

## SUPPLEMENTARY MATERIAL

### Supplementary Experimental Section

#### Preparation and characterization of the lipid formulations and diets

The quantification of the lipid fractions of the two lecithins was evaluated by high-performance thin layer chromatography (HPTLC), using two consecutive plate migrations: the first with petroleum ether and acetone at a ratio of 60:20; the second, with hexane, petroleum ether and acetic acid at a ratio of 80:20:1. The spots corresponding to the TAG and PL fractions were then visualized under UV-light after vaporization of 2,7-DCF in ethanol (0.2%, w/v). Their relative proportions were determined using the area of the spots.

#### Plasma and hepatic lipid analyses

Plasma and liver samples were thawed to room temperature. Free FA were extracted according to the technique described by Bligh et Dyer <sup>[35]</sup>. PL and TAG were separated by thin layer chromatography (TLC) using hexane/diethyl-ether/acetic acid (80:20:1, v/v/v) as a migration solvent. They were then derived into FAME by transmethylation, as previously described (references 36 and 37 in the manuscript). Diheptadecanoyl-glycerophosphoethanolamine and triheptadecanoyl-glycerol were added as internal standards for the quantification of TAG and PL, respectively.

Subsequent FAME were separated using GC-FID (TRACE GC, Thermo Fisher Scientific). Automatic injection was used, with a split injection ratio of 1:33. A fused-silica capillary column (BPX 70, 60m×0.25mm i.d., 0.25µm film; SGE, France) was used with hydrogen as a carrier gas (inlet pressure: 120kPa). The column temperature program was as follows: the temperature increased from 160°C to 180°C at a rate of 1.3°C/min, and was maintained for 65 minutes before increasing at a rate of 25°C/min for 15 minutes until it reached 230°C. Injector and detector temperatures were maintained at 250°C and 280°C, respectively. GC peaks were integrated using the Chromquest software (ThermoFinnigan).

**Supplementary Table S1.** Composition of the experimental diets.

<b>Ingredients (g/100g)</b>	<b>Control</b>	<b>1% RL</b>	<b>3% RL</b>	<b>10% RL</b>	<b>20% SL</b>
<b>Lipid mixture*</b>	<b>5</b>	<b>5</b>	<b>5</b>	<b>5</b>	<b>5</b>
Among which:					
Rapeseed lecithin (RL)	-	0.05	0.15	0.5	-
Soy lecithin (SL)	-	-	-	-	0.5
<b>Fat-free diet base:</b>	<b>95</b>	<b>95</b>	<b>95</b>	<b>95</b>	<b>95</b>
Among which:					
Dextrose	42.7	42.7	42.7	42.7	42.7
Casein (defatted)	32.3	32.3	32.3	32.3	32.3
Cellulose (crude)	8.6	8.6	8.6	8.6	8.6
Mineral mix	10.0	10.0	10.0	10.0	10.0
Vitamin mix	1.4	1.4	1.4	1.4	1.4
<b>Energy content (kJ/g)</b>	<b>14.1</b>	<b>14.1</b>	<b>14.1</b>	<b>14.1</b>	<b>14.1</b>
<b>Energy (ME Atwater, %)**</b>					
Proteins	34.2	34.2	34.2	34.2	34.2
Lipids	13.4	13.4	13.4	13.4	13.4
Carbohydrates	52.4	52.4	52.4	52.4	52.4

\*See detailed lipid composition in Table 1.

