**Supplementary Table 1.**

Composition of the experimental diets (g/kg)

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
|  |  | | CON | FRU | FJA |
|  | JA powder a | | ***-*** | ***-*** | 100 |
|  | Cornstarch | | 650 | 72.8 | ***-*** |
|  | Fructose | | ***-*** | 577.2 | 577.2 |
|  | Fiber (Cellulose) | | 50 | 50 | 38 |
|  | Casein | | 200 | 200 | 186.9 |
|  | Soybean oil | | 50 | 50 | 48.7 |
|  | Mineral Mix AIN-93G | | 35 | 35 | 35 |
|  | Vitamin Mix AIN-93G | | 10 | 10 | 10 |
|  | Methionine | | 3 | 3 | 3 |
|  | Choline bitartrate | | 2 | 2 | 2 |
|  | tert-Butylhydroquinone (TBHQ) | | 0.01 | 0.01 | 0.01 |
| Total amount | | | 1000 | 1000 | 1000 |
| Energy (kJ) | | (CHO + Fiber) | 10584 | 10584 | 10447.9 |
|  | | Protein | 2822.4 | 2822.4 | 2822.4 |
|  | | Lipid | 1757.7 | 1757.7 | 1757.7 |
| Total Energy | | | 15164.1 | 15164.1 | 15028.0 |

a JA powder: JA (100g) contains 63.8g carbohydrates, 12.0g fiber, 13.1g protein, and 1.3g fat. JA (52.8% of fructans) was added to diet by replacing cornstarch.

b All the diets were adjusted to keep energy balance.

Ingredient composition per 100g of JA powder

|  |  |
| --- | --- |
|  | /100g of JA powder |
| Water | 4.0 |
| Protein | 13.1 |
| Fat | 1.3 |
| Ash | 5.8 |
| Carbohydrates | 75.8 |
| Energy | 1376.8 kJ |

**Supplementary Table 2.** Oligonucleotide sequences used in the real-time PCR analysis

|  |  |  |  |
| --- | --- | --- | --- |
| Gene Symbol | Full name |  | Oligonucleotide sequences |
| *Acc* | Acetyl-CoA carboxylase | F | ACTGACTACAGGTTCTTTGTTCGTG |
| R | GCAGTCGCTCTCCTTCATTTT |
| *Fas* | Fatty acid synthase | F | CTTGGGTGCCGATTACAACC |
| R | GCCCTCCCGTACACTCACTC |
| *Evovl6* | Elongation of very long chain fatty acid 6 | F | CTCAGCAAAGCACCCGAAC |
| R | GGAGTACCAAGAGTACAGGAGCACA |
| *Me1* | Malic enzyme 1 | F | GCCGGCTCTATCCTCCTTTG |
| R | CTTCTTTGTTTTGGGGTTCAGG |
| *Igfbp1* | Insulin-like growth factor binding protein 1 | F | GGAATTAACCTGGTGCTGGA |
| R | CATTCAGACCACCTCGACAA |
| *Dcn* | Decorin | F | GGAATTAACCTGGTGCTGGA |
| R | TTCAGACCACCTCGACAATG |
| *Ctgf* | Connective tissue growth factor | F | GTTCCTGGCAATACGTT |
| R | CATTCAGACCACCTCGACAA |
| *Fads2* | Fatty acid desaturase 2 | F | ATCTGCCCTACAACCACCAG |
| R | TGTGACCCACACAAACCAGT |
| *Acaca* | Acetyl-CoA carboxylase alpha | F | AGGAGGGAAGGGAATCAGAA |
| R | CCATACTGATCCGCCAGAAT |
| *Cyp1a2* | Cytochrome P450, family 1, subfamily a, polypeptide 2 | F | ACAACTCTGCCAGTCTCCAG |
| R | TTCAGACCTTTGGGAACCTG |
| *Nampt* | Nicotinamide phosphoribosyltransferase | F | GGACCTTTGTCACCCTTGAA |
| R | ACAACCACCCACTCACACAA |

