**Appendix**

**Table S1 Primers used for validation**

|  |  |  |
| --- | --- | --- |
| **Gene ID** | **Gene Name** | **Primers (5' to 3')** |
| transcript\_90 | myosin heavy chain type 1a | GGTGAACCGCACTTTGA |
| CTGGCTGACTTGGCTTT |
| transcript\_91 | myosin heavy chain type 1b | CGCAACTTGGAACACGATA |
| CGCCCTCGGACTCATACTT |

**Table S2 DEPs statistics of SG40 vs. FG40**

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| **ID** | **Annotation** | **Species** | **log2FC** | **regulated** |
| transcript\_50 | myosin heavy chain type a | *Marsupenaeus japonicus* | 0.81 | up |
| transcript\_5822 | actin 1a | *Fenneropenaeus chinensis* | 0.56 | up |
| transcript\_2192 | heat shock protein 21 | *Macrobrachium rosenbergii* | 0.53 | up |
| transcript\_1516 | glycerol-3-phosphate dehydrogenase | *Nasonia vitripennis* | 0.52 | up |
| transcript\_4523 | LOC103524650 | *Diaphorina citri* | 0.52 | up |
| transcript\_3934 | sarcoplasmic calcium-binding protein | *Litopenaeus vannamei* | 0.51 | up |
| transcript\_4029 | actin 1 | *Fenneropenaeus chinensis* | 0.50 | up |
| transcript\_2405 | glucose-6-phosphate isomerase | *Spodoptera exigua* | 0.44 | up |
| transcript\_6139 | phosphorylase b kinase regulatory subunit alpha-like isoform 2 | *Megachile rotundata* | 0.44 | up |
| transcript\_15197 | skeletal muscle actin 6 | *Homarus americanus* | 0.42 | up |
| transcript\_15574 | Coiled-coil domain-containing protein 47 | *Stegodyphus mimosarum* | 0.40 | up |
| transcript\_3182 | triose-phosphate isomerase | *Litopenaeus vannamei* | 0.37 | up |
| transcript\_10217 | phosphorylase b kinase regulatory subunit beta | *Zootermopsis nevadensis* | 0.32 | up |
| transcript\_3403 | 2,3-bisphosphoglycerate-dependent phosphoglycerate mutase | *Daphnia pulex* | 0.31 | up |
| transcript\_3624 | fructose 1,6-bisphosphatase | *Marsupenaeus japonicus* | 0.30 | up |
| transcript\_1085 | mediator of RNA polymerase II transcription subunit 31 | *Solenopsis invicta* | 0.29 | up |
| transcript\_2330 | AaeL\_AAEL000536 | *Aedes aegypti* | 0.27 | up |
| transcript\_1312 | nucleotide excision repair protein | *Marsupenaeus japonicus* | 0.24 | up |
| transcript\_353 | calcineurin subunit A | *Eriocheir sinensis* | 0.23 | up |
| transcript\_10625 | Myosin light chain kinase | *Toxocara canis* | 0.23 | up |
| transcript\_1536 | protein lethal (2) essential for life-like | *Megachile rotundata* | 0.23 | up |
| transcript\_10565 | Cytoplasmic dynein 1 light intermediate chain 2 | *Zootermopsis nevadensis* | 0.23 | up |
| transcript\_4213 | LOTGIDRAFT\_232738 | *Lottia gigantea* | 0.23 | up |
| transcript\_12761 | 2-oxoglutarate dehydrogenase | *Culex quinquefasciatus* | 0.20 | up |
| transcript\_4302 | DJ-1 protein | *Litopenaeus vannamei* | 0.18 | up |
| transcript\_4936 | ubiquitin | *Procambarus clarkii* | 0.14 | up |
| transcript\_14792 | DAPPUDRAFT\_320916 | *Daphnia pulex* | 0.14 | up |
| transcript\_1495 | SINV\_80052 | *Solenopsis invicta* | 0.13 | up |
| transcript\_516 | EH domain-containing protein 1-like | *Daphnia pulex* | -0.08 | down |
| transcript\_6604 | actin 2 | *Penaeus monodon* | -0.09 | down |
| transcript\_2268 | cyclophilin A | *Litopenaeus vannamei* | -0.12 | down |
| transcript\_4790 | ribosomal protein L10a | *Fenneropenaeus merguiensis* | -0.17 | down |
| transcript\_10514 | 14-3-3 epsilon-like | *Litopenaeus vannamei* | -0.19 | down |
| transcript\_2496 | proliferation-associated protein 2G4-like | *Megachile rotundata* | -0.21 | down |
| transcript\_4729 | heat shock protein 10 | *Scylla paramamosain* | -0.21 | down |
| transcript\_5905 | Shootin-1 | *Zootermopsis nevadensis* | -0.25 | down |
| transcript\_12151 | Tubulin beta-2 chain | *Homarus americanus* | -0.29 | down |
| transcript\_4902 | NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 9 | *Zootermopsis nevadensis* | -0.30 | down |
| transcript\_4982 | ribosomal protein L24 | *Marsupenaeus japonicus* | -0.31 | down |
| transcript\_10357 | histone H1-delta-like | *Aplysia californica* | -0.35 | down |
| transcript\_5097 | ribosomal protein S25 | *Ixodes scapularis* | -0.35 | down |
| transcript\_4971 | 60s ribosomal protein l27a | *Ascaris suum* | -0.36 | down |
| transcript\_11264 | clottable protein | *Marsupenaeus japonicus* | -0.40 | down |
| transcript\_5111 | ribosomal protein L44 | *Procambarus clarkii* | -0.43 | down |
| transcript\_4483 | sarcoplasmic calcium-binding protein, beta chain | *Penaeus sp.* | -0.49 | down |
| transcript\_4129 | T265\_13221 | *Opisthorchis viverrini* | -0.52 | down |
| transcript\_10746 | myosin heavy chain type 2 | *Penaeus monodon* | -0.54 | down |
| transcript\_11623 | myosin heavy chain type b | *Marsupenaeus japonicus* | -0.66 | down |
| transcript\_6703 | GM19733 | *Drosophila sechellia* | -0.69 | down |
| transcript\_10737 | actin 2 | *Penaeus monodon* | -0.81 | down |
| transcript\_91 | myosin heavy chain type 1b | *Litopenaeus vannamei* | -0.95 | down |
| transcript\_90 | myosin heavy chain type 1a | *Litopenaeus vannamei* | -1.00 | down |

