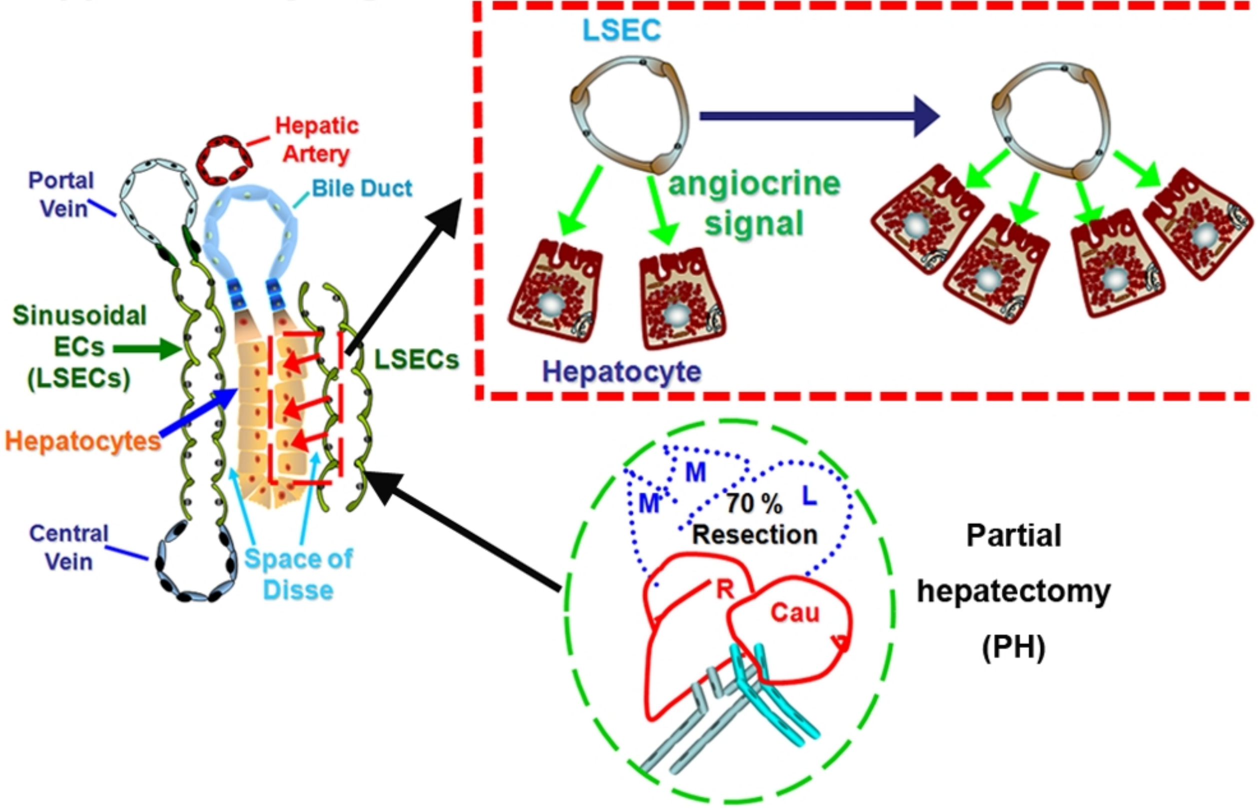
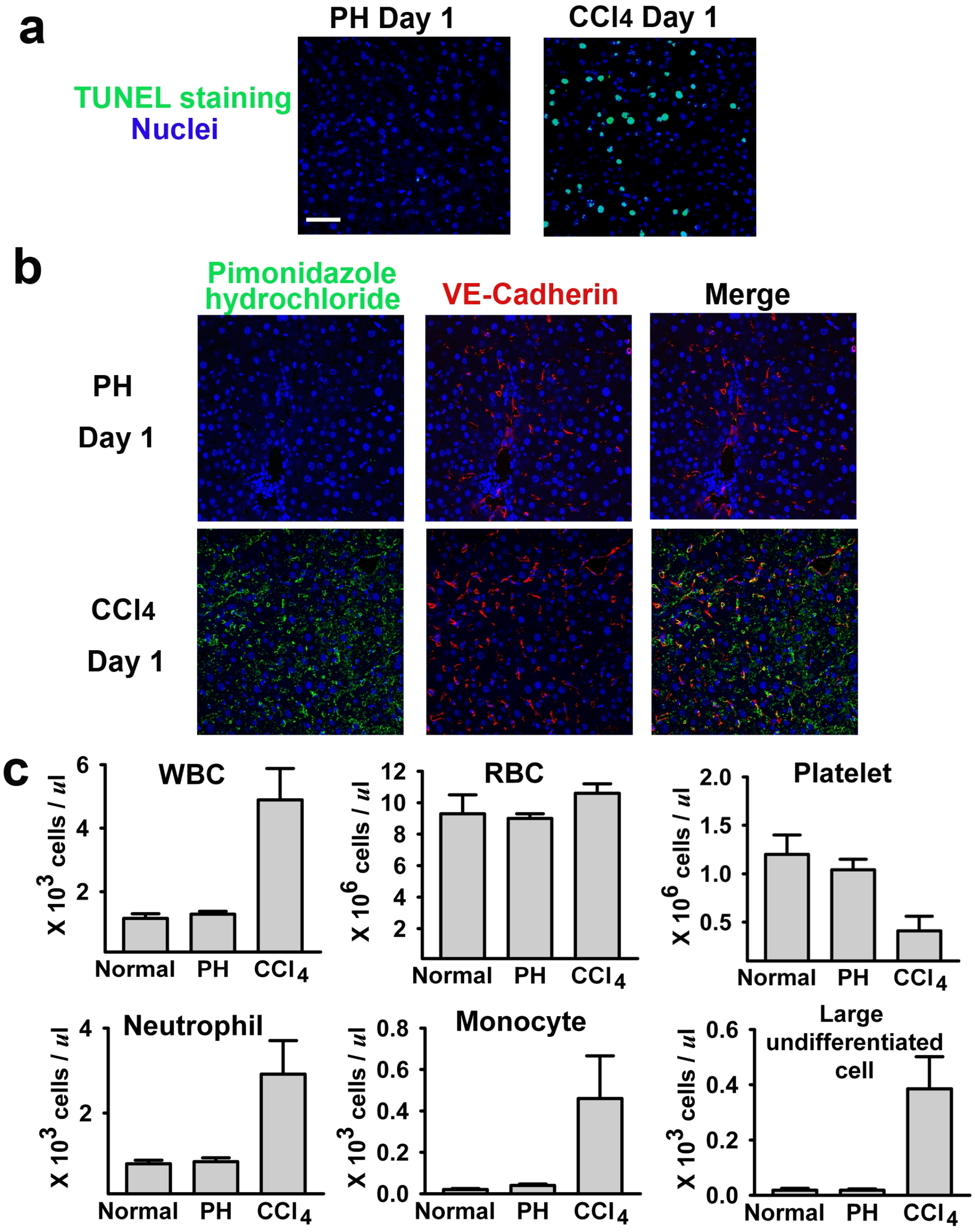
Ding *et al.* supplementary information

Supplementary Fig. 1



Supplementary Fig. 1 Inductive role of liver sinusoidal endothelial cell (LSEC)-derived angiocrine signal in liver regeneration. LSECs lining the liver sinusoid are positioned to the vicinity of hepatocytes. Upon resection of 70% of liver mass (partial hepatectomy, PH), inductive angiogenic but non-proliferative LSECs initiate and sustain the regeneration of proximal hepatocytes, through the elaboration of specific angiocrine signals. M, R, L, and Cau; median, right, left, and caudate lobes of the liver.

