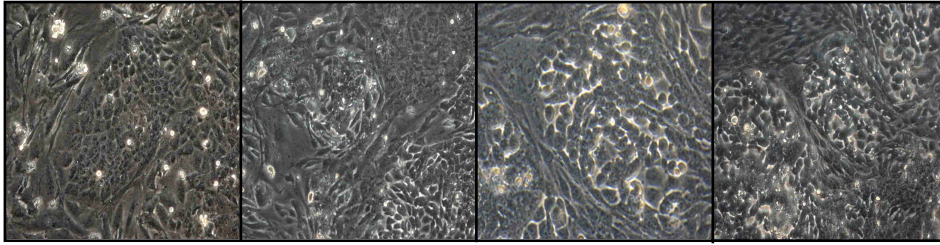
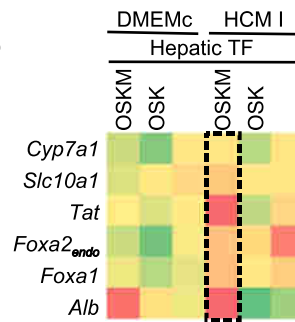
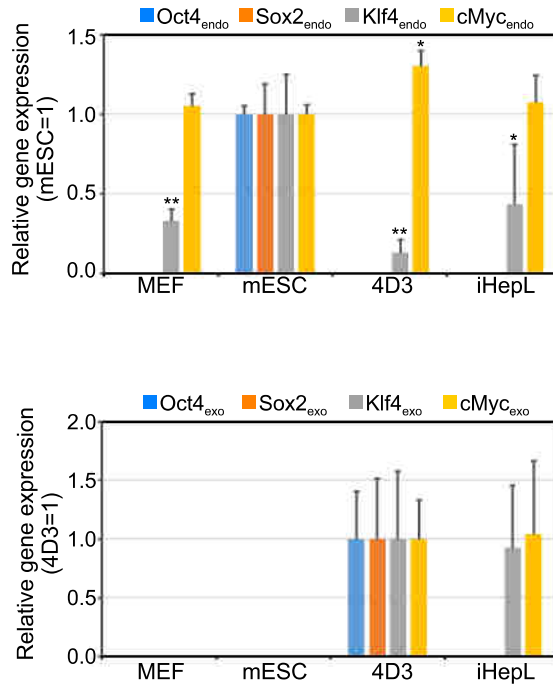
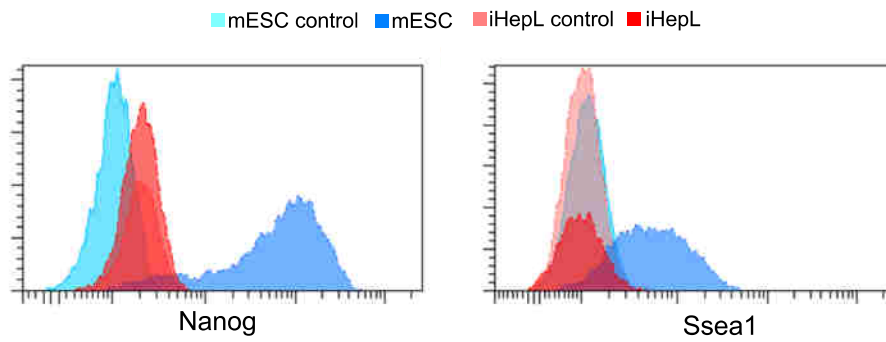
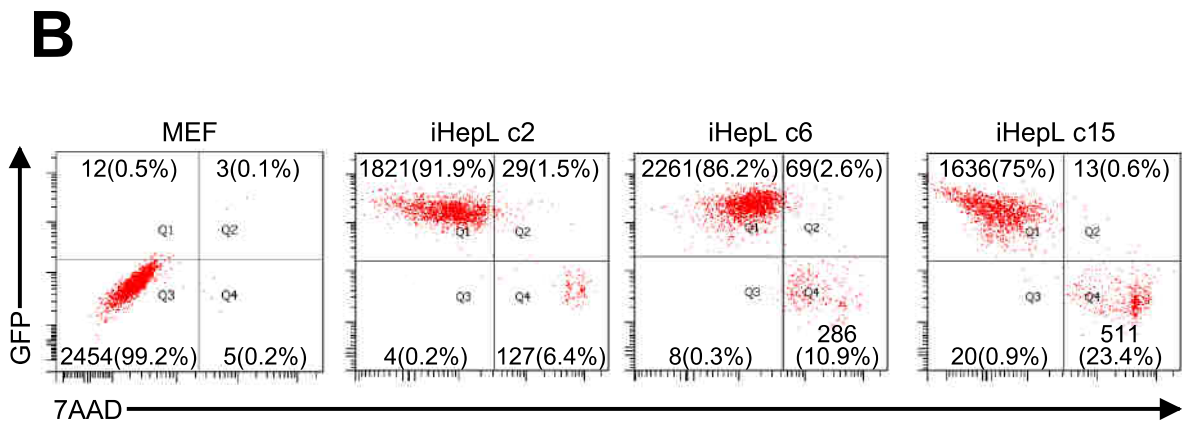
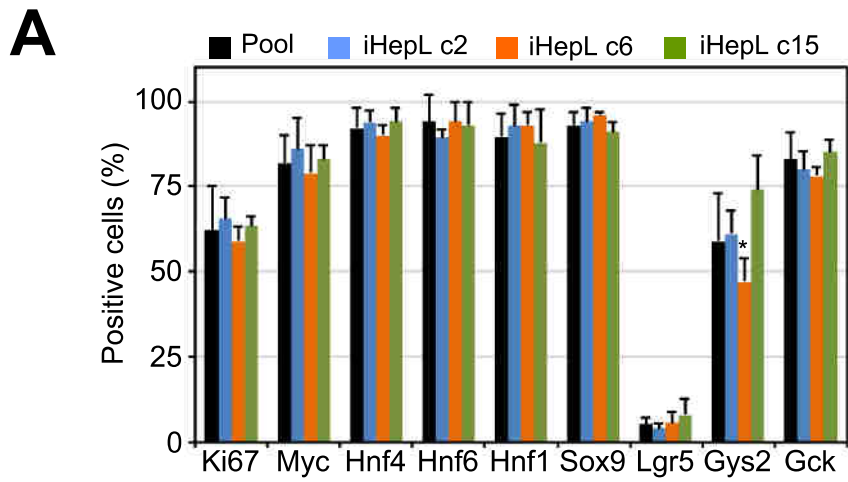