**Supplementary Table 3.** Differentially expressed genes in liver

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| Down-regulated Genes in FJA as compared to FRU | | | Fold Change | |
| Probe ID | Gene Symbol | Gene name | FJA vs. FRU | FRU vs. CON |
| 1385016\_at | *RGD1560784* | similar to RIKEN cDNA B630019K06 | 0.3 | 2.0 |
| 1368877\_at | *Zfp354a* | zinc finger protein 354A | 0.4 | 1.9 |
| 1387703\_a\_at | *Usp2* | ubiquitin specific peptidase 2 | 0.4 | 1.3 |
| 1388166\_at | *Igh-6* | immunoglobulin heavy chain 6 | 0.4 | 3.7 |
| 1372685\_at | *Cdkn3* | cyclin-dependent kinase inhibitor 3 | 0.5 | 2.0 |
| 1372966\_at | *Mfsd2a* | major facilitator superfamily domain containing 2A | 0.5 | 1.2 |
| 1373011\_at | *Fam134b* | family with sequence similarity 134, member B | 0.5 | 1.7 |
| 1373758\_at | *Flad1* | flavin adenine dinucleotide synthetase | 0.5 | 2.0 |
| 1367836\_at | *Cpt1a* | carnitine palmitoyltransferase 1a, liver | 0.5 | 1.1 |
| 1374962\_at | *Rtn4ip1* | reticulon 4 interacting protein 1 | 0.5 | 1.5 |
| 1377885\_at | *LOC685203* | hypothetical protein LOC685203 | 0.5 | 1.9 |
| 1379238\_at | *Ctdspl* | CTD (carboxy-terminal domain, RNA polymerase II, polypeptide A) small phosphatase-like | 0.5 | 1.5 |
| 1389014\_at | *Nampt* | nicotinamide phosphoribosyltransferase | 0.5 | 1.4 |
| 1389408\_at | *Rrm2* | ribonucleotide reductase M2 | 0.5 | 2.5 |
| 1367982\_at | *Alas1* | aminolevulinate, delta-, synthase 1 | 0.6 | 1.4 |
| 1368947\_at | *Gadd45a* | growth arrest and DNA-damage-inducible, alpha | 0.6 | 1.5 |
| 1371091\_at | *Irs2* | insulin receptor substrate 2 | 0.6 | 1.5 |
| 1391635\_at | *Ctdspl* | CTD (carboxy-terminal domain, RNA polymerase II, polypeptide A) small phosphatase-like | 0.6 | 1.5 |
| 1369958\_at | *Rhob* | ras homolog gene family, member B | 0.6 | 1.2 |
| 1379582\_a\_at | *Ccna2* | cyclin A2 | 0.6 | 2.0 |
| 1370209\_at | *Klf9* | Kruppel-like factor 9 | 0.7 | 1.2 |
| 1370397\_at | *Cyp4a3* | cytochrome P450, family 4, subfamily a, polypeptide 3 | 0.7 | 1.5 |
| 1373692\_at | *Eif4ebp3* | eukaryotic translation initiation factor 4E binding protein 3 | 0.7 | 1.4 |
| 1379606\_at | *Rab30* | RAB30, member RAS oncogene family | 0.7 | 1.5 |
| 1383401\_at | *Tes* | testis derived transcript | 0.7 | 1.3 |
| 1384580\_at | *C6* | complement component 6 | 0.7 | 1.4 |
| 1393148\_at | *Gpr137b* | G protein-coupled receptor 137B | 0.7 | 1.4 |
| 1395358\_at | *Rhobtb3* | Rho-related BTB domain containing 3 | 0.7 | 1.6 |
| 1367725\_at | *Pim3* | pim-3 oncogene | 0.7 | 1.2 |
| 1368308\_at | *Myc* | myelocytomatosis oncogene | 0.7 | 1.9 |
| 1370067\_at | *Me1* | malic enzyme 1, NADP(+)-dependent, cytosolic | 0.7 | 2.5 |
| 1370080\_at | *Hmox1* | heme oxygenase (decycling) 1 | 0.7 | 1.3 |
| 1370286\_at | *Slc38a2* | solute carrier family 38, member 2 | 0.7 | 1.2 |
| 1372462\_at | *Acat3* | acetyl-Coenzyme A acetyltransferase 3 | 0.7 | 1.4 |
| 1374584\_at | *Stk24* | Serine/threonine kinase 24 | 0.7 | 1.5 |
| 1375852\_at | *Hmgcr* | 3-hydroxy-3-methylglutaryl-CoA reductase | 0.7 | 1.1 |