\*\* Metabolisable energy

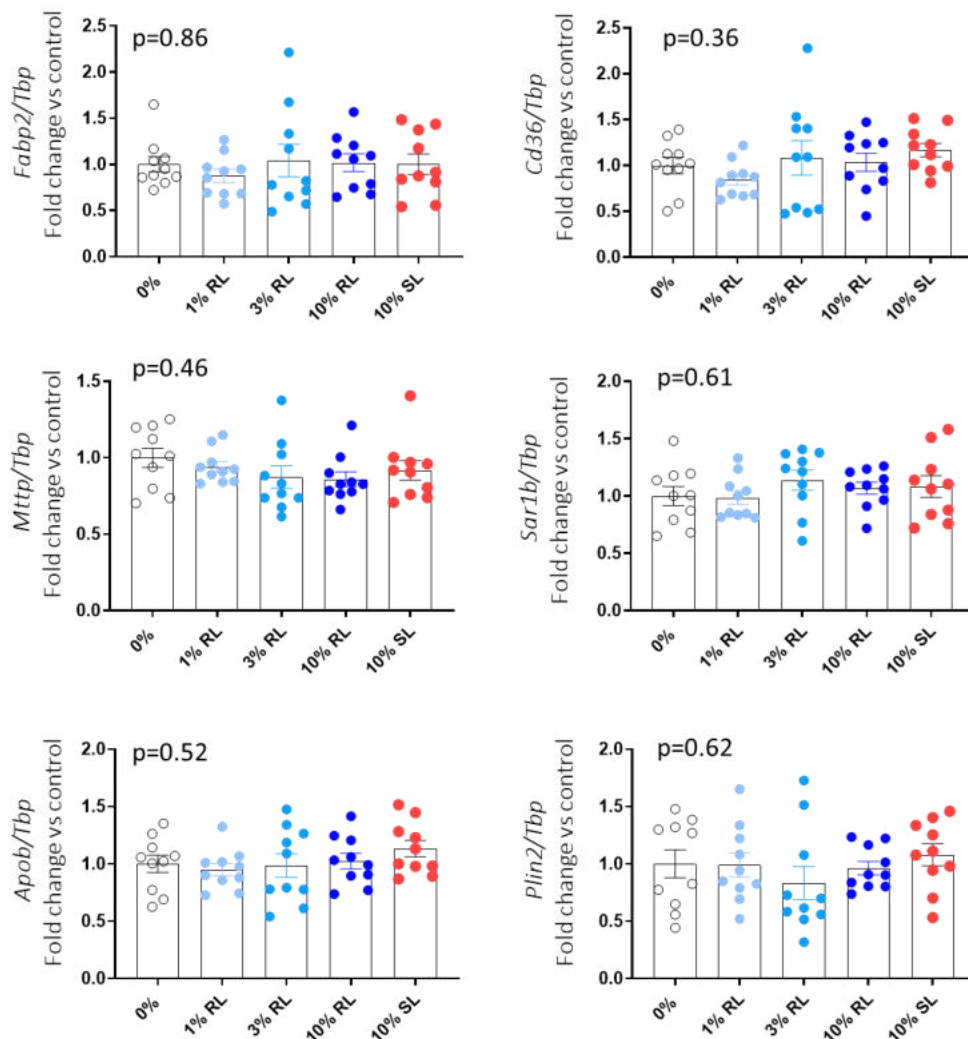
**Supplementary Table S2.** The sequences of forward and reverse primers used for RT-PCR analysis.

Gene name*	Forward primers (5' – 3')	Reverse primers (5' - 3')
<i>Apob</i>	CCTCTCCTGGGTGTTCTAGAC	GTTTCTCCAGATCCTTGCAC
<i>Slc10a2</i> (Abst)	ACCTCAGTGTTAGCATGACC	ATCCAGGCACTTTGGTACAG
<i>Cd36</i>	GTCCTGGCTGTGTTTGGAGG	AAGATCCAAAACGTGTCTGTA
<i>Cpt1a</i>	ACGTATGAGGCTTCCATGAC	GGTGAGTCGACTGCCAGATA
<i>Cyp27a1</i>	TCTGGCTACCTGCACTTC	ACCACACCAGTCACTTCC
<i>Cyp7a1</i>	CAATGAAAGCAGCCTCTGAAG	AAAAGTCAAAGGGTCTGGG
<i>Elovl2</i>	GGTAGCCAAGGTCTTGTGGT	GAAGCTTTGACCACAAGGTA
<i>Elovl5</i>	ATCCACGTCCTCATGTACTC	GTCTGGATGATTGTCAGCAC
<i>Fads1</i>	CACGACCGGAATGTGGACTG	GGTGAAGGTAAGCGTCCAAC
<i>Fads2</i>	TATCAGGTTCTTGAGAGCC	GGAAGAGGTGGTGCTCAATC
<i>Fapb2</i>	ACCTCTCGGACAGCAATCAG	CTTTCCCTACAGTCTAGCAG
<i>Fgf15</i>	GAGGAGGACCAAAACGAACG	GAAGGTACAGTCTTCCTCCG
<i>Nr1h4</i> (Fxr)	GCAACCTGTTGGAAGAAAG	GTCTGTCTGGAGAGAGGATG
<i>Mttp</i>	GGAGAAGTAACCTGAACATC	ACAGGTCTGAGCTGAACATC
<i>Slc5a1</i> (Osta)	GCTCCTTGACCTCCATCTTC	CAGGCAATGCTGATGCCAAT
<i>Adfp</i> (Plin2)	CCTATTCTGAACCAGCCAAC	CTGCTCCTTTGGTCTTATCC
<i>Ppara</i>	TCTCTCCGTAATGGAAGACC	GCATTATGAGACATCCCCAC
<i>Pparδ</i>	CGGGTGTGCGGGGACAAGGC	GCCTTCTTTTTGGTCATGTTG
<i>Sar1b</i>	ATTGCTGGCATGACGTTTAC	TGCCATTGATAGCAGGAAGG
<i>Sult2a1</i>	CAGATGAGCTGGATCTCGTCC	GTGATTCTTCCAGTCCCCAA
<i>Sult2a8</i>	TGGAATCAGGGGAAGTGGAG	TATCAAAGGCTTCAGCCTGG
<i>Tbp</i>	TGGTGTGCACAGGAGCCAAG	TTCACATCACAGCTCCCCAC
<i>Gpbar1</i> (Tgr5)	GTCAGTCTTGGCCTATGAGC	AGTGCTGGGGCCTGGATTG