**A****B**

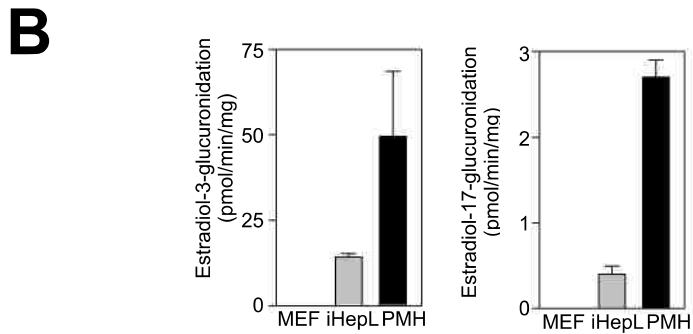
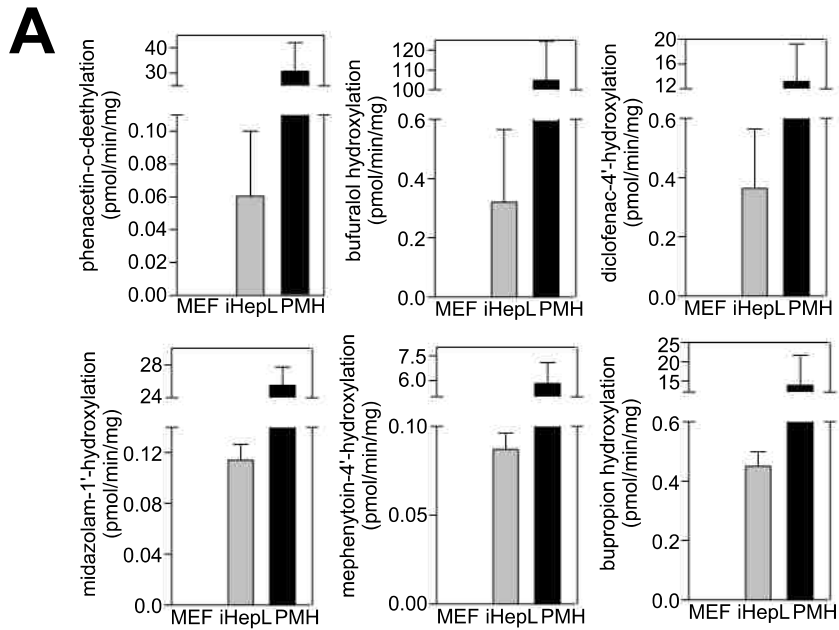
SUPPLEMENTARY FIGURE S1  
(Serrano et al)