| 1386927\_at | *Cpt2* | carnitine palmitoyltransferase 2 | 0.7 | 1.3 |
| 1389566\_at | *Ccnb2* | cyclin B2 | 0.7 | 2.0 |
| 1394844\_s\_at | *Cyp4a2* | cytochrome P450, family 4, subfamily a, polypeptide 2 | 0.7 | 1.3 |
| 1398296\_at | *Gde1* | glycerophosphodiester phosphodiesterase 1 | 0.7 | 1.3 |
| 1367659\_s\_at | *Eci1* | enoyl-CoA delta isomerase 1 | 0.8 | 1.3 |
| 1367676\_at | *Hmgb2* | high mobility group box 2 | 0.8 | 1.3 |
| 1367950\_at | *Slc22a5* | solute carrier family 22 (organic cation/carnitine transporter), member 5 | 0.8 | 1.3 |
| 1368509\_at | *Bbs2* | Bardet-Biedl syndrome 2 | 0.8 | 1.2 |
| 1368659\_at | *Agxt2* | alanine-glyoxylate aminotransferase 2 | 0.8 | 1.1 |
| 1369972\_at | *Fbxo21* | F-box protein 21 | 0.8 | 1.5 |
| 1370281\_at | *Fabp5* | fatty acid binding protein 5, epidermal | 0.8 | 1.6 |
| 1370870\_at | *Me1* | malic enzyme 1, NADP(+)-dependent, cytosolic | 0.8 | 2.5 |
| 1370883\_at | *RT1-Da* | RT1 class II, locus Da | 0.8 | 1.1 |
| 1371012\_at | *Hacl1* | 2-hydroxyacyl-CoA lyase 1 | 0.8 | 1.2 |
| 1371209\_at | *LOC100364956* | MHC class Ib alpha chain-like | 0.8 | 1.2 |
| 1373566\_at | *LOC679357* | similar to interferon regulatory factor 2 binding protein 2 | 0.8 | 1.1 |
| 1374190\_at | *Clybl* | citrate lyase beta like | 0.8 | 1.4 |
| 1375428\_at | *Creg1* | cellular repressor of E1A-stimulated genes 1 | 0.8 | 1.3 |
| 1377014\_at | *Nim1* | serine/threonine-protein kinase NIM1 | 0.8 | 1.5 |
| 1377037\_at | *Acot3* | acyl-CoA thioesterase 3 | 0.8 | 1.4 |
| 1378032\_at | *Nfkbiz* | nuclear factor of kappa light polypeptide gene enhancer in B-cells inhibitor, zeta | 0.8 | 1.3 |
| 1379719\_at | *Syde2-ps1* | Synapse defective 1, Rho GTPase, homolog 2 (C. elegans), pseudogene 1 | 0.8 | 1.4 |
| 1385263\_at | *Myo7b* | myosin VIIb | 0.8 | 2.5 |
| 1386885\_at | *Ech1* | enoyl CoA hydratase 1, peroxisomal | 0.8 | 1.4 |
| 1388340\_at | *Ns5atp9* | NS5A (hepatitis C virus) transactivated protein 9 | 0.8 | 1.6 |
| 1391433\_at | *Acot2* | acyl-CoA thioesterase 2 | 0.8 | 1.3 |
| 1394401\_at | *Elovl6* | ELOVL fatty acid elongase 6 | 0.8 | 2.1 |
| 1367584\_at | *Anxa2* | annexin A2 | 0.8 | 1.4 |
| 1367631\_at | *Ctgf* | connective tissue growth factor | 0.8 | 1.4 |
| 1368160\_at | *Igfbp1* | insulin-like growth factor binding protein 1 | 0.8 | 1.2 |
| 1368446\_at | *Spink3* | serine peptidase inhibitor, Kazal type 3 | 0.8 | 1.7 |
| 1368453\_at | *Fads2* | fatty acid desaturase 2 | 0.8 | 1.1 |
| 1368934\_at | *Cyp4a1* | cytochrome P450, family 4, subfamily a, polypeptide 1 | 0.8 | 1.2 |
| 1370893\_at | *Acaca* | acetyl-CoA carboxylase alpha | 0.8 | 1.2 |
| 1370956\_at | *Dcn* | decorin | 0.8 | 1.2 |
| 1371081\_at | *Rapgef4* | Rap guanine nucleotide exchange factor (GEF) 4 | 0.8 | 1.2 |
|  |  |  |  |  |
| Up-regulated Genes in FJA as compared to FRU | | | Fold Change | | |
| Probe ID | Gene Symbol | Gene name | FJA vs. FRU | FRU vs. CON | |
| 1367775\_at | *Amacr* | alpha-methylacyl-CoA racemase | 1.2 | 0.8 | |
| 1368490\_at | *Cd14* | CD14 molecule | 1.2 | 0.8 | |
