 11.16 | Up | PREDICTED: serine/threonine-protein kinase MARK2 [*Amyelois transitella*] |
| CL17028.Contig1\_All | 11.16 | Up | PREDICTED: calphotin-like [*Amyelois transitella*] |
| Unigene31610\_All | 11.21 | Up | Metallothionein-like protein type 3 [*Trichinella patagoniensis*] |
| CL6851.Contig1\_All | 11.26 | Up | Myosin-XVIIIa [*Papilio xuthus*] |
| CL8069.Contig6\_All | 11.35 | Up | PREDICTED: ejaculatory bulb-specific protein 3-like [*Plutella xylostella*] |
| CL920.Contig3\_All | 11.36 | Up | PREDICTED: shematrin-like protein 2 [*Bombyx mori*] |
| CL12767.Contig6\_All | 11.40 | Up | hypothetical protein RR48\_13663 [*Papilio machaon*] |
| CL12822.Contig3\_All | 11.42 | Up | Chlorophyll a-b binding protein 40, chloroplastic [*Trichinella nelsoni*] |
| CL2462.Contig4\_All | 11.44 | Up | PREDICTED: uncharacterized protein LOC106711210 isoform X3 [*Papilio machaon*] |
| Unigene6793\_All | 11.47 | Up | PREDICTED: keratinocyte proline-rich protein-like [*Papilio polytes*] |
| Unigene10416\_All | 11.54 | Up | PREDICTED: catalase-like [*Amyelois transitella*] |
| Unigene24702\_All | 11.58 | Up | PREDICTED: trans-1,2-dihydrobenzene-1,2-diol dehydrogenase-like isoform X2 [*Papilio polytes*] |
| CL13109.Contig2\_All | 11.61 | Up | PREDICTED: titin [*Bombyx mori*] |
| CL4544.Contig7\_All | 11.64 | Up | PREDICTED: uncharacterized protein LOC106139265 [*Amyelois transitella*] |
| CL2266.Contig2\_All | 11.66 | Up | PREDICTED: uncharacterized protein LOC101739678 [*Bombyx mori*] |
| CL4833.Contig1\_All | 11.80 | Up | PREDICTED: cuticle protein 19.8-like [*Papilio machaon*] |
| CL3960.Contig1\_All | 11.83 | Up | PREDICTED: titin-like [*Amyelois transitella*] |
| CL17028.Contig5\_All | 11.84 | Up | PREDICTED: calphotin-like [*Amyelois transitella*] |
| CL14877.Contig1\_All | 11.86 | Up | PREDICTED: uncharacterized protein LOC106143533 [*Amyelois transitella*] |
| CL11037.Contig1\_All | 11.99 | Up | Glucose dehydrogenase [acceptor] [Papilio machaon] |
| CL9610.Contig5\_All | 11.99 | Up | larval cuticle protein A1A-like precursor [*Papilio polytes*] |
| CL7418.Contig2\_All | 12.09 | Up | PREDICTED: peroxidase-like isoform X1 [*Bombyx mori*] |
| Unigene19983\_All | 12.10 | Up | PREDICTED: cuticular protein RR-2 motif 106 isoform X1 [*Bombyx mori*] |
| CL9610.Contig1\_All | 12.11 | Up | PREDICTED: calphotin-like [*Amyelois transitella*] |
| CL8069.Contig3\_All | 12.12 | Up | PREDICTED: ejaculatory bulb-specific protein 3-like [*Plutella xylostella*] |
| CL632.Contig12\_All | 12.13 | Up | PREDICTED: PDZ and LIM domain protein 3 isoform X5 [*Plutella xylostella*] |
| Unigene30854\_All | 12.19 | Up | putative cuticle protein [*Manduca sexta*] |
| CL10202.Contig2\_All | 12.21 | Up | PREDICTED: uncharacterized protein LOC106134414 [*Amyelois transitella*] |
| CL14877.Contig3\_All | 12.22 | Up | PREDICTED: uncharacterized protein LOC106143533 [*Amyelois transitella*] |
| CL12445.Contig6\_All | 12.23 | Up | PREDICTED: TBC1 domain family member 24 isoform X4 [*Papilio polytes*] |
| CL14877.Contig2\_All | 12.25 | Up | PREDICTED: uncharacterized protein LOC106101210 isoform X2 [*Papilio polytes*] |
| CL13006.Contig2\_All | 12.27 | Up | PREDICTED: catalase-like [*Bombyx mori*] |
| CL2266.Contig1\_All | 12.30 | Up | PREDICTED: uncharacterized protein LOC101739678 [*Bombyx mori*] |
| Unigene6324\_All | 12.30 | Up | hypothetical protein RR46\_09325 [*Papilio xuthus*] |
| CL12581.Contig1\_All | 12.36 | Up | PREDICTED: uncharacterized protein LOC106136348 [*Amyelois transitella*] |
| CL17028.Contig6\_All | 12.36 | Up | PREDICTED: calphotin-like [*Amyelois transitella*] |
| CL10195.Contig3\_All | 12.45 | Up | unnamed protein product [*Tetraodon nigroviridis*] |
| CL15909.Contig3\_All | 12.46 | Up | PREDICTED: endocuticle structural glycoprotein ABD-5-like [*Papilio polytes*] |
| Unigene13431\_All | 12.48 | Up | PREDICTED: catalase-like [*Bombyx mori*] |
| Unigene23942\_All | 12.54 | Up | PREDICTED: uncharacterized family 31 glucosidase KIAA1161-like [*Amyelois transitella*] |
| Unigene17667\_All | 12.57 | Up | PREDICTED: vegetative cell wall protein gp1-like [*Papilio machaon*] |
| Unigene21007\_All | 12.59 | Up | PREDICTED: catalase-like [*Papilio xuthus*] |
| CL12581.Contig2\_All | 12.67 | Up | PREDICTED: uncharacterized protein LOC106136348 [*Amyelois transitella*] |
| CL12767.Contig1\_All | 12.72 | Up | PREDICTED: larval/pupal cuticle protein H1C-like [*Papilio xuthus*] |
| Unigene27353\_All | 12.74 | Up | Uncharacterized protein OBRU01\_15710 [*Operophtera brumata*] |
| CL9121.Contig1\_All | 12.84 | Up | PREDICTED: cuticle protein 16.5, isoform B-like [*Papilio xuthus*] |
| CL1794.Contig8\_All | 12.89 | Up | PREDICTED: apoptosis-stimulating of p53 protein 1 isoform X2 [*Papilio xuthus*] |
| Unigene20194\_All | 12.95 | Up | PREDICTED: cuticle protein 64-like [*Plutella xylostella*] |
| CL13006.Contig1\_All | 13.00 | Up | PREDICTED: catalase-like [*Bombyx mori*] |
| Unigene10298\_All | 13.07 | Up | TPA: Uncharacterized ATP-dependent helicase [*Neospora caninum Liverpool*] |
| CL19667.Contig1\_All | 13.07 | Up | PREDICTED: cuticle protein 76-like [*Amyelois transitella*] |
| CL19667.Contig2\_All | 13.08 | Up | PREDICTED: cuticle protein 76-like [*Amyelois transitella*] |
| CL14919.Contig1\_All | 13.14 | Up | PREDICTED: flightin [*Amyelois transitella*] |
| CL10195.Contig1\_All | 13.15 | Up | PREDICTED: histidine-rich glycoprotein-like [*Papilio polytes*] |
| CL11036.Contig1\_All | 13.20 | Up | PREDICTED: trypsin-3-like [*Amyelois transitella*] |
| Unigene21041\_All | 13.47 | Up | PREDICTED: fibrohexamerin-like [*Bombyx mori*] |
| CL10931.Contig1\_All | 13.54 | Up | PREDICTED: catalase-like [*Bombyx mori*] |
| CL9531.Contig2\_All | 13.74 | Up | PREDICTED: glutamate receptor ionotropic, kainate 2-like [*Plutella xylostella*] |
| Unigene10354\_All | 14.07 | Up | PREDICTED: uncharacterized protein LOC106716514 [*Papilio machaon*] |
| CL10195.Contig2\_All | 14.07 | Up | PREDICTED: histidine-rich glycoprotein-like [*Papilio xuthus*] |
| CL16710.Contig1\_All | 14.20 | Up | PREDICTED: histidine-rich glycoprotein-like [*Bombyx mori*] |
| CL7324.Contig6\_All | 14.30 | Up | troponin T isoform F [*Spodoptera frugiperda*] |
| CL15909.Contig2\_All | 14.53 | Up | PREDICTED: endocuticle structural glycoprotein ABD-5-like [*Papilio polytes*] |
| CL169.Contig111\_All | 14.56 | Up | PREDICTED: transmembrane protease serine 9-like [*Papilio xuthus*] |
| CL11993.Contig9\_All | 14.62 | Up | PREDICTED: probable malate dehydrogenase, mitochondrial [*Papilio machaon*] |
| CL13109.Contig1\_All | 15.85 | Up | PREDICTED: uncharacterized protein LOC105384628 [*Plutella xylostella*] |
| CL920.Contig6\_All | 16.92 | Up | PREDICTED: cuticle protein 64-like [*Papilio polytes*] |

