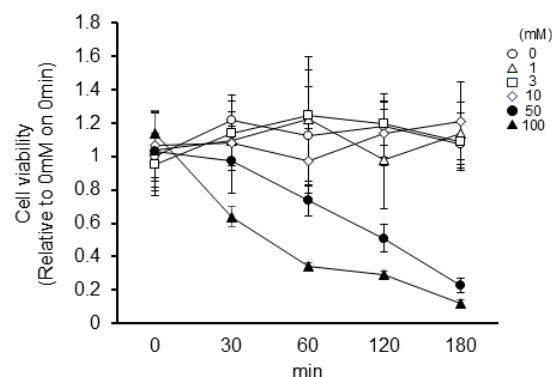
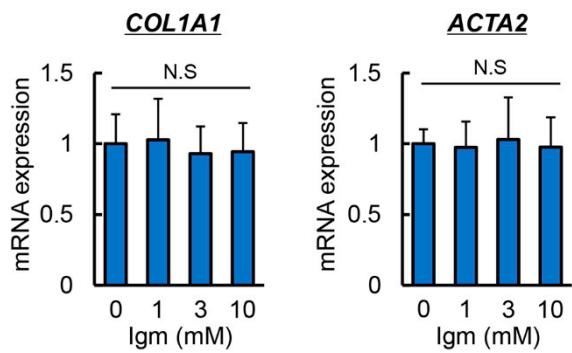


## Supplementary materials



**Supplementary Figure S1. Cell viability by treatment with imeglimin in palmitic acid-stimulated HepG2 cells.** HepG2 cells were treated with different imeglimin concentrations (0, 1, 3, 10, 50 and 100 mM) starting 9 h after the start of palmitic acid exposure. Cell viability was determined using The Premix Water-Soluble Tetrazolium salt (WST)-1 Cell Proliferation Assay system. Quantitative values are indicated as fold changes to the values of imeglimin 0mM-treated group on 0 min. Data are the mean  $\pm$  SD ( $n = 8$ ).



**Supplementary Figure S2. Imeglimin had no direct effect on activated hepatic stellate cells.** Intracellular mRNA expression of *COL1A1* and *ACTA2* in cultured LX-2 cells. LX-2 cells were treated with 0, 1, 3, 10 mM of imeglimin. *GAPDH* was used as an internal control for qRT-PCR. Quantitative values are indicated as fold changes to the values of Igm 0mM-treated group. Data are the mean  $\pm$  SD ( $n = 8$ ). N.S, not significant.

**Supplementary Table S1 List of primary antibodies**

Antibody	Source (catalog number)	Application (Dilution)
<b>mouse</b>		
4-HNE	JalCA (MHN-100P)	IHC (1:4)
PGC-1α	Abcam (ab188102)	WB (1:1000)
mtTFA	Abcam (ab47517)	WB (1:1000)
F4/80	Abcam (ab111101)	IHC (1:100)
α-SMA	Abcam (ab5694)	IHC (1:50), WB (1:100)
COL1A	Santa Cruz (sc-59772)	WB (1:1000)
Actin	Cell Signaling (4967)	WB (1:1000)
<b>Human</b>		
p-JNK1( <sup>Thr183</sup> )	Abcam (ab47337)	WB (1:1000)
JNK1	Abcam (ab199380)	WB (1:1000)
BAX	Cell Signaling (2772)	WB (1:1000)
BCL-2	Abcam (ab182858)	WB (1:2000)
α-SMA	Abcam (ab5694)	WB (1:100)
COL1A	Santa Cruz (sc-59772)	WB (1:1000)
PGC-1 α	Abcam (ab188102)	WB (1:1000)
mtTFA	Abcam (ab47517)	WB (1:1000)
Actin	Cell Signaling (4967)	WB (1:1000)