| 1368733\_at | *Sult1e1* | sulfotransferase family 1E, estrogen-preferring, member 1 | 1.2 | 0.8 | |
| 1369238\_at | *Inhbe* | inhibin beta E | 1.2 | 0.8 | |
| 1369655\_at | *Pik3c3* | phosphoinositide-3-kinase, class 3 | 1.2 | 0.8 | |
| 1369746\_a\_at | *Slco1b3* | solute carrier organic anion transporter family, member 1b3 | 1.2 | 0.8 | |
| 1370363\_at | *Ces1d* | carboxylesterase 1D | 1.2 | 0.8 | |
| 1371016\_at | *LOC100364854 /// LOC290071* | similar to RIKEN cDNA A430107P09 gene-like | 1.2 | 0.7 | |
| 1372316\_at | *Pkdcc* | protein kinase domain containing, cytoplasmic homolog | 1.2 | 0.8 | |
| 1372920\_at | *Prodh* | proline dehydrogenase (oxidase) 1 | 1.2 | 0.6 | |
| 1373438\_at | *Ube2o* | ubiquitin-conjugating enzyme E2O | 1.2 | 0.7 | |
| 1374657\_at | *Anks4b* | ankyrin repeat and sterile alpha motif domain containing 4B | 1.2 | 0.8 | |
| 1381993\_at | *Clic2* | chloride intracellular channel 2 | 1.2 | 0.8 | |
| 1382735\_at | *Atg12* | autophagy related 12 | 1.2 | 0.6 | |
| 1387609\_at | *Car5a* | carbonic anhydrase 5a, mitochondrial | 1.2 | 0.7 | |
| 1387669\_a\_at | *Ephx1* | epoxide hydrolase 1, microsomal | 1.2 | 0.8 | |
| 1388172\_at | *Slc22a25* | solute carrier family 22, member 25 | 1.2 | 0.8 | |
| 1389377\_at | *Insig2* | insulin induced gene 2 | 1.2 | 0.9 | |
| 1391932\_at | *Mab21l3* | mab-21-like 3 (C. elegans) | 1.2 | 0.8 | |
| 1392417\_s\_at | *LOC685619 /// Tp53rk* | similar to TP53-regulating kinase (p53-related protein kinase) (Nori-2) /// TP53 regulating kinase | 1.2 | 0.6 | |
| 1392972\_at | *Trio* | triple functional domain (PTPRF interacting) | 1.2 | 0.8 | |
| 1393690\_at | *Insig2* | insulin induced gene 2 | 1.2 | 0.8 | |
| 1394865\_at | *Rtp3* | receptor (chemosensory) transporter protein 3 | 1.2 | 0.8 | |
| 1398759\_at | *Tsc22d1* | TSC22 domain family, member 1 | 1.2 | 0.9 | |
| 1367826\_at | *Nfe2l2* | nuclear factor, erythroid derived 2, like 2 | 1.3 | 0.7 | |
| 1371104\_at | *Srebf1* | sterol regulatory element binding transcription factor 1 | 1.3 | 0.8 | |
| 1373797\_at | *Hyal3* | hyaluronoglucosaminidase 3 | 1.3 | 0.8 | |
| 1376144\_at | *Parp9* | poly (ADP-ribose) polymerase family, member 9 | 1.3 | 0.8 | |
| 1379888\_at | *LOC100912602* | uncharacterized LOC100912602 | 1.3 | 0.5 | |
| 1387297\_at | *Klrg1* | killer cell lectin-like receptor subfamily G, member 1 | 1.3 | 0.8 | |
| 1390800\_a\_at | *Cav2* | caveolin 2 | 1.3 | 0.7 | |
| 1390873\_at | *Btbd11* | BTB (POZ) domain containing 11 | 1.3 | 0.7 | |
| 1391489\_at | *Irgm* | immunity-related GTPase family, M | 1.3 | 0.8 | |
| 1393510\_at | *Sybu* | syntabulin (syntaxin-interacting) | 1.3 | 0.3 | |
| 1398307\_at | *Cyp3a18* | cytochrome P450, family 3, subfamily a, polypeptide 18 | 1.3 | 0.8 | |
| 1368155\_at | *Cyp2c12* | cytochrome P450, family 2, subfamily c, polypeptide 12 | 1.4 | 0.6 | |
| 1369044\_a\_at | *Pde4b* | phosphodiesterase 4B, cAMP specific | 1.4 | 0.8 | |
| 1371542\_at | *Tuba4a* | tubulin, alpha 4A | 1.4 | 0.8 | |
| 1372091\_at | *Mid1ip1* | MID1 interacting protein 1 (gastrulation specific G12 homolog (zebrafish)) | 1.4 | 0.6 | |