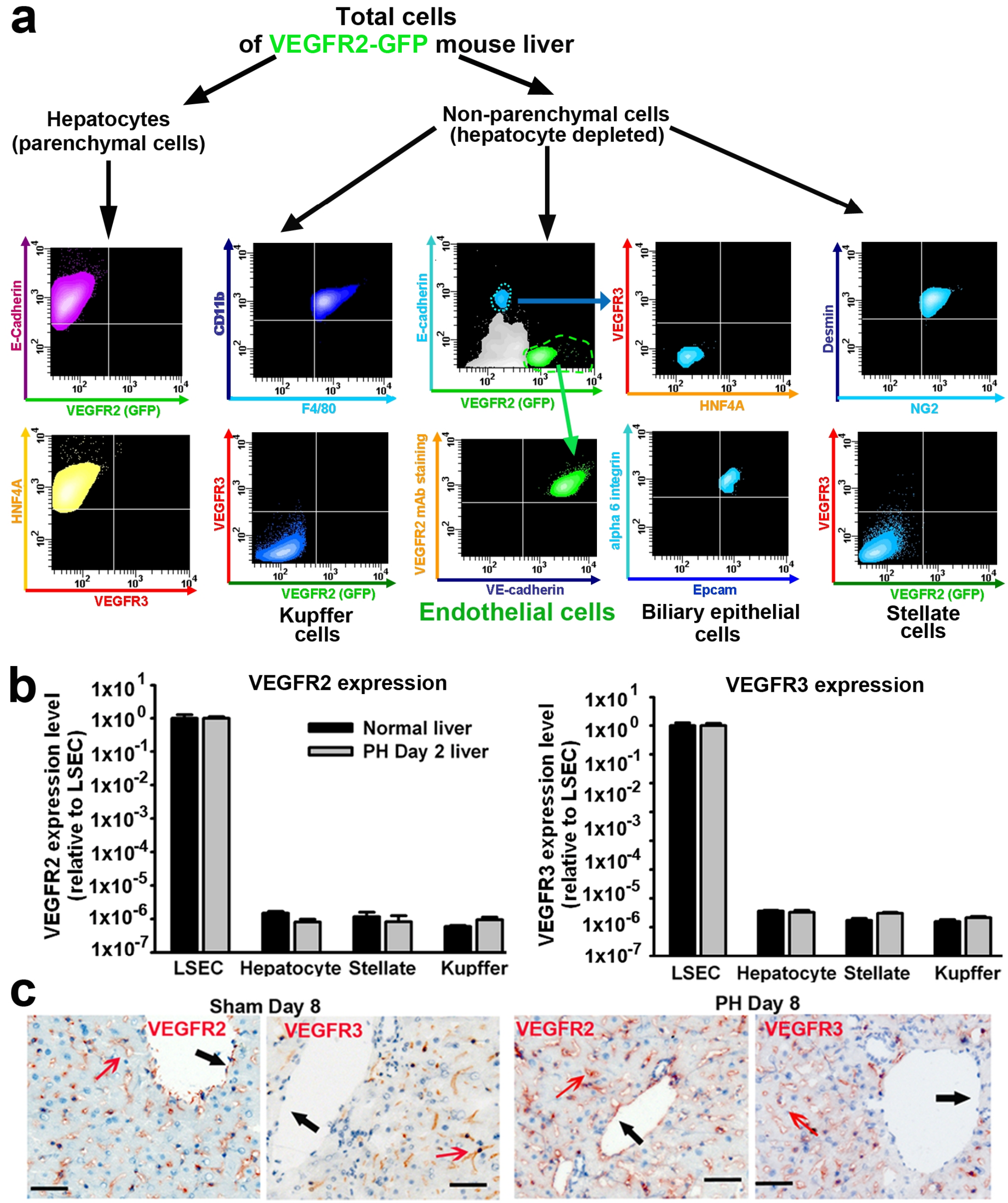
Supplementary Fig. 2



Supplementary Fig. 2. Carbon tetrachloride (CCl_4) injection, but not PH, induces cell apoptosis and hypoxia in the liver and promotes hematopoietic cell mobilization.

a) In contrast to CCl_4 injection that induces remarkable apoptosis in the liver, PH causes little apoptosis, as illustrated by TUNEL staining. TUNEL staining was performed using *In Situ* Cell Death Detection Kit (Roche Applied Science). Scale bar, 50µm**. b)** While significant hypoxia occurs in the liver 24 hours after CCl4 injection, the residual liver lobes remains non-hypoxic 24 hours after PH. Tissue hypoxia was determined by Hypoxyprobe™-1 Kit (Chemicon, Billerica, MA). **c**) CCl_4 injection but not PH induces mobilization of inflammatory cells 24 hours after injury. Blood cell counting was performed using Advia 120 analyzer (Bayer, Germany). WBC, white blood cells; RBC, red blood cells.