**A****B**

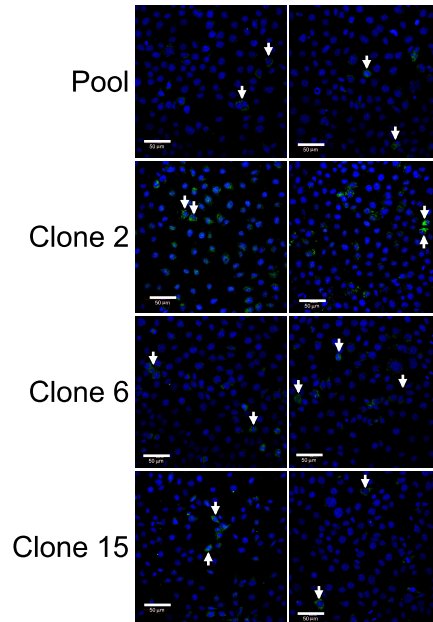
SUPPLEMENTARY FIGURE S2  
(Serrano et al)



SUPPLEMENTARY FIGURE S3  
(Serrano et al)

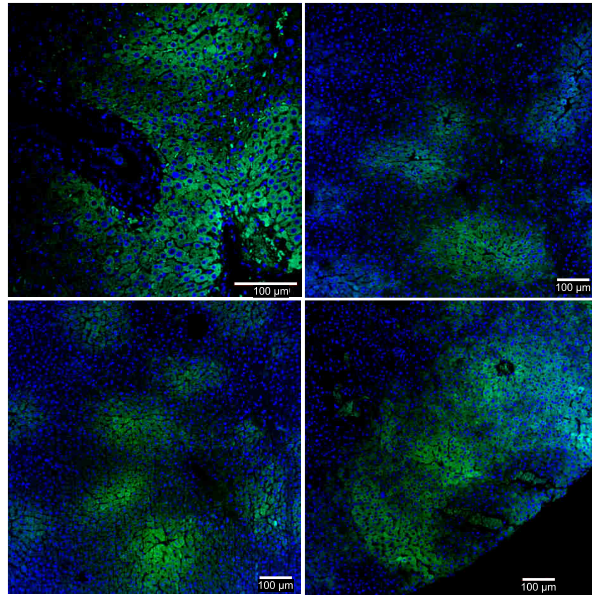


SUPPLEMENTARY FIGURE S4  
(Serrano et al)

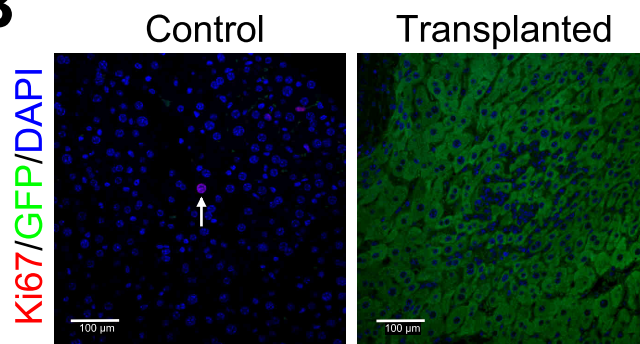


SUPPLEMENTARY FIGURE S5  
(Serrano et al)

