

Figure S1. Additional Analysis of SOD2 Knock-down in iSOD2 Embryos and Mice, Related to Figure 1.

A) Western blot of iSOD2-KD embryos (with both rtTA and shRNA transgenes) compared to negative-control embryos (rtTA transgene only) without doxycycline (DOX). Actin was probed as a loading control.

B) Western blot for mitochondrial OXPHOS components, including mtDNA-encoded COX1 and COX III in negative-control mice (with rtTA transgene only) with (+) and without (-) doxycycline (DOX). GAPDH was probed as a loading control.

C) Body weight (grams) of iSOD2-KD mice that had SOD2 knocked down from day 0.5 to day 12.5e in utero is plotted as a function of time (days post birth through weaning). Error bars represent +/- SEM.

All calculations for statistical significance were completed using a non-parametric, unpaired, two- tailed t-test. n=3-7.



		. B						
PPARa-PPARy-PGC1a	NRF2	1						
UCP2	AKR1C18	1		14-	•		***	rtTA
MPC1	GST3		5	12-			Ι	rtTA + shRNA
МАОВ	GST1	-	mRNA Expression	10-				
CISD3	CHGB	-	les					
Slc25a4	TCN2		Ä	81 7	-	*		
PMVK	CdC34	-	Ā	4-	*	** T		
IDH3B	NFE2L3		RN	3-	***	гЦ	*	
PDK1	BGLAP		ε	2-	. 1			
Slc25a11				1-		L Ó I		
MDH2					 ∾ ♪		N 61	
ECHS1				GST	"estre	ક્ર ¹⁸ હ	JLM HRS1	
MUP1				•	•••		·	
HNF4A		С						
GST1								
GCK				1.5-				
ARHGDIA			ы С					
AKR1C18			cel			ns		
ACSS2			res	1.0-			T	
GOT1			<u>9</u>					
PTGR1			MitoSOX Fluorescence					
HPGD			õ	0.5-				
GAPDH			ĝ					
SLC2A2			Ϊ					
IRF1				0.0				
LTB4R			shF	RNA		-	+	
DOK1			rtT/	4	-	÷	+	
C4A/C4B			DO	х	-	+	+	

Figure S2. Additional Analysis of "Adapted" Liver from iSOD2 mice that experienced embryonic SOD2 knock-down, Related to Figure 2.

A) Top **upregulated PPARα**, **PPARy**, **PGC1α**, and NRF2 driven genes as predicted by gene expression profiling of liver from iSOD2 adapted animals.

B) RNA expression (normalized to tubulin) of redox-related genes in adapted liver normalized to that in negative controls. Error bars represent +/- SEM. GSTMu, glutathione s-transferase mu; GSTP-1, glutathione s-transferase pi-1; GSTA-1, glutathione s-transferase alpha 1; GCLM, glutamate cysteine ligase; DHRS7, dehydrogenase/reductase 7.

C) MitoSox staining in adapted hepatocytes compared to negative controls, which were given a value of 1.0.

All calculations for statistical significance were completed using a non-parametric, unpaired, two- tailed t-test. n=3-6.

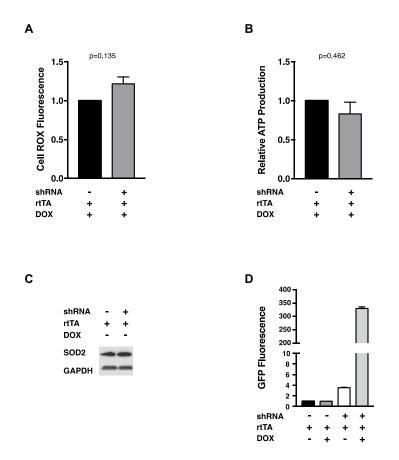


Figure S3. Additional Analysis of SOD2 Knock-down in MEFs from iSOD2-KD Mice, Related to Figure 3.

A) CellROX staining in iSOD2 MEFs in the presence of doxycycline (DOX) relative to that in negative controls, which were given a value of 1.0.

B) ATP levels in iSOD2 MEFs in the presence of doxycycline (DOX) relative to that in negative controls, which were given a value of 1.0 that equates to an ATP concentration of 1.2 nmol/ μ l.

C) Western blot for SOD2 in iSOD2 MEFs in the absence of doxycycline (DOX). GAPDH was probed as a loading control.

D) IRES-GFP expression from the shRNA construct in iSOD2 and negative-control MEFs with (+) and without (-) doxycycline (DOX). Error bars represent +/-SEM. All calculations for statistical significance were completed using a non-parametric, unpaired, two- tailed t-test. n=4-6.