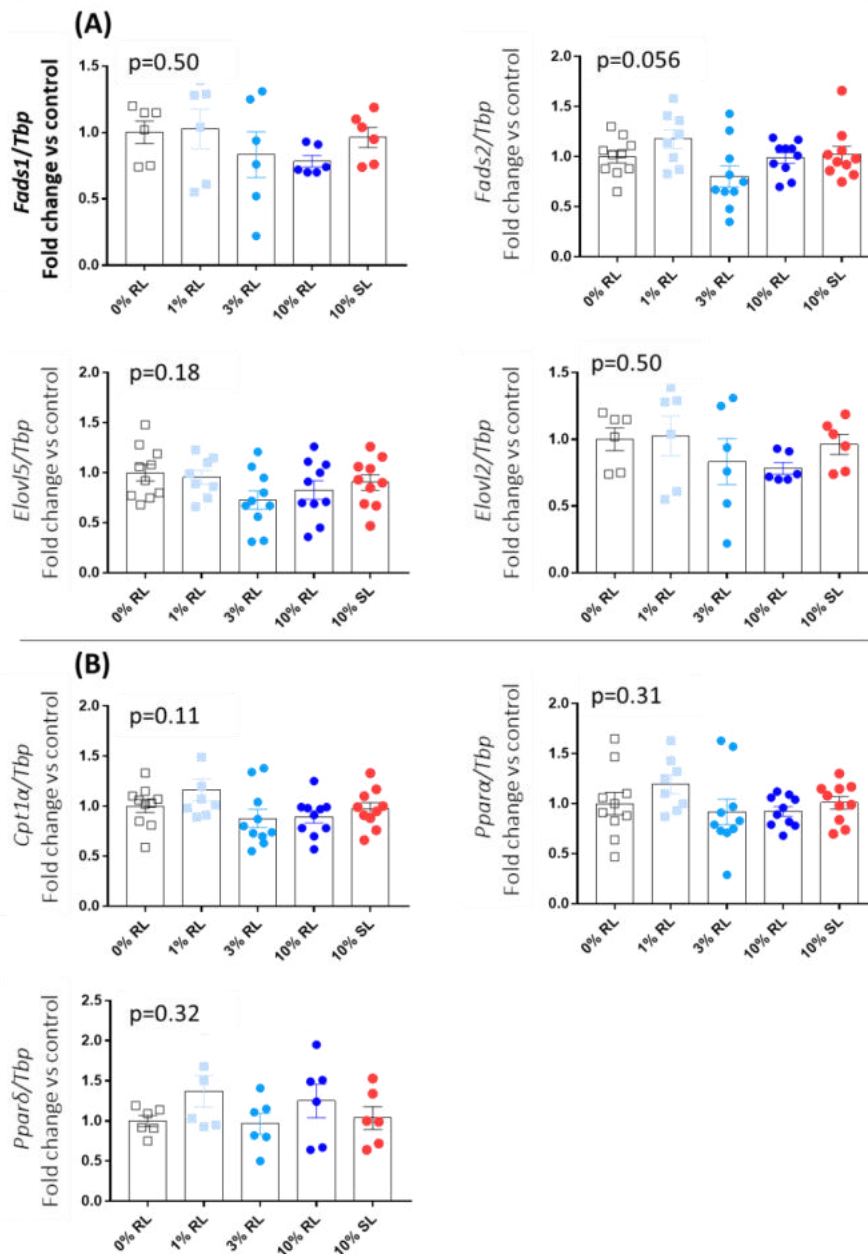
\* the protein for which the gene codes is presented in brackets when the names of the gene and of the protein differ

