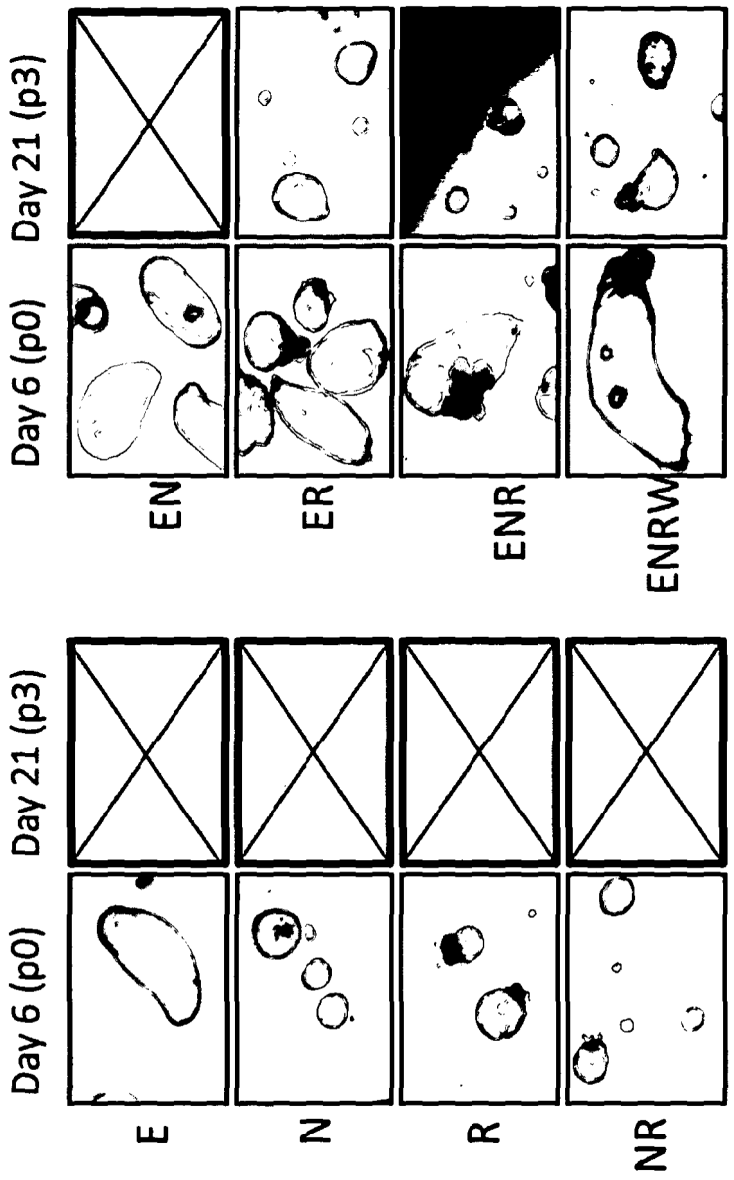


Fig 1a

Fig 1b

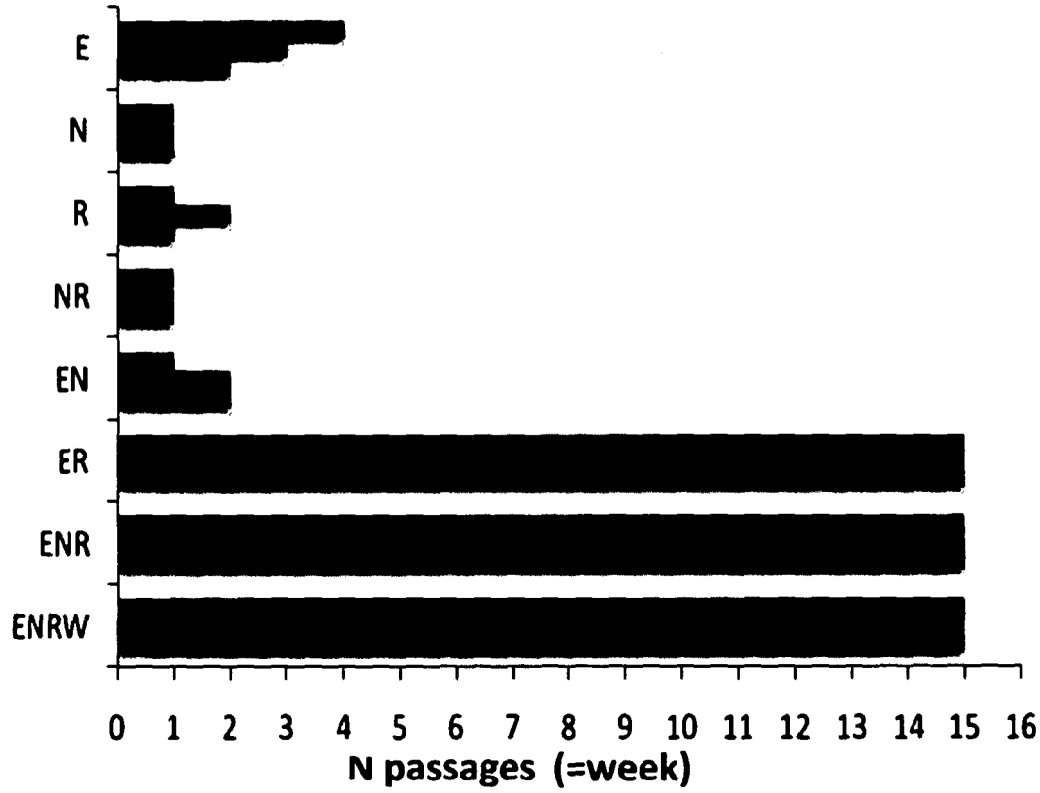

E
N
R
NR
EN
ER
ENR
ENRW
0 1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16
N passages (=week)

Fig 1c

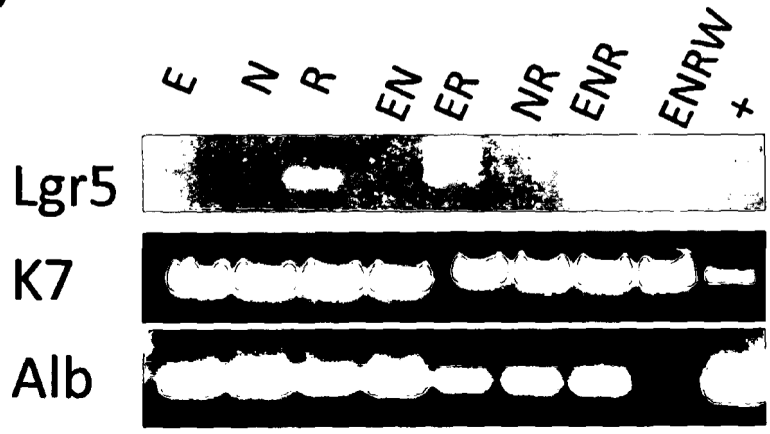

E
N
R
EN
ER
NR
ENR
ENRW
+
Lgr5
K7
Alb

Fig 1d

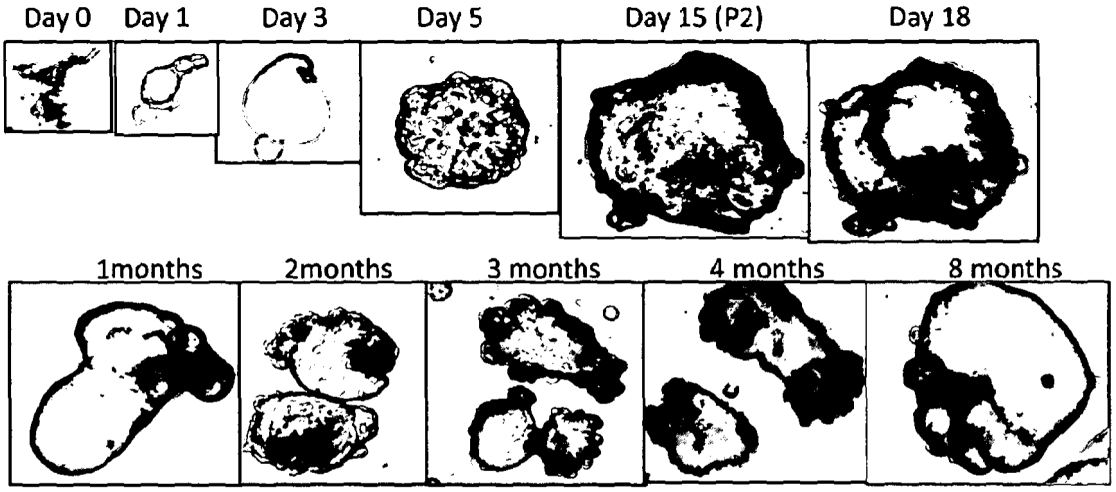

Day 0
Day 1
Day 3
Day 5
Day 15 (P2)
Day 18
1months
2months
3 months
4 months
8 months