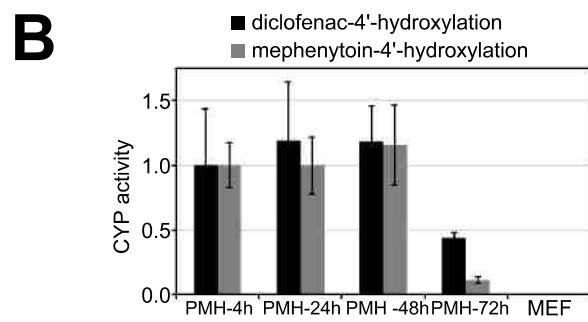
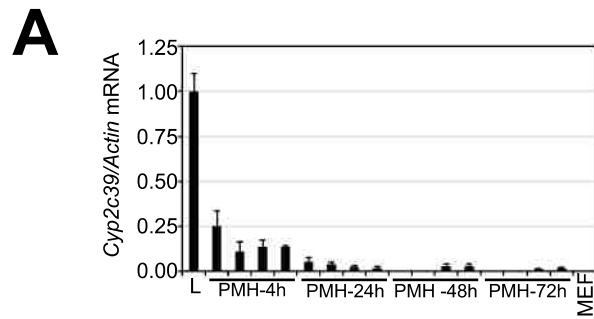
**A**



**B**



SUPPLEMENTARY FIGURE S6  
(Serrano et al)



SUPPLEMENTARY FIGURE S7  
(Serrano et al)

**Supplementary Figure S1. Formation of epithelial colonies in infected MEF.** **A.** Phase contrast photographs of several epithelial colonies (7 days after infection) formed in MEF infected with the retroviral mixture. **B.** Heat map depicting relative expression levels of the mRNAs analyzed in Figure 1B. Red: higher expression; green: lower expression.

**Supplementary Figure S2. iHepL cells do not express endogenous pluripotency factors Oct4 and Sox2.** **A.** Expression levels of endogenous and exogenous (transgenic) transcripts for Oct4, Klf4, Sox2 and c-Myc were measured by qRT-PCR in total RNA extracted from MEF, mESC (CGR8 strain), iHepL and 4D3 (MEF infected with lentiviral vectors expressing OSKM for 3 days) cells. Data is represented as mean  $\pm$  s.d. from MEF (n=3), mESC (n=3), iHepL cells (n=6) and 4D3 (n=3). Student's t test was performed between mESC (upper panel) or 4D3 (lower panel) and the other groups; \* p<0.05; \*\*p<0.01. **B.** Expression of Nanog and Ssea1 in mESC (CGR8 strain) and iHepL analyzed by flow cytometry. Controls were incubated with normal serum instead of the primary antibody.

**Supplementary Figure S3. Characterization of iHepL isolated clones.** **A.** Original unselected pool of iHepL cells and isolated clones from three different infections (see below) were immunostained as shown in Figure 3. The percentage of positive cells was calculated using the CellC software {Selinummi, 2005 #551} and high content screening imaging station Scan<sup>R</sup> from Olympus. Total cell number ranged from 1000 to 4000. Total cell numbers were estimated with DAPI staining. No statistically significant difference was found between the pool and any of the clones except for Gys2 immunostaining in clones 6 and 15, p<0.05. **B.** Cells (MEF and iHepL clones) were incubated for 30 min in media containing 50  $\mu$ g/ml of 7-amino actinomycin D (7-AAD) and analyzed for viability (7AAD-negative) and GFP expression by FACSCanto Flow Cytometer (Becton Dickinson). FACSCanto. iHepL c2: clone 2 from infection #1, iHepL c6: clone 6 from infection #2 and iHepL c15: clone 15 from infection #3.



**Supplementary Figure S4. Limited Cyp450 activities in iHepL cells.** **A.** Cells were incubated with a mixture of 8 substrates and the corresponding metabolites measured by LC-MS. Formation of 6-hydroxychlorzoxazone and 7-hydroxycoumarin were not detected. **B.** Formation of estradiol-3-glucuronide (Ugt1a1) and estradiol-17-glucuronide (Ugt2b) in iHepL incubated with estradiol. Data is represented as mean  $\pm$  s.d. from iHepL cells (n=6) and PMH (n=3). Student's t test was performed and statistical significance was in all cases  $p < 0.001$ .

