

Table 1

The microarray analysis of mouse liver after feeding HF/HS diet for 20 weeks

No.	Fold changes		Description
	HF/HS	HF/HS+EPA	
1	<b>496.2</b>	<b>4.8</b>	<b>cell death-inducing DFFA-like effector <math>\alpha</math> (Cide-a)</b>
2	307.2	111.0	complement factor D (adipsin)
3	63.4	25.1	sulfotransferase family 1E, member 1
4	59.8	11.1	matrix metalloproteinase 12
5	34.4	4.9	lymphocyte antigen 6 complex, locus D
6	31.1	1.6	toll-like receptor 12
7	30.5	7.7	RIKEN cDNA 2310004N24 gene
8	27.2	6.3	eosinophil-associated, ribonuclease A family, member 3
9	<b>22.1</b>	<b>1.0</b>	<b>cell death-inducing DFFA-like effector c (Cide-c)</b>
10	19.7	0.9	oxysterol binding protein-like 3
11	19.3	7.8	mannosidase 2, alpha B2
12	17.2	6.9	steroidogenic acute regulatory protein
13	16.4	6.7	RIKEN cDNA 2610002J02 gene
14	15.3	0.5	apolipoprotein A-IV
15	15.0	4.0	dual specificity phosphatase 5
16	15.0	3.7	ATP-binding cassette, sub-family D (ALD), member 2
17	13.9	0.9	glycoprotein (transmembrane) nmb
18	13.7	3.4	matrix metalloproteinase 13
19	12.9	4.4	DEAH (Asp-Glu-Ala-His) box polypeptide 30
20	12.7	2.6	solute carrier family 15 (H <sup>+</sup> /peptide transporter), member 2
21	10.4	3.6	ATPase, H <sup>+</sup> transporting, lysosomal V0 subunit D2

The fold changes are comparisons between the control and HF/HS or HF/HS+EPA group

Table 2

Stepwise multiple linear regression analysis of association with plasma ALT and liver parameters

Step	Parameters	Model R <sup>2</sup>	P value
1	Cide-c mRNA	0.8074	<0.001
2	Cide-a mRNA	0.8762	<0.001
3	SREBP-1c mRNA	0.8952	0.002
4	Triglyceride content	0.9231	<0.001

The changes in liver parameters associated significantly with plasma ALT levels in 62 samples were listed. Step no. shows the rank of possible relation with plasma ALT levels.