Fig 2a

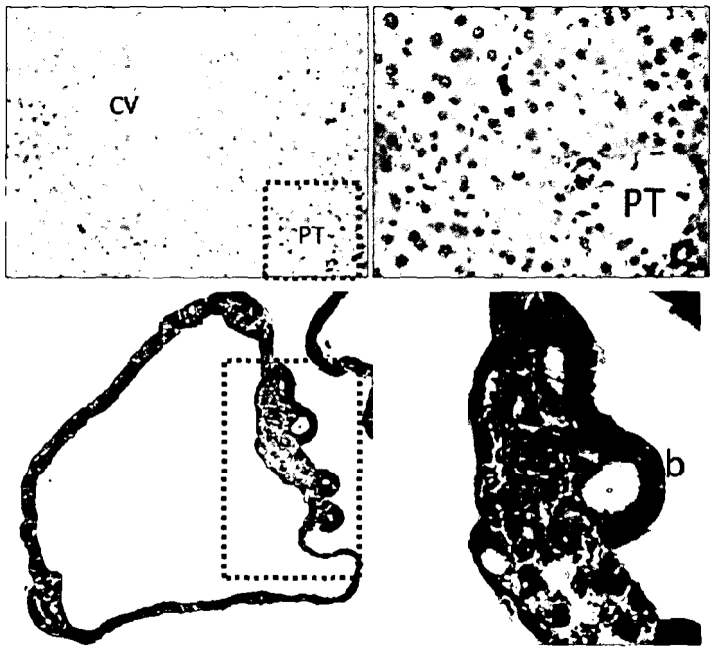

CV
PT
PT
b

Fig 2b

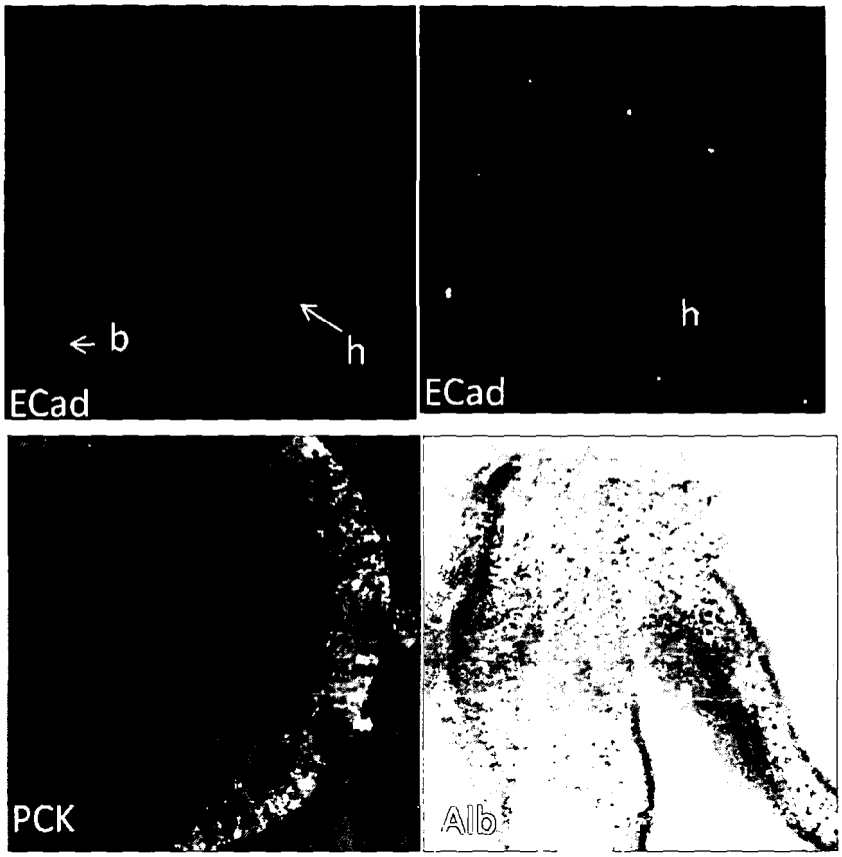


Fig 3

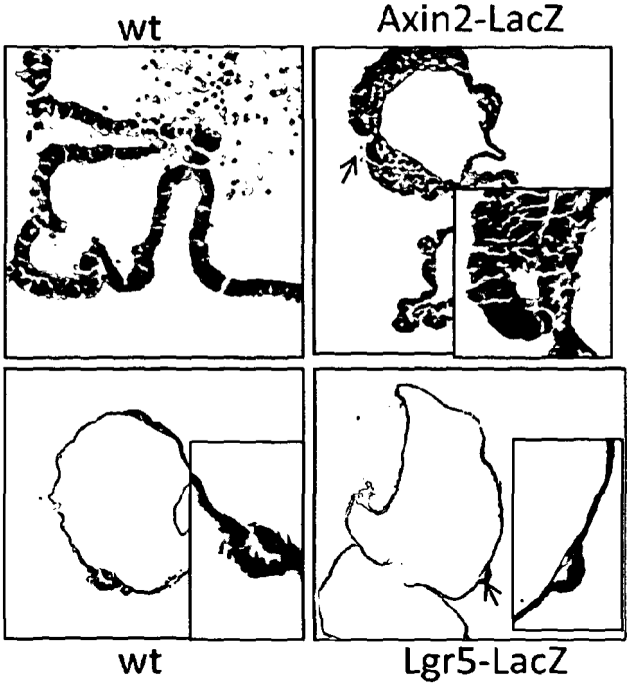


Fig 4a

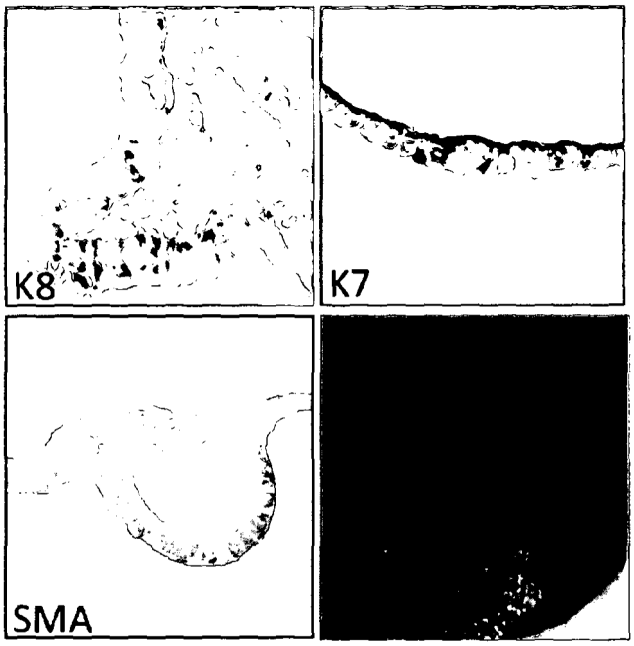

K8
K7
SMA

Fig 4b

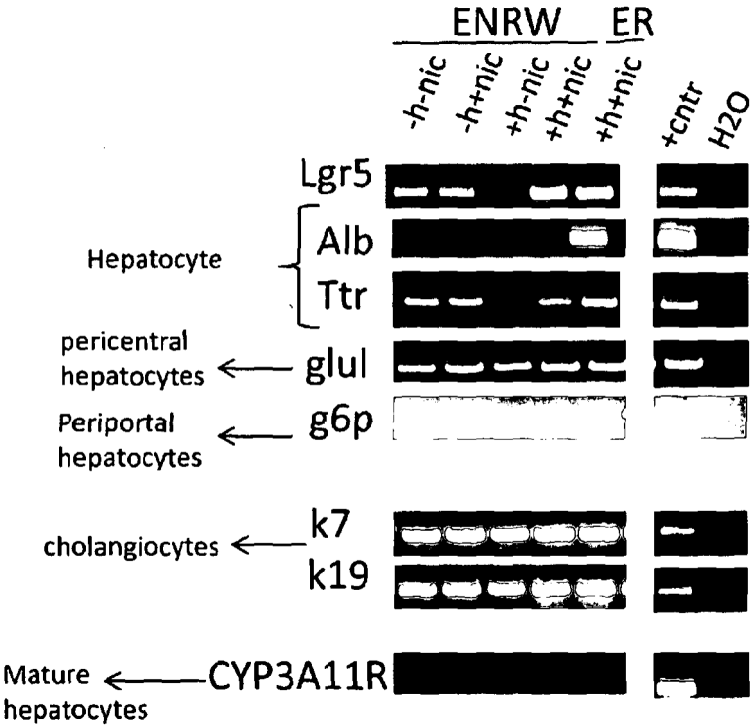

ENRW
ER
-h-nic
-h+nic
+h-nic
+h+nic
+h+nic
+cntr
H2O
Lgr5
Hepatocyte
Alb
Ttr
pericentral hepatocytes
glul
Periportal hepatocytes
g6p
cholangiocytes
k7
k19
Mature hepatocytes
CYP3A11R

Fig 5a

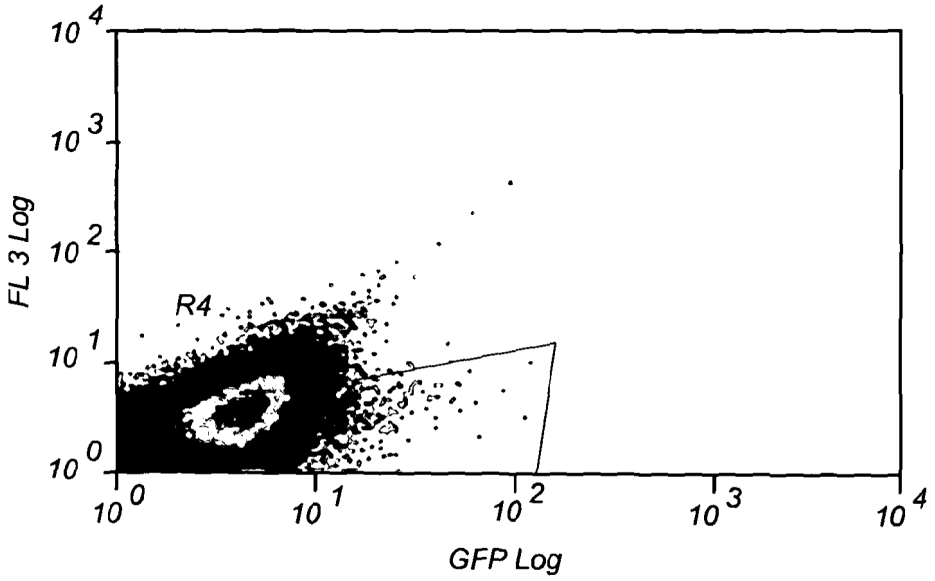

10 4
10 3
10 2
10 1
10 0
FL 3 Log
R4
10 0
10 1
10 2
10 3
10 4
GFP Log

Fig 5b

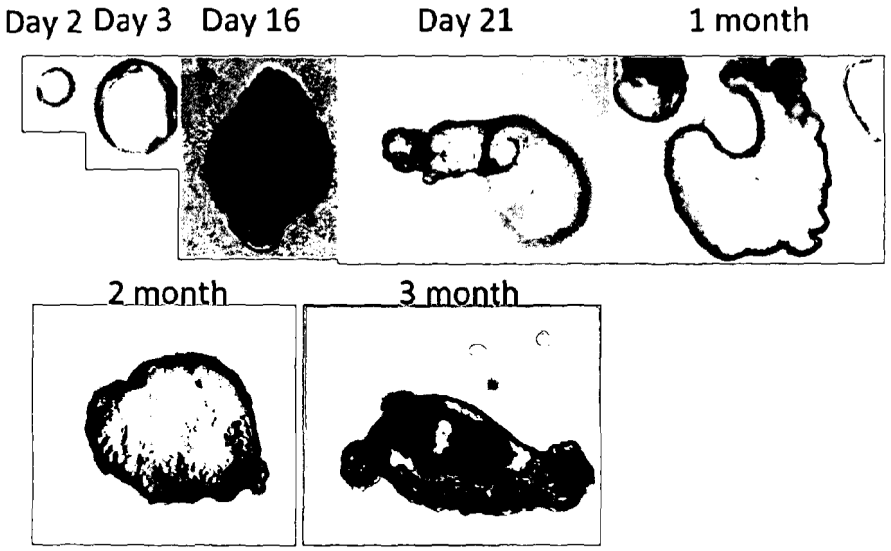
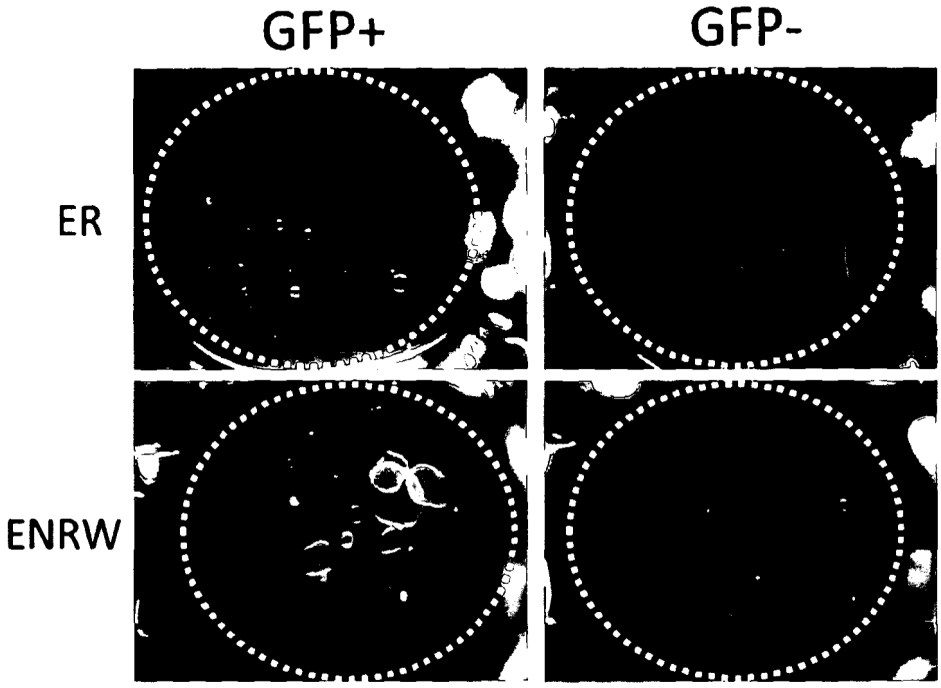

Day 2 Day 3
Day 16
Day 21
1 month
2 month
3 month

Fig 5c



Day 10 after sort

Fig 5d

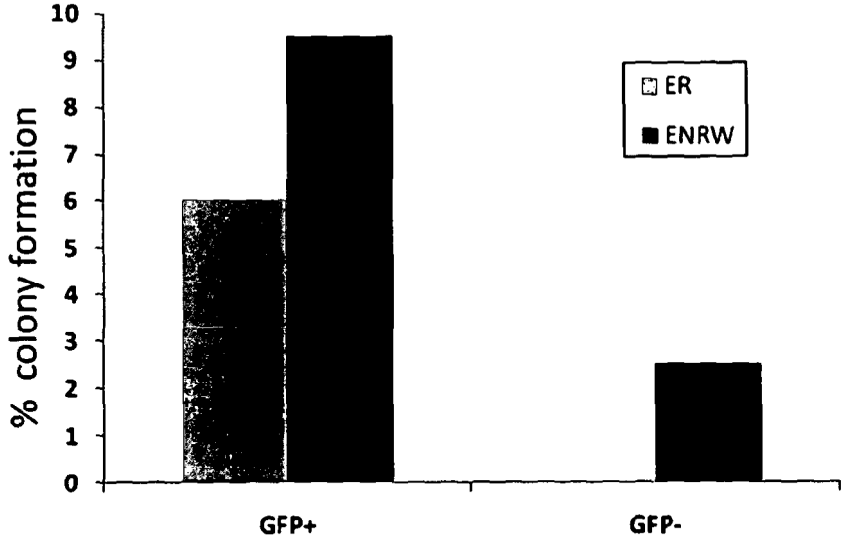


Fig 6a

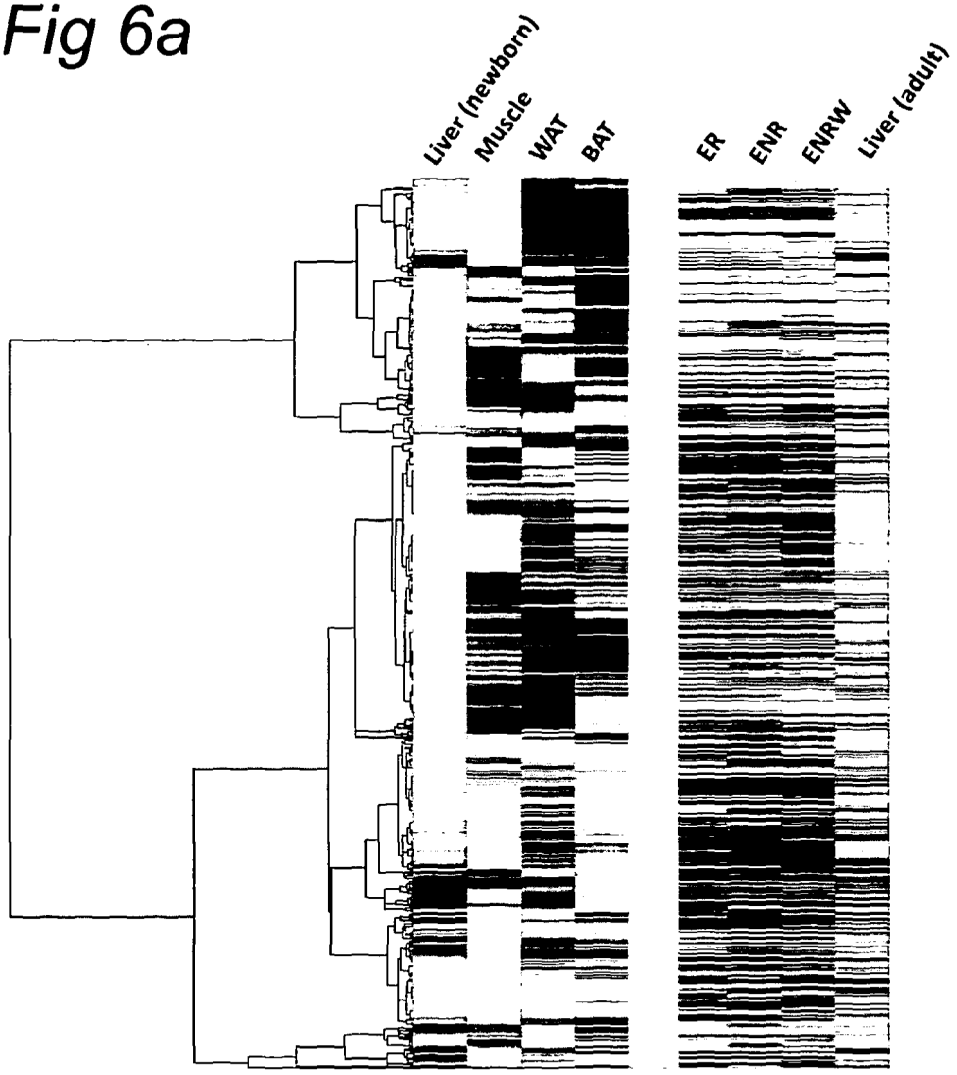


Fig 6b

	ER	ENR	ENRW	Liver (adult)
G6pc2	119.5	122	125	117.5
G6pc3	4679.5	4340.5	4139.5	685.5
Glul	923.5	839.5	1387	18345
Met	5337	5743.5	4122	1828.5
Hnf1a	10980	9865	6176	8334
Hnf1b	2357	2632	2770.5	361
Hnf4a	1336	1283	1086	4033
Cyp39a1	1190.5	1167	1391	1051
Cyp2j6	938.5	918	998.5	1164
Cyp3a13	344	426.5	244	10787
Cyp4b1	1567	1567	370.5	2247
Lap3	4704	4659.5	5069.5	20262
Krt7	163790	161041	195354	386.5
Krt19	88264	79467.5	54949.5	347