**Supplementary Figure S5. Expression of hepatic progenitor marker Lgr5 in pool iHepL and isolated clones.** Representative fluorescence images of iHepL cells immunostained with an antibody against Lgr5. Two images per cell type are shown. Nuclei were made visible with DAPI.

**Supplementary Figure S6. iHepL cells (GFP-positive) engraftment in mouse livers.** **A.** Low magnification representative fluorescent images showing engraftment of iHepL cells in the mouse liver after three weeks. **B.** Serial sections of transplanted livers were stained by Ki67. Only sporadic positive cells (arrow in control) were detected among resident and transplanted cells. Nuclei were made visible with DAPI.

**Supplementary Figure S7. mRNA and activity decay in cultured hepatocytes.** **A.** Total RNA was extracted from cultured primary mouse hepatocytes (PMH) at the indicated times and the expression of *Cyp2c39* was assessed by qPCR and represented as relative gene expression normalized to total mouse liver (L). Data are represented as mean  $\pm$  s.d. (L, n=5; MEF, n=3; PMH, n=4). **B.** Graph showing Cyp450 activity in PMH. Diclofenac and mephenytoin 4 hydroxylation by primary cultured mouse hepatocytes (n=4) at different culture times. Cells were incubated with a diclofenac and mephenytoin and the corresponding metabolites measured by LC-MS.

**Supplementary Table S1. Primers used for cloning**

Primer	Sequence 5'-3'
pMIGR1-Hhex-XhoI-F	AACTCGAGATGCAGTTCCCGCACCCGGGG
pMIGR1-Hhex-EcoRI-R	GGGAATTCTCATCCAGCATTAAAGTAGCC
pMIGR1-Hnf1a-XhoI-F	AACTCGAGACCATGGTTTCTAAACTGAGCCAG
pMIGR1-Hnf1a-EcoRI-R	GGGAATTCTTACTGGGAGGAAGAGGCCAT
pMIGR1-Hnf6a-XhoI-F	AACTCGAGACCATGAACGCGCAGCTGACCATG
pMIGR1-Hnf6a-EcoRI-R	GGGAATTCTCATGCTTTGGTACAAGTGC

**Supplementary Table S2. Retroviral plasmids used in this study.**

Plasmid	Backbone	Developed by	Addgene
pMSx-Oct4	pMXs	Dr Shinya Yamanaka	#13366
pMXs-Sox2	pMXs	Dr Shinya Yamanaka	#13367
pMXs-Klf4	pMXs	Dr Shinya Yamanaka	#13370
pMXs-cMyc	pMXs	Dr Shinya Yamanaka	#13375
pBabe-Foxa2	pBabe-PURO	Dr Ken Zaret	
pBabe-Gata4	pBabe-PURO	Dr Ken Zaret	
pBabe-Foxa2	pBabe-PURO	Dr Ken Zaret	
pMIGR1-Hhex	pMIGR1-IRESGFP	In house	
pMIGR1-Hnf1a	pMIGR1-IRESGFP	In house	
pMIGR1-Hnf6a	pMIGR1-IRESGFP	In house	