| 1374932\_at | *LOC100361444* | rCG31799-like | 1.4 | 0.5 | |
| 1375224\_at | *Phlda3* | pleckstrin homology-like domain, family A, member 3 | 1.4 | 0.8 | |
| 1376646\_at | *Popdc2* | popeye domain containing 2 | 1.4 | 0.4 | |
| 1380383\_at | *Arl4d* | ADP-ribosylation factor-like 4D | 1.4 | 0.7 | |
| 1381859\_at | *Fam91a1* | Family with sequence similarity 91, member A1 | 1.4 | 0.7 | |
| 1383732\_at | *RGD1307603* | similar to hypothetical protein MGC37914 | 1.4 | 0.8 | |
| 1386261\_x\_at | *Cav2* | caveolin 2 | 1.4 | 0.7 | |
| 1388426\_at | *Srebf1* | sterol regulatory element binding transcription factor 1 | 1.4 | 0.7 | |
| 1388654\_at | *Mrpl52* | mitochondrial ribosomal protein L52 | 1.4 | 0.8 | |
| 1388674\_at | *Cdkn1a* | cyclin-dependent kinase inhibitor 1A | 1.4 | 0.5 | |
| 1390591\_at | *Slc17a3* | solute carrier family 17 (sodium phosphate), member 3 | 1.4 | 0.7 | |
| 1393221\_at | *RGD1564865* | similar to 20-alpha-hydroxysteroid dehydrogenase | 1.4 | 0.6 | |
| 1393902\_at | *Akr1c1* | aldo-keto reductase family 1, member C1 (dihydrodiol dehydrogenase 1; 20-alpha (3-alpha)-hydroxysteroid dehydrogenase) | 1.4 | 0.5 | |
| 1368870\_at | *Id2* | inhibitor of DNA binding 2 | 1.5 | 0.7 | |
| 1370336\_at | *Osgin1* | oxidative stress induced growth inhibitor 1 | 1.5 | 0.8 | |
| 1374871\_at | *Asrgl1* | asparaginase like 1 | 1.5 | 0.8 | |
| 1389199\_at | *RGD1309079* | similar to Ab2-095 | 1.5 | 0.8 | |
| 1369591\_at | *Csn3* | casein kappa | 1.6 | 0.8 | |
| 1371152\_a\_at | *Oas1a* | 2'-5' oligoadenylate synthetase 1A | 1.6 | 0.7 | |
| 1373992\_at | *MGC108823* | similar to interferon-inducible GTPase | 1.6 | 0.7 | |
| 1374334\_at | *Igha* | immunoglobulin heavy chain, alpha | 1.6 | 0.7 | |
| 1387243\_at | *Cyp1a2* | cytochrome P450, family 1, subfamily a, polypeptide 2 | 1.6 | 0.8 | |
| 1390192\_at | *Slc27a3* | solute carrier family 27 (fatty acid transporter), member 3 | 1.6 | 0.7 | |
| 1368168\_at | *Slc34a2* | solute carrier family 34 (sodium phosphate), member 2 | 1.7 | 0.5 | |
| 1373108\_at | *Ppp1r3c* | protein phosphatase 1, regulatory subunit 3C | 1.7 | 0.5 | |
| 1374157\_at | *Pde4b* | Phosphodiesterase 4B, cAMP specific | 1.7 | 0.7 | |
| 1383564\_at | *Irf7* | interferon regulatory factor 7 | 1.7 | 0.8 | |
| 1387902\_a\_at | *Igkv28* | Immunoglobulin kappa chain variable 28 (V28) | 1.7 | 0.7 | |
| 1395236\_at | *Ppp1r3c* | protein phosphatase 1, regulatory subunit 3C | 1.7 | 0.4 | |
| 1368778\_at | *Slc6a6* | solute carrier family 6 (neurotransmitter transporter, taurine), member 6 | 1.9 | 0.6 | |
| 1389034\_at | *Usp18* | ubiquitin specific peptidase 18 | 1.9 | 0.7 | |
| 1367802\_at | *Sgk1* | serum/glucocorticoid regulated kinase 1 | 2.1 | 0.6 | |
| 1373718\_at | *Tubb2a* | tubulin, beta 2A class IIa | 2.1 | 0.7 | |
| 1390672\_at | *Rprm* | reprimo, TP53 dependent G2 arrest mediator candidate | 2.1 | 0.5 | |
| 1387283\_at | *Mx2* | myxovirus (influenza virus) resistance 2 | 2.3 | 0.5 | |
| 1382314\_at | *Isg15* | ISG15 ubiquitin-like modifier | 2.6 | 0.5 | |