Figure 7

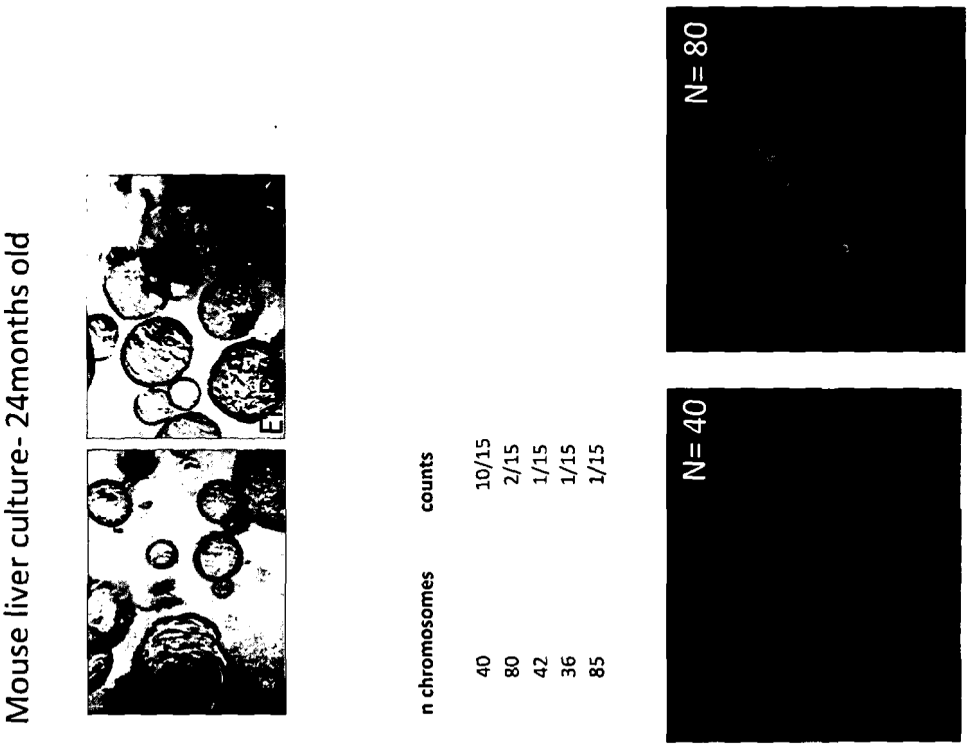
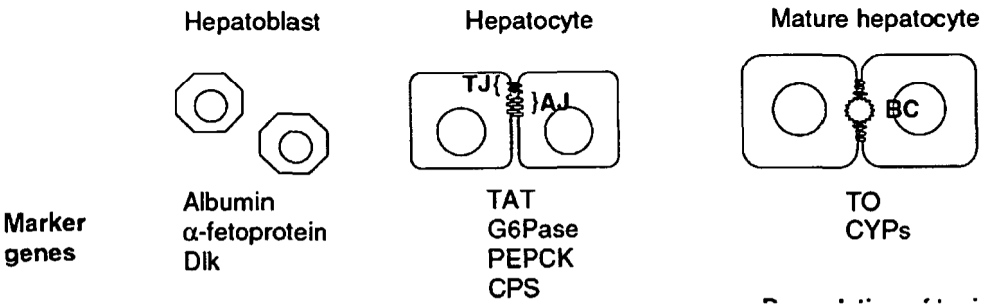

Mouse liver culture- 24months old
A
B
n chromosomes counts
40 10/15
80 2/15
42 1/15
36 1/15
85 1/15
N= 40
N= 80

Figure 8

A


Hepatoblast
Hepatocyte
Mature hepatocyte
TJ
AJ
BC
Marker genes
Albumin
α-fetoprotein
Dlk
TAT
G6Pase
PEPCK
CPS
TO
CYPs

B

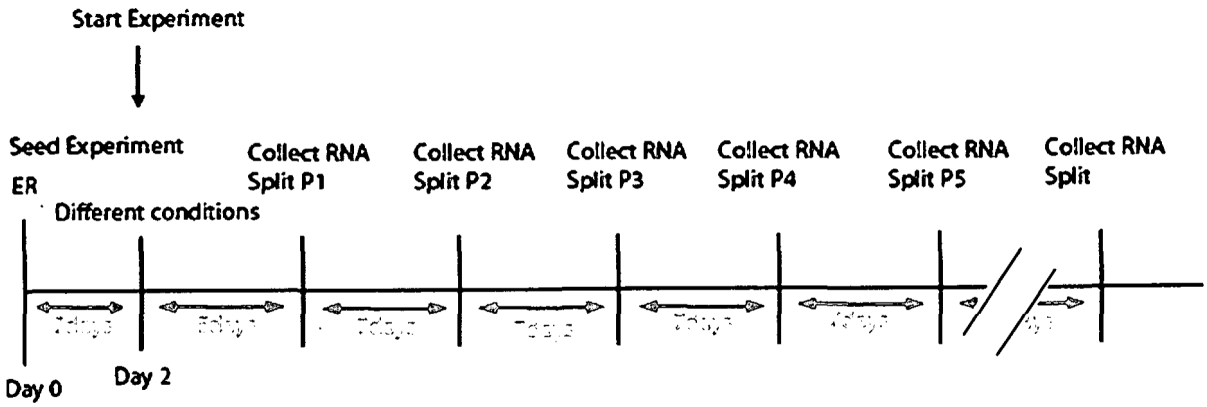

Start Experiment
Seed Experiment
ER
Different conditions
Collect RNA Split P1
Collect RNA Split P2
Collect RNA Split P3
Collect RNA Split P4
Collect RNA Split P5
Collect RNA Split
Day 0
Day 2

Figure 8

C After first split

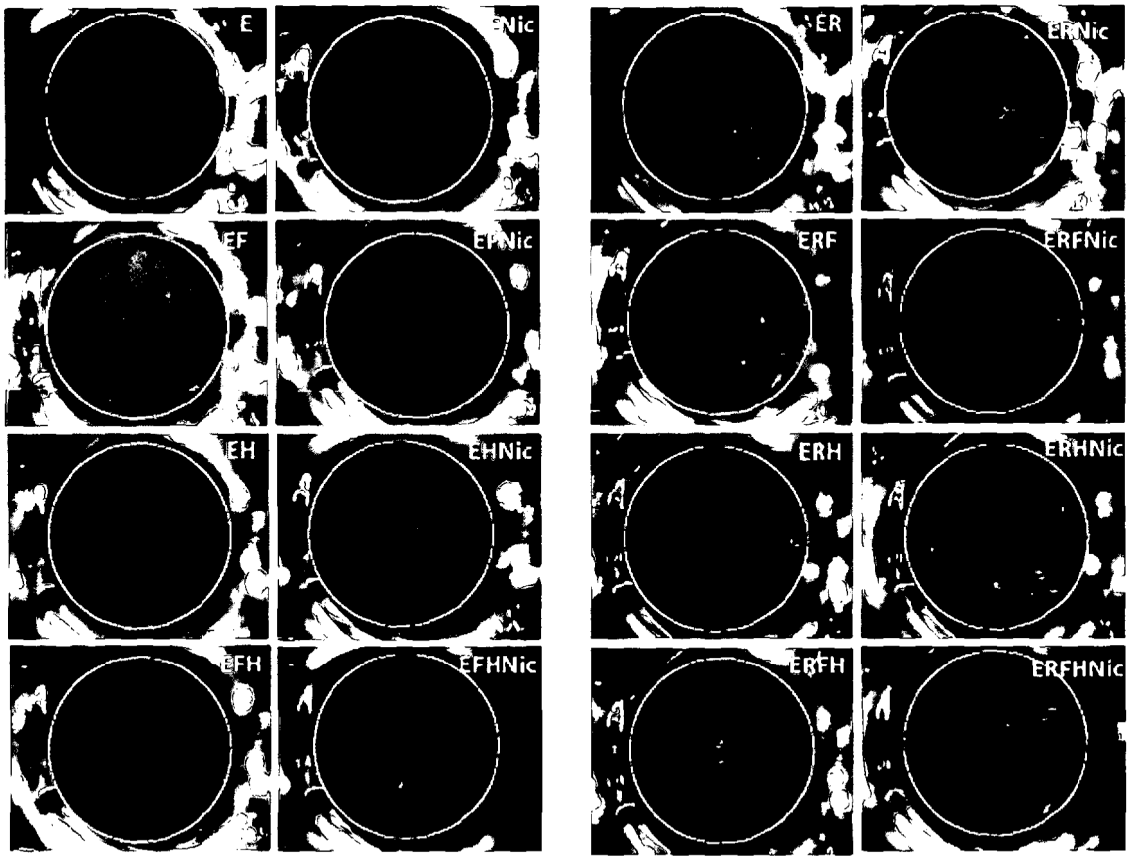


Figure 8

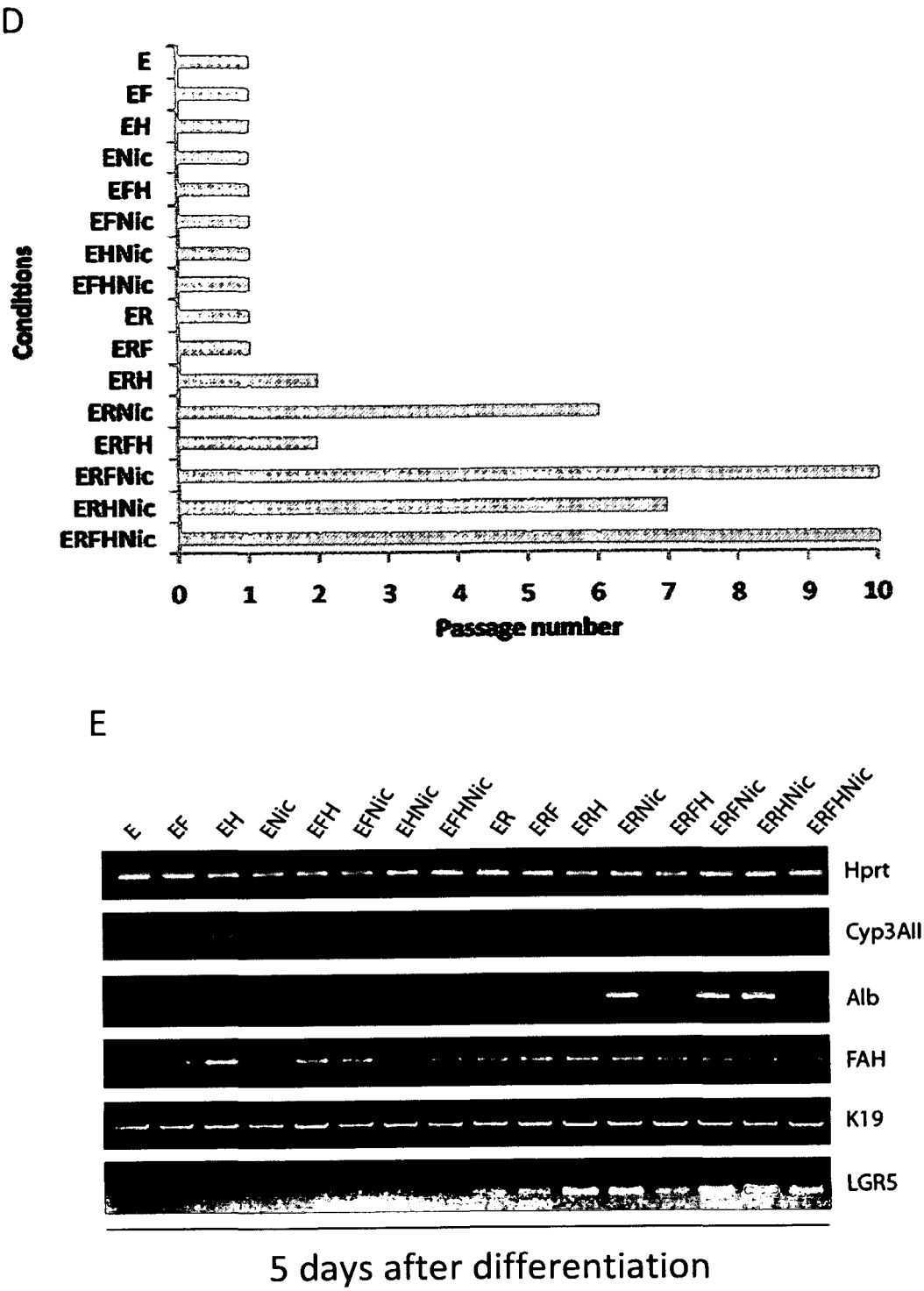
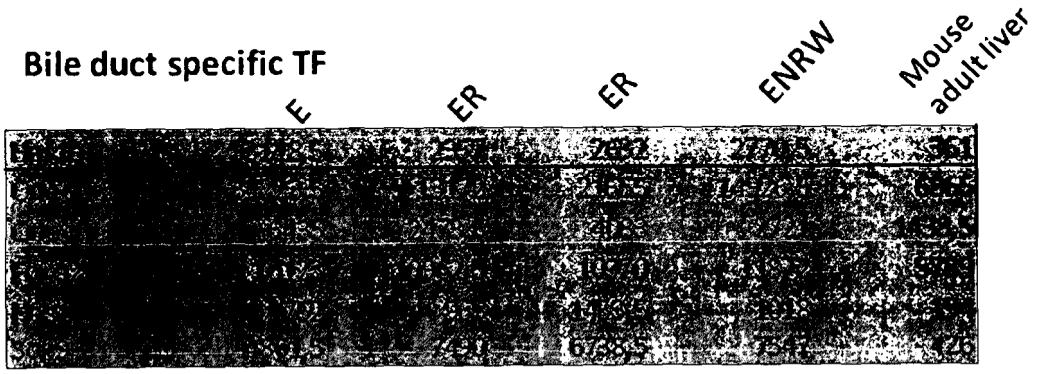