Fig. 1

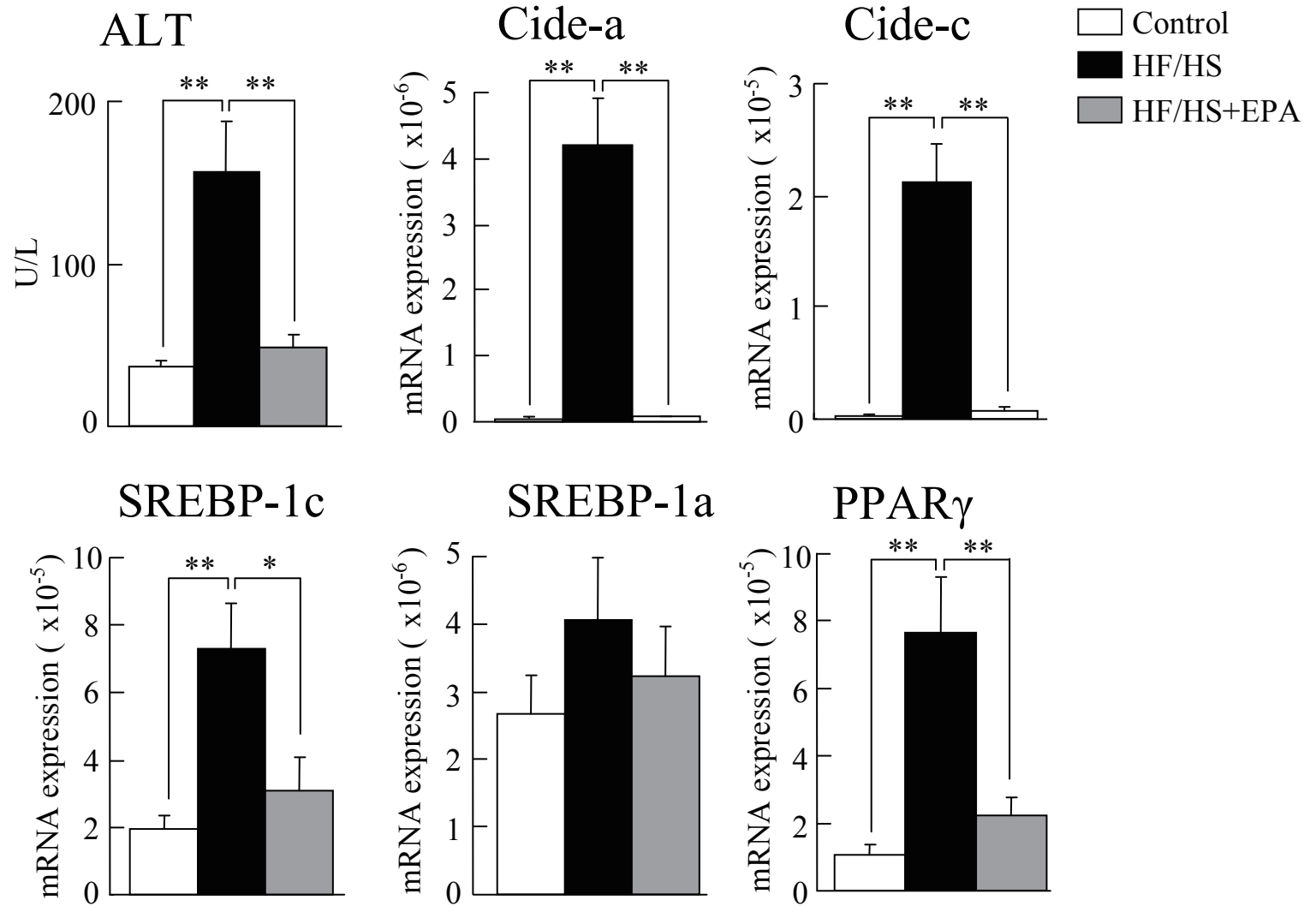
