

S7 Table. The KEGG pathway enrichment for differentially expressed genes in RNA-seq ($p \leq 0.05$).

| Pathways | ID | Input number | Background number | P-Value | Corrected P-Value |
|---|----------|--------------|-------------------|----------|-------------------|
| Folate biosynthesis | tru00790 | 6 | 19 | 1.61E-07 | 9.04E-06 |
| Melanogenesis | tru04916 | 10 | 131 | 1.90E-06 | 5.31E-05 |
| Neuroactive ligand-receptor interaction | tru04080 | 11 | 379 | 0.002331 | 0.043509408 |
| Tyrosine metabolism | tru00350 | 3 | 35 | 0.006939 | 0.078470987 |
| Cytokine-cytokine receptor interaction | tru04060 | 6 | 158 | 0.007006 | 0.078470987 |
| Butanoate metabolism | tru00650 | 2 | 21 | 0.023155 | 0.180845259 |
| Hedgehog signaling pathway | tru04340 | 3 | 57 | 0.023907 | 0.180845259 |
| Purine metabolism | tru00230 | 6 | 213 | 0.025835 | 0.180845259 |
| Dorso-ventral axis formation | tru04320 | 2 | 26 | 0.033461 | 0.208202432 |