Table S1. All primers used for RT-qPCR in this study.

|  |  |  |  |
| --- | --- | --- | --- |
| **Gene ID** | **Best match** | **Primer sequences (5’ to 3’)** | **Length (bp)** |
| DcitrP055490.1 | E3 ubiquitin-protein ligase | CGGGAAATGAACCCCAATGA | 202 |
| CGCAGGTCTGACAGGAAGTAATG |
| DcitrP062105.1 | Proteasome activator complex subunit 3-like | GAAATGAAAATGAGAGCAAAGAGA | 110 |
| CGATGGAGTGAGAATCAGAGTGG |
| DcitrP026550.1 | Ubiquitin-associated domain-containing protein 1 | AAGCACCCTTGGATTTCAGTATG | 199 |
| TGTGGAGGTATTGGAGGTTTAGC |
| DcitrP080605.1 | Ubiquitin-conjugating enzyme E2 J2 | GTCATAGCAGAACCAAACCCAGC | 127 |
| TGAATGGGAAATCTCTTGGAAAA |
| DcitrP013835.1 | 40S ribosomal protein S9 | GTGAGAATTGGAGTGCTTGATGA | 207 |
| GCGTACTACGAAACTTGGGATGT |
| DcitrP037015.1 | 28S ribosomal protein S27, mitochondrial | GTCTTGGACTAACAAAGGATGCC | 155 |
| ACTCTCATTGCTACTGCTGGGTG |
| DcitrP036095.1 | Spondin-2-like | TACATTCTACGCTCCACCCATCA | 147 |
| CACAAATCCAAACTATCCACTCCA |
| DcitrP022220.1 | Apolipophorin-III | CCGAGACCGTCAAATCTATCCA | 221 |
| GACGACTTGCTTGCTCAACTTCT |
| DcitrP017415.1 | Heat shock protein 70 | TCATCACAGTCCCCGCCTATT | 184 |
| GTTCCGCCTCCCAAGTCAAA |
| DcitrP034560.1 | Partitioning defective 6 like protein gamma | TGGAACACCTGGGAAGACAAAA | 196 |
| ACCAGTAGAAGTGACACGCAGG |
| DcitrP079275.1 | Cytochrome P450 CYP4C4 | GCTGGTCTCTCTTCCTCCTGG | 110 |
| ATCTCGCATCGTGATTTTCCG |
| DcitrP045800.1 | Probable cytochrome P450 6a14 | TCTTATCAACTTCCCAACACCG | 217 |
| GCTGAGCGAATCTTTTACCAATG |
| DcitrP098450.1 | Acetylcholine receptor subunit alpha | CCTGGGTGTATGACGGGAAC | 182 |
| TCTGAGTCGGAAGTGAATGGTG |
| DcitrP034805.1 | Gelsolin | GTGACTGTCGCCTTATTTGGTG | 119 |
| AGGAACTCTCCCAGCATTTACAA |
|  | GAPDH | CATGGCAAGTTCAACGGTGA | 171 |
| CGATGCCTTCTCAATGGTGG |