**Supplementary Table S3.** The sequences of forward and reverse primers used for the analysis of the gut microbiota.

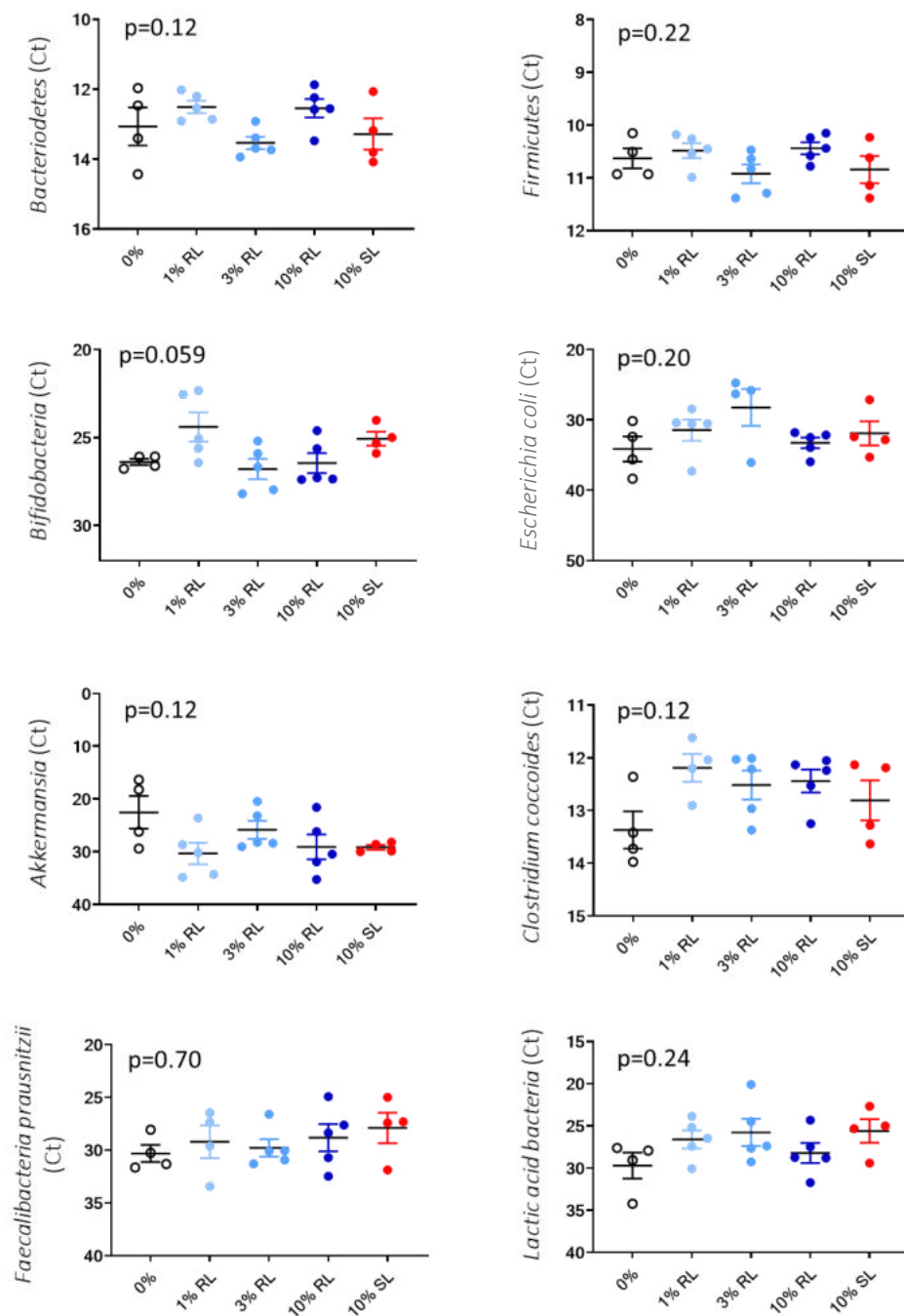
Population	Forward and reverse primers (5' – 3')
Total bacteria (HDA)	F : ACTCCTACGGGAGGCAGCAG R : GTATTACCGCGGCTGCTGGCAC
<i>Bacterioidetes</i>	F : GGARCATGTGGTTTAATTTCGATGAT R : AGCTGACGACAACCATGCAG
<i>Firmicutes</i>	F : GGAGYATGTGGTTTAATTTCGAAGCA R : AGCTGACGACAACCATGCAC
<i>Bifidobacterium spp.</i>	F : TCGCGTCYGGTGTGAAAG R : CCACATCCAGCRTCCAC
<i>Escherichia coli</i>	F : CATGCCGCGTGTATGAAGAA R : CGGGTAACGTCAATGAGCAAA
<i>Akkermansia muciniphila</i>	F : CAGCACGTGAAGGTGGGGAC R : CCTTGCGGTTGGCTTCAGAT
<i>Clostridium coccoides</i> group	F : CGGTACCTGACTAAGAAGC R : CTTCTCCGTTTTGTCAA
<i>Clostridium leptum</i> group	F : GCACAAGCAGTGGAGT R : CTTCTCCGTTTTGTCAA
<i>Faecalibacterium praunsnitzii</i>	F : AGATGGCCTCGCGTCCGA R : CCGAAGACCTTCTTCTCC
<i>Lactobacillus</i> group	F : AGCAGTAGGGAATCTTCCA R : ATTYCACCGCTACACATG



