Supporting information

Contents

1. Method

Histopathology of livers

Liver samples were collected. After fixation in 10% neutral buffered formalin for approximately 48h, the livers were dehydrated with a graded series of alcohol solutions (70%–100%), cleared in xylene, embedded in paraffin, and sectioned along the transverse plane at 3 μm thickness. Serial sections were mounted on glass slides, stained with hematoxylin and eosin, and covered with glass coverslips. Finally, the sections were examined with a light microscopy.

2. Results

2.1 Histopathology

Table S1 Analysis and statistics of liver histopathology(*N* = 3).

Histological damage	Control	OF	LVFX
Fat vacuole	/	+ +	+ + +
Nuclear deviation and dissolution	/	+	+ + +
Loss of hepatic plate structure	/	+	+ + +
Hepatocytes lose their inherent morphology as a whole	/	+	+ +
The basic structure of the liver is unclear	/	/	+ +

Notes: / indicates that this phenomenon has not occurred. + indicates that this phenomenon occurs more often. + + or + + + indicates that this phenomenon has occurred many times.

2.2 Gene transcriptome analysis

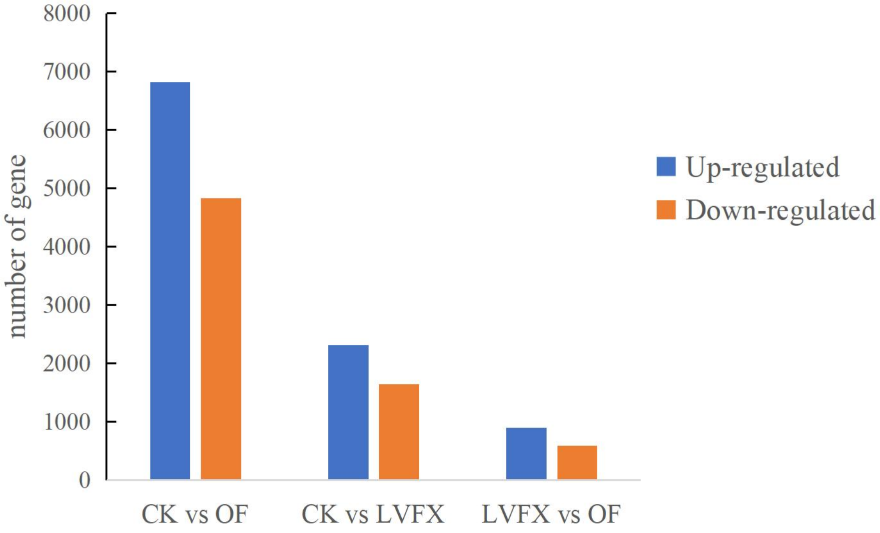

Fig. S1 Expression difference analysis result statistics.