**Supplementary Table S3. Primers used for qRT-PCR**

Transcript	Forward (5'-3')	Reverse (5'-3')	Size (bp)
Albumin	gcatgggcagtagctcgct	ggcaaggtccgcctgtcat	150
Slc10a1	tggtacctctcctgatgcc	cctgttccatgctgatggtgct	108
Cyp7a1	caacgggttgattccatacc	attccccatcagttgcag	118
Foxa1	acgaggagccccatcgagcc	accaggtggccatgcagaca	124
Foxa2 <sub>endo</sub>	cgaacaagcgggctggat	cctctattccctgtcccagct	142
Foxa3	ctctattcccgtctctgctt	ggcagttaccacagtagccaa	179
Cebp	ccatgccgggagaactctaac	tggaggtgactgctcatcgg	86
Hhex <sub>endo</sub>	cccagcctctcaggaagacccc	gtccggtctctaaacatggccga	125
Hnf4a <sub>endo</sub>	tgaatcctacaagctcctgcc	taggttactcccaggtgctct	164
Oct4 <sub>endo</sub>	gtggacctcaggttgactgg	ttctgcagggcttcatgcc	199
Sox2 <sub>endo</sub>	tagagctagactccggcgatga	ttgcttaacaagaccagaaa	296
Klf4 <sub>endo</sub>	ccaactgaacatcccggactt	tctgcttaaaggcactatggga	498
cMyc <sub>endo</sub>	tgacctaacctgaggagagctggaatc	aagtttgaggcagttaaaattatggctgaagc	142
Oct4 <sub>exo</sub>	ttgggctagagaaggtatgtggtc	ttatcgtcgaccactgtgctg	421
Sox2 <sub>exo</sub>	ggttacctctctcccactccag	ttatcgtcgaccactgtgctg	376
Klf4 <sub>exo</sub>	gcgaactcacacaggcgagaacc	ttatcgtcgaccactgtgctg	406
cMyc <sub>exo</sub>	cagaggaggaacgagctgaagcgc	ttatcgtcgaccactgtgctg	426
Afp	gttgccaaggaaactcgtg	ggtttgacgccattctctgc	163

MaoB	acctagcaagcagcatgagc	gtaagtcctgcctctacacg	146
Fmo1	ttaccaccgccaagtgtcat	gatgctcagagccagtcgtg	195
Nat2	cccgggtgcagtcctggtag	tagcccgtatctggctgta	132
Cyp1a2	cccctgccctcagtggtaca	agcacgtccccatactgctg	246
Cyp2e1	gacgtgcggaggtttccct	ttcaggggtgcacagccaat	164
Cyp2c39	ggccagtgatgcctgatcacaat	aatcgggaaaggagtggggc	159
Cyp3a11	acctgggtgctcctagcaat	acagcaaggagaggcgtttgac	221
Ugt1a1	tgggaggctgttagtgtccc	accacgcgcagcagaaaaga	249
Tat	acctcaatcccaccca	tcccactggataggtag	205
Aat1	atcccccttggtcccat	ttcagcttgcctccagag	96
Otc	gctgcgtcgtactggacatt	gcttctggagcacaggtgag	175
Cdh1	aacaactgcataagggcgggaatc	cctgtgcagctggctcaaatcaaa	246
Ocln	cctccaatggcaaagtgaatggca	tgtttcatagtgtcagggtccgt	227
Snai1	ttgtgtcgcacgacctgggaaa	tcttcacatccagtggtttgga	167
Zeb1	tgctcactgcccgtattgtgata	agtgcactgaactgcggttcc	224
Thy1	accgagcacacgtaccgct	tgccccacactgaccagc	190
Nanog	ccactagggaaagccatgctgc	aggaacctggctttgccctgac	135
Lin28	ggagtgagcggcgccaaaa	gctggggtggcagctgcat	116
Ggt1	ttgcctatccaagaggacc	ctgggtgggtggtttcatca	132
Slc51a	tggccatcctttccgtaaa	agcgaacaagcctcataccc	286
Krt19	gtgccaccattgacaactcc	aatccactccacactgacc	287
Spp1	agccacaagtccacagcca	aggaactgtgttttgcctct	147
Aqp5	gtcacactgggcatctgt	cgatcggtcctaccagaag	130
CD24a	ttcgcagtgtcacacactga	acacacacagtagcttcggg	124
Cftr	ttgcccgatcagttctcag	gcctgaaggagctgtactg	221
Actin	ccaccatgtaccaggcatt	agggtgtaaacgcagctca	250

