**Table S1.** Primers of RT-qPCR validation.

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| **Gene name** | **Gene symbol** | **Primers** | **Primer sequences (5'-3')** | **TM/°C** | **Gene ID** |
| *fatty acid synthase* | *FAS* | Forward | TCCTTCTTCAGCGTCTCT | 53.0 | Cluster-67591.17008 |
|  |  | Reverse | CCATACTTCTTCACTCTCACT |  |  |
| *acyl-coenzyme A thioesterase* | *ACOT* | Forward | TCCACTGTCCTGTCTTCAT | 56.8 | Cluster-67591.33303 |
|  |  | Reverse | CGTCAACCTCACCATTCC |  |  |
| *acetyl CoA carboxylase* | *ACC* | Forward | TGGCAGCATTGGAGGTGTA | 60.8 | Cluster-67591.43403 |
|  |  | Reverse | GATGAGATGATGGCAGCAGAA |  |  |
| *mitochondrial enoyl-[acyl-carrier protein] reductase* | *MECR* | Forward | GGCACTGGAGATGTTGTT | 53.0 | Cluster-67591.46559 |
|  |  | Reverse | CTTCTGTTACCACCACTGT |  |  |
| *3-oxoacyl-[acyl-carrier-protein] synthase II* | *FabF* | Forward | GCTGGTATGGTAGTCTTGG | 59.1 | Cluster-67591.6543 |
|  |  | Reverse | GAGGTGCTGTGTAATGGAA |  |  |
| *malonyl-CoA-acyl carrier protein transacylase* | *FabD* | Forward | GCATTGGTGTAGCAGGTT | 63.0 | Cluster-67591.23513 |
|  |  | Reverse | GTCTTGAATCTGGTCCGTAT |  |  |
| *long-chain fatty acid CoA ligase* | *ACSL* | Forward | TGCGGATTACTCAGATGTG | 53.0 | Cluster-67591.28717 |
|  |  | Reverse | TGTAGATGCGGTCAAGGA |  |  |
| *carnitine O-palmitoyltransferase 1* | *CPT1* | Forward | TTCCTTGGTGCTCTAACAG | 56.8 | Cluster-67591.38584 |
|  |  | Reverse | TGCCTTCTTCATCGTATCC |  |  |
| *carnitine O-palmitoyltransferase 2* | *CPT2* | Forward | GTTGGAGACTGTAGCCTTC | 59.3 | Cluster-67591.35527 |
|  |  | Reverse | ACGGTGTGGTGGATATGA |  |  |
| *enoyl-CoA hydratase* | *echA* | Forward | GGCTCTCAATGCTCTATGT | 59.3 | Cluster-67591.24041 |
|  |  | Reverse | CCTGCTGTGCTGTAATCA |  |  |
| *18s* | *18s* | Forward | TATACGCTAGTGGAGCTGGAA | / | / |
|  |  | Reverse | GGGGAGGTAGTGACGAAAAAT |  |  |