D
E
EF
EH
ENic
EFH
EFNic
EHNic
EFHNic
ER
ERF
ERH
ERNic
ERFH
ERFNic
ERHNic
ERFHNic
Conditions
0 1 2 3 4 5 6 7 8 9 10
Passage number
E
E EF EH ENic EFH EFNic EHNic EFHNic ER ERF ERH ERNic ERFH ERFNic ERHNic ERFHNic
Hprt
Cyp3All
Alb
FAH
K19
LGR5
5 days after differentiation

Figure 9



HC specific TF

Gata6	4981,5	5381	5124	5184	740
Cebpa	1431	1188	856	946	10640
Hnf1a	11640	10980	9865	6176	8334
Hnf4a	2573	1336	1283	1086	4033

Prox1	495	219,5	379,5	319	2139
Tbx3	196,5	214	208	180	1840,5
Nr5a2	132	139	131,5	141	1234

Notch signaling

Jag1	**6832,5**	**3638,5**	**4111**	**3394**	**343**
Dll1	4035	3758	2791,5	2714,5	415,5
Notch3	557	718	476	788	234

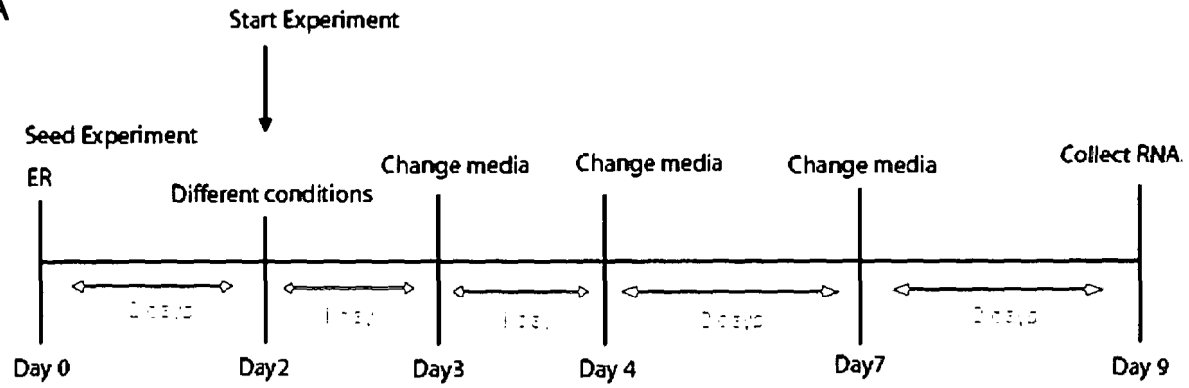
TGFb signaling

Tgfbr1	3439	2971	4281	3664	733
Tgfbr1	245	234	243	210	116

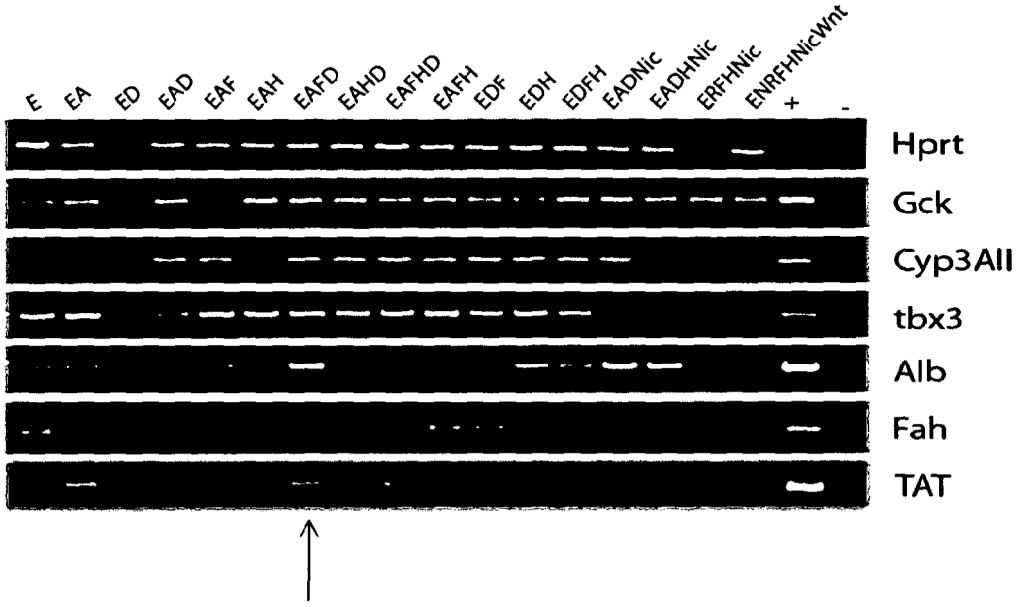
Tgfbr2	8442	9942	13874	11392	1364

Figure 10

A



B



E=EGF 50ng/ml

A=A8301 50nM

D=DAPT 10nM

F=FGF10 100ng/ml

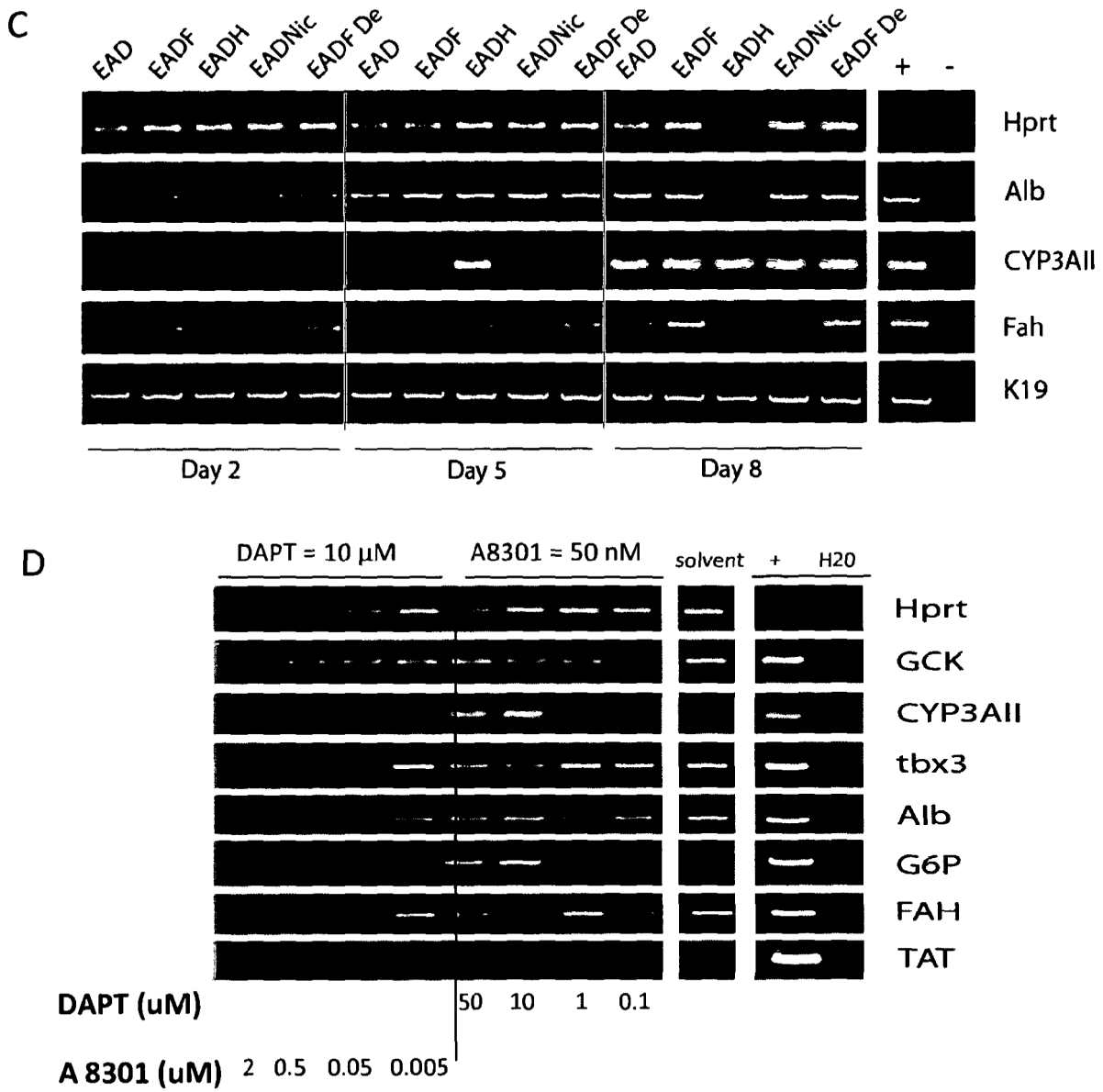
H=HGF 50ng/ml

Nic=Nicotinamide 10nM

R=Rspondin1 500ng/ml

Wnt= Wnt conditioned media 50%

Figure 10



E=EGF 50ng/ml

A=A8301 50nM

D=DAPT 10nM

F=FGF10 100ng/ml

H=HGF 50ng/ml

Nic=Nicotinamide 10nM

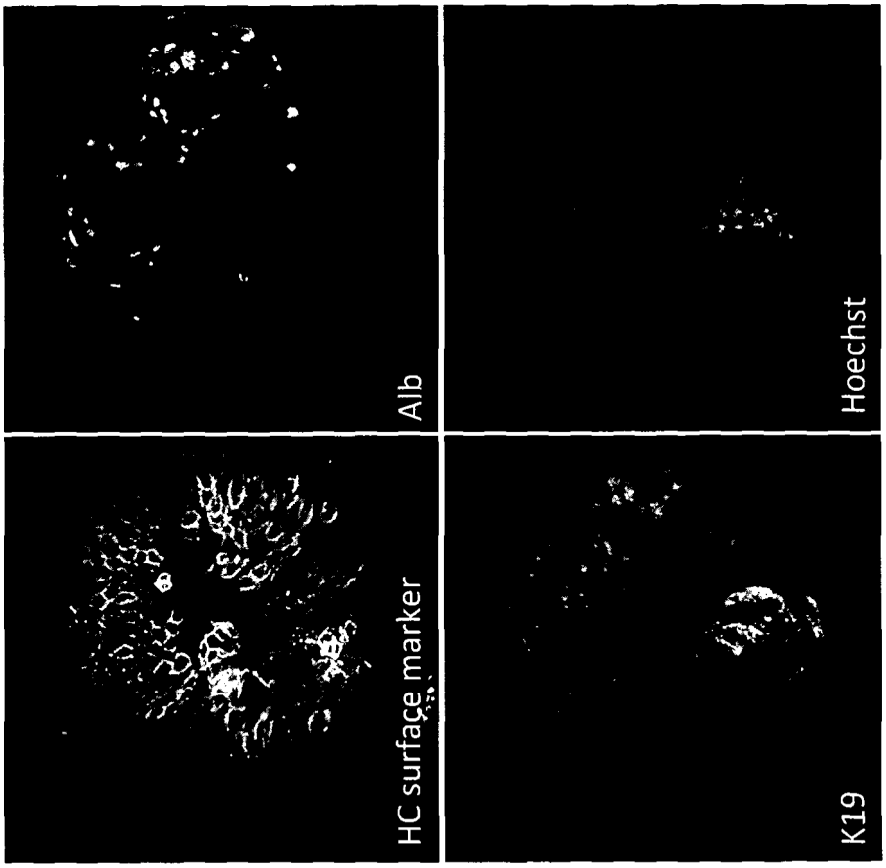
R=Rspondin1 500ng/ml

Wnt= Wnt conditioned media 50%

De= dexamethasone 10mM

Figure 10E

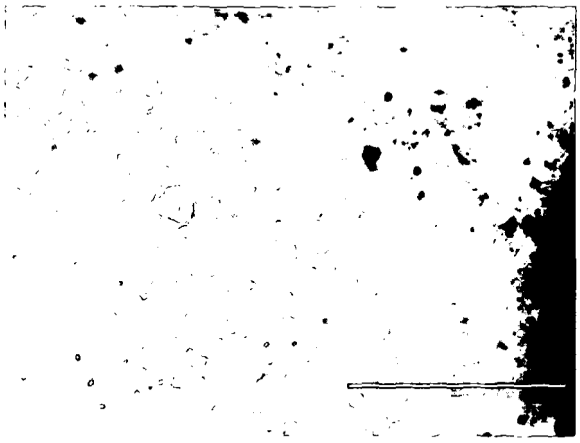
Staining for liver markers after 8 days of differentiation condition EADF



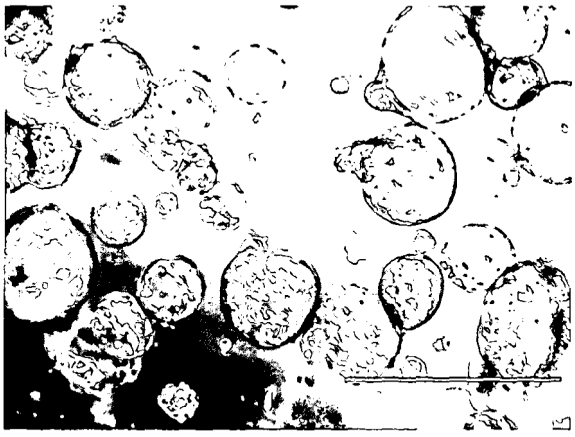

F Albcreert2LacZ derived organoids, (tamoxifen inducible system)
Control not induced with tamoxifen
Tamoxifen induced culture