**Table S3 DEPs statistics of SG70 vs. FG70**

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| **ID** | **Annotation** | **Species** | **log2FC** | **regulated** |
| transcript\_7770 | cactus protein | *Litopenaeus vannamei* | 0.75 | up |
| transcript\_2449 | pyruvate kinase 3 | *Litopenaeus vannamei* | 0.48 | up |
| transcript\_1516 | glycerol-3-phosphate dehydrogenase | *Nasonia vitripennis* | 0.41 | up |
| transcript\_11514 | glycogen debranching enzyme isoform X2 | *Microplitis demolitor* | 0.40 | up |
| transcript\_2405 | glucose-6-phosphate isomerase | *Spodoptera exigua* | 0.29 | up |
| transcript\_1121 | YQE\_04268 | *Dendroctonus ponderosae* | 0.28 | up |
| transcript\_4212 | COP9 signalosome complex subunit 7a | *Zootermopsis nevadensis* | 0.22 | up |
| transcript\_5955 | Deoxyribonuclease tatD | *Lepeophtheirus salmonis* | 0.15 | up |
| transcript\_2268 | cyclophilin A | *Litopenaeus vannamei* | -0.11 | down |
| transcript\_1118 | GTP-binding protein CG1354-like | *Bombus terrestris* | -0.12 | down |
| transcript\_2070 | Phosphoglycolate phosphatase | *Cerapachys biroi* | -0.14 | down |
| transcript\_9510 | protein ROP | *Pediculus humanus corporis* | -0.16 | down |
| transcript\_4776 | prefoldin subunit 4-like | *Aplysia californica* | -0.18 | down |
| transcript\_1590 | BRAFLDRAFT\_122807 | *Branchiostoma floridae* | -0.18 | down |
| transcript\_935 | integrin | *Litopenaeus vannamei* | -0.19 | down |
| transcript\_12360 | Protein transport protein Sec24B | *Cerapachys biroi* | -0.19 | down |
| transcript\_4552 | prefoldin | *Ixodes scapularis* | -0.19 | down |
| transcript\_12753 | DAPPUDRAFT\_41019 | *Daphnia pulex* | -0.20 | down |
| transcript\_352 | 10-formyltetrahydrofolate dehydrogenase | *Zootermopsis nevadensis* | -0.20 | down |
| transcript\_2759 | eukaryotic initiation factor 4A | *Litopenaeus vannamei* | -0.21 | down |
| transcript\_4915 | ribosomal protein L11 | *Triatoma infestans* | -0.21 | down |
| transcript\_4802 | ribosomal protein L14 | *Lysiphlebus testaceipes* | -0.21 | down |
| transcript\_4440 | proteasome subunit beta type-1 | *Tribolium castaneum* | -0.23 | down |
| transcript\_1982 | BRAFLDRAFT\_285686 | *Branchiostoma floridae* | -0.25 | down |
| transcript\_13573 | Tyrosine-protein kinase CSK | *Stegodyphus mimosarum* | -0.25 | down |
| transcript\_15296 | DAPPUDRAFT\_189511 | *Daphnia pulex* | -0.25 | down |
| transcript\_9605 | patatin-like phospholipase domain-containing protein 2-like isoform X2 | *Ceratitis capitata* | -0.26 | down |
| transcript\_9952 | H+ transporting ATP synthase O subunit | *Antheraea yamamai* | -0.26 | down |
| transcript\_2496 | proliferation-associated protein 2G4-like | *Megachile rotundata* | -0.26 | down |
| transcript\_894 | DAPPUDRAFT\_321849 | *Daphnia pulex* | -0.26 | down |
| transcript\_9625 | myosin heavy chain type b | *Marsupenaeus japonicus* | -0.27 | down |
| transcript\_2525 | DAPPUDRAFT\_306997 | *Daphnia pulex* | -0.27 | down |
| transcript\_12854 | tropomodulin isoform X6 | *Tribolium castaneum* | -0.28 | down |
| transcript\_3589 | rRNA 2&apos;-O-methyltransferase fibrillarin | *Zootermopsis nevadensis* | -0.28 | down |
| transcript\_4691 | BRAFLDRAFT\_59133 | *Branchiostoma floridae* | -0.29 | down |