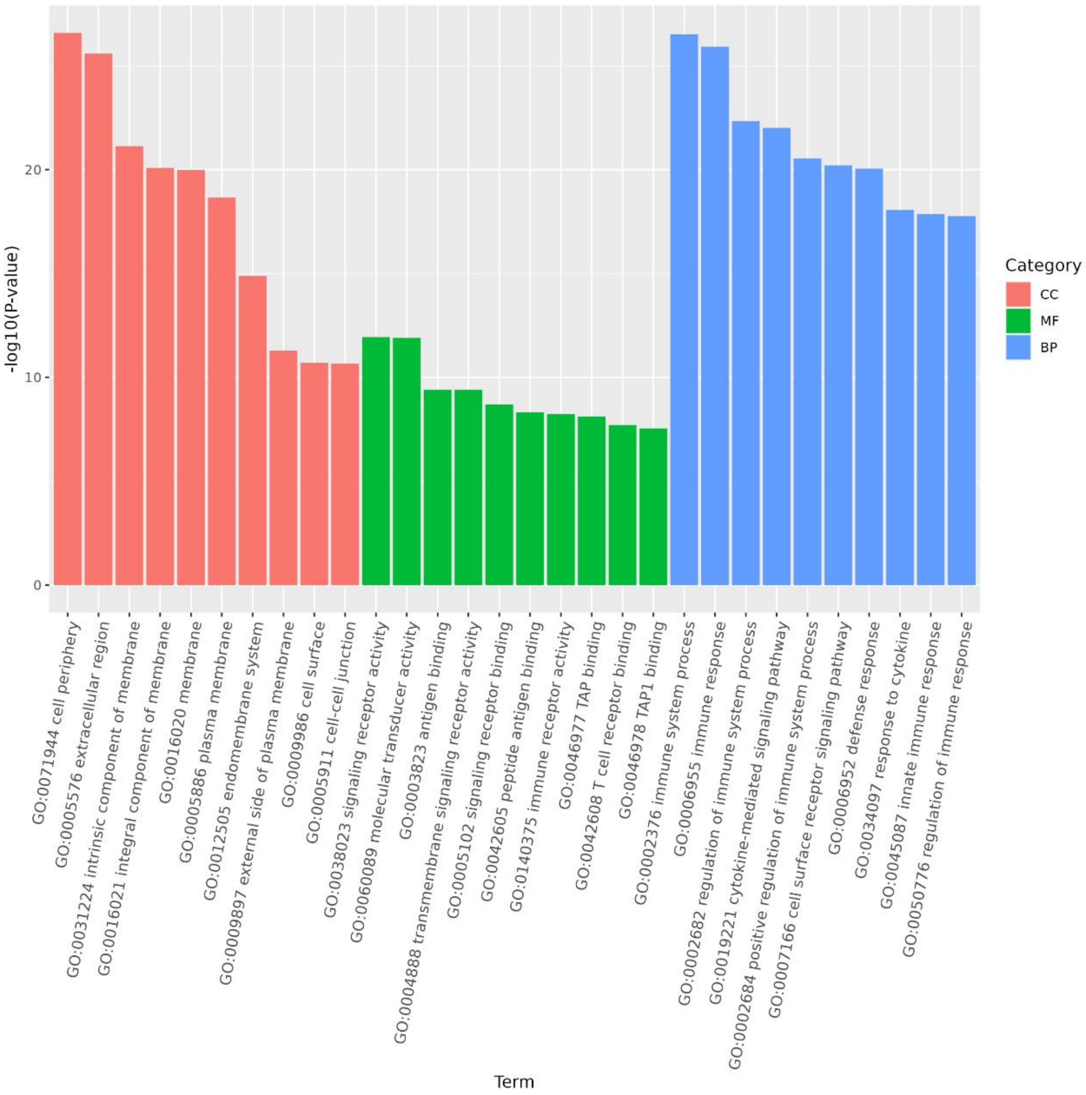

Fig. S2 Histogram of GO Pathway enrichment results in LVFX vs OF.

