Table S1. List of reference and target genes investigated in the analysis

Gene symbol	Gene name	Sequence accession number	Primer sequence (5′ → 3′)	Start	Stop	Amplicon length (base pairs)
Gak	cyclin G-associated kinase	NM_153569.2	Fwd: TTGTAAAGGACAGCTGGTGGAG Rev: TGATGGGTGGTTTCTGCCTG	507 640	528 621	134
Srebf1	sterol regulatory element-binding transcription factor 1	NM_011480.4	Fwd: GGAACTTTTCCTTAACGTGGGC Rev: GAGCTGGAGCATGTCTTCGAT	33 189	54 169	157
Fasn	fatty acid synthase	NM_007988.3	Fwd: TGCACCTCACAGGCATCAAT Rev: GTCCCACTTGATGTGAGGGG	2935 3038	2954 3019	104
Fads1	fatty acid desaturase 1	NM_146094.2	Fwd: ACGCGCTACTTTACTTGGGA Rev: CACAAAAGGATCCGTGGCAT	219 389	238 370	171
Fads2	fatty acid desaturase 2	NM_019699.2	Fwd: TTCCAGATTGAGCACCACCTC Rev: GCAACGGCTTCTCCTGGTAT	1215 1332	1235 1313	118
Oat	ornithine aminotransferase	NM_016978.2	Fwd: GGCGGTTTATACCCTGTGTCT Rev: TAGTGGGTTTCCGCCGTATG	1026 1124	1046 1105	99
Fbp1	fructose bisphosphatase 1	NM_019395.4	Fwd: GCATCGCACAGCTCTATGGT Rev: ACAGGTAGCGTAGGACGACT	276 397	295 378	122
Prdx6	peroxiredoxin 6	NM_001303408.1	Fwd: TTTCCTGGGAGATTCCTGCTGA Rev: GTTGGCTTGGCCTTGAAGTTAG	175 237	196 216	63

Table S2. Haematology of the male mice fed for six months with a standard diet (STD group), high saturated fatty acid diet (SFA group), high polyunsaturated fatty acid diet with an LA:ALA ratio of 14:1 (14:1 group) and high-polyunsaturated fatty acid diet with an LA:ALA ratio of 5:1 (5:1 group)

Parameter	STD	SFA	14:1	5:1
WBC (10^9/L)	25.28 (12.12)	21.50 (9.66)	20.31 (11.84)	25.22 (10.58)
LYM (10^9/L)	19.76 (8.15)	15.28 (6.20)	13.45 (6.33)	19.17 (7.87)
MON (10^9/L)	0.71 (0.86)	0.25 (0.35)	0.79 (1.49)	0.26 (0.33)
NEU (10^9/L)	4.81 (5.56)	5.97 (3.88)	6.06 (4.47)	5.79 (3.45)
HCT (%)	55.91 (2.46)	53.56 (2.65)	52.93 (2.76)	53.42 (2.09)
MCHC (g/L)	32.35 (1.23)	33.20 (0.89)	32.91 (1.33)	33.88 (1.90)
MCV (fL)	62.13 (1.13)	63.25 (2.12)	64.00 (2.83)	62.75 (2.77)
RDWcv (%)	17.28 (0.75)	16.84 (0.46)	16.91 (0.63)	17.36 (0.70)
PLT (10^9/L)	752.25 (108.06)	463.88 (219.81)	513.00 (240.96)	670.88 (254.00)

HCT – haematocrit; LYM – lymphocyte count; MCHC – mean corpuscular haemoglobin concentration; MCV – mean corpuscular volume; MON – monocyte count; NEU – neutrophil count; PLT – platelet count; RDWcv – red cell distribution width related to corpuscular volume; WBC – white blood cell count. Data are expressed as mean ± standard deviation; n = 8 mice per group

Table S3. Protein spots expressed differentially between the standard diet (STD) and high-fat diet groups (saturated fatty acid–rich (SFA), polyunsaturated fatty acid–rich with a linoleic acid:α linolenic acid ratio of 14:1 (14:1), and similar but with this ratio 5:1 (5:1) in mouse liver after six months' feeding