| transcript\_5223 | 40S ribosomal protein S28-like | *Strongylocentrotus purpuratus* | -0.29 | down |
| transcript\_516 | EH domain-containing protein 1-like | *Daphnia pulex* | -0.30 | down |
| transcript\_10954 | LIM and senescent cell antigen-like-containing domain protein 1-like isoform X1 | *Ceratitis capitata* | -0.31 | down |
| transcript\_10514 | 14-3-3 epsilon-like | *Litopenaeus vannamei* | -0.31 | down |
| transcript\_4939 | ribosomal protein S17 | *Branchiostoma belcheri* | -0.31 | down |
| transcript\_1029 | glycosyl-phosphatidylinositol-linked carbonic anhydrase | *Litopenaeus vannamei* | -0.32 | down |
| transcript\_2651 | Protein msta, isoform A | *Zootermopsis nevadensis* | -0.32 | down |
| transcript\_2202 | DAPPUDRAFT\_309332 | *Daphnia pulex* | -0.32 | down |
| transcript\_2531 | COP9 signalosome complex subunit 2 | *Nasonia vitripennis* | -0.33 | down |
| transcript\_8699 | DAPPUDRAFT\_305817 | *Daphnia pulex* | -0.36 | down |
| transcript\_3099 | CAPTEDRAFT\_177589 | *Capitella teleta* | -0.36 | down |
| transcript\_14551 | 25-kDa subunit RNA polymerase | *Ornithodoros parkeri* | -0.36 | down |
| transcript\_422 | Eukaryotic translation initiation factor 5-like | *Daphnia pulex* | -0.36 | down |
| transcript\_1989 | BRAFLDRAFT\_270056 | *Branchiostoma floridae* | -0.36 | down |
| transcript\_10484 | ribosomal protein S18 | *Procambarus clarkii* | -0.38 | down |
| transcript\_3286 | bifunctional methylenetetrahydrofolate dehydrogenase/cyclohydrolase, mitochondrial | *Acyrthosiphon pisum* | -0.38 | down |
| transcript\_9552 | TOM1-like protein 2 | *Zootermopsis nevadensis* | -0.39 | down |
| transcript\_2785 | TNF superfamily ligand Eiger homologue | *Marsupenaeus japonicus* | -0.41 | down |
| transcript\_2463 | UMP-CMP kinase | *Zootermopsis nevadensis* | -0.41 | down |
| transcript\_4248 | ribosomal protein rpl6 | *Glycera tridactyla* | -0.41 | down |
| transcript\_13987 | ubiquitin-conjugating enzyme E2 b | *Eriocheir sinensis* | -0.42 | down |
| transcript\_53 | myosin heavy chain type 1 | *Litopenaeus vannamei* | -0.42 | down |
| transcript\_11202 | protein OPI10 homolog | *Apis mellifera* | -0.44 | down |
| transcript\_4729 | heat shock protein 10 | *Scylla paramamosain* | -0.44 | down |
| transcript\_2025 | vacuolar protein-sorting-associated protein 25-like | *Saccoglossus kowalevskii* | -0.46 | down |
| transcript\_91 | myosin heavy chain type 1b | *Litopenaeus vannamei* | -0.50 | down |
| transcript\_10921 | DAPPUDRAFT\_222043 | *Daphnia pulex* | -0.52 | down |
| transcript\_1831 | beta-tubulin | *Mythimna separata* | -0.52 | down |
| transcript\_12024 | muscle M-line assembly protein unc-89 isoform X2 | *Acromyrmex echinatior* | -0.55 | down |
| transcript\_4982 | ribosomal protein L24 | *Marsupenaeus japonicus* | -0.60 | down |
| transcript\_1980 | -- | *--* | -0.70 | down |
| transcript\_4833 | crustacyanin subunit C | *Fenneropenaeus merguiensis* | -0.82 | down |
| transcript\_90 | myosin heavy chain type 1a | *Litopenaeus vannamei* | -0.84 | down |
| transcript\_2418 | DAPPUDRAFT\_302108 | *Daphnia pulex* | -1.17 | down |
| transcript\_141 | paramyosin | *Papilio xuthus* | -1.49 | down |