**Supplementary Table S4. Primers used for genomic qPCR**

Transcript	In plasmid	Forward (5'-3')	Reverse (5'-3')	Size (bp)
Cnd1 <sub>In1</sub>		tggattggaggaacctgctc	cctgagtcctctgctgaac	85
Cnd1 <sub>In2</sub>		atcctgtaggccaggtgatg	aggctcaagggttttaagg	81
GFP	pMIGR1-IRES-GFP derived	tatatcatggccgacaagca	gttgtggcggatctgaagt	60
Hnf1 <sub>exo</sub>	pMIGR1-Hnf1a-IRES-GFP	atggcctctctcccagta	acaccgcccttattccaag	80
Hnf6a <sub>exo</sub>	pMIGR1-Hnf6a-IRES-GFP	tcaagcactgtaccaagca	accgcccttattccaagc	81
Hhex <sub>exo</sub>	pMIGR1-Hhex-IRES-GFP	tcgagggggataaaggctac	acaccgcccttattccaag	94
Oct4 <sub>exo</sub>	pMXs-Oct4	gtggtgttacgggaaatcac	cgaagtctgaagccaggtgt	82
Sox2 <sub>exo</sub>	pMXs-Sox2	gtggtgttacgggaaatcac	ttcagctccgtctccatca	71
Klf4 <sub>exo</sub>	pMXs-Klf4	gtggtgttacgggaaatcac	gctggacgcagctgtcttct	146
cMy <sub>cexo</sub>	pMXs-cMyc	gtggtgttacgggaaatcac	agggtgtacggagctcgtag	127

**Supplementary Table S5. Antibodies used in this study.**

Antibody	Raised in	Dilution	Reference	Use
Albumin	Mouse	1/100	AB1455; Merck Millipore	IC, IHC
Ck17-19	Rabbit	1/50	12434; Cell Signalling Technology	IC, IHC
E-cadherin	Rabbit	1/500	3195; Cell Signalling Technology	IC, IHC
GFP	Goat	1/200	Ab6673; Abcam	IC, IHC
Glucokinase	Rabbit	1/50	Orb38697; Biorbyt	IC, IHC
Haptoglobin	Rabbit	1/50	Orb28600; Biorbyt	IHC
Gys2	Rabbit	1/250	HPA039482; Sigma	IC
Hnf1	Rabbit	1/200	8986; Santa Cruz Biotechnology	IC, IHC
Hnf1	Goat	1/200	6547; Santa Cruz Biotechnology	IC, IHC
Hnf4	Goat	1/200	6556; Santa Cruz Biotechnology	IC, IHC
Hnf6	Rabbit	1/200	13050; Santa Cruz Biotechnology	IC
Ki67	Rabbit	1/200	9106; Thermo Scientific	IC, IHC
Lgr5	Rabbit	1/50	Ab75732; Abcam	IC
Myc	Rabbit	1/200	Ab32072; Abcam	IC, IHC
Nanog	Rabbit	1/100	REC-RCAB0001P; Cosmo Bio Ltd	IC, FC
Oct4	Rabbit	1/400	2840; Cell Signalling Technology	IC, FC
pH3	Rabbit	1/200	9701S; Cell Signalling Technology	IC, IHC
Sox9	Rabbit	1/100	AB5535; Merck Millipore	IC, IHC
Ssea1	Mouse	1/100	4744; Cell Signalling Technology	IC, FC
Ugt1a1	Rabbit	1/750	AV44294; Sigma	IC

**Supplementary Table S6. Statistical significance of relative transgene copy number.** The following table shows the statistical significance calculated by unpaired Student's t-test between iHepL cells and each of the samples included in Figure 6D. A fragment of intron 2 from Ccnd1 gene was used as a secondary normalization control.

	TARGET GENES							
	Ccnd1 <sub>in2</sub>	GFP	Hnf1a <sub>exo</sub>	Hhex <sub>exo</sub>	Oct4 <sub>exo</sub>	Sox2 <sub>exo</sub>	Klf4 <sub>exo</sub>	Myc <sub>exo</sub>
<b>T1874</b>	0.149	0.528	0.059	0.445	N.D.	N.D.	0.102	<u>0.000</u>
<b>T1875</b>	0.188	0.102	<u>0.001</u>	0.386	N.D.	N.D.	<u>0.019</u>	<u>0.001</u>
<b>T1878</b>	<u>0.010</u>	<u>0.038</u>	<u>0.006</u>	0.144	N.D.	N.D.	0.297	<u>0.001</u>
<b>T1881</b>	<u>0.005</u>	0.203	<u>0.000</u>	0.778	N.D.	N.D.	0.687	<u>0.000</u>
<b>Control</b>	0.065	N.D.	N.D.	N.D.	N.D.	N.D.	N.D.	N.D.

N.D: not detected