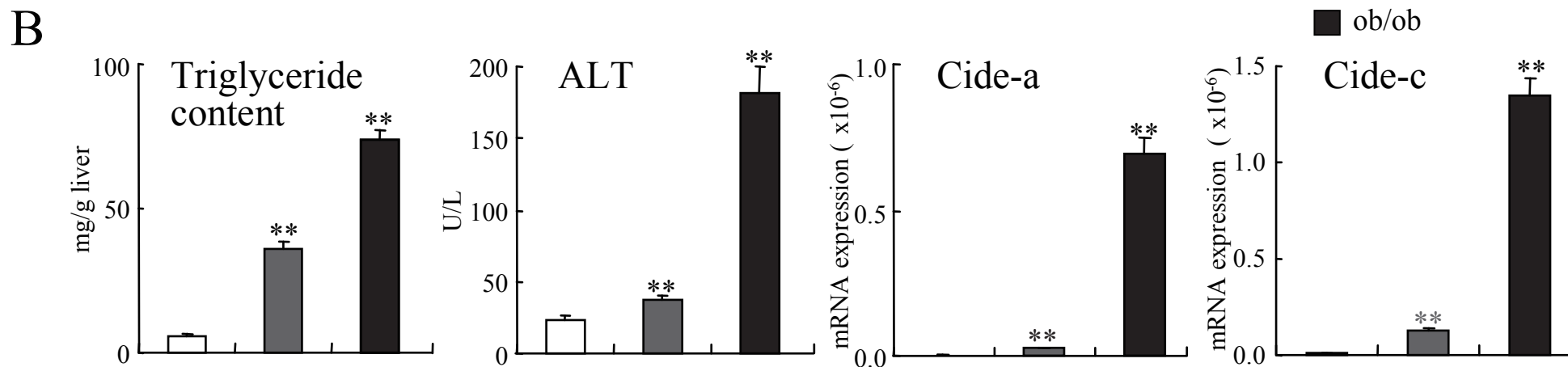
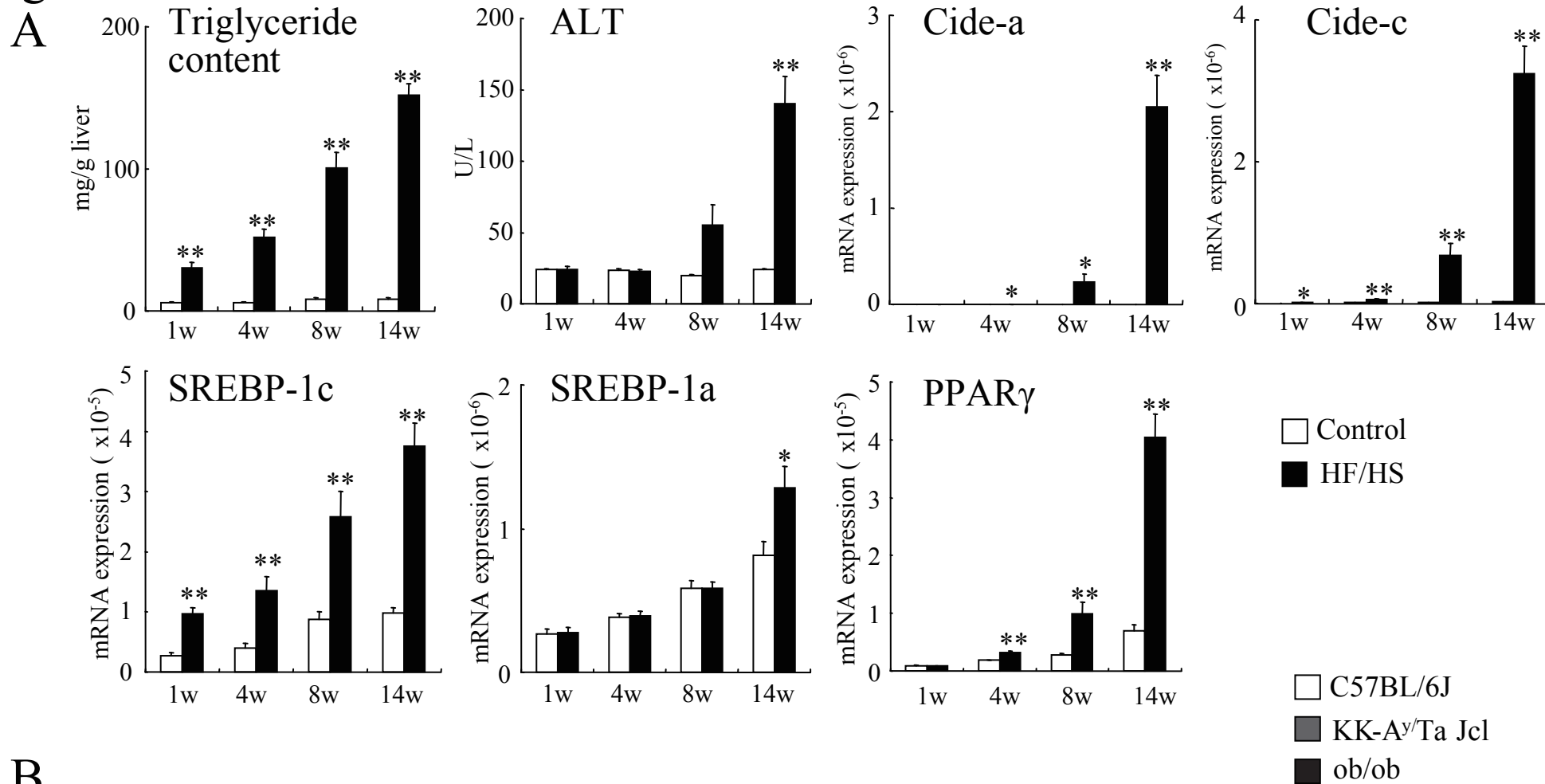


