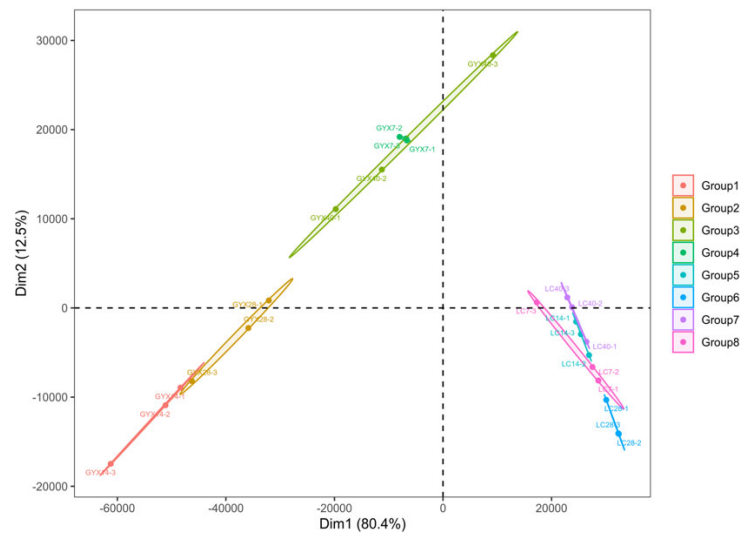
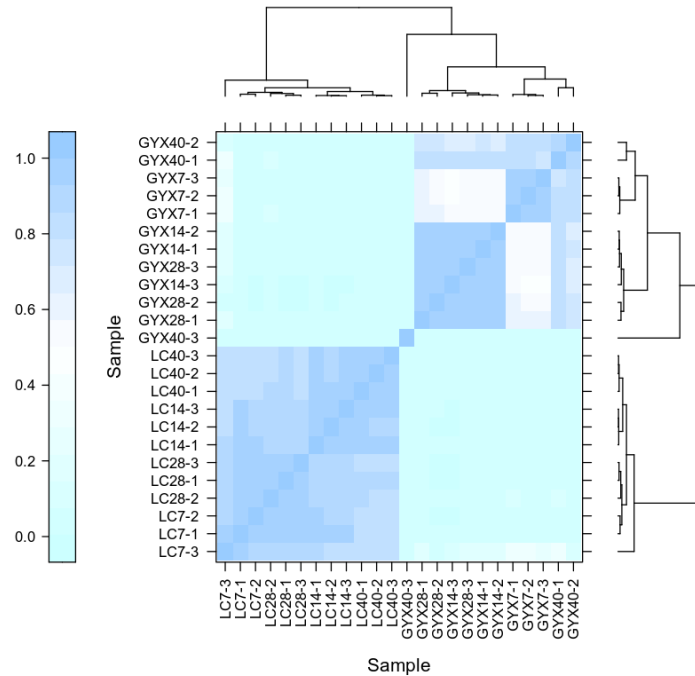


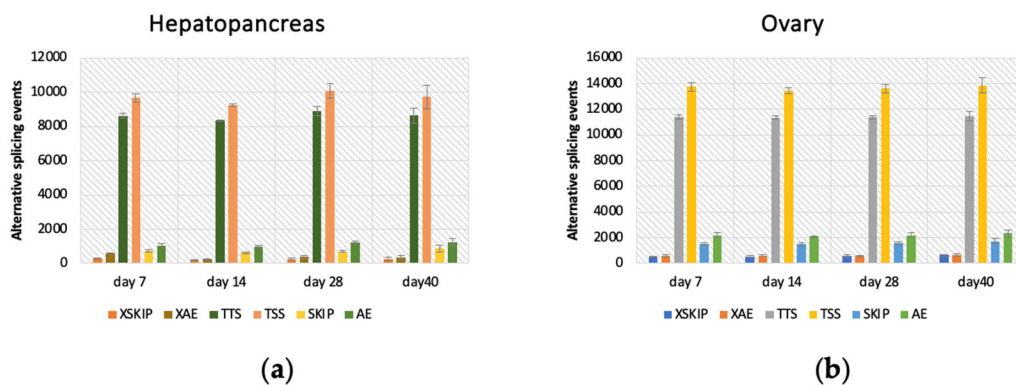
**Figure S1.** Dynamics of selected serum biomarkers in female *Scylla paramamosain* under imposed starvation. **(a)** hepatopancreas function transaminases; **(b)** serum lipids; **(c)** serum glucose. ALT, glutamic-pyruvic transaminase; AST, glutamic oxaloacetic transaminase; TG, serum triglycerides; TC, serum total cholesterol. Data are presented as mean  $\pm$  SE (n=3). Different letters of the bar/line with the same color indicate significant difference ( $P < 0.05$ ).