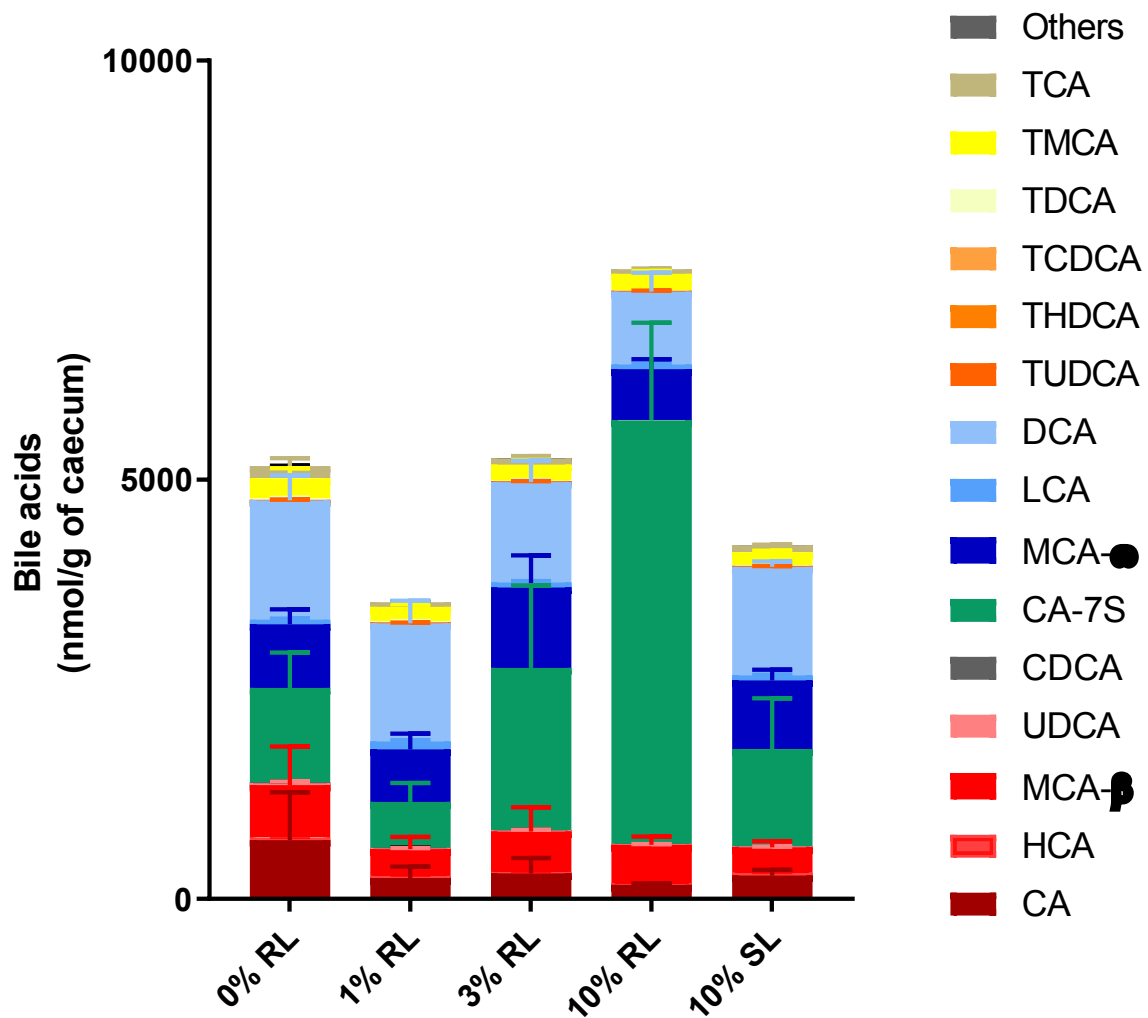
**Supplementary Figure S4.** The mRNA expression of genes involved in lipid absorption in the jejunum of mice. Values are normalized to the levels of the mRNA expression of *Tbp* and expressed as relative amount compared with control (0% lecithin). Bars represent mean  $\pm$  SEM, n=7-9. To test the impact of lecithin on the expression of these genes, all groups were analyzed by one-way ANOVA. *Apob*=apolipoprotein B; *Cd36*=cluster of differentiation 36; *Fapb2*=fatty acid binding protein 2; *Mttp*=microsomal triglyceride transport protein; *Plin2*=perilipin 2; RL=rapeseed lecithin; *Sar1b*=secretion associated Ras related GTPase 1B; SL=soybean lecithin; *Tbp*=TATA box binding protein.