Supplementary Fig. 3



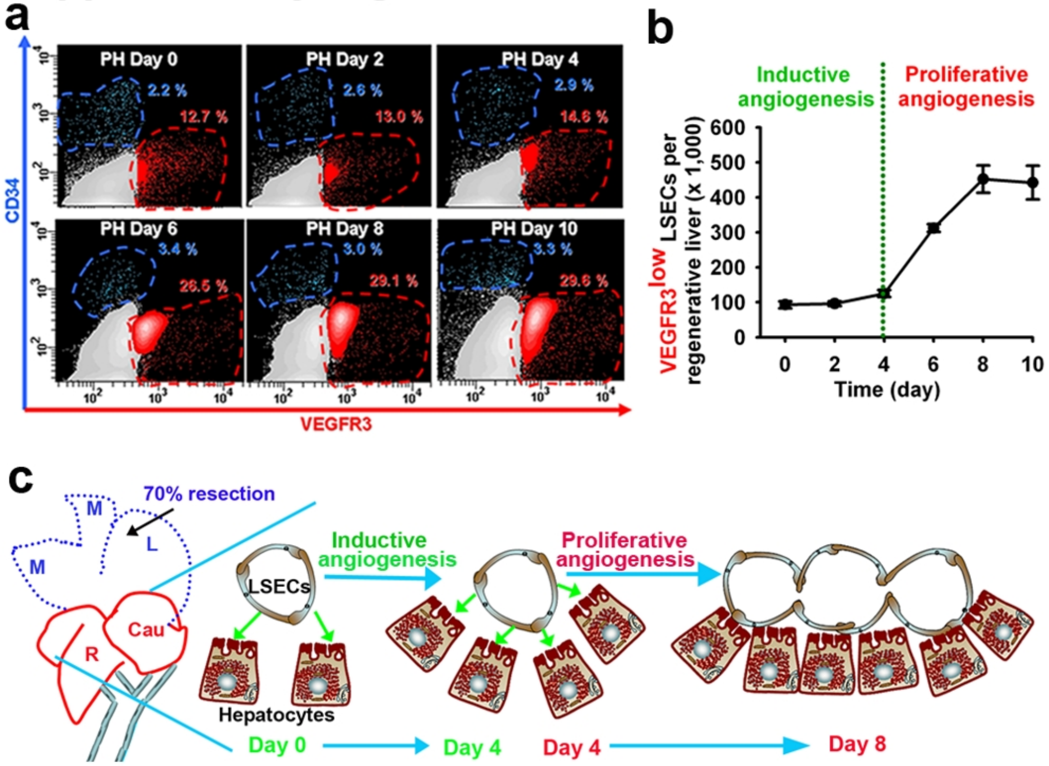
Supplementary Fig. 3 Restricted expression of VEGFR2 and VEGFR3 to the liver ECs.

a) In VEGFR2-GFP mouse whereby endogenous VEGFR2 promoter drives GFP expression, VEGFR2 (GFP) is only expressed by VE-cadherin^{+} ECs but not other cell types, including E-cadherin^{+}hepatocyte nuclear factor 4α (HNF4A)$^{+}$ hepatocytes, E-cadherin^{+}α6 integrin^{+}Epcam^{+} biliary epitheial cells, NG2^{+}desmin^{+} stellate cells, and F4/80^{+}CD11b^{+} Kupffer cells.

b) Expression profile of VEGFR2 and VEGFR3 in hepatocytes, LSECs, Stellate and Kupffer cells. Note the logarithmic axis of the expression level that clearly demonstrates the absence of VEGFR2 and VEGFR3 in other non-LSEC liver cell types.

c) Immunohistochemical staining on liver frozen sections reveals VEGFR2 expression by both sinusoids (red arrow) and portal veins (black arrow), while VEGFR3 is primarily expressed on the sinusoids but absent in portal vein (black arrow), in either sham-operated (Sham) or PH liver. Scale bar, 100 µm.

Supplementary Fig. 4



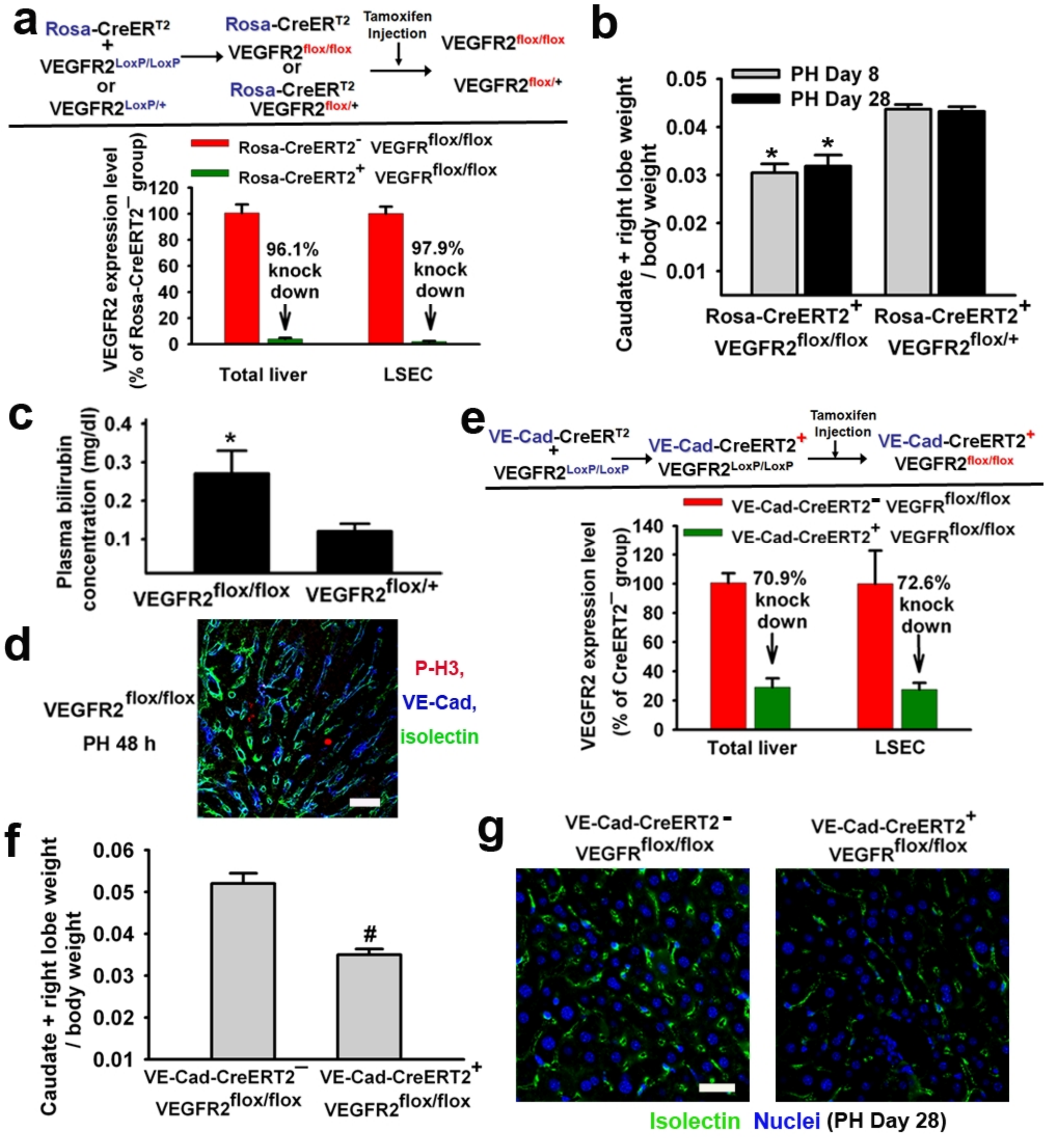
Supplementary Fig. 4 Characterization of normal and regenerative LSECs.

a) Increase in VEGFR3^{+}CD34^{-} LSECs represents the predominant expanding vascular populations during liver regeneration. Although proliferation of the LSECs is low during the early inductive phases (days 1-3 after PH) of liver regeneration, the number of the LSECs increases during the proliferative angiogenic phase (days 4-8 after PH) of the liver regeneration.

b) Kinetics of VEGFR3^{low}CD34^{-} LSECs expansion during liver regeneration. The numbers of VEGFR3^{low}CD34^{-} population were quantified at the indicated time points, respectively.

c) Proposed schema describing the roles of LSECs in liver regeneration. Upon PH (day 0), LSECs initiate the proliferation of proximal hepatocytes by exerting "inductive signals", possibly by releasing angiocrine factors. Day 4 post PH, there is a significant LSEC expansion (proliferative angiogenesis) to sustain hepatic reconstitution.