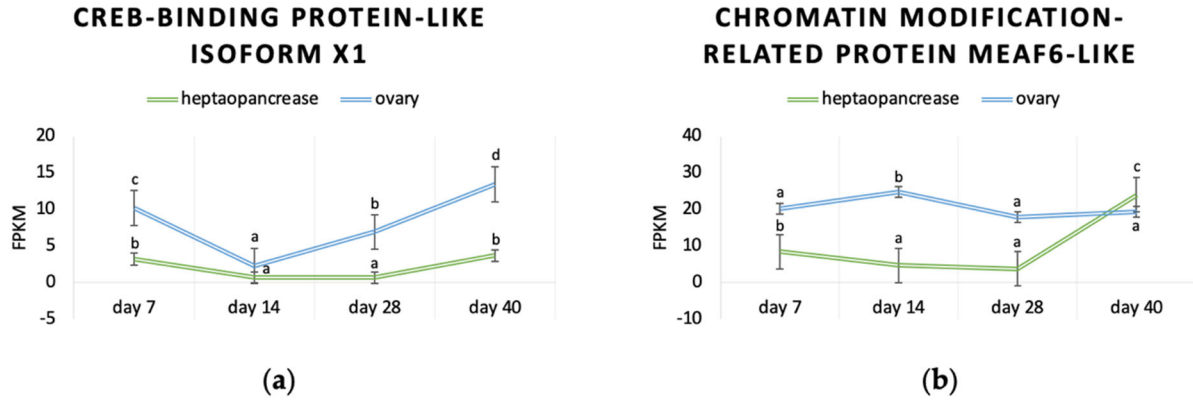
**Figure S2.** Principal component analysis of gene expression for all samples.



**Figure S3.** Heatmap of the mosaic gene expression patterns between each two samples with the clustering results of sample correlation. Use Pearson's Correlation Coefficient  $r$  as an evaluation indicator for biological repeated correlations. The closer the absolute value of  $R$  is to 1, the stronger the correlation between two samples.



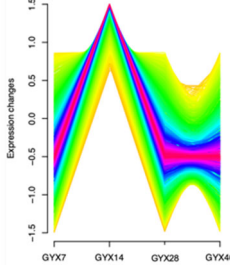
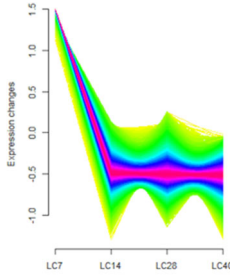
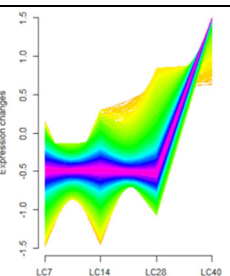
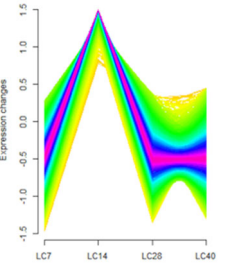
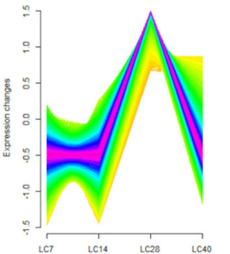
**Figure S4.** Specific patterns of alternative splicing events in mud crab (a) hepatopancreas and (b) ovary under imposed starvation. Colors indicate different alternative splicing events. Data are presented as mean  $\pm$  SE ( $n=3$ ).



**Figure S5.** Features of epigenetic modifications. Temporal expression trends of (a) CREB-binding protein-like isoform X1 and (b) chromatin modification-related protein MEAF6-like in *Scylla paramamosain* hepatopancreas (green line) and ovary (blue line) under imposed starvation. Data are presented as mean  $\pm$  SE (n=3). Different letters of the same line indicate significant difference ( $P < 0.05$ ).

**Table S1.** Selective clusters with diverse patterns in hepatopancreas and ovary of female *Scylla paramamosain* under imposed starvation

| Cluster name | Number of DEGs | KEGG enrichment (Corrected $P$ -value <0.05)  | Organ          | Expression trends (color from orange to red indicates gene cluster membership) |
|--------------|----------------|---|----------------|--|
| H-C5         | 3404           | D-Glutamine and D-glutamate metabolism;<br>mTOR signaling pathway;<br>RNA transport;<br>Arginine biosynthesis;<br>Longevity regulating pathway - multiple species | Hepatopancreas |  |
| H-C10        | 2646           | Proteasome;<br>RNA degradation;<br>Autophagy - other;<br>Basal transcription factors;<br>RNA polymerase;<br>Spliceosome   | Hepatopancreas |  |
| H-C8         | 2365           | Ribosome;<br>Other glycan degradation;<br>Sphingolipid metabolism;<br>Lysosome;<br>Glycosphingolipid biosynthesis - globo and isoglobo series                     | Hepatopancreas |  |

|             |      |   |                |  |
|-------------|------|---|----------------|--|
| <b>H-C6</b> | 1817 | Ribosome;<br>Ubiquinone and other terpenoid-quinone biosynthesis;<br>RNA transport;<br>Phenylalanine metabolism;<br>Biosynthesis of unsaturated fatty acids;<br>Tyrosine metabolism   | Hepatopancreas |    |
| <b>O-C8</b> | 3927 | Lysosome;<br>Sphingolipid metabolism;<br>Ubiquinone and other terpenoid-quinone biosynthesis;<br>Retinol metabolism;<br>Glycosphingolipid biosynthesis - globo and isoglobo series;<br>Linoleic acid metabolism;<br>Glycosphingolipid biosynthesis - lacto and neolacto series;<br>Starch and sucrose metabolism;<br>Amino sugar and nucleotide sugar metabolism;<br>Ascorbate and aldarate metabolism;<br>Other glycan degradation | Ovary          |    |
| <b>O-C1</b> | 2765 | Inositol phosphate metabolism;<br>Phenylalanine metabolism;<br>Phosphatidylinositol signaling system  | Ovary          |   |
| <b>O-C6</b> | 2703 | Ribosome;<br>Oxidative phosphorylation;<br>Glutathione metabolism   | Ovary          |  |
| <b>O-C9</b> | 2541 | Lysine degradation  | Ovary          |  |