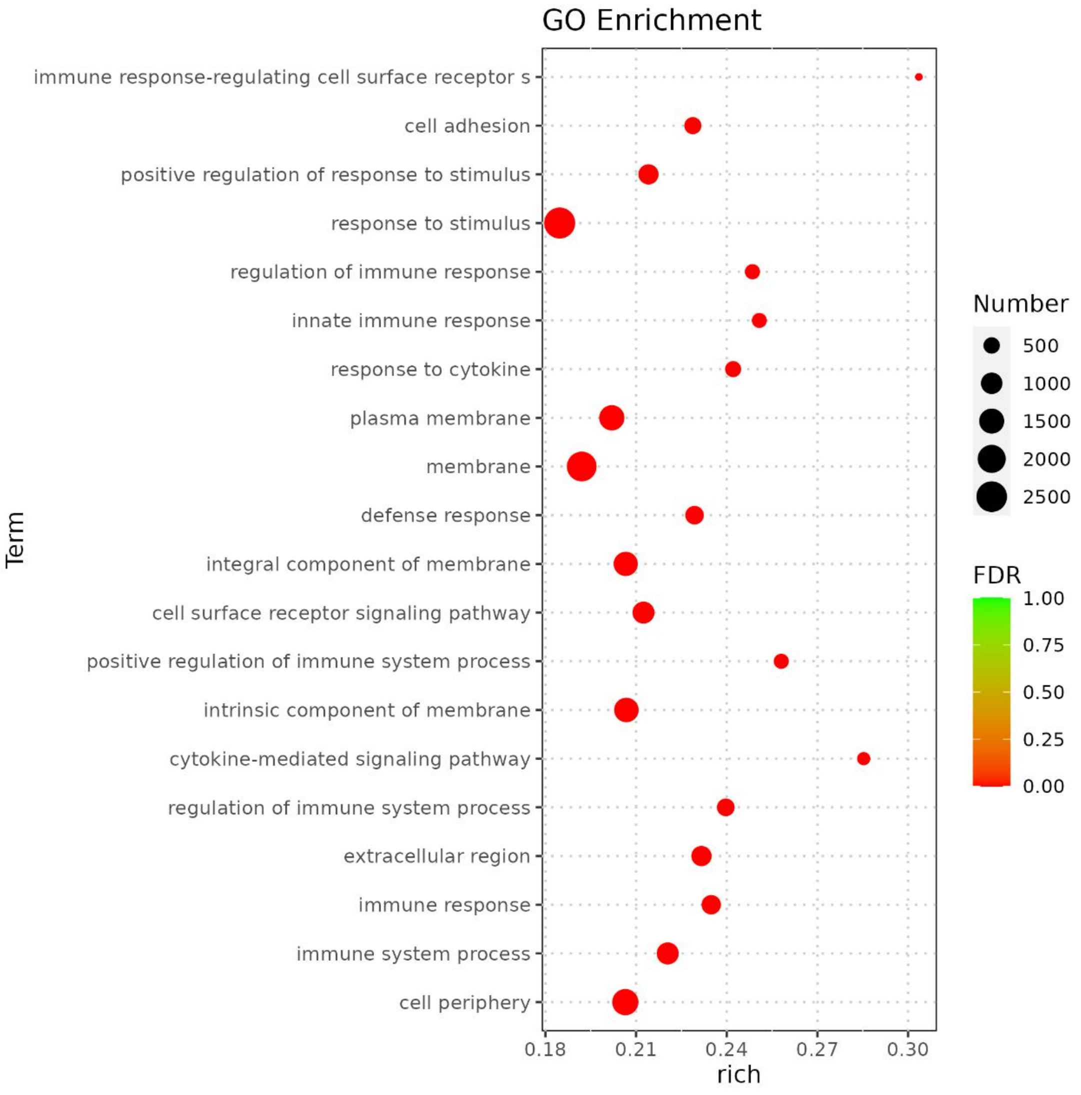

Fig. S3 GO enrichment analysis bubble chart in LVFX vs OF.