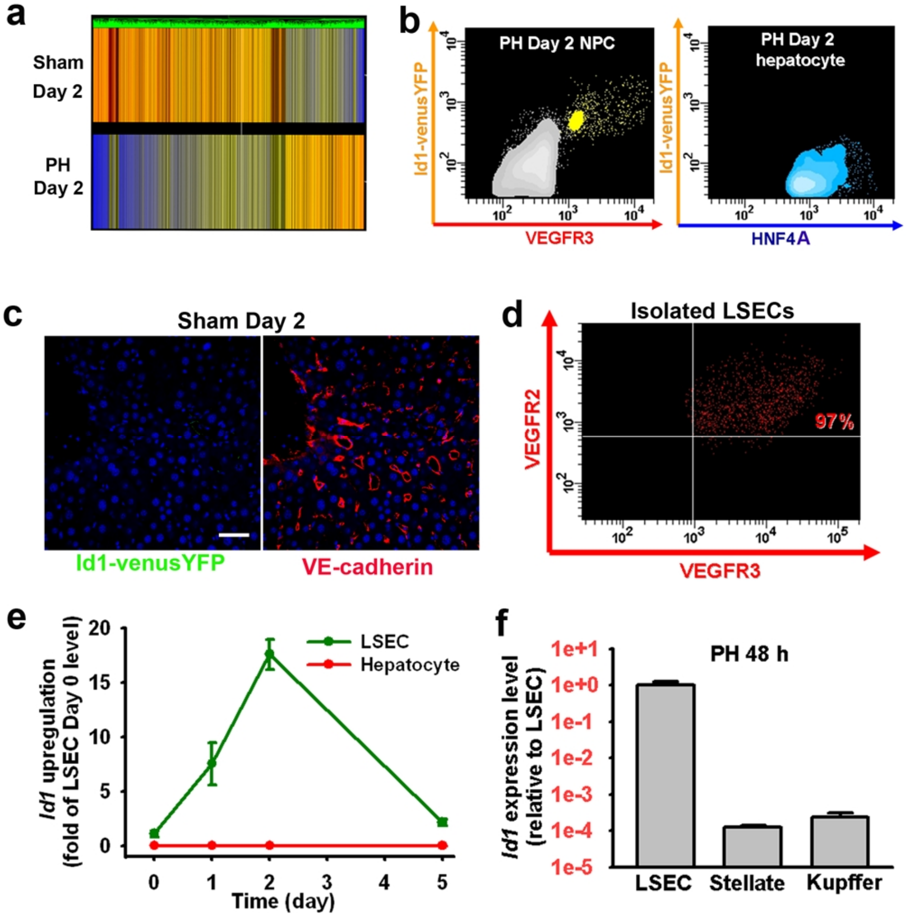
Supplementary Fig. 5



Supplementary Fig. 5 Endothelial-specific knock down of VEGFR2 results in impaired liver regeneration.

a) Selective knockdown of VEGFR2 in liver endothelial cells after tamoxifen treatment of *Rosa-CreER*^{T2}*VEGFR2*$^{flox/flox}$ mice, *n* = 4. **b**) Sustained inhibition of liver mass recovery in *Rosa-CreER*^{T2}*VEGFR2*$^{flox/flox}$ with endothelial knockdown of VEGFR2. *, P < 0.05, versus *VEGFR2*$^{flox/+}$ group, *n* = 4. **c**) Impaired regeneration of liver function (increased plasma bilirubin level) in *VEGFR2*$^{flox/flox}$ mice after PH. *, P < 0.05, versus *VEGF*$^{flox/+}$ group, *n* = 4. **d**) Despite the presence of intact functional VE-cadherin^{+}isolectin^{+} vasculature, there is profound absence of mitotic P-H3^{+} hepatocytes in *Rosa-CreER*^{T2}*VEGFR2*$^{flox/flox}$ mice. **e**) Generation of endothelial-specific VEGFR2 knockout mice. *VE-cadherin-CreER*^{T2} mice were crossed with *VEGFR2*$^{LoxP/LoxP}$ mice. Treatment of tamoxifen to the resultant *VE-cadherin-CreER*^{T2}*VEGFR2*$^{loxP/loxP}$ leads to *VE-cadherin-CreER*^{T2}*VEGFR2*$^{flox/flox}$ mice that have endothelial-selective VEGFR2 deficiency. Quantification of endothelial-specific VEGFR2 knockdown in *VE-cadherin-CreER*^{T2}*VEGFR2*$^{flox/flox}$ mice is shown in the bar graph. **f & g**) Impaired regeneration of liver mass (f) and isolectin^{+} functional vessel (g) in *VE-cadherin-CreER*^{T2}*VEGFR2*$^{flox/flox}$ mice. Scale bar, 50 μm.

Supplementary Fig. 6



Supplementary Fig. 6 Endothelial-specific upregulation of *Id1* in the regenerative liver.

a) Tree view of the comparison of microarray gene expression between the livers after PH and sham operation at day 2.

b) 48 hours after PH, in *Id1*-venusYFP reporter mice whereby YFP is driven by Id1 expression, Id1 (YFP) is only detected in VEGFR3$^+$ LSECs but not HNF4A$^+$ hepatocyte or other nonparenchymal cells.

