Supplementary Table 1 Fatty acid composition of experimental dietsf

|  |  |  |  |
| --- | --- | --- | --- |
| Fatty acid (% total fatty acids) | FO | VO | C |
| 14:0 | 12.10 | 6.38 | 11.69 |
| 16:0 | 34.81 | 29.10 | 37.05 |
| 18:0 | 4.66 | 5.00 | 10.41 |
| 20:0 | 0.33 | 0.23 | 0.19 |
| ∑SFAa | 51.90 | 40.71 | 59.34 |
| 16:1n-7 | 3.38 | 1.49 | 2.8 |
| 18:1n-9 | 6.69 | 9.74 | 6.38 |
| ∑MUFAb | 10.07 | 11.23 | 9.18 |
| 18:2n-6 | 11.35 | 20.74 | 3.36 |
| 20:4n-6 | 0.31 | 0.12 | 0.39 |
| ∑n-6 PUFAc | 11.66 | 20.86 | 3.75 |
| 18:3n-3 | 1.88 | 11.64 | 1.07 |
| 20:5n-3 | 6.59 | 3.79 | 7.21 |
| 22:6n-3 | 5.74 | 3.02 | 6.74 |
| ∑n-3 PUFAd | 14.21 | 18.45 | 15.02 |
| n-3/n-6PUFA | 1.22 | 0.88 | 4.01 |
| Σn-3LC-PUFAe | 12.33 | 6.81 | 13.95 |

a SFA: saturated fatty acids.

b MUFA: mono-unsaturated fatty acids.

c n-6 PUFA: n-6 polyunsaturated fatty acids.

d n-3 PUFA: n-3 polyunsaturated fatty acids.

e LC-PUFA: long chain-polyunsaturated fatty acids.

f Some fatty acids, of which the contents are minor, trace amount or not detected, such as 4:0, 6:0, 8:0, 10:0, 11:0, 12:0, 13:0, 24:0, 14:1, 20:1n-9, 22:1n-11, 20:2n-6, 23:0, 20:3n-6, are not listed in the table.

Supplementary Table 2 Sequences of the primers for RT-qPCR

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| --- | --- | --- | --- | --- | --- |
| Gene name | Abbreviation | Forward (5'-3') | Reverse (5'-3') | roles | Accession number |
| sterol-regulatory element binding protein-1c | *srebp1c* | TCTCCTTGCAGTCTGAGCCAAC | TCAGCCCTTGGATATGAGCCT | fatty acid and triglyceride biosynthesis | KP342262.1 |
| acetyl CoA carboxylase | *acc1* | GACTTGGCGGAATACCTACTGG | GCTTGCTGGATGATCTTTGCTT | fatty acid and lipid biosynthesis | XM\_027273319.1 |
| diacylglycerol acyltransferases | *dgat1* | GGTATCTTGGTGGACCCCATTCA | TGAGCACCGTGGCTGAAGGAAAGA | triglyceride biosynthesis | XM\_019254827.2 |
| fatty acid synthase | *fas* | CAGCCACAGTGAGGTCATCC | TGAGGACATTGAGCCAGACAC | fatty acid biosynthesis | XM\_010741011.3 |
| carnitine palmitoyl transferase-1 | *cpt1* | GCTGAGCCTGGTGAAGATGTTC | TCCATTTGGTTGAATTGTTTACTGTCC | fatty acid oxidation | XM\_019255573.2 |
| adipose triglyceride lipase | *atgl* | CCATGCATCCGTCCTTCAACC | GAGATCCCTAACCGCCCACT | catabolism of triglycerides | HQ916211.1 |
| acyl-CoA oxidase | *aco* | AGTGCCCAGATGATCTTGAAGC | CTGCCAGAGGTAACCATTTCCT | catabolism of fatty acid | XM\_010748324.3 |
| peroxisome proliferators-activated receptor α | *pparα* | GTCAAGCAGATCCACGAAGCC | TGGTCTTTCCAGTGAGTATGAGCC | fatty acid oxidation | XM\_027291871.1 |
| *fatty acid desaturase 2* | *△6fad* | TTCGCTTCCTCTGCTGCTATG | CCAGTCACGGTGCTTCTCG | desaturation of fatty acids | XM\_027272512.1 |
| Elongation of very long chain fatty acids protein 5 | *elovl5* | ATCACCTTCCTTCACATCTATCACC | GAGGCACCGAAGTACGAATGG | elongation of fatty acids | XM\_019268506.2 |
| Elongation of very long chain fatty acids protein 4 | *elovl4* | GGGCTCTTATTGGCTATGCT | TGCTTCTTCCCGTTATCCTC | elongation of fatty acids | XM\_010739301.3 |
| microsomal triacylglycerol transfer protein | *mtp* | CTTGAGTCGCTGATTGCTGC | TGAGGTCGCTGTAACCCTTG | transferring neutral lipids | XM\_010744909.3 |
| apolipoprotein b100 | *apob100* | AGAGTGTTGTCCAGGATAAAGATGC | CAGGGCTCAGGGTCTCAGTC | moving cholesterol | XM\_027284282.1 |
| apolipoprotein AI | *apobAI* | TTGCTCTCGCCCTTCTCCTG | CACGCTGTCCTTGATCTCCTTG | transporting cholesterol and certain fats | XM\_010745246.3 |
| nuclear factor erythroid 2-related factor 2 | *nrf2* | TCTGATGTGCGTCTCTCCAG | GCCTCATTCATTTGGTGCTT | regulator of cellular resistance to oxidants | XM\_010737768.3 |
| superoxide dismutase 1 | *sod1* | GCGGGACCGTGTTCTTTGAG | GCTACCAGCGTTGCCAGTCTTT | an antioxidant enzyme protecting the cell from reactive oxygen species toxicity | NM\_001303360.1 |
| superoxide dismutase 2 | *sod2* | GGCACTGGCAAAGGGAGAC | CACAAGCGGCGATACGAAG | an antioxidant enzyme protecting the cell from reactive oxygen species toxicity | NM\_001303364.1 |
| superoxide dismutase3 | *sod3* | CCTGGAGACTTTGGTAACTTTG | TCCCTATTATACTGCTTATGGTG | an antioxidant enzyme protecting the cell from reactive oxygen species toxicity | NM\_001303353.1 |
| glutathione peroxidase | *gpx* | CTGCTGGAGAAGGTGGATGT | TGGAAGTTGTTGAACGGGATA | an antioxidant enzyme class with the capacity to scavenge free radicals | XM\_010745288.3 |
| beta-actin | *β-actin* | GACCTGACAGACTACCTCATG | AGTTGAAGGTGGTCTCGTGGA | reference gene | GU584189.1 |