Figure 10F

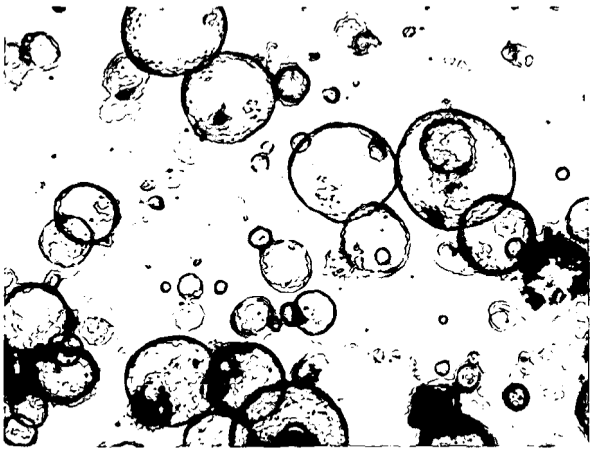
Figure 11 - Human-derived liver cultures ERFHNic culture conditions



5 days after seeding 4x



P1 (day 10) 4x



P2 (day 20) 4x

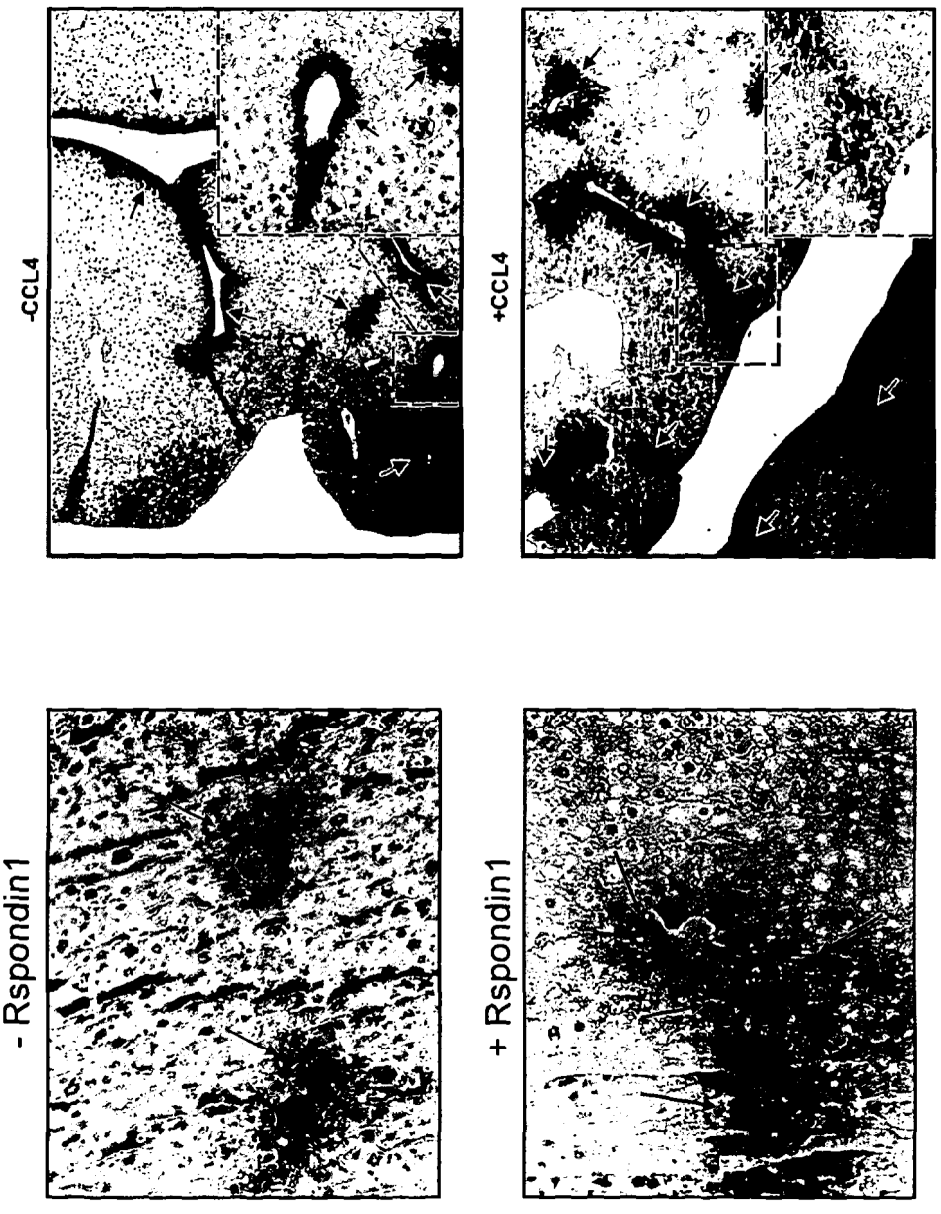


Figure 12

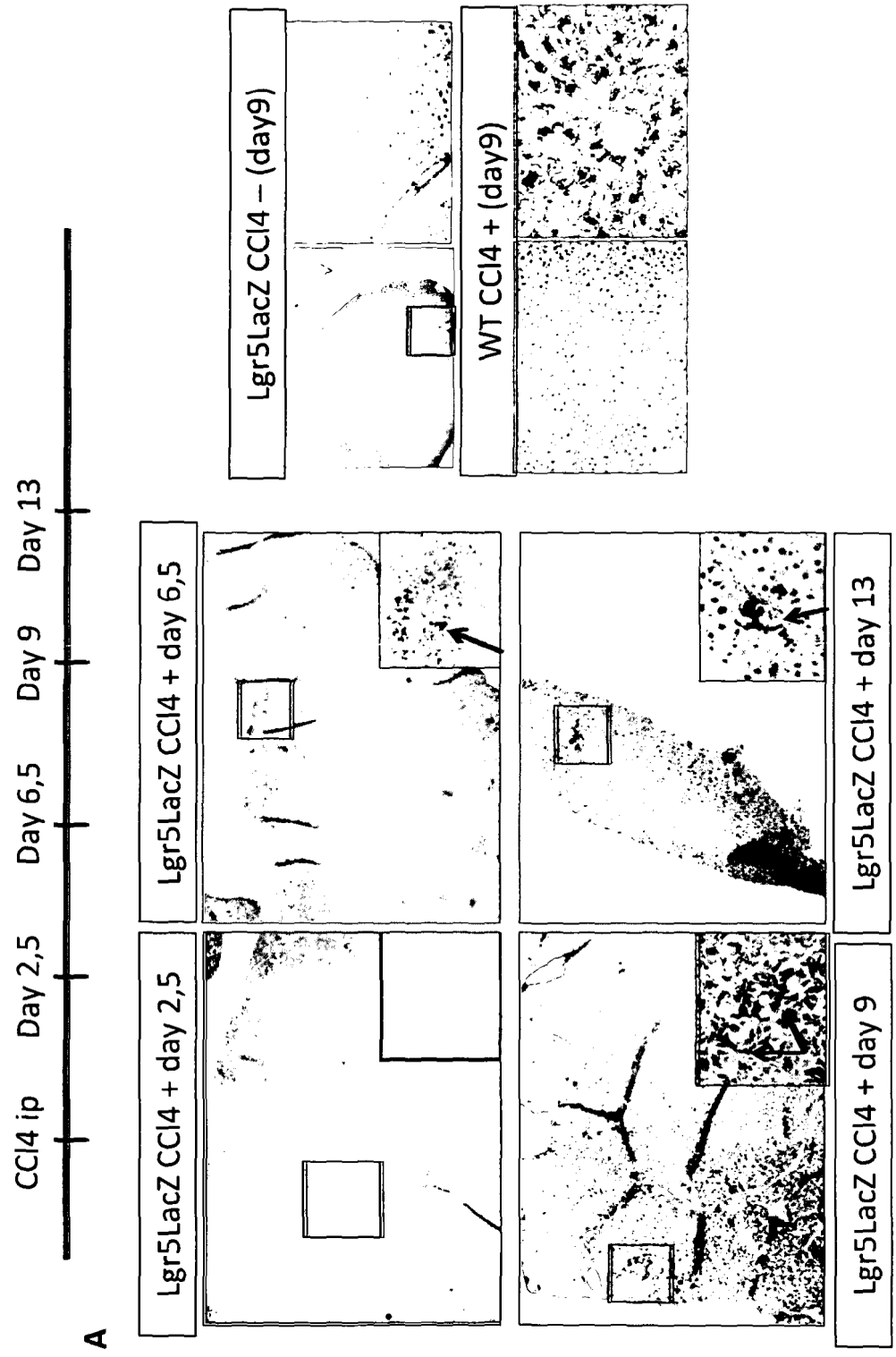

A
CCl4 ip
Day 2,5
Day 6,5
Day 9
Day 13
Lgr5LacZ CCl4 + day 2,5
Lgr5LacZ CCl4 + day 6,5
Lgr5LacZ CCl4 + day 9
Lgr5LacZ CCl4 + day 13
Lgr5LacZ CCl4 – (day9)
WT CCl4 + (day9)

Figure 13A

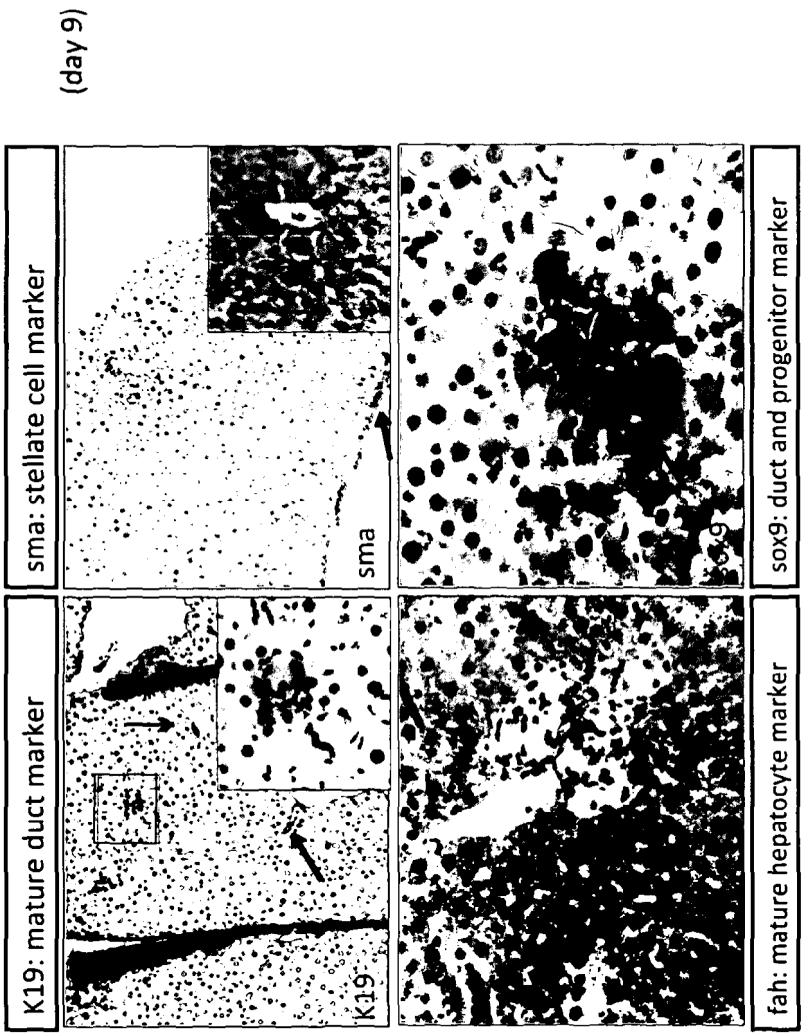

(day 9)
K19: mature duct marker
sma: stellate cell marker
K19
sma
fah: mature hepatocyte marker
sox9: duct and progenitor marker
sox9

Figure 13B



Figure 14

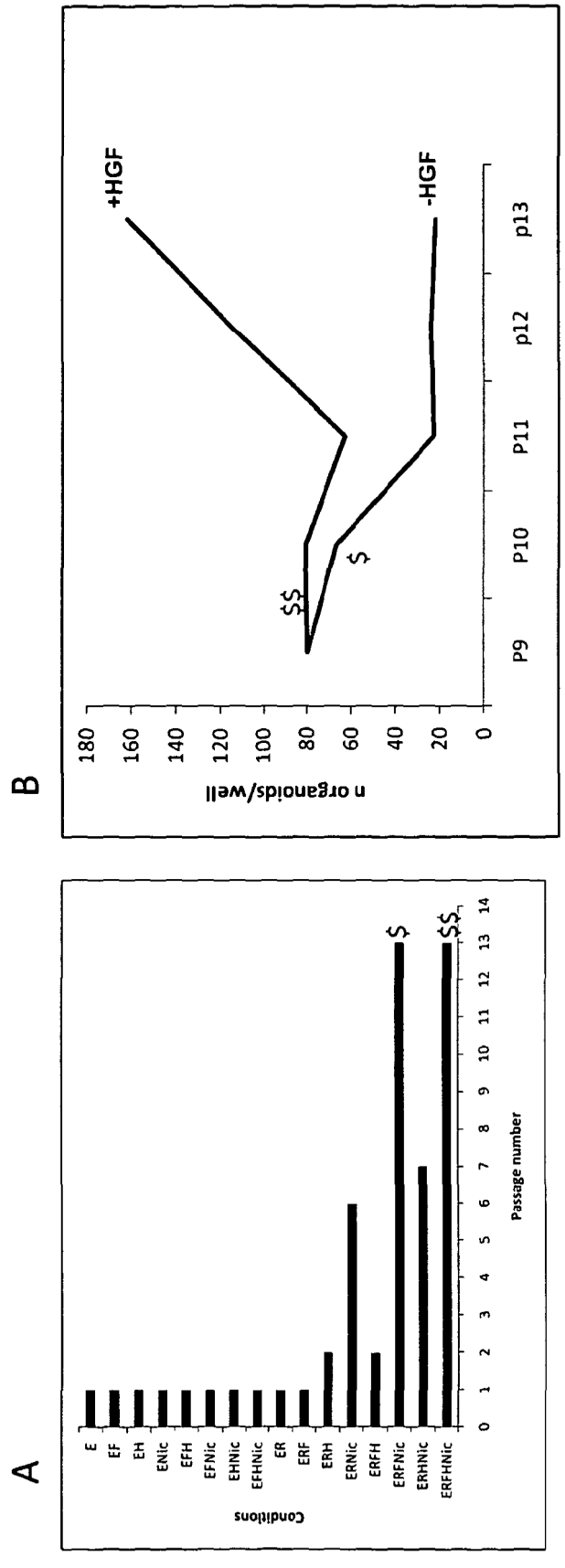

A
Conditions
E
EF
EH
ENic
EFH
EFNic
EHNic
EFHNic
ER
ERF
ERH
ERNic
ERFH
ERFNic
ERHNic
ERFHNic
$
$$
0 1 2 3 4 5 6 7 8 9 10 11 12 13 14
Passage number
B
n organoids/well
180 160 140 120 100 80 60 40 20 0
+HGF
-HGF
$$
$
P9 P10 P11 p12 p13