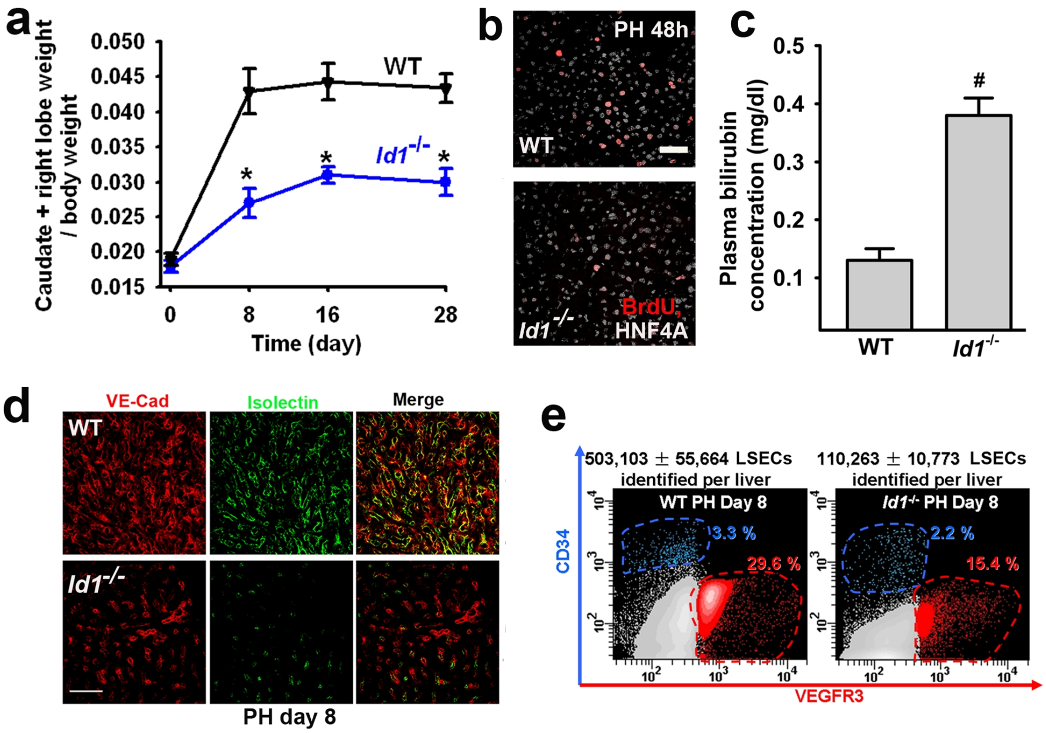
c) Absence of *Id1* (YFP) upregulation in the liver of sham-operated Id1-YFP mouse two days after PH. Scale bar, 50 μm.

d) Isolation and characterization of LSECs. Flow cytometry shows that the majority of the isolated cells are LSECs that coexpress VEGFR2 and VEGFR3.

e) Kinetics of *Id1* upregulation in LSECs during liver regeneration. LSECs and hepatocytes were isolated from the mouse liver at the indicated time points after PH, and *Id1* expression level was measured by quantitative PCR and compared to the baseline levels at day 0. There was no Id1 expression in hepatocytes at all the time points.

f) Absence of *Id1* activation in stellate and Kupffer cells after PH. Note the logarithmic axis of the expression level that clearly demonstrates the absence of Id1 in other cell types.

Supplementary Fig. 7



Supplementary Fig. 7 Liver regeneration is impaired in *Id1*-deficient (*Id1*$^{-/-}$) mice.

a) Sustained inhibition of liver mass recovery in *Id1*$^{-/-}$ mice. Throughout the indicated period, VEGF-A$_{164}$ injection failed to rescue the hepatic reconstitution. *$P < 0.05$ versus WT, $n = 4$.

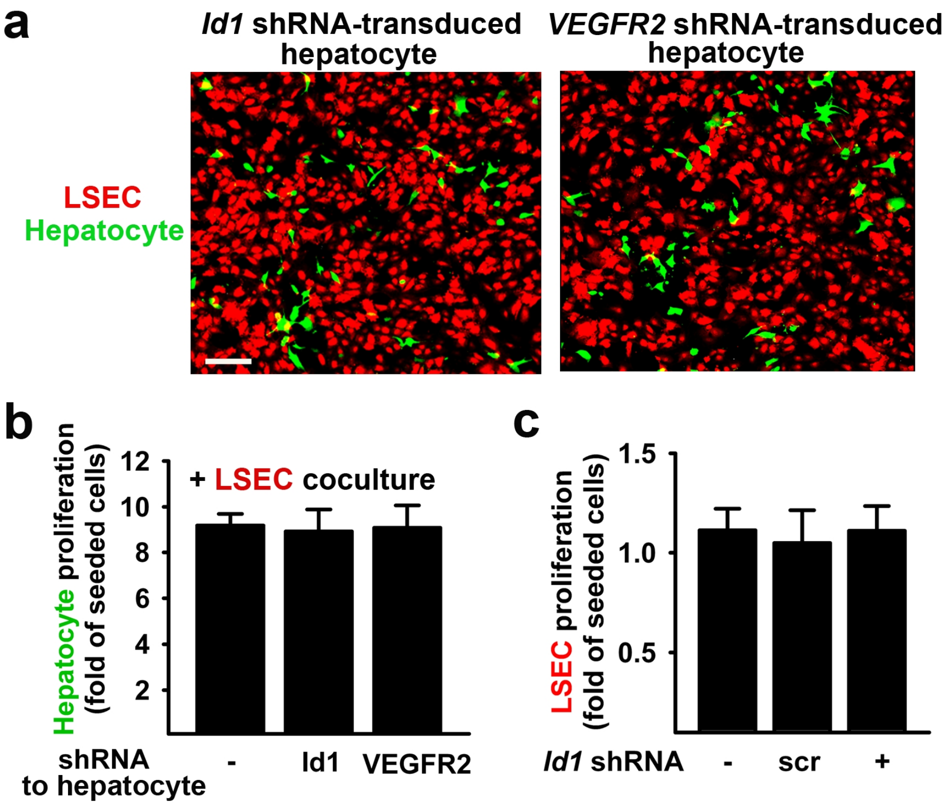
b) Impairment of HNF4A^{+} hepatocyte proliferation in the *Id1*$^{-/-}$ mice 48 hours after PH (PH 48h), revealed by the decreased incorporation of BrdU. Representative image of BrdU incorporation of each group is shown. Scale bar, 50 µm.

c) Impaired regeneration of liver function (increased plasma bilirubin level) in *Id1*$^{-/-}$ mice after PH. #, P < 0.01, versus WT group, $n = 3$.

d) The generation of both VE-cadherin^{+} and functional (isolectin^{+}) vessels are inhibited in *Id1*$^{-/-}$ mice after PH. Representative image is shown. Scale bar, 50 µm. Quantification of the inhibited assembly of VE-cadherin^{+} and functional (isolectin^{+}) vessels in *Id1*$^{-/-}$ mice after PH is shown in Fig. 3c in the text.

e) Polyvariate flow cytometry shows the impaired regeneration of VEGFR3^{+}CD34^{-} LSECs in the *Id1*$^{-/-}$ mice at day 8 after PH. Representative image is shown, and the blunted increase of VEGFR3^{+}CD34^{-} cell population per regenerative *Id1*$^{-/-}$ liver was compared to that of WT mice (top text panel).

