Snider et al., http://www.jcb.org/cgi/content/full/jcb.201102142/DC1

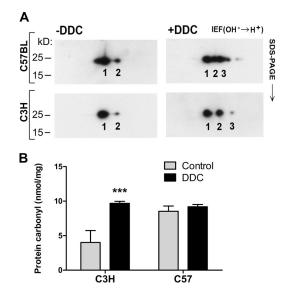


Figure S1. Strain differences in PRDX6 modification and total protein carbonylation in C3H and C57BL livers. (A) 2D gel electrophoresis and immunobloting of PRDX6 in C3H and C57BL mouse livers under basal (-DDC) conditions and after DDC treatment. Note the increased intensity of the acidic PRDX6 isoforms in C57BL livers after DDC exposure. The numbers denote different charged isoforms of PRDX6. IEF, isoelectric focusing. (B) Quantification of total carbonylated protein in the livers of C3H and C57BL control and DDC-treated mice based on dinitrophenylhydrazine reactivity with protein carbonyl groups. ***, P < 0.001 using a two-way analysis of variance. Each tested group included three to four mice, and samples were analyzed in triplicates. Results are represented as the mean and the SD.

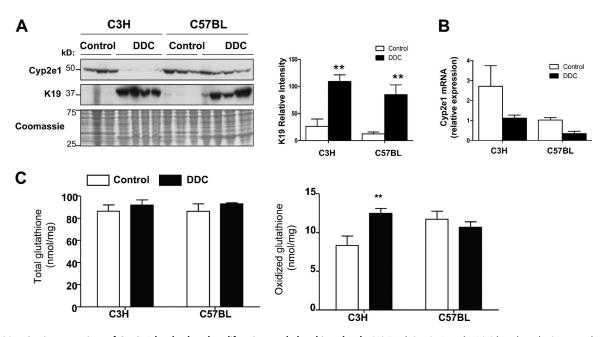


Figure S2. Strain comparison of Cyp2e1 levels, ductal proliferation, and glutathione levels. (A) Total Cyp2e1 and K19 (ductal marker) protein levels (left) and quantification of K19 band intensities (right). Coomassie stain serves as a loading control. (B) Relative mRNA expression for Cyp2e1 in C3H and C57BL livers before and after DDC treatment. (C) Liver levels of total and oxidized glutathione were quantified by an enzymatic recycling method using glutathione reductase, as described in Materials and methods. **, P < 0.01 using a two-way analysis of variance. Each tested group included three to four mice, and samples were analyzed in triplicates. Results are represented as the mean and the SD.

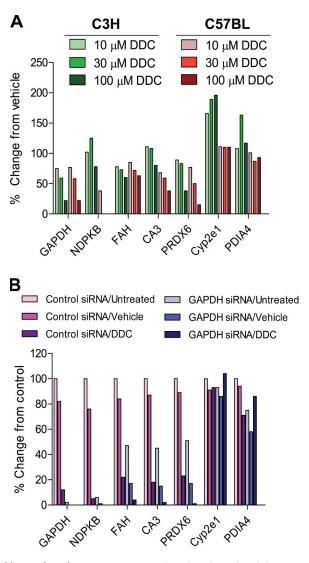


Figure S3. Quantification of the immunoblotting data shown in Fig. 7. (A and B) The relative band densities were estimated using Photoshop CS2 software. Data are representative of three experimental repeats.

Table S1. Relative mRNA expression of selected genes in untreated and DDC-treated C3H and C57BL mice