Figure 15

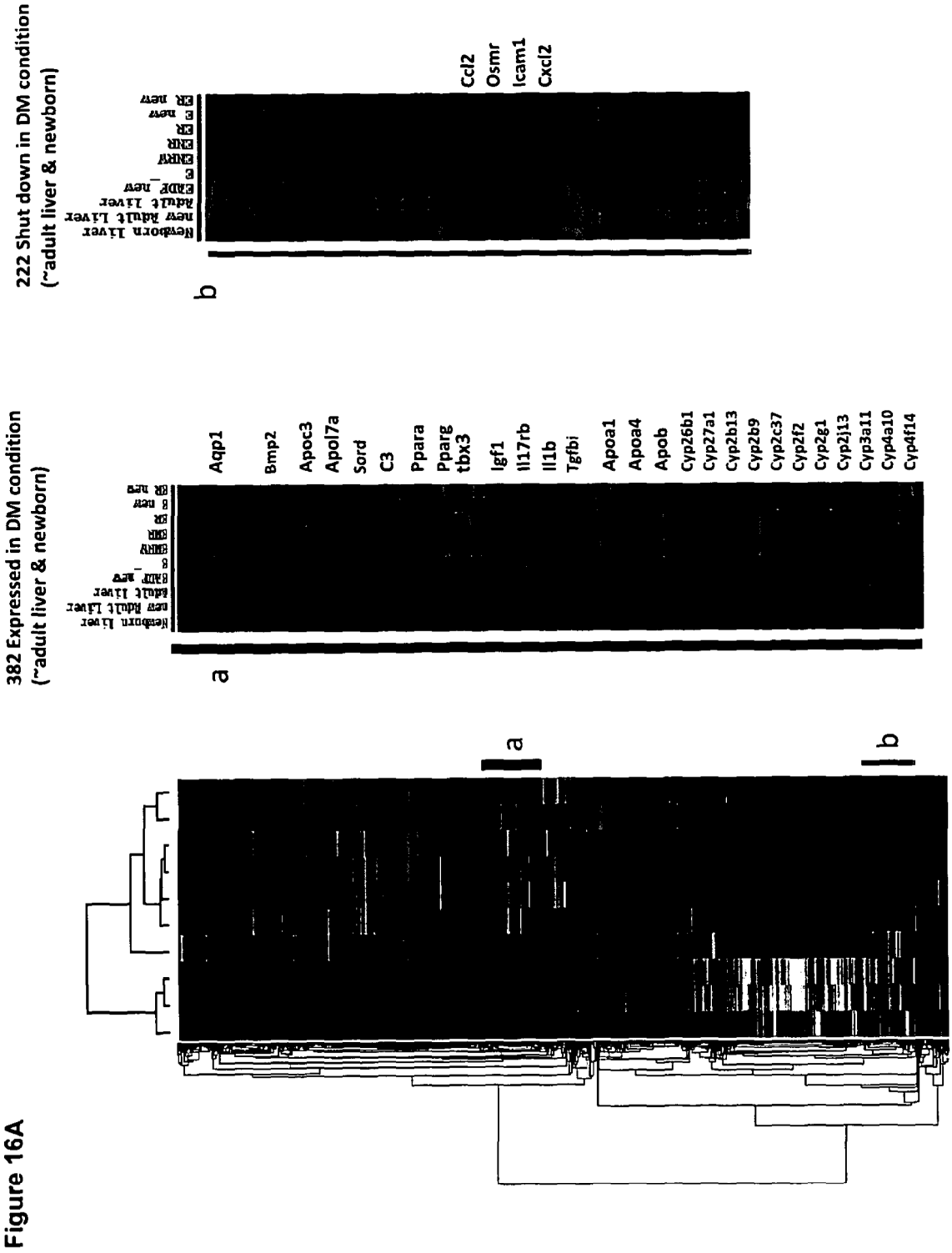

382 Expressed in DM condition
("adult liver & newborn)
Aqp1
Bmp2
Apoc3
Apol7a
Sord
C3
Ppara
Pparg
tbx3
Igf1
Il17rb
Il1b
Tgfbi
Apoa1
Apoa4
Apob
Cyp26b1
Cyp27a1
Cyp2b13
Cyp2b9
Cyp2c37
Cyp2f2
Cyp2g1
Cyp2j13
Cyp3a11
Cyp4a10
Cyp4f14
a
b
222 Shut down in DM condition
("adult liver & newborn)
Ccl2
Osmr
Icam1
Cxcl2
a
b

Figure 16A

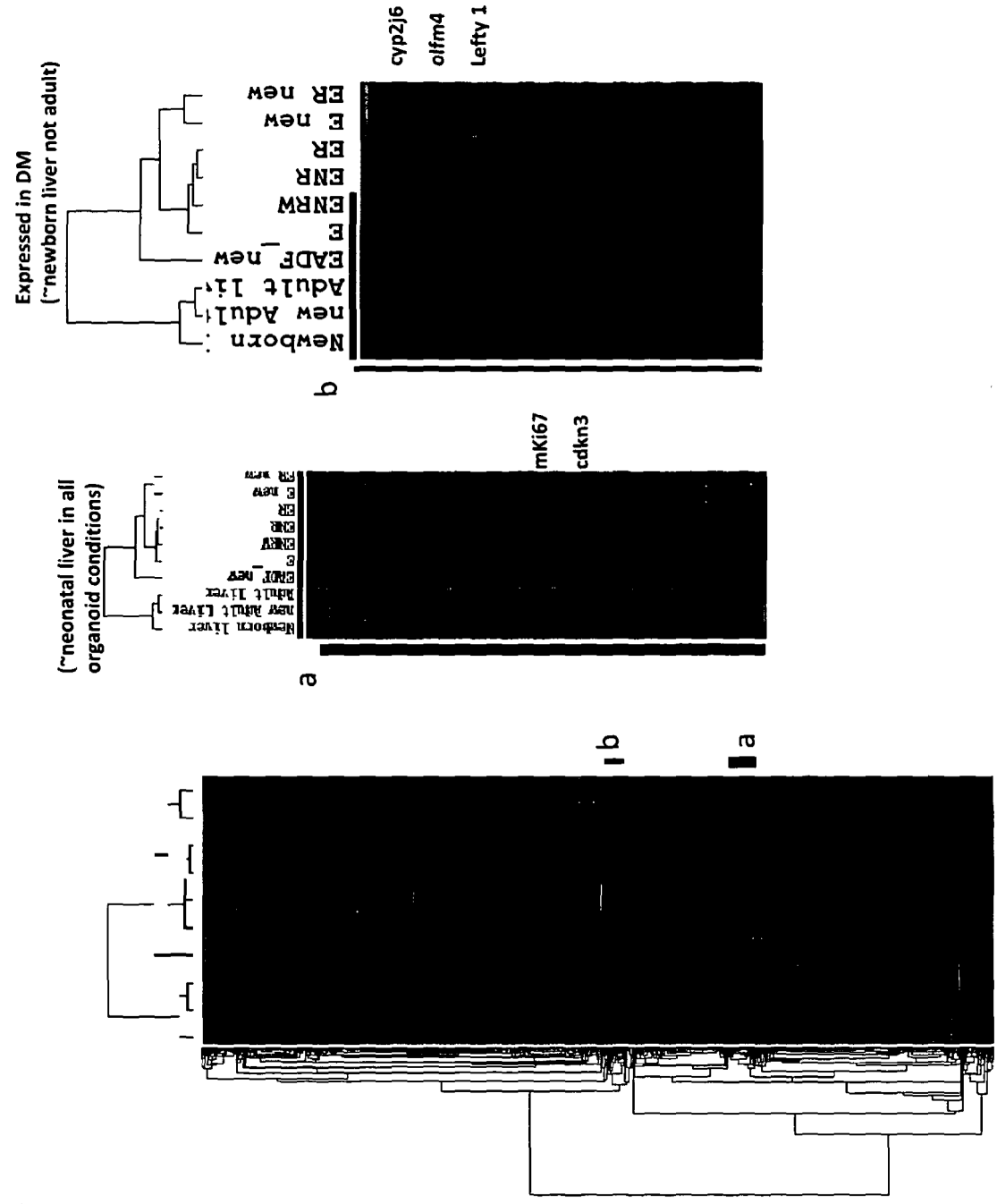

Expressed in DM
(~newborn liver not adult)
cyp2j6
olfm4
Lefty 1
Newborn
new Adult
Adult li
EADF_new
E
ENRW
ENR
ER
E new
ER new
b
(~neonatal liver in all
organoid conditions)
mKi67
cdkn3
a
b
a

Figure 16B

Figure 16C

		Adult liver	Adult pancreas	Pancreas organoid	Liver organoid
Ductal markers					
ref|Mus musculus leucine aminopeptidase 3 (Lap3), mRNA [NM_024434]	Lap3	11826	922	3286	2655
ref|Mus musculus keratin 19 (Krt19), mRNA [NM_008471]	Krt19	302	566	76191	29904
ref|Mus musculus keratin 7 (Krt7), mRNA [NM_033073]	Krt7	237	369	147227	108352
ref|Mus musculus SRY-box containing gene 9 (Sox9), mRNA [NM_011448]	Sox9	235	185	2365	2492
ref|Mus musculus HNF1 homeobox B (Hnf1b), mRNA [NM_009330]	Hnf1b	234	115	608	764
ref|Mus musculus one cut domain, family member 1 (Onecut1), mRNA [NM_008262]	Hnf6	1239	120	1297	1454
Transcription Factors necessary for Ngn3 expression					
ref|Mus musculus SRY-box containing gene 9 (Sox9), mRNA [NM_011448]	Sox9	235	185	2365	2492
ref|Mus musculus forkhead box A2 (Foxa2), mRNA [NM_010446]	Foxa2	8695	1415	12948	9579
ref|Mus musculus HNF1 homeobox B (Hnf1b), mRNA [NM_009330]	Hnf1b	234	115	608	764
ref|Mus musculus one cut domain, family member 1 (Onecut1), mRNA [NM_008262]	Hnf6	1239	120	1297	1454
Endocrine markers					
ref|Mus musculus neurogenin 3 (Neurog3), mRNA [NM_009719]	Neurog3	226.5	108	110	118
gb|Mouse hepatocyte nuclear factor 1 (HNF-1) mRNA, complete cds. [M57966]	Hnf1a	5709.5	693	4929	6185
ref|Mus musculus hepatic nuclear factor 4, alpha (Hnf4a), mRNA [NM_008261]	Hnf4a	2947	90.5	385	404
ref|Mus musculus pancreatic and duodenal homeobox 1 (Pdx1), mRNA [NM_008814]	Pdx1	137	102	201.5	198.5
ref|Mus musculus neurogenic differentiation 1 (Neurod1), mRNA [NM_010894]	Neurod1	87	76	88	78.5
ref|Mus musculus ISL1 transcription factor, LIM/homeodomain (Isl1), mRNA [NM_021459]	Isl1	82	88.5	93	239
ref|Mus musculus NK2 transcription factor related, locus 2 (Drosophila) (Nkx2-2), mRNA [NM_010919]	Nkx2-2	100	105	158	76
ref|Mus musculus NK2 transcription factor related, locus 6 (Drosophila) (Nkx2-6), mRNA [NM_010920]	Nkx2-6	159	93	94	99
ref|Mus musculus paired box gene 6 (Pax6), mRNA [NM_013627]	Pax6	157	88.5	100.5	114
ref|Mus musculus insulin II (Ins2), mRNA [NM_008387]	Ins2	195.5	113183	107.5	85.5
ref|Mus musculus solute carrier family 2 (facilitated glucose transporter), member 2 (Slc2a2), mRNA [NM_031197]	Slc2a2	1212.5	100	188	143
ref|Mus musculus pyruvate kinase liver and red blood cell (Pklr), transcript variant 1, mRNA [NM_013631]	Pklr	237	124.5	288	186
ref|Mus musculus glucokinase (Gck), mRNA [NM_010292]	Gck	1771	184	261	162

