

Table S1: Characteristics of primers used in RT-qPCR according to MIQE guidelines.

Gene symbol	Accession	Sequence	Amplicon length	Exons	[Primer]	Efficiency
Cyp7a1	NM_007824.3	Sense CATTACAGAGTGCTGGCCAAGA Antisense CTGTCCGGATATTCAAGGATGC	144	4/5	0.1 μ M	97%
Lcn2	NM_008491.1	Sense GGAACGTTTCACCCGCTTTG Antisense TGAACCATTGGGTCTCTGCG	140	5/6	0.1 μ M	104%
Lpin1	NM_001355598.1	Sense TACCCCCAGTCAGCATCGTA Antisense CTTTTTGGTGTTGAGGGCCG	89	5/6	0.1 μ M	96%
Resf1	NM_001289662.1	Sense AATCCCGACGGAGGGACTAA Antisense GCTTTGGAGGTGGCTGTAT	232	3	0.1 μ M	98%
Rhobtb1	NM_001081347.1	Sense CGGGAGCGAGAGCTTTGTAA Antisense CAGCAGCTGGTACTGTGTCA	158	2/3	0.1 μ M	101%
Saa1	NM_009117.4	Sense TTAGCTCAGTAGGTTGTGCTGG Antisense ACAATGTTTCCCCAGAGAGCA	92	4	0.1 μ M	97%
Saa2	NM_011314.3	Sense CTGGCTGGAAAGATGGAGAC Antisense TGTCTCTCGTGTCTCTGC	147	3/4	0.1 μ M	104%
Slc4a1	NM_011403.2	Sense GATCCCAGATCGAGACAGCG Antisense CACATAGACCTGACCGGAGC	184	3/5	0.1 μ M	107%
Txndc5	NM_145367.4	Sense CAGGCTTGTCTCAGATGTCACCAT Antisense TAACCTCGTACCGAGTACTTGCTG	82	8/9	0.2 μ M	100%
Ppib	NM_011149	Sense GGAGATGGCACAGGAGGAA Antisense GTAGTGCTTCAGCTTGAAGTTCTCAT	72	3/4	0.1 μ M	103%

Table S2: Sequence quality metrics and genome mapping of GSE185515.

Group	Total Raw Reads (M)	Total Clean Reads (M)	Clean Reads (%)	Mapping Ratio (%)
Wildtype (n=3)	48,31 \pm 1,44	44,69 \pm 1,08	44,69 \pm 1,08	92,86 \pm 1,0652
Knock-out (n=3)	49,97 \pm 1,44	45,73 \pm 1,08	45,73 \pm 0,36	93,34 \pm 0,42

Supplementary Table S3: Summary of SNP variant type of GSE185515.

Group	A-G	C-T	Transition	A-C	A-T	C-G	G-T	Transversion	Total
Wildtype	1673 ± 342	1677 ± 351	3350 ± 692	365 ± 93	336 ± 64	301 ± 80	319 ± 78	1321 ± 306	4670 ± 989
Knock-out	1621 ± 342	1635 ± 351	3256 ± 692	350 ± 93	277 ± 64	297 ± 80	328 ± 78	1252 ± 306	4509 ± 989

A-G: The amount of A-G variant type; C-T: The amount of C-T variant type; Transition: The amount of A-G and C-T variant type; A-C: The amount of A-C variant type; A-T: The amount of A-T variant type; C-G: The amount of C-G variant type; G-T: The amount of G-T variant type; Transversion: The amount of A-C, A-T, C-G and G-T variant type
Total: The amount of all variant type

Supplementary Table S4: Summary of splice variant type of GSE185515.

Group	SE	MXE	A5SS	A3SS	RI
Wildtype	3353 ± 1019	275 ± 85	693 ± 122	831 ± 150	338 ± 54
Knock-out	3508 ± 1019	302 ± 85	718 ± 122	905 ± 150	346 ± 54

SE: Skipped Exon, MXE: Mutually exclusive exons, A5SS and A3SS: Alternative 5' or 3' Splicing Site respectively and RI: Retained Intron.

Supplementary Table S5. Changes in hepatic *Txndc5* expression.

Experimental condition	Type of change	Signal log ₂ ratio	Accession number
Fish oil	Increased	0.6	GDS1307
Iron deficient, LPS injected mice	Increased	0.5	GDS5271
TGFβ-activated kinase 1 deficiency	Increased	0.5	GDS5474
Very low-fat diet in mice	Increased	0.3	GDS1517
Alcoholic hepatitis	Increased	0.1	GDS4389
Dexamethasone	Decreased	-0.6	GDS5035
NF-E2-related factor 2 Nrf2 deficiency	Decreased	-0.3	GDS3476
Sphingosine 1-phosphate lyase deficiency	Decreased	-0.12	GDS3654
Caspase-1 deficiency	No change	-0.06	GDS4922
Dicer1 deficiency	No change	-0.05	GDS3685
Steroid receptor coactivator-2 deficiency	No change	0.05	GDS4785
Interleukin 6	No change	0.02	GSD3773

Data obtained from Genome Expressed Omnibus data bank and Array express. <https://www.ncbi.nlm.nih.gov/geoprofiles/> <https://www.ebi.ac.uk/arrayexpress/>.