Supplementary Fig. 8

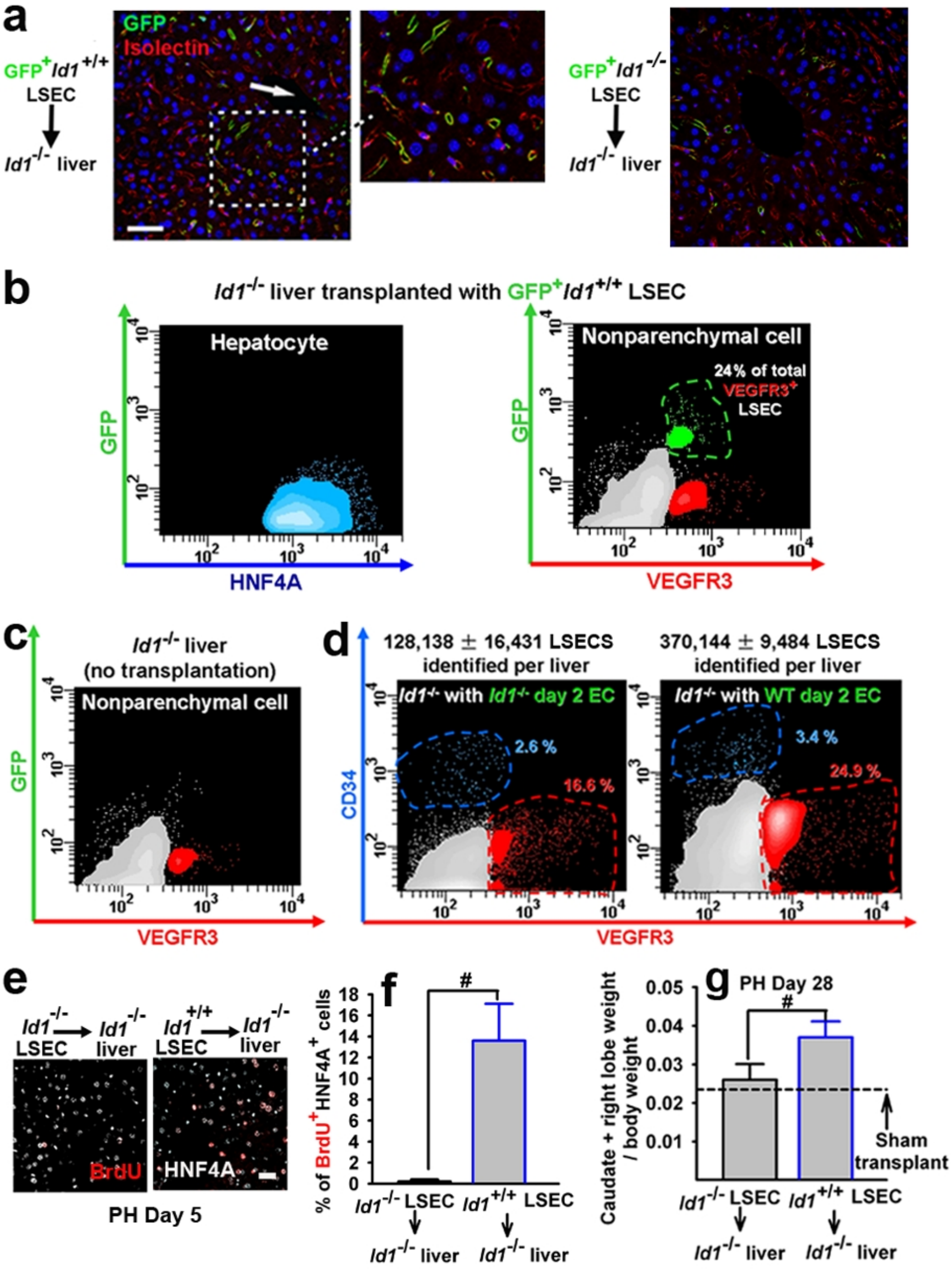


Supplementary Fig. 8 *Id1*-dependent angiocrine effects on hepatocyte proliferation.

a & b) The EC-dependent stimulation of hepatocyte proliferation is not affected by *Id1* or *VEGFR2* gene knockdown in hepatocytes. Representative image (a) and the quantification of hepatocyte proliferation after incubation of LSEC (b) are shown. Primary hepatocytes were isolated from mouse liver, transduced with albumin-GFP reporter, and co-cultured with mCherry labeled LSEC monolayer for 2 weeks as described in "Methods". Scale bar, 50 µm; *n* = 4.

c) Absence of LSEC proliferation in the coculture system and endothelial survival was not influenced by *Id1* knockdown. Scr, scrambled shRNA; *n* = 4.

Supplementary Fig. 9



Supplementary Fig. 9 Incorporation of the transplanted LSECs into the regenerating *Id1*$^{-/-}$ liver post PH.

a) *Id1*$^{+/+}$ or *Id1*$^{-/-}$ LSECs were isolated from WT mice at day 2 after PH, marked with lenti-GFP, and transplanted into the *Id1*$^{-/-}$ mice at day 2 after PH as described in the “Methods” and Fig. 3f. Regenerative *Id1*$^{+/+}$ LSECs incorporated into the *Id1*$^{-/-}$ liver sinusoid. Alexa 568-conjugated isolectin B4 (red) was i.v. injected to reveal the functional liver vasculature. Scale bar, 50 µm.

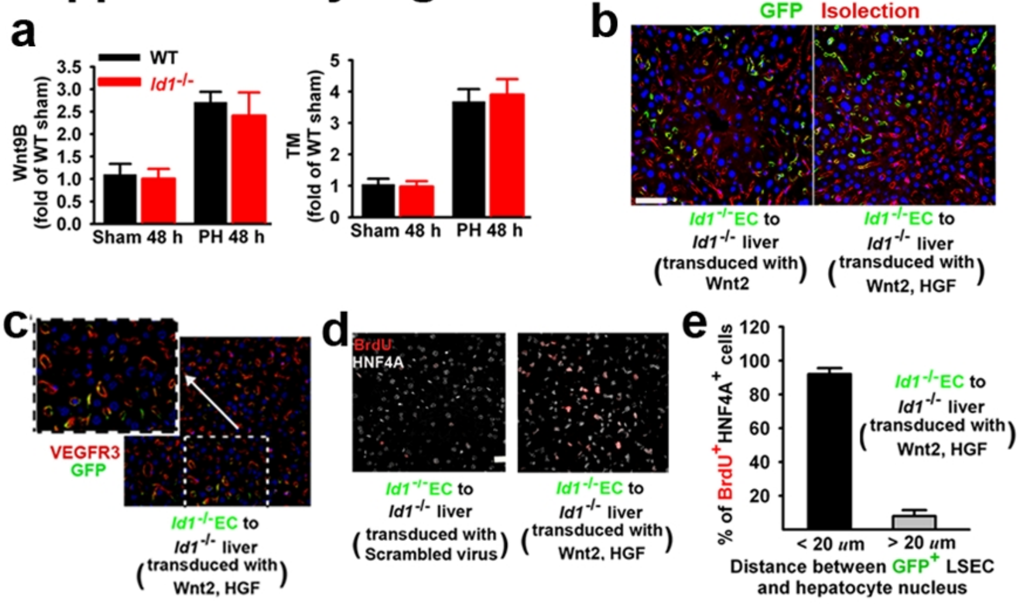
b) Engrafted GFP^{+}*Id1*$^{+/+}$ LSECs exclusively reside in VEGFR3^{+} LSEC population, but not other nonparenchymal cells or hepatocytes.