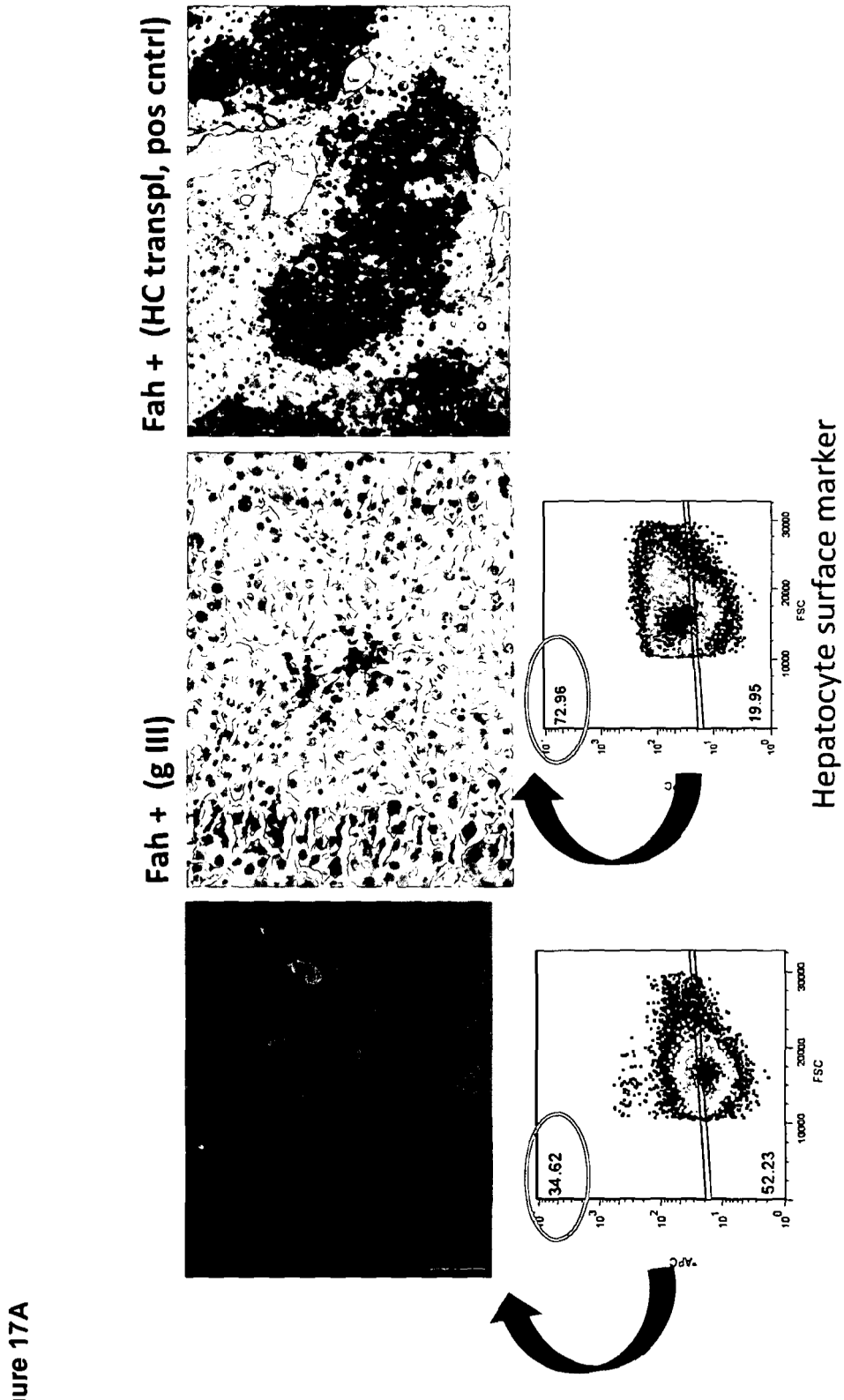
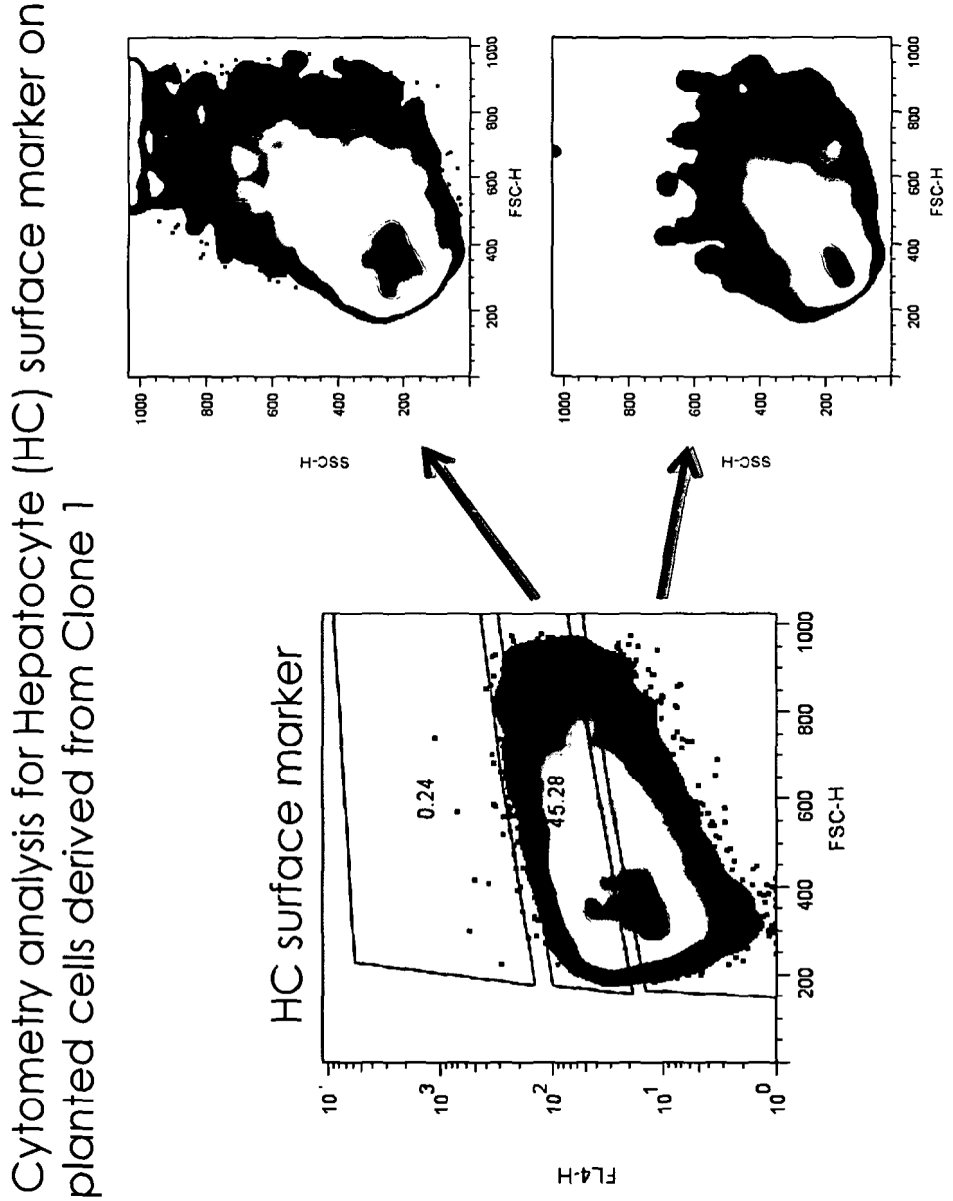

Fah + (HC transpl, pos cntrl)
Fah + (g III)
72.96
19.95
34.62
52.23
FSC
FSC
Hepatocyte surface marker

Figure 17A

Figure 17B


Flow Cytometry analysis for Hepatocyte (HC) surface marker on transplanted cells derived from Clone 1
HC surface marker
0.24
45.28
FL4-H
FSC-H
SSC-H

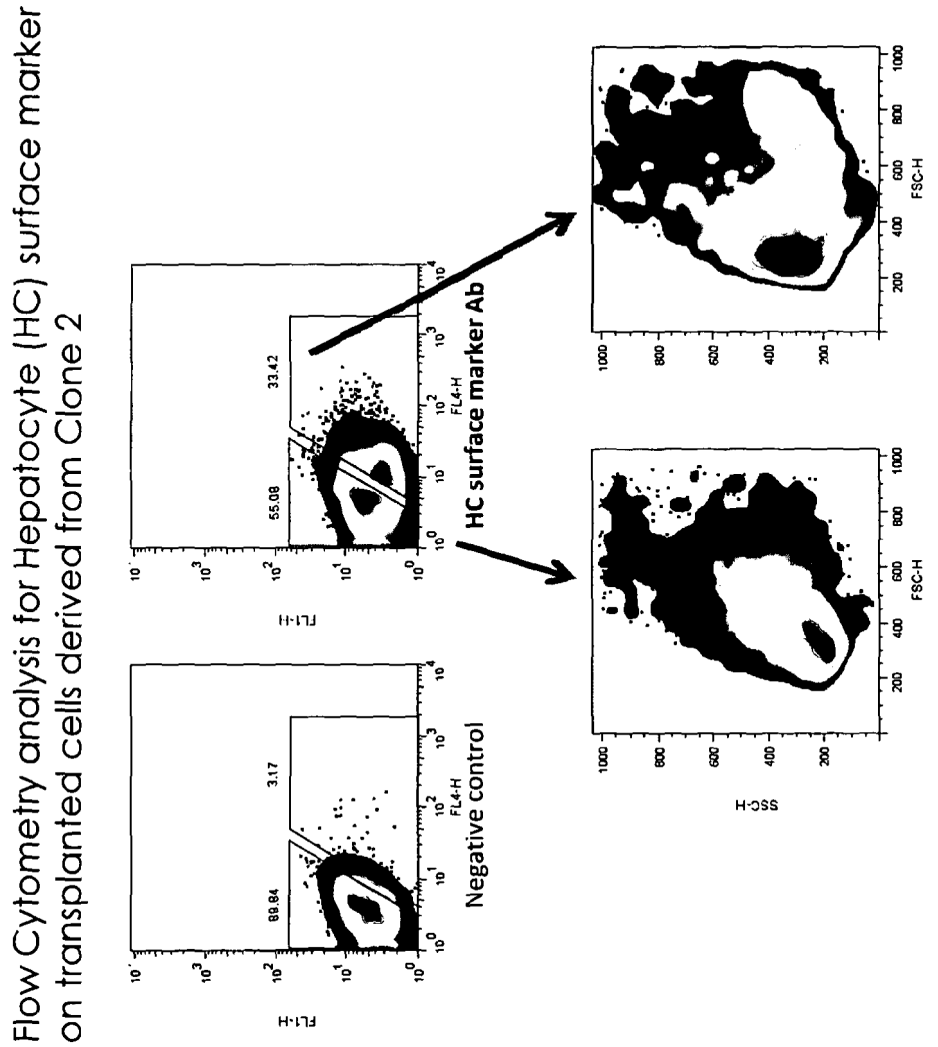
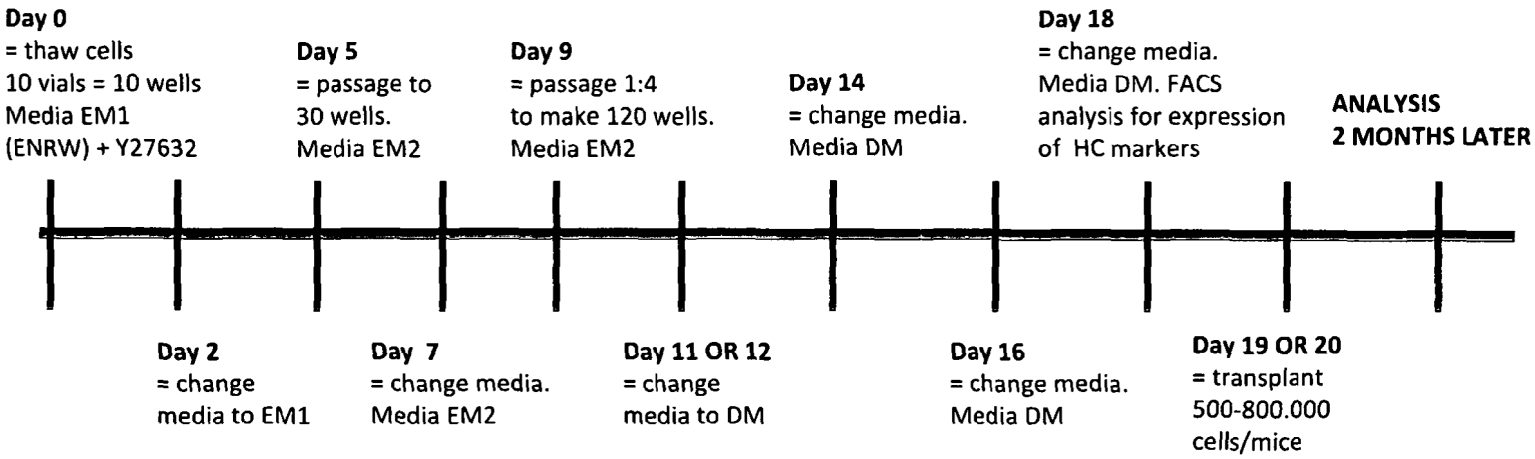

Flow Cytometry analysis for Hepatocyte (HC) surface marker on transplanted cells derived from Clone 2
FL1-H
FL4-H
89.84
3.17
Negative control
55.08
33.42
HC surface marker Ab
SSC-H
FSC-H

Figure 17C

Figure 17D

Mouse model: adult FGR MICE (FAH-/-RAG-/-IL2R-/-). Transplant of organoids or hepatocytes as Control

Transplantation schedule---



EM1= expansion media 1=ENRWFHNic

EM2= expansion media 2= ERFHNic

DM= differentiation media= EADF

Figure 18

stem cell signature mouse liver		liver/HC CG specific signature		reprograming genes	
positive for	negative for	positive for in expansion	negative for	positive	negative
lgr5	lgr6	Hnf1a	afp	Klf4	Pou5f1
lgr4		Hnf1b	Ins1	Myc	Sox2
epcam		Hnf4a	Ins2		
Cd44		Hhex	Gcg		
Tnfrsf19		Onecut1	Ptf1a		
Sox9		Onecut2	Cela1		
Sp5		Prox1	Cela2a		
Cd24a		Cdh1	Cela3b		
Prom1		Foxa2	Neurod1		
Cdca7		Gata6	Neurod2		
Elf3		Foxm1	Neurog1		
		Cebpa	Neurog2		
		Cebpb	Neurog3		
		Cebpd	Amy2a4		
		Cebpg	Igf1r		
		Glul	Igf2		
		Krt7	Cd34		
		Krt19			
		Met			

