**Supplemental Table S6.** KEGG Pathways of the genes that are differentially methylated and differentially spliced between bacteriocyte and body samples

|  |  |
| --- | --- |
| **Description** | **Set sizea** |
| Metabolic pathways | 40 |
| RNA transport | 14 |
| Spliceosome | 12 |
| Protein processing in endoplasmic reticulum | 12 |
| Wnt signaling pathway | 12 |
| mTOR signaling pathway | 10 |
| Endocytosis | 9 |
| Hippo signaling pathway - fly | 9 |
| Ubiquitin mediated proteolysis | 8 |
| Ribosome biogenesis in eukaryotes | 7 |
| mRNA surveillance pathway | 7 |
| RNA degradation | 7 |
| Glycerophospholipid metabolism | 6 |
| Biosynthesis of amino acids | 6 |
| Lysosome | 6 |
| Jak-STAT signaling pathway | 6 |

aNumber of genes that belong to the pathway