c) Absence of GFP^{+} cells in the *Id1*$^{-/-}$ liver without transplantation.

d) Restored regeneration of VEGFR3^{+}CD34^{-} LSECs in the *Id1*$^{-/-}$ mouse liver after transplantation of *Id1*$^{+/+}$GFP^{+} LSECs. Representative flow cytometry image is shown, and the number of the regenerating VEGFR3^{+}CD34^{-} LSECs per liver post transplantation was quantified (top text panel).

e & f) Intrasplenic transplantation of regenerative *Id1*$^{+/+}$ LSECs, but not *Id1*$^{-/-}$ LSECs, effectively restores the proliferation of HNF4A^{+} hepatocyte in the *Id1*$^{-/-}$ liver. Representative image (e) and the quantification of hepatocyte proliferation (f) are shown. **g**) Long-term restoration of *Id1*$^{-/-}$ liver mass reconstitution after transplantation of regenerative *Id1*$^{+/+}$ LSECs. Dashed line, the level of regenerative *Id1*$^{-/-}$ liver underwent PBS injection and splenectomy (sham transplant). #$P < 0.05$; $n = 3$.

Supplementary Fig. 10



Supplementary Fig. 10. Identification of Wnt2 and HGF as Id1-mediated paracrine factors derived from LSEC for liver regeneration.

a) 48 hours after PH, upregulation of paracrine cytokine Wnt2 and HGF but not Wnt9B and TM is inhibited in *Id1*$^{-/-}$ LSECs, as compared to WT LSECs. Alteration in the expression of Wnt2 and HGF in *Id1*$^{-/-}$ LSECs after PH is shown in Fig. 4.

b) Incorporation of the transplanted *Id1*$^{-/-}$ LSECs expressing various transduced genes into the *Id1*$^{-/-}$ liver. GFP$^+$Wnt2$^+$ LSEC and GFP$^+$Wnt2$^+$HGF$^+$ LSEC showed similar levels of incorporation into the *Id1*$^{-/-}$ liver sinusoidal vasculature. Scale bar, 50 µm.

c) Incorporation of the engrafted GFP$^+$ LSECs into the lumen of VEGFR3$^+$ sinusoidal vasculature.

d) Intrasplenic transplantation of *Id1*$^{-/-}$Wnt2$^+$HGF$^+$ LSECs, but not *Id1*$^{-/-}$ LSECs, restores HNF4A$^+$ hepatocyte proliferation in the *Id1*$^{-/-}$ liver. Representative image is shown. Quantification of hepatocyte proliferation is shown in Fig. 4c. Scale bar, 25 µm.

e) Essential role of cellular proximity between transplanted LSECs and hepatocytes in stimulating hepatocyte mitosis by the transplanted GFP$^+$*Id1*$^{+/+}$Wnt2$^+$HGF$^+$ vasculature in the *Id1*$^{-/-}$ liver.

Supplementary Table 1 Genetic alteration in the regenerative liver

Upregulated and downregulated genes in the liver 2 days after PH (Altered Fold after PH) were compared to the sham-operated liver.

Genes that are upregulated 5-fold and downregulated to 30% of sham liver level are listed.

Gene Name	Altered Fold after PH	Description
1430811_a_at	19.67	cell division cycle associated 1
1448899_s_at	19.53	RAD51 associated protein 1
1419764_at	18.88	chitinase 3-like 3
1418457_at	18.11	chemokine (C-X-C motif) ligand 14
1419669_at	18.08	proteinase 3
1435575_at	17.58	kinetochore associated 1
1448453_at	16.86	hydroxysteroid dehydrogenase-1, delta<5>-3-beta
1449708_s_at	16.73	checkpoint kinase 1 homolog (S. pombe)
1417938_at	15.98	RAD51 associated protein 1
1422651_at	15.81	adiponectin, C1Q and collagen domain containing
1451246_s_at	15.8	aurora kinase B
1434734_at	15.6	RAD54 homolog B (S. cerevisiae)
1430574_at	15.58	cyclin-dependent kinase inhibitor 3
1416930_at	15.07	lymphocyte antigen 6 complex, locus D
1423774_a_at	14.77	protein regulator of cytokinesis 1
1417867_at	14.39	adipsin
1419513_a_at	14.33	ect2 oncogene
1416802_a_at	13.29	cell division cycle associated 5
1417910_at	13.27	cyclin A2
1416309_at	12.98	nucleolar and spindle associated protein 1
1419394_s_at	12.93	S100 calcium binding protein A8 (calgranulin A)
1417926_at	12.82	leucine zipper protein 5
1450677_at	12.68	checkpoint kinase 1 homolog (S. pombe)
1418026_at	12.61	exonuclease 1
1448205_at	12.1	cyclin B1, related sequence 1 ; cyclin B1
1452954_at	12.1	ubiquitin-conjugating enzyme E2C
1424638_at	11.98	cyclin-dependent kinase inhibitor 1A (P21)
1448756_at	11.95	S100 calcium binding protein A9 (calgranulin B)
1454694_a_at	11.89	topoisomerase (DNA) II alpha
1417911_at	11.42	cyclin A2
1424278_a_at	11.05	baculoviral IAP repeat-containing 5
1436723_at	10.99	FSH primary response 1
1417541_at	10.91	helicase, lymphoid specific
1424128_x_at	10.87	aurora kinase B