Figure 19

*background cutoff >3.5fold (gMedian); dyeswap to Cy3/Cy5 (Cy3-samples; Cy5-reference RNA)				25148506_7708_1	25148506_7708_2	25148506_7708_3	25148506_7708_4		ENRW_pat10511	ER_pat10511	EADF_pat10511	liver tissue_pat10511
Feature Number	**Systematic Name**	**Description**	**Gene Name**	**ENRW_pat10511**	**ER_pat10511**	**EADF_pat10511**	**liver tissue_pat10511**		**gMedian Signal**	**gMedianSignal**	**gMedianSignal**	**gMedianSignal**
Stem cell signature human liver												
40197	NM_003667	ref|Homo sapiens leucine-rich repeat-containing G protein-coupled receptor 5 (LGR5), mRNA [NM_003667]	**LGR5**						85	82.5	83	80
40602	NM_018490	ref|Homo sapiens leucine-rich repeat-containing G protein-coupled receptor 4 (LGR4), mRNA [NM_018490]	**LGR4**	1.3710	1.5826	1.8852	1.1145		1602	1684	2689	190.5
4087	NM_002354	ref|Homo sapiens tumor-associated calcium signal transducer 1 (TACSTD1), mRNA [NM_002354]	**TACSTD1/Epcam**	3.0978	3.5264	4.2412	-3.2251		16341	23939	42144	118
18697	NM_000610	ref|Homo sapiens CD44 molecule (Indian blood group) (CD44), transcript variant 1, mRNA [NM_000610]	**CD44**	0.8742	0.8495	-1.5025	-3.8418		10117	11624.5	2586.5	148.5
31576	NM_018647	ref|Homo sapiens tumor necrosis factor receptor superfamily, member 19 (TNFRSF19), transcript variant 1, mRNA [NM_018647]	**TNFRSF19**						83	85.5	81	81
2504	NM_000346	ref|Homo sapiens SRY (sex determining region Y)-box 9 (campomelic dysplasia, autosomal sex-reversal) (SOX9), mRNA [NM_000346]	**SOX9**	2.2553	2.3538	1.5394	-2.0445		484	448.5	355	88
6370	NM_001003845	ref|Homo sapiens Sp5 transcription factor (SP5), mRNA [NM_001003845]	**SP5**	-0.0509	0.4409	0.0402	3.3653		162	217.5	199	239.5
40879	A_23_P85250	gb|Homo sapiens CD24 signal transducer mRNA, complete cds and 3' region. [L33930]	**CD24**	3.2316	3.5288	1.9579	-2.4236		15141.5	17882	7049	125
1705	NM_006017	ref|Homo sapiens prominin 1 (PROM1), mRNA [NM_006017]	**PROM1**	3.2512	2.6437	2.4209	-1.5556		445	340	346	84

43572	NM_031942	ref|Homo sapiens cell division cycle associated 7 (CDCA7), transcript variant 1, mRNA [NM_031942]	**CDCA7**	-2.4618	-3.6148	-7.7368	-5.0979		476	218	87	83
1226	NM_004433	ref|Homo sapiens E74-like factor 3 (ets domain transcription factor, epithelial-specific) (ELF3), transcript variant 1, mRNA [NM_004433]	**ELF3**	3.3588	3.9163	4.2213	0.4499		6378.5	8700.5	14527	161
Reprogramming genes												
19017	NM_004235	ref|Homo sapiens Kruppel-like factor 4 (gut) (KLF4), mRNA [NM_004235]	**KLF4**	0.3754	2.3397	1.9646	-0.9306		291	1176.5	919	105
6084	NM_002467	ref|Homo sapiens v-myc myelocytomatosis viral oncogene homolog (avian) (MYC), mRNA [NM_002467]	**MYC**	-1.1416	-0.8254	-3.3457	-2.1032		3006	3896	871	323
11740	NM_002701	ref|Homo sapiens POU class 5 homeobox 1 (POU5F1), transcript variant 1, mRNA [NM_002701]	**POU5F1**	-3.9024	-3.5281	-3.8577	-1.8681		1643	2251.5	2261	1173
34630	NM_003106	ref|Homo sapiens SRY (sex determining region Y)-box 2 (SOX2), mRNA [NM_003106]	**SOX2**	-4.0411	-4.0509	-4.3534	-2.6317		131	131.5	129	98
Liver/HC CG specific signature: positive for expansion												
22258	NM_000545	ref|Homo sapiens HNF1 homeobox A (HNF1A), mRNA [NM_000545]	**HNF1A**	0.1593	0.4237	0.3115	2.1337		287.5	366.5	367.5	240
19971	NM_000458	ref|Homo sapiens HNF1 homeobox B (HNF1B), mRNA [NM_000458]	**HNF1B**	3.3524	3.3315	3.1792	0.0000		200.5	200	141	86
7418	NM_000457	ref|Homo sapiens hepatocyte nuclear factor 4, alpha (HNF4A), transcript variant 2, mRNA [NM_000457]	**HNF4A**	-0.9981	1.7168	1.0493	2.0374		84.5	119.5	108	103
25738	NM_002729	ref|Homo sapiens hematopoietically expressed homeobox (HHEX), mRNA [NM_002729]	**HHEX**	0.8347	0.9290	1.4544	0.2789		1025	1263	1931	178
28260	NM_004498	ref|Homo sapiens one cut homeobox 1 (ONECUT1), mRNA [NM_004498]	**ONECUT1**	0.5189	2.1647	2.9438	5.8053		120	211	327	387

30379	NM_004852	ref|Homo sapiens one cut homeobox 2 (ONECUT2), mRNA [NM_004852]	**ONECUT2**	3.4671	3.7373	3.5642	2.8300		4693	6965	6460	498
20882	NM_002763	ref|Homo sapiens prospero homeobox 1 (PROX1), mRNA [NM_002763]	**PROX1**	2.4930	1.0227	1.1415	2.4817		98	98	97.5	101
12860	NM_004360	ref|Homo sapiens cadherin 1, type 1, E-cadherin (epithelial) (CDH1), mRNA [NM_004360]	**CDH1**	3.3253	3.6614	4.1391	2.4935		10803	16648	25328	1076.5
33903	NM_021784	ref|Homo sapiens forkhead box A2 (FOXA2), transcript variant 1, mRNA [NM_021784]	**FOXA2**	2.8637	3.2434	3.0108	2.6774		289.5	306	398	129.5
39806	NM_005257	ref|Homo sapiens GATA binding protein 6 (GATA6), mRNA [NM_005257]	**GATA6**	3.0052	3.5536	3.8552	1.2789		1620	2038	3585	136
16668	NM_202002	ref|Homo sapiens forkhead box M1 (FOXM1), transcript variant 1, mRNA [NM_202002]	**FOXM1**	-1.9203	-3.6288	-5.0418	-4.5112		329	156.5	117.5	94
9214	NM_004364	ref|Homo sapiens CCAAT/enhancer binding protein (C/EBP), alpha (CEBPA), mRNA [NM_004364]	**CEBPA**	-0.9322	1.2903	-0.0086	4.2303		304	1257	647	1586.5
14125	NM_005194	ref|Homo sapiens CCAAT/enhancer binding protein (C/EBP), beta (CEBPB), mRNA [NM_005194]	**CEBPB**	-0.1111	-0.2252	0.4127	2.5221		5257	5653.5	10124	5163.5
37458	NM_005195	ref|Homo sapiens CCAAT/enhancer binding protein (C/EBP), delta (CEBPD), mRNA [NM_005195]	**CEBPD**	-0.1615	0.9115	0.4583	4.1610		1525	3232	2733	2661
145	NM_001806	ref|Homo sapiens CCAAT/enhancer binding protein (C/EBP), gamma (CEBPG), mRNA [NM_001806]	**CEBPG**	0.9187	2.0261	1.8780	0.7494		2185	4317.5	4980	364
41435	NM_002065	ref|Homo sapiens glutamate-ammonia ligase (glutamine synthetase) (GLUL), transcript variant 1, mRNA [NM_002065]	**GLUL**	-0.1834	0.0758	-0.8704	0.4736		1365.5	1338	876	311
30469	NM_005556	ref|Homo sapiens keratin 7 (KRT7), mRNA [NM_005556]	**KRT7**	5.1396	4.8373	4.3723	-0.0401		7538.5	4712	2627	96
13920	NM_002276	ref|Homo sapiens keratin 19 (KRT19), mRNA [NM_002276]	**KRT19**	4.1830	3.7196	3.6914	-2.4731		365708	424094	308350	1571
5427	NM_000245	ref|Homo sapiens met proto-oncogene (hepatocyte growth factor receptor) (MET), mRNA [NM_000245]	**MET**	1.3614	1.0945	1.2510	-0.3692		7623.5	6639	8627	406

Liver/HC CG specific signature: negative												
16839	NM_001134	ref|Homo sapiens alpha-fetoprotein (AFP), mRNA [NM_001134]	**AFP**	-8.2963	-6.4426	-8.2926	-5.5894		95	141	107	103
33640	NM_002054	ref|Homo sapiens glucagon (GCG), mRNA [NM_002054]	**GCG**	0.0000	0.0000	0.6162	0.0000		85	90	88	78
34885	NP233946	gb|Homo sapiens bHLH transcription factor p48 mRNA, partial cds. [AF181999]	**PTF1A**	0.1838	0.4898	0.4317	0.7839		105	111	112	93
40134	NM_024019	*ref|Homo sapiens neurogenin* 2 (NEUROG2), mRNA [NM_024019]	**NEUROG2**						73	79.5	81.5	75
5505	NM_000875	ref|Homo sapiens insulin-like growth factor 1 receptor (IGF1R), mRNA [NM_000875]	**IGF1R**						78.5	81	82.5	78
5632	NM_001773	ref|Homo sapiens CD34 molecule (CD34), transcript variant 2, mRNA [NM_001773]	**CD34**						74	70	75	79
Hepatocyte specific gene signature												
991	NM_000371	ref|Homo sapiens transthyretin (prealbumin, amyloidosis type I) (TTR), mRNA [NM_000371]	**TTR**	-0.5692	0.0924	0.1884	9.0077		1243.5	1660	2331	107880
23323	NM_000477	ref|Homo sapiens albumin (ALB), mRNA [NM_000477]	**ALB**	-3.0821	-2.9215	-3.2544	6.3642		5970	10841	7266	306897
10807	NM_000137	ref|Homo sapiens fumarylacetoacetate hydrolase (fumarylacetoacetase) (FAH), mRNA [NM_000137]	**FAH**	-0.1297	-0.5453	-0.2095	2.2811		716	520	783	618
29558	NM_000353	ref|Homo sapiens tyrosine aminotransferase (TAT), nuclear gene encoding mitochondrial protein, mRNA [NM_000353]	**TAT**	0.1829	0.3011	-0.8291	6.6911		97	101	95	381.5
2423	NM_000765	*ref|Homo sapiens cytochrome* P450, family 3, subfamily A, polypeptide 7 (CYP3A7), mRNA [NM_000765]	**CYP3A7**	5.5511	7.1260	6.6750	8.9567		3649	10927	9853	5989

1710	NM_000039	ref|Homo sapiens apolipoprotein A-I (APOA1), mRNA [NM_000039]	**APOA1**	-3.5478	-2.8913	-2.1400	5.2314		370	536	1014.5	24580
8511	NM_002130	ref|Homo sapiens 3-hydroxy-3-methylglutaryl-Coenzyme A synthase 1 (soluble) (HMGCS1), transcript variant 2, mRNA [NM_002130]	**HMGCS1**	1.9834	1.8579	-1.2536	1.9013		1518	1248	264	271
2331	NM_138711	ref|Homo sapiens peroxisome proliferator-activated receptor gamma (PPARG), transcript variant 3, mRNA [NM_138711]	**PPARG**	1.9376	3.5421	1.0259	-0.9723		794	2235	489	102
42261	NM_000767	ref|Homo sapiens cytochrome P450, family 2, subfamily B, polypeptide 6 (CYP2B6), mRNA [NM_000767]	**CYP2B6**	3.1696	3.8429	3.7438	7.0424		691	835	1376	23535
40086	NM_000772	ref|Homo sapiens cytochrome P450, family 2, subfamily C, polypeptide 18 (CYP2C18), mRNA [NM_000772]	**CYP2C18**	7.6099	8.9559	7.5195	8.1267		441	938	458.5	231
18649	NM_000771	ref|Homo sapiens cytochrome P450, family 2, subfamily C, polypeptide 9 (CYP2C9), mRNA [NM_000771]	**CYP2C9**	7.4072	9.3744	7.5571	10.9138		371.5	1144	765	3195
1249	NM_000775	ref|Homo sapiens cytochrome P450, family 2, subfamily J, polypeptide 2 (CYP2J2), mRNA [NM_000775]	**CYP2J2**	2.6839	2.5692	2.5672	5.4100		839	595.5	802	682.5
37457	NM_017460	ref|Homo sapiens cytochrome P450, family 3, subfamily A, polypeptide 4 (CYP3A4), mRNA [NM_017460]	**CYP3A4**	6.0960	6.9956	7.3093	9.3567		400.5	1260	1142	496.5
33810	ENST00000439761	gb|Homo sapiens CYP3A5 mRNA, allele CYP3A5*3, exon 4B and partial cds, alternatively spliced. [AF355801]	**CYP3A5**	-0.3739	0.1067	0.0937	1.4438		736	962.5	1172	403.5
2423	NM_000765	ref|Homo sapiens cytochrome P450, family 3, subfamily A, polypeptide 7 (CYP3A7), mRNA [NM_000765]	**CYP3A7**	5.5511	7.1260	6.6750	8.9567		3649	10927	9853	5989
14586	NM_007253	ref|Homo sapiens cytochrome P450, family 4, subfamily F, polypeptide 8 (CYP4F8), mRNA [NM_007253]	**CYP4F8**	2.7132	4.1535	2.5950	5.9628		686	2541.5	825.5	1176
14415	NM_207352	ref|Homo sapiens cytochrome P450, family 4, subfamily V, polypeptide 2 (CYP4V2), mRNA [NM_207352]	**CYP4V2**	2.9194	2.9333	2.7663	5.2822		853	995	923.5	822
29103	NM_005505	ref|Homo sapiens scavenger receptor class B, member 1 (SCARB1), transcript variant 1, mRNA [NM_005505]	**SCARB1**	-0.6468	-0.4215	-1.0325	2.0324		14042	23763	13137	22012