# Supplementary Figure Captions

**Supplementary Figure 1.** Overview of the experimental design and analysis pipeline. Three biological replicates per condition were sampled for the mRNA and miRNA sequencing. The raw data were assessed and filtered using FastQC and were assembled using Trinity to obtain the reference genome.

**Supplementary Figure 2.** Details of transcriptome sequencing, assembly, and annotation. (**A**) Statistics of the top 10 species with the largest number of reads for sequence alignment (an example from sample HC1). (**B**) Venn diagram showing the overlap of NR, KEGG, KOG, GO, and SwissProt; numbers in each circle indicate the number of annotated unigenes. (**C**) GC content frequency distribution of assembled unigenes. (**D**) Length distribution of assembled unigenes.

**Supplementary Figure 3.** Details of the miRNA sequencing and analysis. (**A**) Length distribution of clean reads from sample HC1. (**B**) Length distribution statistics of known miRNAs detected in nine samples.

**Supplementary Figure 4.** Differentially expressed genes (DEGs) and differentially expressed miRNAs (DEMs) in the three pairwise comparisons. (**A**) DEG distribution in the three pairwise comparisons. (**B**)Validation of the differential expression of 12 genes from qPCR and RNA-Seq (HC vs LC). (**C**) DEM distribution in the three pairwise comparisons (numbers on the bar graph represent the number of DEGs or DEMs). (**D**) Validation of the differential expression of six miRNAs from qPCR and miRNA-Seq (HC vs LC).



**Supplementary Figure 1.**



**Supplementary Figure 2.**



**Supplementary Figure 3.**



**Supplementary Figure 4.**

**Supplementary Table 1.** Primer list for the selected DEGs and DEMs in the qRT-PCR validation experiments.

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| --- | --- |
| Gene/miRNA | Forward/reverse primer (5′-3′) |
| Troponin C2 (TC2) | F:5'GCTGATTCCACAGGCAAG3' R:5'CTCGCCTCGAAGTGCCTA3' |
| Calmodulin (Cal) | F:5'GATCAGAGAAGCTGATGTCG3' R:5'ACAACAGGTCCAGTTGTAAG3' |
| Chloride channel protein-like isoform X4 (CCP4) | F:5'ACACCTGTGAACTGTGATCTAA3' R:5'ATGTCTGGTGATGCCAAC3' |
| Kazal type protease inhibitor (Kazal) | F:5'TACAACAACGACTGCGAAC3' R:5'GCCTTGAGGCATTCACAT3' |
| Metallothionein (Met) | F:5'CCCTGTGAGAAATGCACAAC3' R:5'CTTGGAGCAAGTCTTGGC3' |
| Myosin heavy chain (MHC) | F:5'CCGACGAGAAGGAAAGTTATG3' R:5'TCTCCTCCCGGAATGCTA3' |
| Neuroparsin (Neu) | F:5'GAGACTCTCCCGGAAGATTG3' R:5'TCGACAGACTTCGCAGCA3' |
| Na+/K+/2Cl- cotransporter (NKC) | F:5'CAGACACAAAGAGTGCGTAAT3' R:5'ACAATGGAGTAGAAGCTACGA3' |
| PP2A catalytic (PP2Ac) | F:5'ACGAGAAGATTGTCACGG3' R:5'CGACCATGTAACCAGCTAGA3' |
| prophenoloxidase 2 (Prop) | F:5'AAGCTCACCTTGAATAACTCAG3' R:5'CTGCATTGTGGTATCGTCC3' |
| sarcoplasmic calcium-binding protein (SCB) | F:5'AGGTTGGCCTCGATGAGTA3' R:5'TTCACCTCAGCAAAGGCAGA3' |
| sodium/potassium-transporting ATPase (SPA) | F:5'GCCAAAGTACACTCCAACG3' R:5'GGATGTTCTTGGGCGAAT3' |
| EF-1α | F:5'ATTGGAGGTATTGGAACAGTGCC3' R:5'TCGGTAAGAGCTTCGTGGTGC3' |
| efu-miR-133-3p | TGGTCCCCTTCAACCAGCTGTA |
| efu-miR-152 | GTCAGTGCATGACAGAACTTGGGC |
| aae-miR-34-5p | TGGCAGTGTGGTTAGCTGGTTG |
| bbe-miR-10a-5p | TACCCTGTAGATCCGAATTTGT |
| ccr-miR-100 | AACCCGTAGATCCGAACTTGT |
| odi-miR-1c | GCTGGAATGTAAAGAAGTATGTGA |
| U6 | CAAGGATGACACGCAAATTCG |