**Supplementary Table S2 List of primers used in q-PCR**

gene	Sense (5'-3')	Antisense (5'-3')
<b>Mouse</b>		
<i>Ppara</i>	ATGCCAGTACTGCCGTTTC	TTGCCAGAGATTGAGGTC
<i>Cpt1a</i>	ATGCTCTCGCTGTTGGTGA	GTCAGCTGGTAGTGGTGTG
<i>Acox1</i>	ATGGCTCTCGTGTGCTATCC	TGGGACTCTGCGTTGGTAG
<i>Srebf1c</i>	CGACTACATCCGCTTGCAG	CCTCCATAGACACATCTGTGCC
<i>Fasn</i>	CTGAGATCCCAGCACTCTTG	GCCTCCGAAGCCAATGAG
<i>Scd1</i>	TTCTTGCATACTCTGGTGC	CGGGATTGAATGTTCTGCGT
<i>Gpx1</i>	CGCTCTTACCTCCTGCGGAA	AGTTCCAGGCAATGCGTTGCG
<i>Cybb</i>	TGGCGATCTCAGCAAAGGTGG	GTACTGCCCCACCTCCATTTG
<i>Sod2</i>	TAACCGCGCAGATCATGCAGCTG	AGGCTGAAGAGCGACCTGAGTT
<i>Cat</i>	CGGCACATGAATGGCTATGGATC	AAGCCTCCCTGCCTCTCCAACA
<i>Ncf4</i>	ACTGGAGCTCTGGTTCTGG	AAGTCTGGCTGCTTGTGTC
<i>Ddit3</i>	CTGGAAGCCTGGTATGAGGA	TGGTGCCTGGTAGTGAGA
<i>Hspa5</i>	AGATGAAGGAGGAGGAGGAGGA	AGTGGGTACAGATAGGGGTG
<i>Ppargc1a</i>	GAATCAAGCCACTACAGACACCG	CATCCCTCTTGAGCCTTCGTG
<i>Tfam</i>	GAGGCAAAGGATGATTGGCTC	CGAACCTATCATCTTAGCAAGC
<i>Tnfa</i>	CAGGCGGTGCCTATGTCTC	CGATCACCCCGAAGTTAGTAG
<i>Il6</i>	TACCACTTCACAAGTCGGAGGC	CTGCAAGTGCATCATCGTTGTC
<i>Il1b</i>	TGGACCTCCAGGATGAGGACA	GTTCATCTCGGAGCCTGTAGTG
<i>Il10</i>	TGCACTACCAAAGCCACAAG	TCAGTAAGAGCAGGCAGCAT
<i>Ccl2</i>	AGGTCCCTGTATGCTCTG	TCTGGACCCATTCTCTTG
<i>Ccl3</i>	TGGCTCAGCCAGATGCAATC	AGGCTCCCAGGTCTCTTGG
<i>Nos2</i>	CCTTGTTCAGCTACGCCCTC	CTTCAGAGTCTGCCATTGC
<i>Arg1</i>	GCAGTTGGAAGCATCTCTGG	GAGAAAGGACACAGGTTGCC
<i>Cd163</i>	ATGGGTGGACACAGAATGGT	AGCTCACAGCCACAACAAAG
<i>Timp1</i>	CATGGAAAGCCTCTGGATATG	GATGTCAAATTCCGTTCTT
<i>Ctgf</i>	TGCCATGAGGAGTGGGTGTG	TGGAGATTTGGAGTACGGG
<i>Tgfb1</i>	TTGCTTCAGCTCACAGAGA	TGGTTGAGAGGGCAAGGAC
<i>Lgals3</i>	TGTGAAGGTGATGGATGAG	AAGTGGTCGCTGAAGAGCAG
<i>Gapdh</i>	GACCCCTTCATTGACCTAAC	GATGACCTGCCACAGCCTT
<b>Human</b>		
<i>PPARA</i>	TGGACACAGAGGAAAGAGCC	TGGCATCTGTTGAAGGATGG
<i>CPT1A</i>	GCTGCTCCTGAGTCATGCTG	GGAGGACTGGACACGAAGA
<i>CPT2</i>	GCAGATGATGGTGAGTGCTCC	AGATGCCGCAGAGCAAACAAGTG
<i>ACADC</i>	GAGGAGGAGGAGAAGGAGGC	GTCATCCTCCAGCTCCTCCT
<i>ACAD9</i>	GGCTGTGAGGACGTTGACTT	TGGTCGATGTCAGGTTGTCT
<i>ACAA2</i>	AGGTGGTGGAAAGAGGACTTT	CTTCTGCCTTCATCTGGTGA
<i>SREBFC1</i>	ACTTCTGGAGGCATCGCAAGCA	AGGTTCCAGAGGAGGCTACAAG
<i>FASN</i>	CCTGGAACCGTTATGAAGAT	ATGGCATGGTGATGAGCTT
<i>PPARG</i>	CGAGAAGGAGAAGCTGTTGG	TCAGCGGGAAAGGACTTTATG
<i>DDIT3</i>	AGCGACTTCAGGGTCGTTGCG	AGGCATGGAGCTGCAACGTCC
<i>HSPA5</i>	TAGCGTATGGTGCCTGTC	TGACACCTCCCACAGTTCA
<i>COL1A1</i>	CCAAATCTGCTCCCCAGAA	TCAAAAACGAAGGGAGATG
<i>ACTA2</i>	GAGACCCTGTTCCAGCCATC	TACATAGTGGTGCCCCCTGA
<i>PPARGC1A</i>	CAGAGAGTATGAGAAGCGAGAG	AGCATCACAGGTATAACGGTAG
<i>TFAM</i>	ACCAAAAAGACCTCGTTAGC	CGAGTTCGTCCCTTTAGCA
<i>GAPDH</i>	CCAAGGAGTAAGACCCCTGG	TGGTTGAGCACAGGGTACTT