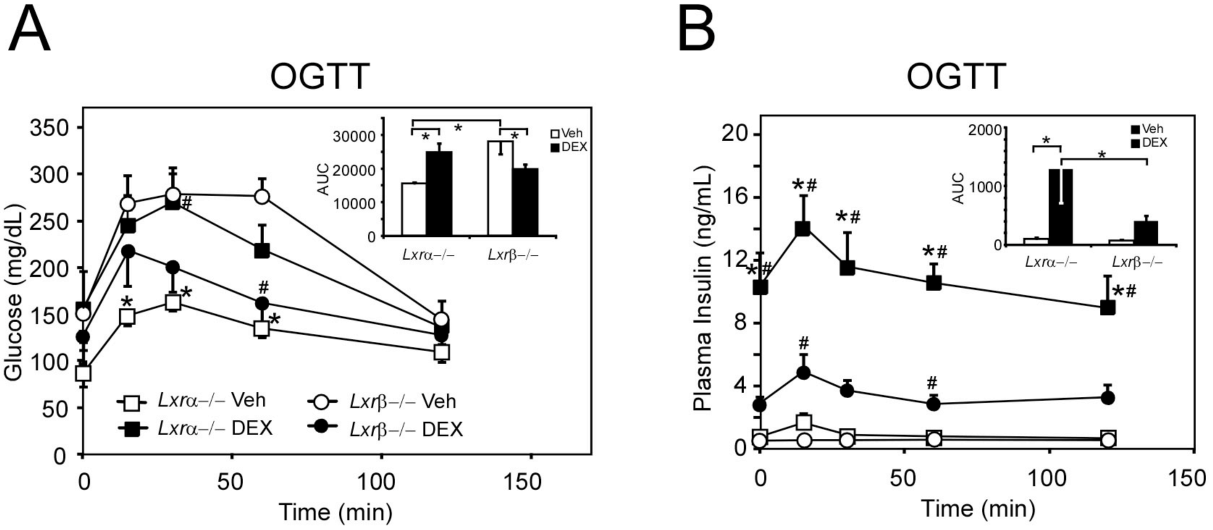
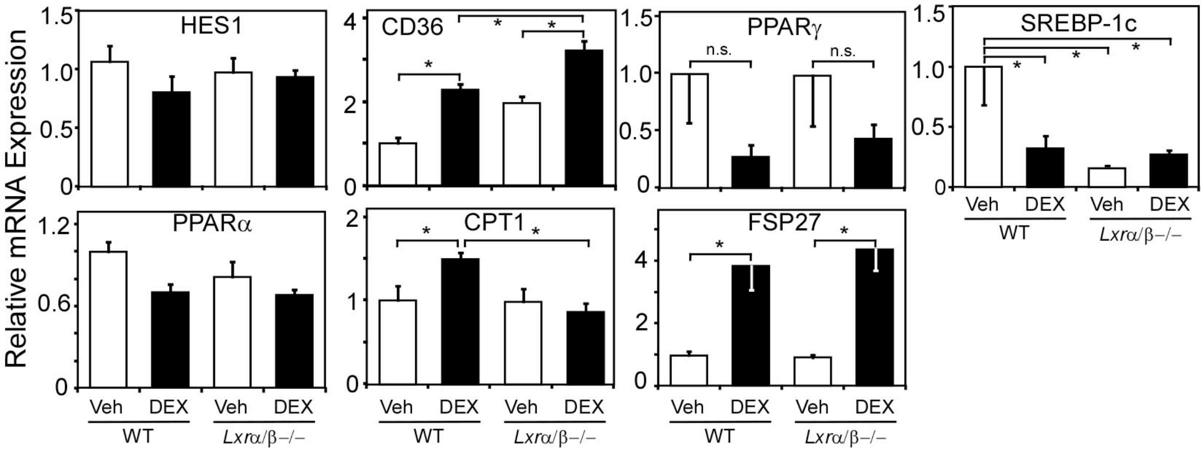
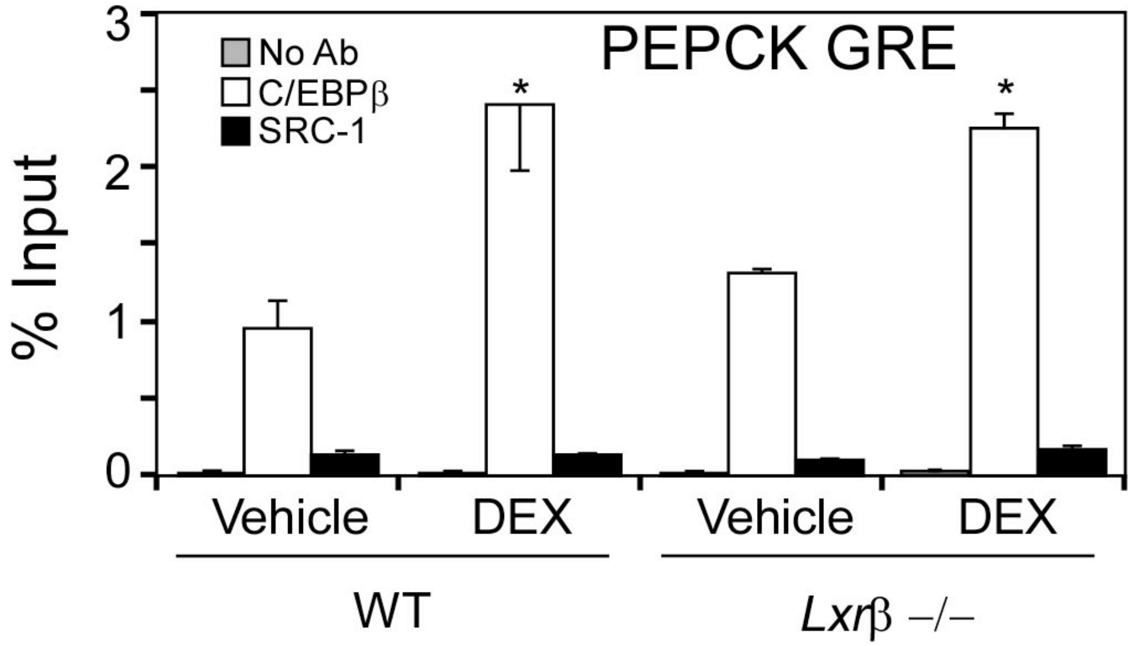