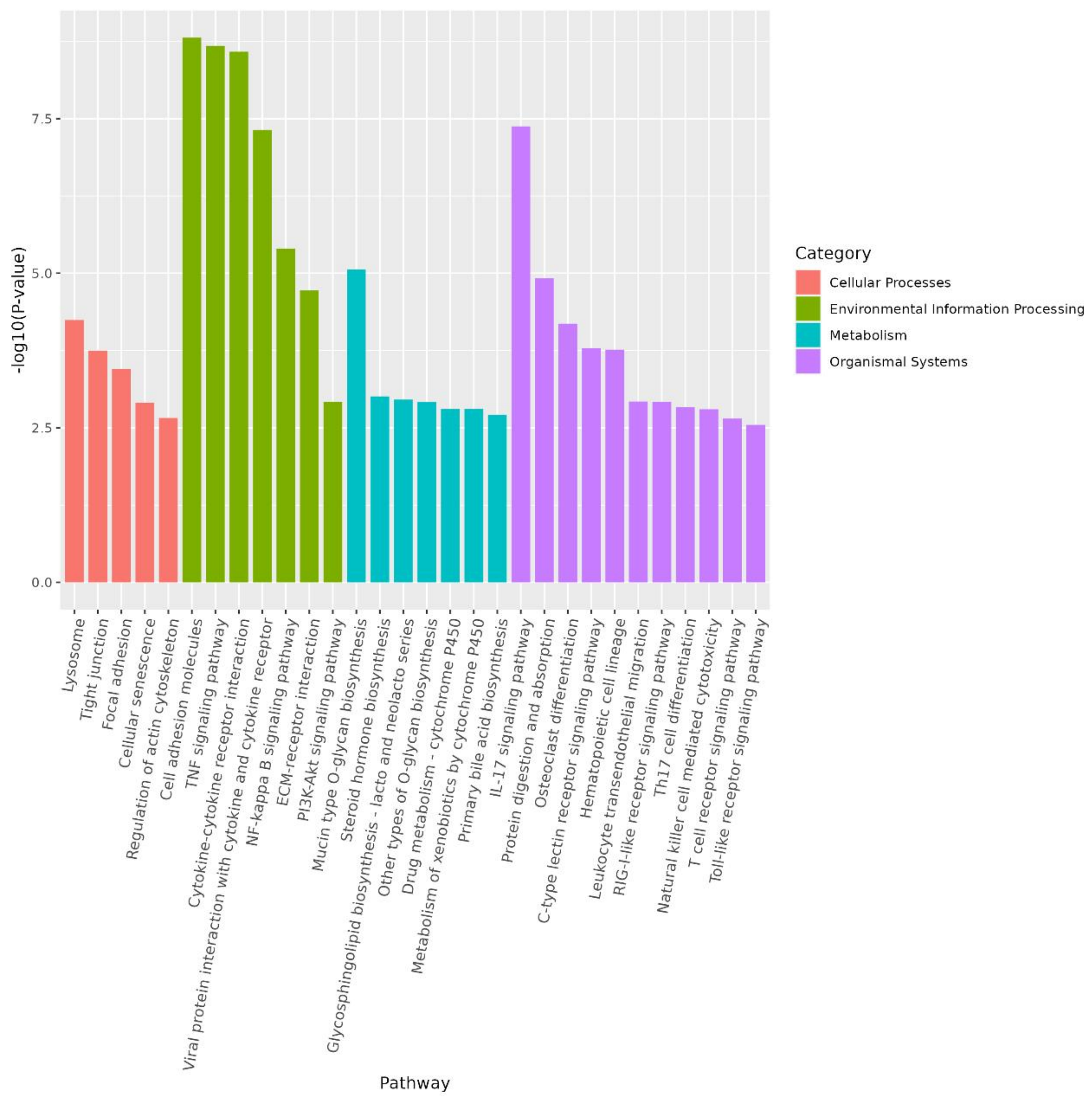

Fig. S4 Histogram of KEGG Pathway enrichment results in LVFX vs OF.

