

Supplementary Information

Figure S1. Confirmation of genotype in *Smad3* and *SMP30* mutant mice. **(A)** Ethidium bromide-stained agarose gel showing polymerase chain reaction (PCR) products of tail DNA from *Smad3* mutant mice. The 431 bp band (lane 1) indicates the wild-type (*Smad3*^{+/+}) and the 284 bp band (lane 4) represents knockout (*Smad3*^{-/-}) mice. Lane designations: lane M, DNA molecular size marker; lane 1, tail DNA of *Smad3*^{+/+} mice with primer 1 plus primer 2 mixture; lane 2, tail DNA of *Smad3*^{+/+} mice with primer 1 plus primer 3 mixture, lane 3, tail DNA of *Smad3*^{-/-} mice with primer 1 plus primer 2 mixture, lane 4, tail DNA of *Smad3*^{-/-} mice with primer 1 plus primer 3 mixture; and **(B)** Ethidium bromide-stained agarose gel showing PCR products of tail DNA from *SMP30* mutant mice. The *SMP30*^{Y/+} and *SMP30*^{Y/-} genes gave 280 bp and 1363 bp PCR products, respectively.

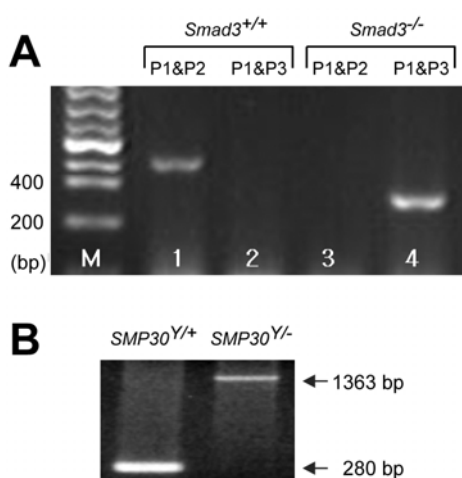


Table S1. Markedly changed hepatic proteins in *Smad3*^{-/-} mice vs. *Smad3*^{+/+} mice.

Spot No.	Protein Name	Accession No. ^A	MOWSE Score ^B	Masses Matched (%)	MW ^C (kDa)	pI ^C	Relative ratios ^D
Down-regulated proteins in livers of <i>Smad3</i> ^{-/-} mice							
1	Semaphorin 3E precursor	P70275	9.84 × 10 ⁴	21	90	8.00	0.00
2	Probable urocanate hydratase	Q8VC12	2.87 × 10 ³	18	75	7.30	0.34
3	Heat shock cognate 71 kDa protein (HSP 70)	P63017	7.85 × 10 ⁹	44	70	5.40	0.36 *
4	Nonspecific lipid-transfer protein	P32020	1.23 × 10 ⁴	13	59	7.20	0.00
5	Ubiquinol-cytochrome-c reductase complex core protein 2	Q9DB77	7.42 × 10 ³	14	48	9.30	0.00 *
6	T-cell ectoADPribosyl-transferase 1 precursor (T-cell differentiation marker Rt6 homolog 1)	P17981	3.32 × 10 ³	11	32	8.40	0.34 *
Up-regulated proteins in livers of <i>Smad3</i> ^{-/-} mice							
18	Perilipin (Lipid droplet-associated protein)	Q8CGN5	4.15 × 10 ³	20	56	6.60	2.20
19	Selenium-binding protein 1(SP56)	P17563	1.24 × 10 ⁴	18	52	6.00	2.86 *
21	Senescence marker protein-30 (<i>SMP30</i>)	Q64374	3.55 × 10 ⁶	22	33	5.20	2.58 *
22,23	Glutathione S-transferase Mu 1	P10649	1.29 × 10 ⁶	21	26	7.70	2.61 *

^A Accession No.: Protein No. of SwissProt database (2007.04.19); ^B MOWSE score: Based on the number of peptides matching the protein in the database and the accuracy of those matches; ^C MW and pI: Obtained from the MS fit search of proteinprospector database; ^D Relative ratio: Relative % volume of spot density in *Smad3*^{-/-} compared to *Smad3*^{+/+} mice (1>, up-regulation in *Smad3*^{-/-} mice; 1<, down-regulation in *Smad3*^{-/-} mice); * Significant differences in the *Smad3*^{+/+} mice (Student's *t* test, *p* value <0.05).