**Supplementary Figure S5.** The mRNA expression of genes involved in (A) bioconversion of ALA to n-3 long chain polyunsaturated fatty acids and (B) beta-oxidation, in the liver of mice. Values are normalized to the levels of the mRNA expression of *Tbp* and expressed as relative amount compared with control (0% lecithin). Bars represent mean±SEM, n=7-9. To test the impact of lecithin on the expression of these genes, all groups were analyzed by one-way ANOVA. *Cpt1α*=Carnitine palmitoyltransferase I-α; *Elovl2-5*=elongase of very-long-chain fatty acids-like 2-5; *Fads1-2*=Fatty Acid Desaturase 1-2; *Pparaα-δ*=peroxisome proliferator-activated receptor α-δ; RL=rapeseed lecithin; SL=soybean lecithin; *Tbp*=TATA box binding protein.



**Supplementary Figure S6.** The DNA expression of *Bacteroidetes*, *Firmicutes*, *Bifidobacteria*, *Escherichia coli*, *Akkermansia*, *Clostridium coccoides*, *Lactic acid bacteria* and *Faecalibacterium prausnitzii* in the feces of mice following 5 days of consumption of diets containing 0 to 10% RL or SL. Bars represent mean±SEM, n=4-5. To test the impact of SL and RL on these parameters, all groups were analyzed by one-way ANOVA. Ct=number of cycles; RL=rapeseed lecithin; SL=soybean lecithin.



**Supplementary Figure S7.** The bile acid profile in the caecum of Swiss mice, after 5 days of consumption of diets containing 0 to 10% RL or SL. Values represent mean  $\pm$  SEM, n=5-7. CA=cholic acid; CDA=deoxycholic acid; CDCA= chenodeoxycholic acid; HCA= hypocholeic acid; HDCA= hyodeoxycholic acid; LCA= lithocholic acid; MCA= muricholic acid; RL=rapeseed lecithin; SL=soybean lecithin; T=taurine-conjugated; UDCA= ursodeoxycholic acid.