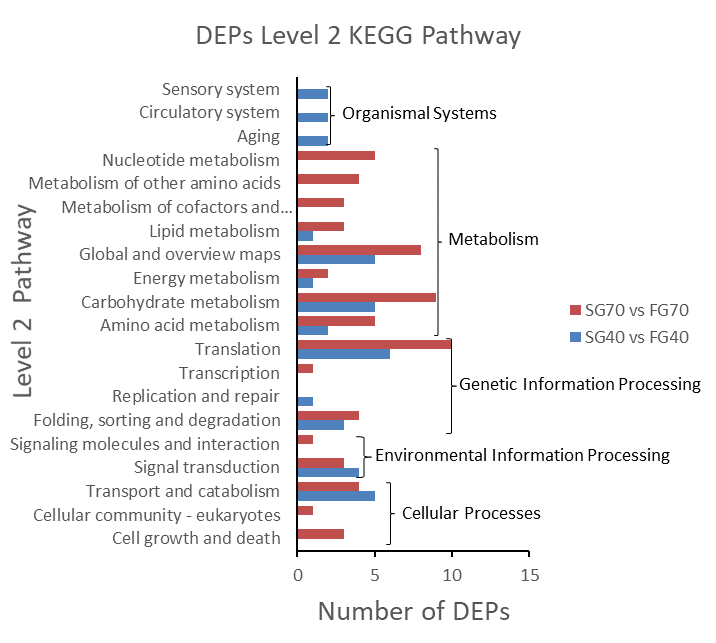


Fig. S1. Level 2 KEGG pathway analysis of DEPs in *M. japonicus*.