Spot number (SSP)	Protein name	Accession number UniProtKB/ NCBI	Gene symbol	MASCOT score	E-value	Sequence coverage	Peptides matched / peptides searched	Theoretical pI/MW (Da)	Ratio					
									SFA/ STD	14:1/ STD	5:1/ STD	14:1/ SFA	5:1/ SFA	5:1/ 14:1
0104	annexin A5	P48036 / NP_033803.1	*Anxa5*	119	8.5e-08	30%	9 / 15	4.72 / 35787	0.99	1.22 (*)	0.85	1.23	0.86	0.69 (***)
0106	regucalcin	Q64374 / NP_033086.1	*Rgn*	188	1.1e-14	61%	16 / 28	5.15 / 33899	1.39 (***)	1.07	1.13	0.77 (*)	0.81 (**)	1.06
0204	eukaryotic translation initiation factor 2 subunit 1	Q6ZWX6 / NP_080390.1	*Eif2s1*	86	1.60e-04	23%	6 / 8	5.02 / 36371	0.83	0.87	0.61 (***)	1.05	0.74	0.70 (*)
0609	serine protease inhibitor A3K	P07759 / NP_035588.2	*Serpina3k*	91	5.1e-05	27%	10 / 21	5.05 / 47021	0.45	0.34 (*)	0.51 (**)	0.75	1.13	1.51
1201	galactokinase	Q9R0N0 / NP_058601.2	*Galk1*	95	2.1e-05	33%	11 / 40	5.17 / 42668	1.26	1.16	0.92	0.92	0.73 (**)	0.79
2607	heat shock 70 kDa protein 1A	Q61696 / NP_034609.2	*Hspa1a*	65	0.021	20%	9 / 22	5.38 / 70321	0.45	0.34 (*)	0.51 (**)	0.75 (**)	1.13	1.51
3010	ferritin light chain 1	P29391 / NP_034370.2	*Ftl1*	108	1.1e-06	53%	8 / 23	5.66 / 20847	1.26	1.31	0.89	1.04	0.70 (*)	0.68 (*)
3103	ketohexokinase	P97328 / NP_032465.2	*Khk*	61	4.90e-02	26%	5 / 14	5.59 / 33300	1.54 (*)	0.93	1.05	0.60 (***)	0.68 (**)	1.12
3417	S-adenosylmethionine synthase isoform type-1	Q91X83 / NP_598414.1	*Mat1a*	82	4.30e-04	22%	7 / 14	5.51 / 44051	0.53 (*)	0.51 (*)	0.58 (*)	0.97	1.10	1.13
3505	sulfite oxidase, mitochondrial	Q8R086 / NP_776094.2	*Suox*	215	2.1e-17	45%	16 / 26	6.07 / 61231	1.18 (*)	0.91	1.05	0.77 (***)	0.89	1.15
3512	formimidoyltransferase cyclodeaminase	Q91XD4 / NP_543121.1	*Ftcd*	210	6.7e-17	60%	22 / 47	5.79 / 59529	1.49 (**)	0.94	0.96	0.63 (***)	0.64 (***)	1.02
3605	albumin	P07724 / NP_033784.2	*Alb*	288	1.1e-24	54%	29 / 55	5.75 / 70700	0.62	0.76 (*)	0.61 (***)	1.22	0.98	0.80
3610	albumin	P07724 / NP_033784.2	*Alb*	140	6.7e-10	32%	15 / 29	5.75 / 70700	0.42 (*)	0.55 (***)	0.44 (***)	1.31	1.04	0.80
3806	cytosolic 10-formyltetrahydrofolate dehydrogenase	Q8R0Y6 / NP_081682.1	*Aldh1l1*	114	2.7e-07	21%	13 / 23	5.64 / 99502	1.26	0.97	1.47 (*)	0.77	1.16	1.51 (*)
4004	peroxiredoxin-4	O08807 / NP_001300640.1, NP_058044.1	*Prdx4*	89	9.3e-05	38%	8 / 25	6.67 / 31261	1.13	1.40 (**)	1.56 (***)	1.24	1.38 (*)	1.11
4101	indolethylamine N-methyltransferase	P40936 / NP_033375.1	*Inmt*	113	3.4e-07	51%	10 / 23	5.75 / 30068	1.19	0.80 (*)	0.87	0.67 (***)	0.74 (***)	1.10
4301	ornithine aminotransferase, mitochondrial	P29758 / NP_058674.1	*Oat*	205	2.1e-16	53%	20 / 36	6.19 / 48723	0.72 (***)	0.53 (***)	0.69 (**)	0.74 (**)	0.97	1.30
5110	peroxiredoxin-6	O08709 / NP_031479.1	*Prdx6*	189	8.5e-15	72%	15 / 33	5.71 / 24969	1.80 (***)	1.56 (***)	1.04	0.87	0.58 (*)	0.66