Gene	СЗН		C57BL	
	Control	DDC	Control	DDC
CBR3	1.19 ± 0.177	16.6 ± 5.65	1.71 ± 0.619	38.1 ± 14.6°,b
GSTA3	1.31 ± 0.297	1.34 ± 0.085	1.07 ± 0.258	1.23 ± 0.338
GSTM1	2.04 ± 0.906	16.8 ± 2.53°	1.02 ± 0.137	$5.93 \pm 2.34^{a,d}$
GSTP1	1.13 ± 0.197	1.80 ± 0.215°	0.990 ± 0.045	1.10 ± 0.267°
GSTP2	1.49 ± 0.506	29.3 ± 14.6^{f}	2.64 ± 2.63	10.2 ± 3.10
PRDX6	1.42 ± 0.361	1.60 ± 0.259	1.09 ± 0.257	1.00 ± 0.208
CA3	1.52 ± 0.450	0.370 ± 0.121^{f}	1.08 ± 0.421	$0.210 \pm 0.020^{\circ}$
GAPDH	1.43 ± 0.373	2.46 ± 0.172^{f}	0.850 ± 0.161	0.697 ± 0.151^{d}
NDPK-A	1.41 ± 0.354	2.45 ± 0.284	1.01 ± 0.012	1.03 ± 0.317
NDPK-B	1.27 ± 0.228	1.46 ± 0.179	0.943 ± 0.191	1.18 ± 0.327
PSMC6	1.77 ± 0.738	2.42 ± 0.058	0.833 ± 0.145	0.630 ± 0.181 ^b
SBP1	1.62 ± 0.566	2.71 ± 0.223	1.24 ± 0.442	1.43 ± 0.592°

One-way analysis of variance and Tukey's multiple comparison tests were used.

 $^{^{}m o}P$ < 0.05, relative to control group of the same strain.

 $^{^{\}text{b}}\text{P}<0.01,$ relative to C3H in the same treatment group.

^cP < 0.001, relative to control group of the same strain.

 $^{^{\}text{d}}\text{P} < 0.001$, relative to C3H in the same treatment group.

 $^{^{\}mathrm{e}}\mathrm{P}$ < 0.05, relative to C3H in the same treatment group.

 $^{^{\}text{f}}\text{P} < 0.01,$ relative to control group of the same strain.

Table S2. Primers used for quantitative real-time PCR

Gene	Primer sequence		
NME1 or NDPK-A			
Forward	5'-GGACCTTCTCAAGGAGCACTAC-3'		
Reverse	5'-ACCACAAGCTGATCTCCTTCTC-3'		
NME2 or NDPK-B			
Forward	5'-TCTGAAGAACACCTGAAGCAGC-3'		
Reverse	5'-TAGTCGATCAGTTCTTCGGG-3'		
CA3			
Forward	5'-GCTCTGCTAAGACCATCC-3'		
Reverse	5'-ATTGGCGAAGTCGGTAGG-3'		
PRDX6			
Forward	5'-TTGATGATAAGGGCAGGGAC-3'		
Reverse	5'-CTACCATCACGCTCTCTCCC-3'		
CBR3			
Forward	5'-TACTTGGCTCTCCTGCCTCC-3'		
Reverse	5'-GACTAGCTGGCCGTGAGGTT-3'		
SELENBP1			
Forward	5'-GTGCAACGTGAGCAGTTT-3'		
Reverse	5'-CTGCATCCCCAGGCTTCT-3'		
PSMC6			
Forward	5'-CGGGTGAAAGTGCTCGTTTG-3'		
Reverse	5'-AGCAAAGCAGGATCCAGTGT-3'		
GSTA3			
Forward	5'-TGGACAACTTCCCTCTCCTGAA-3'		
Reverse	5'-AATCTTCTTTGCTGACTCAACACATT-3'		
GSTM1			
Forward	5'-CCTATGATACTGGGATACTGGAACG-3'		
Reverse	5'-GGAGCGTCACCCATGGTG-3'		
GSTP1			
Forward	5'-GCAAATATGTCACCCTCATCTACACC-3		
Reverse	5'-GCAGGGTCTCAAAAGGCTTCA-3'		
GSTP2			
Forward	5'-CAAATATGGCACCATGATCTACAGA-3'		
Reverse	5'-GCAGGGTCTCAAAAGGCTTCA-3'		
GAPDH			
Forward	5'-TCCACCACCCTGTTGCTGTAG-3'		
Reverse	5'-GACCACAGTCCATGACATCACT-3'		
185			
Forward	5'-ACCTGGTTGATCCTGCCAGTAG-3'		
Reverse	5'-TTAATGAGCCATTCGCAGTTTC-3'		