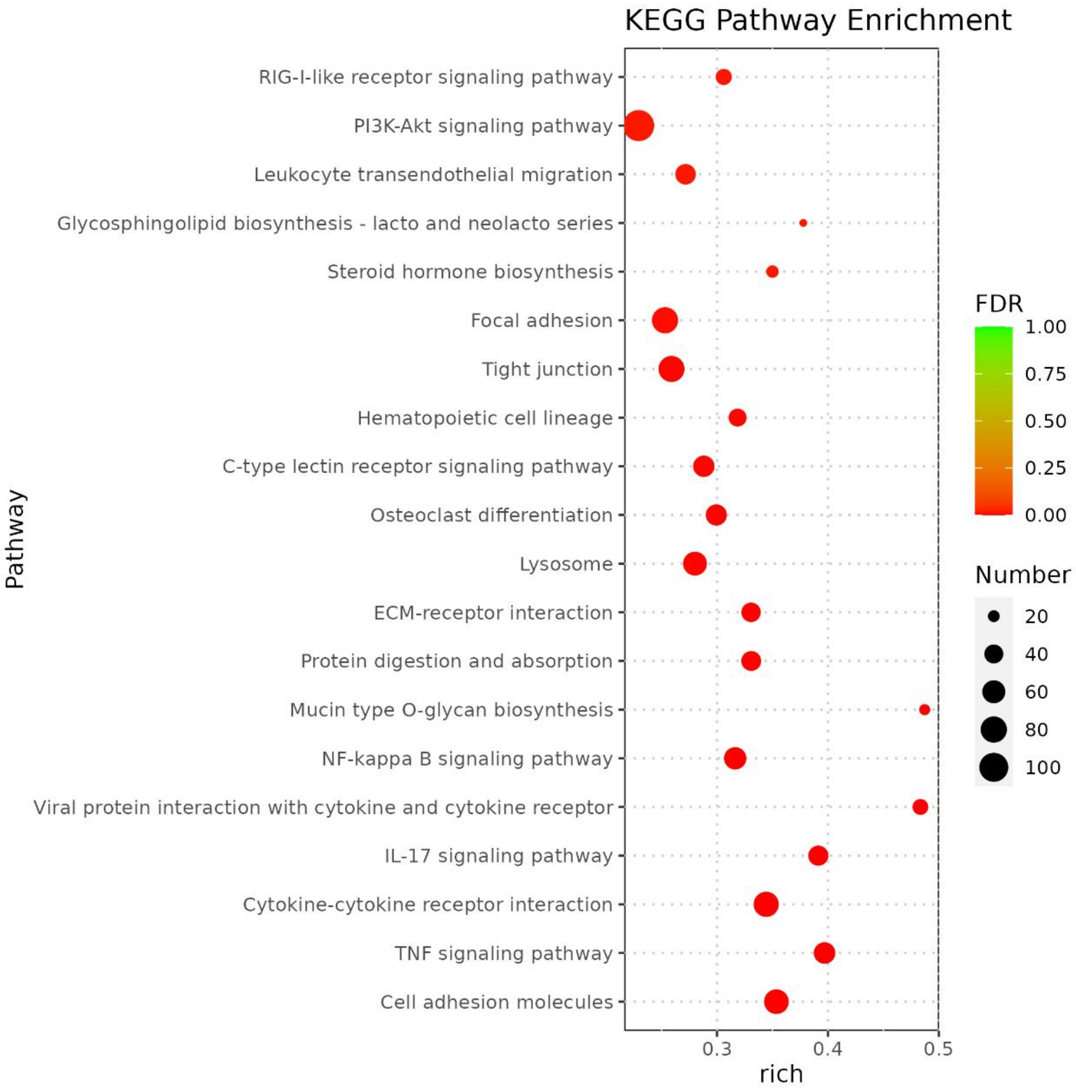

Fig. S5 KEGG enrichment analysis bubble chart in LVFX vs OF.