Fig.2



**Fig. 3**

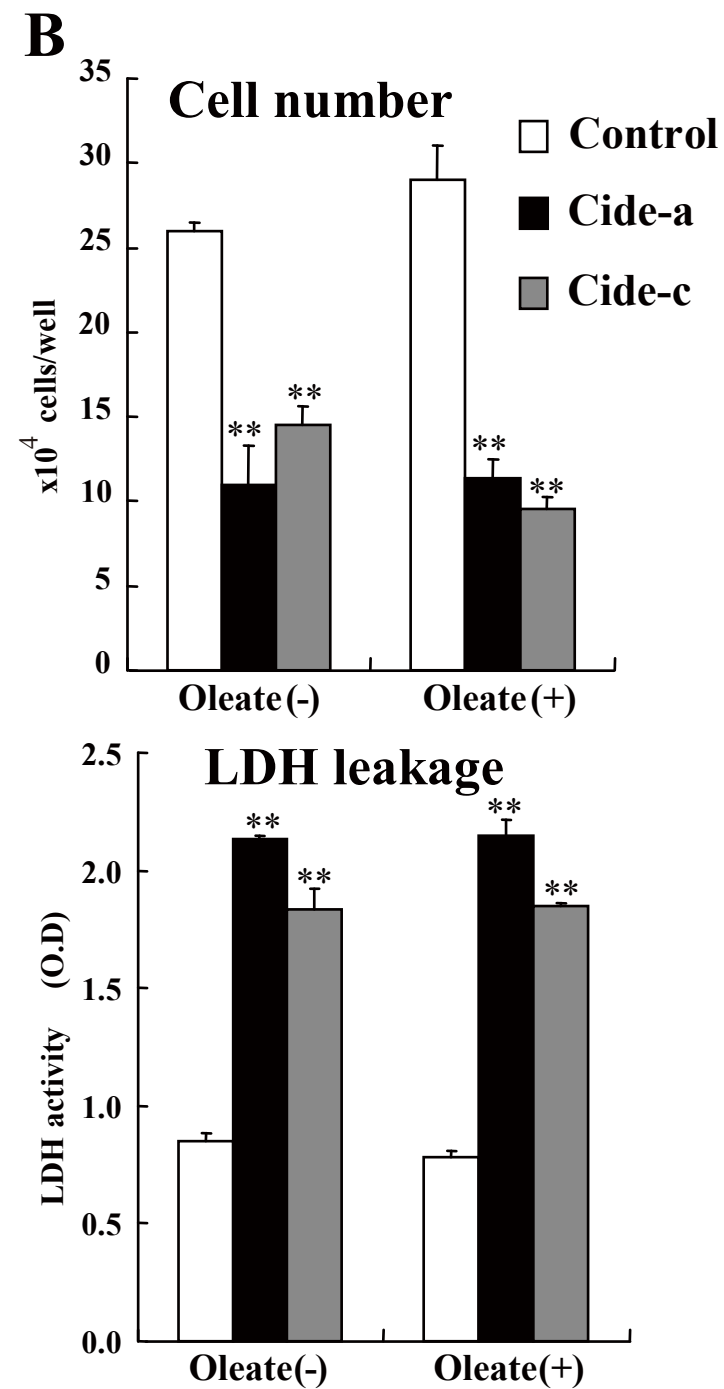
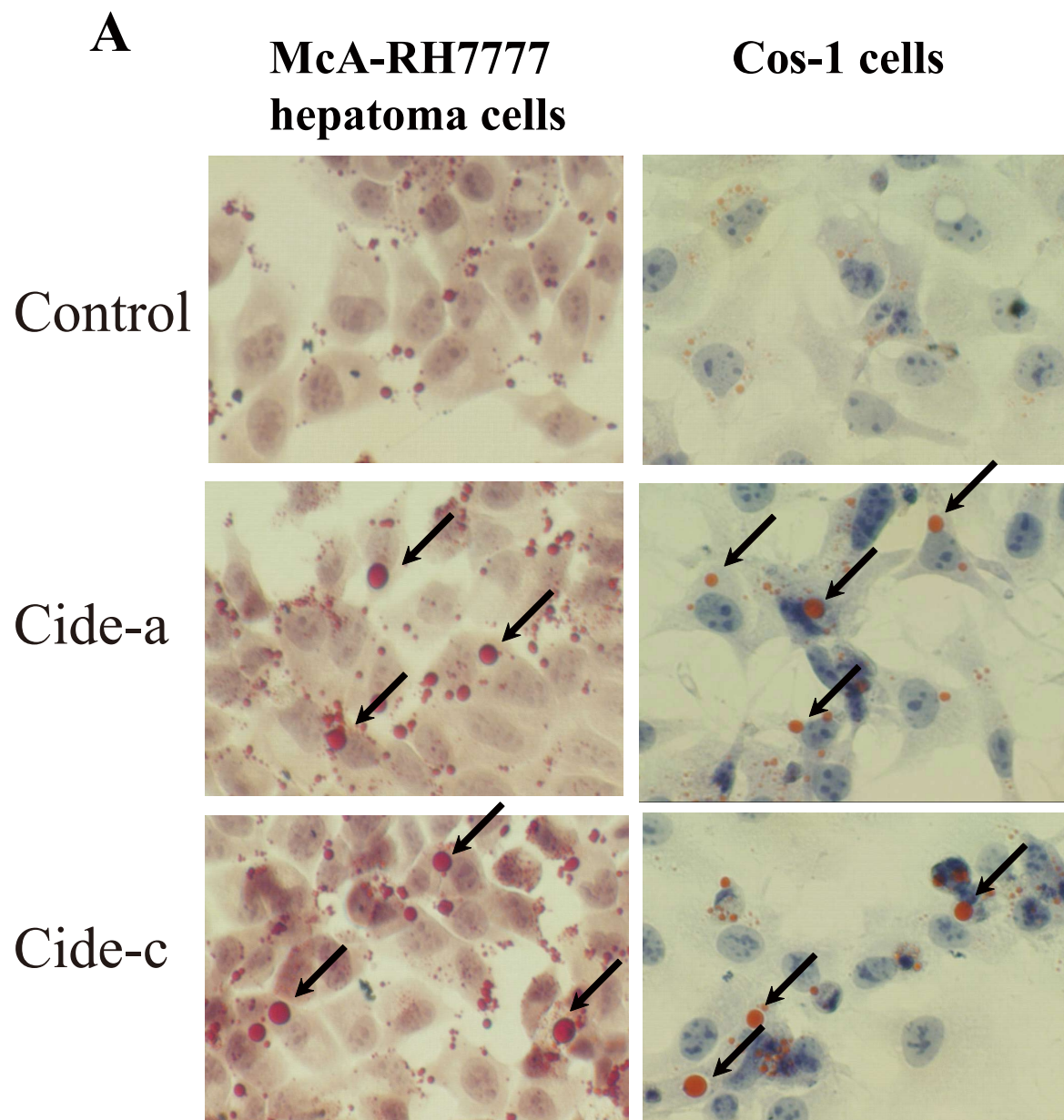
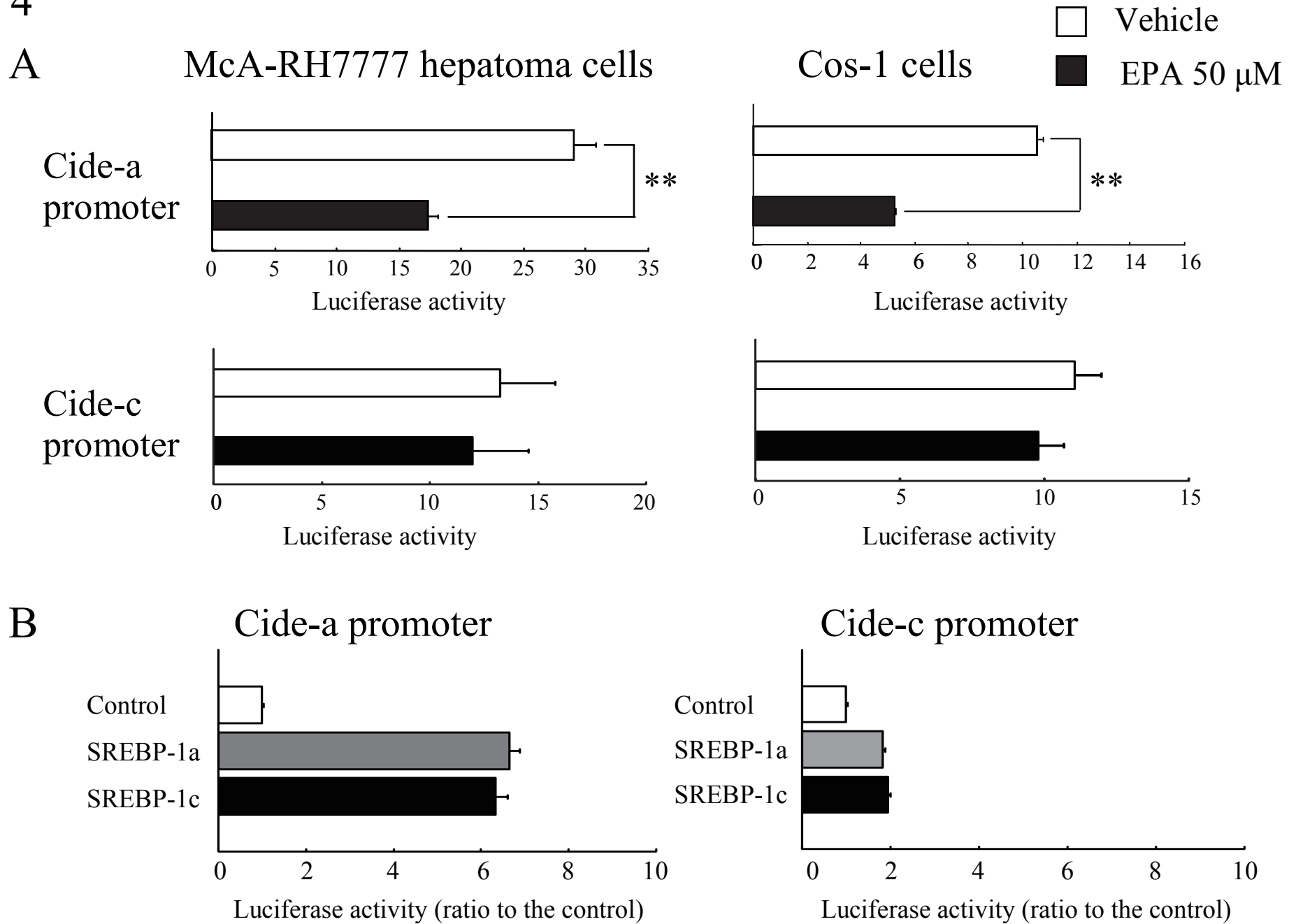


Fig. 4



## Supplementary

Table 1 Sequence of oligonucleotide primers and probes used for quantitative real-time PCR

Gene name	Forward primer (5' - 3')	Reverse primer (5' - 3')	Probe (5' - 3')
SREBP-1a	AGGCGGCTCTGGAACAGA	TCAAACCGCTGTGTCCAGTT	ACTGGCCGAGATGTG
SREBP-1c	CGGCGCGGAAGCTGT	TGCAATCCATGGCTCCGT	CGTCTGCACGCCCTA
PPAR $\gamma$	TTCCACTATGGAGTTCATG CTTGT	TCCGGCAGTTAAGATCACACC TA	TTTTCCGAAGAACCATCCGA TTGAAGC