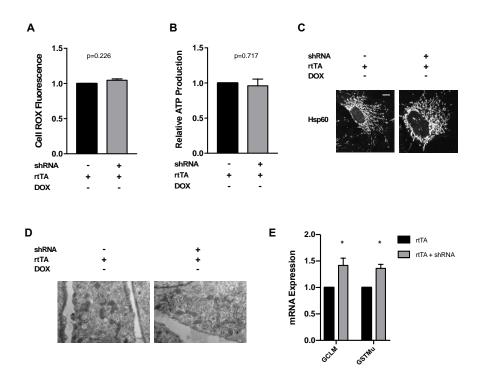


Figure S4. Additional analysis of adapted MEFs from iSOD2 mice, Related to Figure 4.

A) CellROX staining in adapted iSOD2 MEFs compared to negative controls, which were given a value of 1.0.

B) ATP levels in iSOD2 knock-down MEFs compared to negative controls, which were given a value of 1.0 that equates to an ATP concentration of 1.8 nmol/ μ l.

C) Grayscale image of mitochondria in adapted MEFs (day 12) compared to negative controls. Images are z-stack projections of representative cells, fixed and stained with anti-HSP60 to visualize mitochondria. Scale bar represents 10 µm.

D) Electron microscopy of adapted iSOD2 MEFs compared to negative controls. Scale bar = 2 μ M.

E) RNA expression of redox-related genes (normalized to tubulin) in iSOD2 adapted MEFs relative to negative controls. Error bars represent +/- SEM. GCLM, glutamate cysteine ligase; GSTMu, glutathione s-transferase mu.

All calculations for statistical significance were completed using a non-parametric, unpaired, two- tailed t-test. n=3-9.

Oligonucleotides		
GCLM Forward 5'-3' TTGGGAACTCCATTCATTCA	This paper	N/A
GCLM Reverse 5'-3' CGGGAACCTGCTCAACTG	This paper	N/A
NQO1 Forward 5'-3' GTCTTCTCTGAATGGGCCAG	This paper	N/A
NQO1 Reverse 5'-3' CCAATCAGCGTTCGGTATTA	This paper	N/A
GRX Forward 5'-3' ATCGTGCATGAATTCCGAGT	This paper	N/A
GRX Reverse 5'-3' GGTGGTGGAGAGTCACAAGC	This paper	N/A
UCP2 Forward 5'-3' CAGCGCCAGATGAGCTTTG	This paper	N/A
UCP2 Reverse 5'-3' GGAAGCGGACCTTTACCACA	This paper	N/A
PGC1α Forward 5'-3' TGAGGACCGCTAGCAAGTTT	This paper	N/A
PGC1α Reverse 5'-3' TGAAGTGGTGTAGCGACCAA	This paper	N/A
GSTmu Forward 5'-3' AACACAGGTCTTGGGAGGAA	This paper	N/A
GSTmu Reverse 5'-3' CGTATGTTTGAGCCCAAGTG	This paper	N/A
GSTP1 Forward 5'-3' GGGCCTTCACGTAGTCATTC	This paper	N/A
GSTP1 Reverse 5'-3' ATGGGAAAAACCAGAGGGAG	This paper	N/A
GSTA1 Forward 5'-3' CTCTTCAAACTCCACCCCTG	This paper	N/A
GSTA1 Reverse 5'-3' TGGAGAAGAAGCCAGGACTC	This paper	N/A
Col1A1 Rev45 Reverse 5'-3' CACCCTGAAAACTTTGCCCC	This paper	N/A
ROSA C 5'-3' GGAGCGGGAGAAATGGATATG	This paper	N/A
ROSA B 5'-3' GCGAAGAGTTTGTCCTCAACC	This paper	N/A
ROSA D 5'-3' TCAGTAAGGGAGCTGCAGTGG	This paper	N/A
shRNA 835 Forward 5'-3' AAGCCACAGATGTATCTTTCAGTAA	This paper	N/A
shRNA 582 Forward 5'-3' AAGCCACAGATGTATTAAACTTCTC	This paper	N/A
Sod2_835 shRNA 1,	This paper	N/A
5'GAAGGCTCGAGAAGGTATATTGCTGTTGACAGTGAGCGA		
TGGGAGAATGTTACT		
GAAAGATAGTGAAGCCACAGATGTATCTTTCAGTAACATTC		
TCCCAGTGCCTACTG		
CCTCGGACTTCAAGGGGCTAGAATTCGAGCA-3'		

 Table S2. Additional Oligonucleotides Used in the Study, Related to Figures 1-4

 Oligonucleotides

Sod2_582 shRNA 2,	This paper	N/A
5'GAAGGCTCGAGAAGGTATATTGCTGTTGACAGTGAGCGC		
TGGGTCTTTTGAGAA		
GTTTAATAGTGAAGCCACAGATGTATTAAACTTCTCAAAAGA		
CCCAATGCCTACTGC		
CTCGGACTTCAAGGGGCTAGAATTCGAGCA-3'		