2.3 Targeted lipid metabolomics analysis

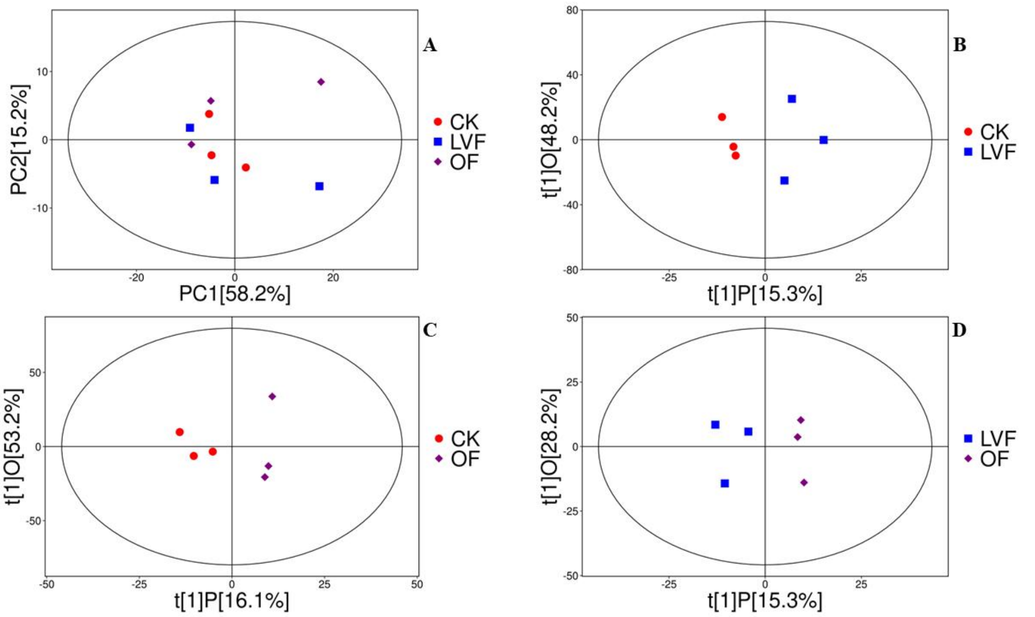

Fig. S6 Score scatter plot for PCA model TOTAL (A). Score scatter plot of PCA model for group CK vs LVF (B), CK vs OF (C) and OF vs LVF (D).

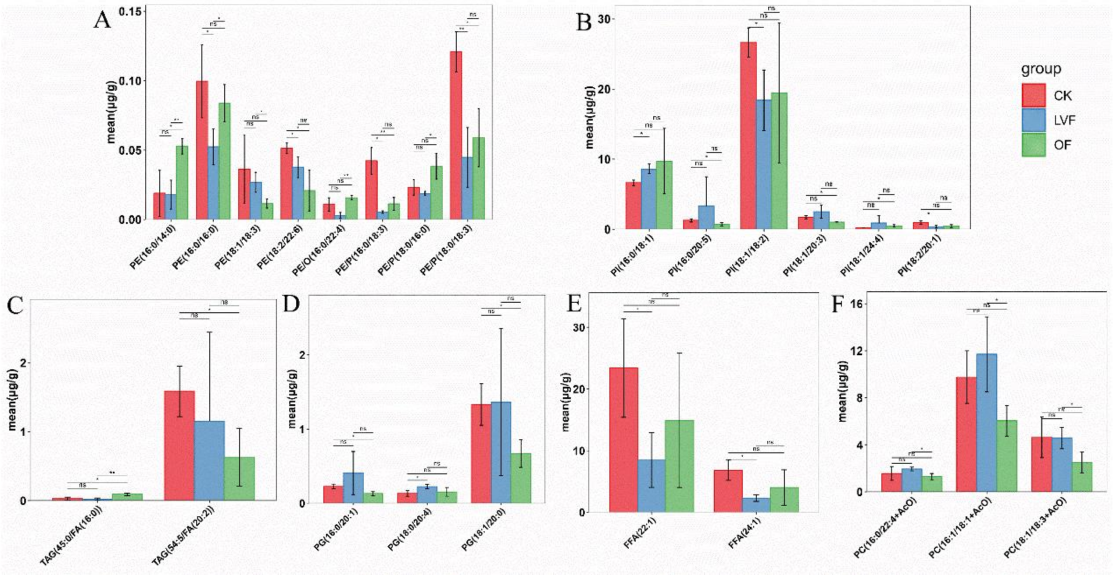

Fig. S7 Unsaturated bonds and carbon chain lengths of PE (A), PI (B), TAG (C), PG (D), FFA (E)and PC (F), respectively.

