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## Supplemental information

#### Metabolic nuclear receptors coordinate energy

# metabolism to regulate Sox9<sup>+</sup> hepatocyte fate

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### **Supplemental information**



Figure S1. Activation of PPAR $\alpha$  or FXR regulates the expression of Sox9

#### in vitro and in vivo, related to Figure 1 and 2.

- (A) Sox9-Immunoblot analysis in HepG2 cells.
- (B) Sox9-Immunoblot analysis in primary mouse hepatocytes cells.
- (C) Sox9-Immunoblot analysis of liver samples.
- (D) Sox9-Immunoblot analysis of liver samples.



Figure S2. Sox9 is a target of PPAR $\alpha$  and FXR, related to Figure 3.

Functional role of IR9 motif in the regulatory region of mouse Sox9 for PPAR $\alpha$ and FXR activity in Hep1-6 cells. Data are expressed as means ± SD. Comparisons between two groups were performed using the two-tailed Student's t-test. Significant difference is presented at the levels of \*p < 0.05 and \*\*p < 0.01.



Figure S3. Activation of PPAR $\alpha$  or FXR regulates the expression of Sox9 in vivo, related to Figure 4.

Representative images from RNAscope® assays for Sox9 mRNA levels in the indicated groups. Graph show quantification of the integrated optical density (IOD) in the indicated groups (n = 5). Scale bar represents 20µm. Data are expressed as means  $\pm$  SD. Comparisons between multiple groups were performed using ordinary one-way ANOVA with the Dunnett's multiple comparison test. Significant difference is presented at the levels of \*p < 0.05 and \*\*p < 0.01.





Figure S4. PPAR $\alpha$  promotes, but FXR prevents proliferation of Sox9<sup>+</sup> BrdU<sup>+</sup> cells in CCl<sub>4</sub>-induced chronic liver injury model, related to Figure 5. The model of CCl<sub>4</sub>-induced chronic liver injury was described in Fig. 4*A*. Sox9/BrdU staining was performed. Arrows depict Sox9<sup>+</sup>BrdU<sup>+</sup> cells. Graphs show percentages of Sox9<sup>+</sup>BrdU<sup>+</sup> cells in the indicated groups (n=5). Scale bar represents 20µm. Data are expressed as means ± SD. Comparisons between multiple groups were performed using ordinary one-way ANOVA with the Dunnett's multiple comparison test. Significant difference is presented at the levels of \*p < 0.05 and \*\*p < 0.01.



Figure S5. Few CK19<sup>+</sup> BrdU<sup>+</sup> cells in CCl<sub>4</sub>-induced chronic liver injury model, related to Figure 5.

The model of CCl<sub>4</sub>-induced chronic liver injury was described in Fig. 4A. CK19/BrdU staining was performed. Scale bar represents 20µm.



Figure S6. Few CK19<sup>+</sup> BrdU<sup>+</sup> cells after CCI4-induced chronic liver injury

#### in Sox9-CreERT2; Rosa26-mTmG mice, related to Figure 7.

The model of CCl₄-induced chronic liver injury was described in Fig. 6B. CK19/BrdU staining was performed. Scale bar represents 20µm.

Table S1. The primer sequences for qPCR, EMSA, ChIP and PlasmidConstruction, related to STAR Methods.

Name	Application	Sequence (5'-3')		
H-Cpt1a-F	qPCR	CATTCAGGCAGCAAGAGC		
H-Cpt1a-R	qPCR	CAGCAGCCGCCCATCATG		
H-GAPDH-F	qPCR	CTCTGGTAAAGTGGATATTG		
H-GAPDH-R	qPCR	GGTGGAATCATATTGGAAC		
H- Acox1-F	qPCR	GTATGGAATCAGTCAGAACGC		
H- Acox1-R	qPCR	CTTGTAAGATTCGTGGACCTC		
H-SHP-F	qPCR	CCCAAGATGCTGTGACCTTT		
H-SHP-R	qPCR	CCAGAAGGACTCCAGACAGC		
H-Sox9-F	qPCR	ACCGACGAGCAGGAGAAGGG		
H-Sox9-R	qPCR	GCGGATGCACACGGGGAACT		
H-PDK4-F	qPCR	GTGATGTGGTAGCAGTGGTC		
H-PDK4-R	qPCR	TCTATTGGTGTAAGGGAAGG		
M-PDK4-F	qPCR	GAGCATCAAGAAAACCGT		
M-PDK4-R	qPCR	ATAACCAAAACCAGCCAA		
M-36B4-F	qPCR	TGGAGACAAGGTGGGAGCC		
M-36B4-R	qPCR	CACAGACAATGCCAGGACGC		
M-Acox1-F	qPCR	CTGAAATCAAGAGAAGCGAG		
M-Acox1-R	qPCR	GAGAAAGTGGAAGGCATAGG		
M-Cpt1a-F	qPCR	ACCTATTCGTCTTCTGGGAT		
M-Cpt1a-R	qPCR	GTGTTGGATGGTGTCTGTCT		
M-SHP-F	qPCR	CGATCCTCTTCAACCCAGATG		
M-SHP-R	qPCR	AGGGCTCCAAGACTTCACACA		
M-Sox9-F	qPCR	TGCAAGCTGGCAAAGTTGAT		
M-Sox9-R	qPCR	TCAGTTCACCGATGTCCACG		

Sox9-probe-F(Labeled)	EMSA	AGTTCAAGGTCGGCGTGGCCC		
Sox9-probe-R(Labeled)	EMSA	GGGCCACGCCGACCTTGAACT		
Sox9-probe-F(Mut)	EMSA	CTACCAAGGTCGGCGCATGCC		
Sox9-probe-R(Mut)	EMSA	GGCATGCGCCGACCTTGGTAG		
Sox9- probe-F(Cold)	EMSA	AGTTCAAGGTCGGCGTGGCCC		
Sox9- probe-R(Cold)	EMSA	GGGCCACGCCGACCTTGAACT		
M-Sox9-IR9-F	ChIP	AGTGGCGAGCCTGACGGTGTTTGTG		
M-Sox9-IR9-R	ChIP	CCGTGGGCCACGCCGACCTTGAACT		
M-SOX9-PGL3-F	Plasmid	CGACGCGTCTCCCTACCTCAAGCCTG		
	Construction	AAGAAT		
M-SOX9- PGL3-R	Plasmid	GAAGATCTGAACCAGCCGAGTCCTCC		
	Construction	GACATG		
M-SOX9-PGL3-Mut-F	Plasmid	ACTTGTCCTACCAAGGTCGGCGCATG		
	Construction	CCACGGGACCGGCCGCA		
M-SOX9- PGL3-Mut -R	Plasmid	TGCGGCCGGTCCCGTGGCATGCGCC		
	Construction	GACCTTGGTAGGACAAGT		

H: Human

M: Mouse

F: Forward

R: Reverse

# Table S2. The probe information for RNAscope<sup>®</sup> assay, related to STARMethods.

Official symbol	Cat No.	SOURCE	Gene ID	Genbank nucleotide accession number	Channel	Detection Kit
Sox9	40105 1-C3	www.acdbio.c om	2068 2	NM_011448 .4	C3	RNAsco pe <sup>®</sup> Multiple x
Pck1	45802 1	www.acdbio.c om	1853 4	NM_011044 .2	C1	Fluoresc ent Reagent Kit v2