**Figure legends**

**Figure S1** Statistics of unigene database. GO: Gene Ontology; COG: Clusters of Orthologous Groups of proteins; KEGG: Kyoto Encyclopedia of Genes and Genomes; NR: non-redundant protein sequences; NT: non-redundant nucleic acid sequence; SwissProt: manual annotation and expected, non-redundant protein database.

**Figure S2** Venn diagram of annotation results against NR, NT, COG, KEGG and SwissProt.

**Figure S3** The top-hits species in the annotated distribution of unigene against NR. The X-axis represents the number of unigene of the corresponding species, and the Y-axis represents the species of NR.

**Figure S4** Statistics of the number of differently expressed genes (DEGs) among the remaining 6 groups of samples.

**Figure S5** Signal transduction. The X-axis represents the number of unigenes and the Y-axis represents the KEGG functional classification.

**Figure S6** Phylogenetic analysis of the cuticular proteins from *M.separata* (Green), *H.armigera* (Red), *S.litura* (Orange), *T.ni* (DarkSalmon), *S.frugiperda* (Pink), *G.mellonella* (Blue) and *B.mori* (Purple). A distance neighbor-joining tree was generated using MEGA 7.0. Nodes with distance bootstrap values (1000 replicates) are shown.

**Figure S7** Phylogenetic analysis of juvenile hormone from *M.separata* (Green), *S.litura* (Orange), *A.dissimilis* (Yellow), *T.ni* (DarkSalmon), *G.mellonella* (Blue) and *B.mori* (Purple). A distance neighbor-joining tree was generated using MEGA 7.0. Nodes with distance bootstrap values (1000 replicates) are shown.

**Figure S8** Phylogenetic analysis of 20-hydroxyecdysone from *M.separata* (Green), *H.armigera* (Red), *A.dissimilis* (Yellow), *S.litura* (Orange) and *S.exigua* (MediumBlue). A distance neighbor-joining tree was generated using MEGA 7.0. Nodes with distance bootstrap values (1000 replicates) are shown.



**Figure S1**

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**Figure S2**

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**Figure S3**

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**Figure S4**

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**Figure S5**

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**Figure S6**

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**Figure S7**

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**Figure S8**