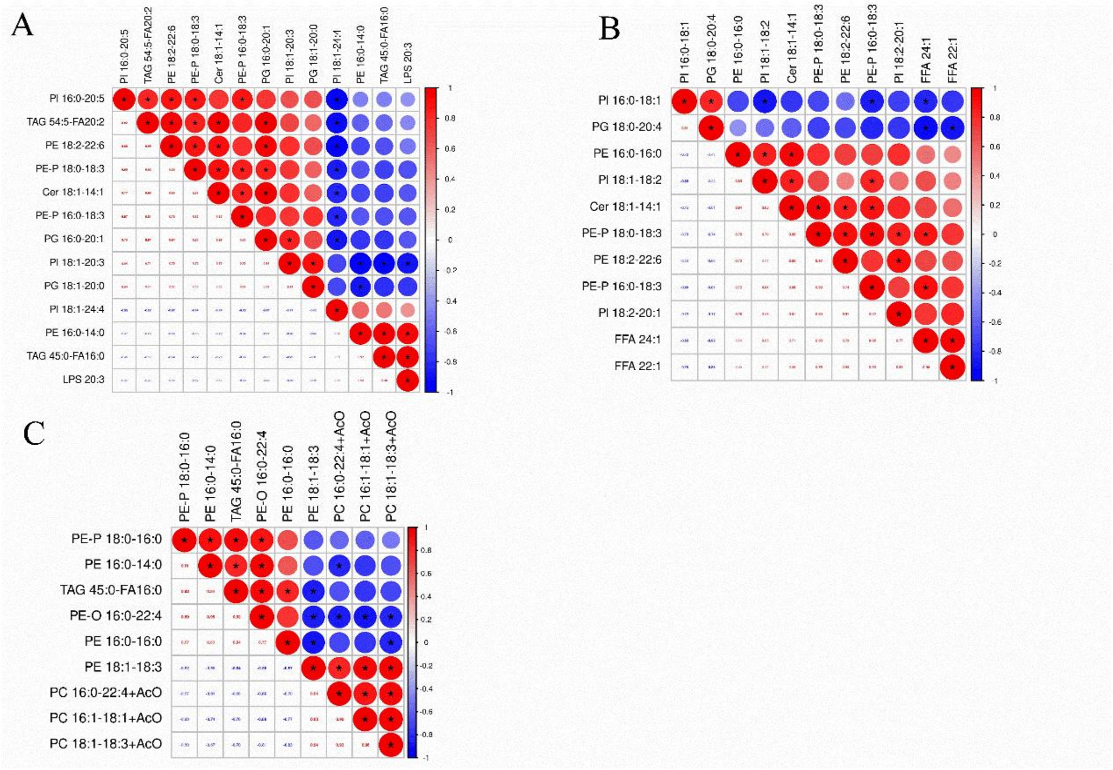

Fig. S8 Heatmap of correlation analysis for group CK vs OF (A), CK vs LVFX (B) and LVFX vs OF (C), respectively.

2.4 Molecular docking: the binding of key proteins to enantiomers

Table S2 Docking score of proteins and chemicals.

Proteins name	Chemicals name	Docking score (kcal/mol)
Acetyl CoA carboxylase	Dextrofloxacin	−6.8
Hormone sensitive triglyceride lipase	Dextrofloxacin	−7.1
Lipoprotein lipase	Dextrofloxacin	−7.4
Hepatic lipase	Dextrofloxacin	−7.5
Acetyl CoA carboxylase	LVFX	−7.9
Hormone sensitive triglyceride lipase	LVFX	−8.3
Lipoprotein lipase	LVFX	−8.5
Hepatic lipase	LVFX	−8.4