**Supplementary Tables**

Table S1. Primers for quantitative PCR.

|  |  |  |  |
| --- | --- | --- | --- |
| **Gene** | **Genbank accession no.** | **Forward primer (5'-3')** | **Reverse primer (5'-3')** |
| *eif3* | DW542195 | caggatgttgttgctggatggg | acccaactgggcaggtcaaga |
| *ef1a* | AF321836 | caccaccggccatctgatctacaa | tcagcagcctccttctcgaacttc |
| *rpol2* | CA049789 | taacgcctgcctcttcacgttga | atgagggaccttgtagccagcaa |
| *scd1* | bt044999 | tgaaatagtgctgtcccgggctc | tggggaaacctcttagccactccg |
| *scd2* | bt059328 | tacgccaccagtgagttcggc | gccagtcttgtggctgccgt |
| *cox2* | AY848944 | cccccgacttacaatgctga | gcggttcccataggtgtagg |
| *FA* | BT048827 | tgcctcagcaccctactctg | gctttacaacctcaggattggc |
| *aco* | DQ364432 | ccttcattgtacctctccgca | catttcaacctcatcaaagccaa |
| *cpt1* | AM230810 | gtaccagccccgatgccttcat | tctctgtgcgaccctctcggaa |
| *hsp70* | BT059361 | cccaccatcgaggaagtcg | gattgggcctctggggttac |
| *bax* | DY722290 | tgacagatttcatctacgagcggg | gccatccagctcatctccaatct |
| *gpx2* | CF753103 | tgtacctcaaggagaagctgccgt  | attaaggccatgggatcgtcgc |
| *cat* | est04a09 | ccagatgtgggccgctacaa | tctggcgctcctcctcattc |
| *sod1s* | BT057716 | ttctgttgtacgctgtcccaaaagc | gcagcttggtacgcaaagtgaaca |
| *nrf2* | BT059007 | ccggactcctcgccttcgga | gtggatagttggcttgtcccttcgt |
| *tnfa* | NM\_001123589 | aggttggctatggaggctgt | tctgcttcaatgtatggtggg |

*eif3: eukaryotic translation initiation factor 3. ef1a: eukaryotic translation elongation factor 1 alpha. rpol2: rna polymerase 2. scd1: stearoyl-coa desaturase 1. scd2: stearoyl-coa desaturase 2. cox2: cyclooxygenase 2. fas: fatty acid synthase. aco: acyl-coa oxidase 1. cpt1: carnitine palmitoyltransferase 1. hsp70: heat shock protein 70. bax: bcl2 associated x. gpx2: glutathione peroxidase 2. cat: catalase. sod1s: superoxide dismutase 1 soluble. nrf2: nuclear factor. erythroid 2 like 2. tnfa: tumor necrosis factor alpha.*

Table S2. Gene expression of markers for fatty acid oxidation (*aco, cpt1*). fatty acid synthesis (*fas, scd1, scd2*), stress (*hsp70*), inflammation (*cox2*), apoptosis (*bax*), and oxidative stress (*nrf2, cat, sod1s, gpx2*) in intestine. Gene expression levels were compared within the Low and the High groups of FO and DHA-CA. Data (n=5) are shown with standard error means.

|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
|   | LOW FO | HIGH FO |  | LOW DHA-CA | HIGH DHA-CA | ANOVA |
| *scd1* | 0.0 | ± | 0.1 | 0.0 | ± | 0.0 |  | -0.2 | ± | 0.1 | 0.2 | ± | 0.1 |  |
| *scd2* | 0.0 | ± | 0.1 | 0.0 | ± | 0.1 |  | 0.0 | ± | 0.2 | 0.0 | ± | 0.1 |  |
| *fas* | 0.0 | ± | 1.1 | 0.0 | ± | 1.1 |  | 1.0 | ± | 0.7 | 0.1 | ± | 0.4 |  |
| *aco* | 0.0 | ± | 0.3 | 0.0 | ± | 0.0 |  | 0.8 | ± | 0.4 | 0.2 | ± | 0.1 |  |
| *cpt1* | 0.0 | ± | 1.0 | 0.0 | ± | 0.8 |  | 2.8 | ± | 0.9 | -0.7 | ± | 0.9 |  |
| *cox2* | 0.0 | ± | 0.5 | 0.0 | ± | 0.4 |  | 0.4 | ± | 0.3 | -0.3 | ± | 0.2 |  |
| *hsp70* | 0.0 | ± | 0.2 | 0.0 | ± | 0.1 |  | 0.3 | ± | 0.0 | 0.1 | ± | 0.0 |  |
| *bax* | 0.0 | ± | 0.3 | -0.2 | ± | 0.1 |  | -0.2 | ± | 0.2 | 0.1 | ± | 0.1 | p < 0.05 |
| *gpx2* | 0.0 | ± | 0.3 | 0.0 | ± | 0.3 |  | 1.2 | ± | 0.5 | 0.3 | ± | 0.2 |  |
| *cat* | 0.0 | ± | 1.6 | 0.0 | ± | 0.5 |  | 1.5 | ± | 0.8 | -0.2 | ± | 1.1 |  |
| *sod1s* | 0.0 | ± | 0.3 | 0.0 | ± | 0.2 |  | 0.7 | ± | 0.4 | -0.1 | ± | 0.1 |  |
| *nrf2* | 0.0 | ± | 0.4 | 0.0 | ± | 0.0 |  | 0.9 | ± | 0.2 | 0.3 | ± | 0.1 |  |

*scd1: stearoyl-coa desaturase 1. scd2: stearoyl-coa desaturase 2. cox2: cyclooxygenase 2. fas: fatty acid synthase. aco: acyl-coa oxidase 1. cpt1: carnitine palmitoyltransferase 1. hsp70: heat shock protein 70. bax: bcl2 associated x. gpx2: glutathione peroxidase 2. cat: catalase. sod1s: superoxide dismutase 1 soluble. nrf2: nuclear factor. erythroid 2 like 2. tnfa: tumor necrosis factor alpha.*