<u>Supplementary Figure 1:</u> Glucose tolerance is preserved in DEX treated *Lxr*β–/– mice. *Lxr*α–/– and *Lxr*β–/– mice were treated with DEX (2.5 mg/kg b.i.d.) or vehicle for 7 days and fasted for 4 h prior to performing the OGTT test. Mice were gavaged with 20% D-glucose and blood sampled at regular intervals into EDTA coated microvette tubes. Plasma glucose (**A**) was assayed using a colorimetric kit. Plasma insulin (**B**) from the glucose tolerance test was assayed by RIA. **B** shares the same figure legend as **A** (Avg±SEM, *n*=6-7). $^{*,\#}$P<0.05, ANOVA followed by Student-Newman-Keuls. * is significantly different from *Lxr*β–/– mice of the same treatment regimen, # is significantly different from vehicle treated control of same genotype, n.s., not statistically significant.



<u>Supplementary Figure 2:</u> QPCR expression analysis of genes known to be involved in hepatic steatosis. Liver RNA was extracted from WT and *Lxr*α/β–/– mice treated with DEX (2.5 mg/kg b.i.d.) for five days, reverse-transcribed and real-time QPCR was performed using SYBR Green I chemistry. CD36, fatty acid translocase; CPT-1, carnitine palmitoyl-transferase I; FSP27, fat specific protein; HES1, hairy and enhancer of split 1. (Avg±SEM, *n*=4-6). *P<0.05 by ANOVA and Student-Newman-Keuls, n.s., not statistically significant.



<u>Supplementary Figure 3:</u> Recruitment of C/EBPβ and SRC-1 to the PEPCK promoter is similar in WT and *Lxr*β−/− mice. Chromatin immunoprecipitation of GR protein from mice perfused with vehicle or 10 nM DEX through the portal vein for 30 min. Chromatin was pooled from 2 mice per treatment and results are expressed relative to % input. Error bars represent PCR amplification variability (Avg±SD, *n*=3). *P<0.05 (Student's t-test, relative to vehicle control of same genotype).

