

## Supplementary data to International Journal of Molecular Sciences

### Deletion of KLF10 Leads to Stress-Induced Liver Fibrosis upon High Sucrose Feeding

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**Supplementary table S1.** Pathological scores for HSD-induced NAFLD.

**Supplementary table S2.** Primer sequences for quantitative real-time PCR.

**Supplementary table S1.** Pathological scores for HSD-induced NAFLD.

<b>Steatosis</b>	<b>definition</b>	<b>Score</b>
0-3	Grade Low- to medium-power evaluation of parenchymal involvement	
	<5%	0
	5-33%	1
	33%-66%	2
	>66%	3
	Predominant distribution pattern	
	Zone3	0
Zone1	1	
Azpm;	2	
Panacinar	3	
<b>Fibrosis</b>		
0-4	None	0
	Perisinusoidal or periportal	1
	Mild, zone 3, perisinusoidal	1.2
	Moderate, zone 3, perisinusoidal	1.4
	Portal/periportal	1.6
	Perisinusoidal and portal/periportal	2
	Bridging fibrosis	3
	Cirrhosis	4
<b>Inflammation</b>		
	Lobular inflammation Overall assessment of all inflammatory foci	
	No foci	0
	<2 foci per 200 field	1
	2-4 foci per 200 field	2
	>4 foci per 200 field	3
	Microgranulomas Small aggregates of macrophages	
	Absent	0
	Present	1
	Large lipogranulomas Usually in portal areas or adjacent to central veins	
	Absent	0
	Present	1
	Portal inflammation Assessed from low magnification	
	None to minimal	0
Greater than minimal	1	
<b>Cell injury</b>		
	Ballooning*	
	None	0
	Few balloon cells	1
	Many cells/prominent ballooning	2
	Acidophil bodies	
	None to rare	0
	Many	1
	Pigmented macrophages	
	None to rare	0
	Many	1
	Megamitochondria*	
	None to rare	0
	Many	1

**Supplementary table S2.** Primer sequences for quantitative real-time PCR

Gene symbol	Forward primers (5' to 3')	Reverse primers (5' to 3')
<i>Apob</i>	CGTGGGCTCCAGCATTCTA	TCACCAGTCATTTCTGCCTTTG
<i>Atf3</i>	TGGAGATGTCAGTCACCAAGTCT'	GCAGCAGCAATTTTATTTCTTTCT''
<i>Catalase</i>	CCGAGTCTCTCCATCAGGTTT	TCATGTGCCGGTGACCAT
<i>Cd36</i>	GGAAGTGTGGGCTCATTGC	CATGAGAATGCCTCCAAACAC
<i>Chop</i>	CACCACACCTGAAAGCAGAAC	GGTGAAAGGCAGGGACTCA
<i>Coll1a1</i>	CCTGAGTCAGCAGATTGAGAACA	CCAGTACTCTCCGCTCTTCCA
<i>Fas</i>	GCTGCGGAAACTTCAGGAAAT	AGAGACGTGTCACTCCTGGACTT
<i>Gadd34</i>	GGCGGCTCAGATTGTTCAA	GAAGTGTACCTTCCGAGCTTTTAGAG
<i>Mcp1</i>	TCTGGGCCTGCTGTTTACA	CCAGCCTACTCATTGGGATCA
<i>Mtp</i>	AGCCAGTGGGCATAGAAAATC	GGTCACTTTACAATCCCCAGA
<i>Noxa</i>	TGGGAAGTCGCAAAGAGCA	CCCTGCTCAGGGAACCAAAA
<i>Nqo1</i>	CCATGGCGGCGAGAAG	TTCATGGCGTAGTTGAATGATGT
<i>Nrf2</i>	CCCGGTTGCCACATTC	TGTCTCTGCCAAAAGCTGCAT
<i>Pai1</i>	GCAAAAGGTCAGGATCGAGGTA	GTGCCGAACCACAAAGAGAAAG
<i>Puma</i>	GCGGCGGAGACAAGAAGA	AGTCCCATGAAGAGATTGTACATGAC
<i>Smad3</i>	GTAATGCACTTGGTGTTCACGTT	TGAAGAAGCTCAAGAAGACGGG
<i>Sod2</i>	CAGACCTGCCTTACGACTATGG	CTCGGTGGCGTTGAGATTGTT
<i>Srxn1</i>	CACAACGTACCAATCGC	CCTTTGATCCAGAGGACGTC
<i>Tgfb1</i>	GCAGTGGCTGAACCAAGGA	AGAGCAGTGAGCGCTGAATC
<i>Tnfa</i>	CTGAGGTCAATCTGCCCAAGTAC	CTTACAGAGCAATGACTCCAAAG
<i><math>\alpha</math>-Sma</i>	CACGGCATCATCACCAACTG	GGCCACACGAAGCTCGTTAT