5202	fructose-1,6-bisphosphatase 1	Q9QXD6 / NP_062268.1	*Fbp1*	239	8.5e-20	78%	27 / 51	6.15 / 37288	1.28 (**)	1.21 (*)	1.01	0.95	0.79 (**)	0.83 (*)
6404	alpha-enolase	P17182 / NP_075608.2	*Eno1*	196	1.7e-15	63%	25 / 85	6.37 / 47453	1.28 (***)	1.15	1.05	0.90	0.82 (**)	0.92
6606	triokinase/FMN cyclase	Q8VC30 / NP_663471.1	*Tkfc*	249	8.5e-21	55%	27 / 40	6.44 / 59938	1.41 (**)	1.11	1.17	0.79 (*)	0.83 (*)	1.05
7102	phosphoglycerate mutase 1	Q9DBJ1 / NP_075907.2	*Pgam1*	149	8.5e-11	62%	16 / 50	6.67 / 28928	1.05	1.06	1.40 (*)	1.01	1.33	1.32
7104	carbonic anhydrase 3	P16015 / NP_031632.2	*Ca3*	231	5.3e-19	81%	16 / 34	6.89 / 29633	1.36 (*)	1.31	1.40 (**)	0.96	1.03	1.07
8013	haemoglobin subunit beta-1	P02088 / NP_001265090.1	*Hbb-b1*	91	5.00e-05	62%	7 / 33	7.12 / 15944	0.52	0.92	0.61 (**)	1.76	1.18	0.67
8014	cytochrome c oxidase subunit 6A1, mitochondrial	P43024 / NP_031774.1	*Cox6a1*	66	0.016	61%	4 / 12	9.97 / 12344	0.34 (*)	0.78	0.42 (*)	2.27 (*)	1.22	0.54
8207	3-ketoacyl-CoA thiolase, mitochondrial	Q8BWT1 / NP_803421.1	*Acaa2*	201	5.3e-16	60%	22 / 42	8.33 / 42260	1.39	0.55	0.91	0.40 (**)	0.65 (**)	1.64 (*)
8211	3-ketoacyl-CoA thiolase, mitochondrial	Q8BWT1 / NP_803421.1	*Acaa2*	142	4.2e-10	42%	16 / 41	8.33 / 42260	0.84	0.64 (*)	1.41	0.75	1.67	2.21 (*)
8302	hydroxymethylglutaryl-CoA synthase, mitochondrial	P54869 / NP_032282.2	*Hmgcs2*	194	2.7e-15	45%	28 / 65	8.65 / 57300	1.33	0.92	0.99	0.69 (*)	0.75	1.08
8303	betaine--homocysteine S-methyltransferase 1	O35490 / NP_057877.1	*Bhmt*	128	1.1e-08	48%	15 / 48	8.01 / 45448	0.50 (**)	1.11	0.81	2.23 (***)	1.63 (*)	0.73
8403	aldehyde dehydrogenase 1A1	P24549 / NP_038495.2	*Aldh1a1*	152	4.2e-11	50%	21 / 68	7.92 / 55060	1.65 (**)	1.18	1.46 (*)	0.71 (*)	0.89	1.24
8406	homogentisate 1,2-dioxygenase	O09173 / NP_038575.2	*Hgd*	103	3.4e-06	28%	11 / 28	6.86 / 50726	1.42 (*)	0.93	1.28	0.66 (**)	0.90	1.37 (**)
8502	aldehyde dehydrogenase family 6, subfamily A1	Q9EQ20 / NP_598803.1	*Aldh6a1*	154	2.7e-11	34%	17 / 40	8.29 / 58335	1.48 (**)	1.02	1.06	0.69 (*)	0.72 (**)	1.04

Spot number indicates the number labelling the spots in Fig 5. The results are the highest identification values from an average of three biological replicates. The statistically significant (P-value < 0.05) value of the average intensity of the SFA, 14:1 and 5:1 groups in relation to the STD group, as well as the 14:1 and 5:1 groups in relation to the SFA group and the 5:1 group in relation to the 14:1 group. Significance of differences was estimated using the model described in the chapter Material and Methods: Statistical analysis. pI – isoelectric point; MW – molecular weight; * – P-value < 0.05; ** – P-value < 0.01; *** – P-value < 0.001