<u>Table S1:</u> Average Change in Body Weight after DEX Treatment as a Function of Dosing Route and Length of Treatment

Treatment Regimen	s.c. injection DEX 5 day treatment		s.c. injection DEX-21-Acetate 7 day treatment		i.p. injection DEX 14 day treatment	
Change in BW	(g)	(% of initial)	(g)	(% of initial)	(g)	(% of initial)
WT	*n*=8-9		*n*=12-14		*n*=4-5	
Veh	-0.7 ± 0.6	-1.3 ± 1.3	-2.0 ± 0.4	-5.4 ± 1.1	-0.3 ± 0.6	-0.5 ± 2
DEX	0.2 ± 0.5	1.2 ± 1.6	-3.4 ± 0.6^{A}	-8.4 ± 1.2^{B}	-2.4 ± 0.9	-6.8 ± 2.3^{B}
Lxrα/β−/−	*n*=11-15		*n*=15		*n*=6	
Veh	0.2 ± 0.3	0.9 ± 1.0	-0.2 ± 0.4	-0.4 ± 1.3	-0.3 ± 1.0	-0.4 ± 3.5
DEX	-0.4 ± 0.2	-1.2 ± 0.8	-1.5 ± 0.5^{A}	-4.5 ± 1.3*	-0.6 ± 0.5	-1.9 ± 1.6
Lxrα−/−			*n*=6		*n*=5	
Veh			-0.5 ± 0.2	-1.9 ± 0.6	-3.0 ± 1.4	-7.6 ± 3.4
DEX			0.3 ± 0.6	0.7 ± 2.2	-0.02 ± 1.1	0.1 ± 2.6
Lxrβ−/−			*n*=6		*n*=4-5	
Veh			-0.03 ± 0.5	-0.1 ± 1.7	0.5 ± 0.4	2.1 ± 1.3
DEX			-0.9 ± 0.5	-3.3 ± 1.8	-2.9 ± 0.6*	-10.2 ± 1.9*

Data shown represent the Avg±SEM

*Significantly different from Veh of same genotype P<0.05 (Student's t-test)

^{A}P=0.05; ^{B}P=0.07

Table S2: **QPCR primer sequences**

Gene Name	Abbrev.	Accession#	Forward and Reverse Primers
CD36 (fatty acid translocase)	CD36	NM_007643.3	5'ggaactgtgggctcattgc3' 5'catgagaatgcctccaaacac3'
Carnitine Palmitoyltransferase I	CPT1	NM_013495.1	5'tgagtggcgtcctctttgg3' 5'cagcgagtagcgcatagtca3'
Cyclophilin B	cyclophilin	NM_011149.2	5’ggagatggcacaggaggaa3’ 5’gcccgtagtgcttcagctt3’
Fat specific gene 27 (CIDEC)	FSP27	NM_178373.3	5’tggcaaaagataccatgttcatg3’ 5’gcttctgggaaagggctagct3’
Forkhead box O1	FOXO1	NM_019739.2	5’tcatggatggagataccttgga3’ 5’cttgacactgtgtgggaagctt3’
Glucose-6-phosphatase	G6Pc	NM_008061.3	5'gtggcagtggtcggagact3' 5'acgggcgttgtccaaac3'
Glucocorticoid Receptor	GR	NM_008173.3	5’catacatgcagggtagagtcattctt3’ 5’gcaagtggaaacctgctatgc3’
Hairy and enhancer of split 1	HES1	NM_008235.2	5'aaccaaagacggcctctga3' 5'cccttcgcctcttctccat3'
Phosphenolpyruvate carboxykinase	PEPCK	NM_011044.2	5'caccatcacctcctggaaga3' 5'gggtgcagaatctcgagttg3'
PPARalpha	PPARα	NM_011144.3	5'acaaggcctcagggtacca3' 5'gccgaaagaagcccttacag3'
PPARgamma	PPARγ	NM_011146.2	5'caagaataccaaagtgcgatcaa3' 5'agctgggtcttttcagaataataag3'
PPAR-gamma coactivator 1α	PGC1α	NM_008904.1	5'tgagagaccgctttgaagtttt3' 5'cggtaggtgatgaaaccatagc3'
Tyrosine aminotransferase	TAT	NM_146214.2	5’tctggagccatgtaccttatgg3’ 5’ttccacgtcattctcaaattctg3’
SREBP-1c	SREBP1c	NM_011480.2	5'ggagccatggattgcacatt3' 5'ggcccgggaagtcactgt3'