1423556_at	10.84	aldo-keto reductase family 1, member B7
1416299_at	10.69	Shc SH2-domain binding protein 1
1417761_at	10.58	apolipoprotein A-IV
1456362_at	9.752	cytochrome P450, family 11, subfamily b, polypeptide 1
1426817_at	9.668	antigen identified by monoclonal antibody Ki 67
1452595_at	9.306	ADAMTS4
1416641_at	9.266	ligase I, DNA, ATP-dependent
1448650_a_at	9.07	polymerase (DNA directed), epsilon
1437580_s_at	8.995	NIMA (never in mitosis gene a)-related expressed kinase 2
1452040_a_at	8.99	cell division cycle associated 3
1449061_a_at	8.783	DNA primase, p49 subunit
1436504_x_at	8.738	apolipoprotein A-IV
1430139_at	8.687	helicase, lymphoid specific
1423809_at	8.511	transcription factor 19
1418369_at	8.458	DNA primase, p49 subunit
1421430_at	8.449	RAD51-like 1 (S. cerevisiae)
1449984_at	8.415	chemokine (C-X-C motif) ligand 2
1415885_at	8.251	chromogranin B
1449133_at	8.183	small proline-rich protein 1A
1450156_a_at	8.149	hyaluronan mediated motility receptor (RHAMM)
1454854_at	8.047	organic solute transporter beta
1452458_s_at	7.943	peptidylprolyl isomerase (cyclophilin) like 5
1450352_at	7.867	melatonin receptor 1A
1433888_at	7.848	ATPase, Ca++ transporting, plasma membrane 2
1448804_at	7.827	cytochrome P450, family 11, subfamily a, polypeptide 1
1419735_at	7.753	casein kappa
1451064_a_at	7.678	phosphoserine aminotransferase 1
1428518_at	7.51	myeloid leukemia factor 1 interacting protein
1452260_at	7.423	cell death-inducing DFFA-like effector c
1448314_at	7.2	cell division cycle 2 homolog A (S. pombe)
1450708_at	7.184	secretogranin II
1422016_a_at	7.153	centromere autoantigen H
1449171_at	7.124	Ttk protein kinase
1422926_at	7.088	melanocortin 2 receptor
1415938_at	7.034	serine peptidase inhibitor, Kazal type 3
1418728_at	7.03	steroidogenic acute regulatory protein
1424629_at	6.967	breast cancer 1
1421546_a_at	6.942	Rac GTPase-activating protein 1
1449201_at	6.899	steroidogenic acute regulatory protein
1422462_at	6.882	ubiquitin-conjugating enzyme E2T (putative)
1418729_at	6.836	steroidogenic acute regulatory protein
1451128_s_at	6.833	kinesin family member 22

1425895_a_at	6.811	inhibitor of DNA binding 1
1438434_at	6.757	Rho GTPase activating protein 11A
1428066_at	6.756	DNA segment, Chr X, Immunex 50, expressed
1437187_at	6.731	E2F transcription factor 7
1450971_at	6.639	growth arrest and DNA-damage-inducible 45 beta
1425451_s_at	6.541	chitinase 3-like 3 ; chitinase 3-like 4
1455983_at	6.538	cell division cycle associated 2
1434748_at	6.5	cytoskeleton associated protein 2
1415949_at	6.463	carboxypeptidase E
1435306_a_at	6.287	kinesin family member 11
1424143_a_at	6.283	retroviral integration site 2
1419127_at	6.213	neuropeptide Y
1422878_at	6.197	synaptotagmin XII
1439695_a_at	6.194	M-phase phosphoprotein 1
1424144_at	6.19	retroviral integration site 2
1450920_at	6.185	cyclin B2
1451204_at	6.064	scavenger receptor class A, member 5 (putative)
1449207_a_at	6.061	kinesin family member 20A
1417939_at	6.037	RAD51 associated protein 1
1423920_at	6.036	barren homolog (Drosophila)
1454607_s_at	6.027	phosphoserine aminotransferase 1
1423525_at	6.024	microtubule associated serine/threonine kinase-like
1422916_at	6.015	fibroblast growth factor 21
1427167_at	5.984	expressed sequence AI448196
1437611_x_at	5.958	kinesin family member 2C
1436847_s_at	5.928	cell division cycle associated 8
1449877_s_at	5.921	kinesin family member C1
1448113_at	5.86	stathmin 1
1424156_at	5.859	retinoblastoma-like 1 (p107)
1434195_at	5.856	protease, serine, 35
1440924_at	5.826	M-phase phosphoprotein 1
1433892_at	5.815	sperm associated antigen 5
1437093_at	5.798	dynein, axonemal, intermediate chain 1
1448466_at	5.721	cell division cycle associated 5
1422960_at	5.658	steroid 5 alpha-reductase 2
1439436_x_at	5.601	inner centromere protein
1419944_at	5.595	DNA segment, Chr 4, ERATO Doi 639, expressed
1437716_x_at	5.571	kinesin family member 22
1427102_at	5.554	schlafen 4
1417625_s_at	5.469	chemokine orphan receptor 1
1429273_at	5.42	BMP-binding endothelial regulator
1418149_at	5.394	chromogranin A

1434473_at	5.339	solute carrier family 16 (monocarboxylic acid transporters)
1424321_at	5.313	replication factor C (activator 1) 4
1428481_s_at	5.311	cell division cycle associated 8
1448529_at	5.305	thrombomodulin
1422925_s_at	5.297	acyl-CoA thioesterase 3
1420804_s_at	5.269	C-type lectin domain family 4, member d
1427707_a_at	5.245	Tal1 interrupting locus
1448226_at	5.24	ribonucleotide reductase M2
1416431_at	5.232	tubulin, beta 6
1417419_at	5.206	cyclin D1
1449773_s_at	5.203	growth arrest and DNA-damage-inducible 45 beta
1448834_at	5.173	forkhead box M1
1433966_x_at	5.159	asparagine synthetase
1417273_at	5.133	pyruvate dehydrogenase kinase, isoenzyme 4
1448127_at	5.124	ribonucleotide reductase M1
1459897_a_at	5.073	suprabasin
1420380_at	5.069	chemokine (C-C motif) ligand 2
1437370_at	5.069	shugoshin-like 2 (S. pombe)
1420438_at	5.06	orosomucoid 2
1418456_a_at	5.037	chemokine (C-X-C motif) ligand 14
1448507_at	5.028	EF hand domain containing 1
1449586_at	4.95	plakophilin 1
1448929_at	4.939	coagulation factor XIII, A1 subunit
1427094_at	4.929	polymerase (DNA directed), epsilon 2 (p59 subunit)
1422583_at	4.928	RAB3B, member RAS oncogene family
1425663_at	4.91	interleukin 1 receptor antagonist
1415878_at	4.873	ribonucleotide reductase M1
1417450_a_at	4.871	transforming, acidic coiled-coil containing protein 3
1439827_at	4.818	ADAMTS12
1439208_at	4.807	checkpoint kinase 1 homolog (S. pombe)
1423110_at	4.793	procollagen, type I, alpha 2
1438161_s_at	4.773	replication factor C (activator 1) 4
1421228_at	4.761	chemokine (C-C motif) ligand 7
1451095_at	4.731	asparagine synthetase
1434767_at	4.705	expressed sequence C79407
1425341_at	4.699	potassium channel, subfamily K, member 3
1427161_at	4.67	centromere autoantigen F
1439394_x_at	4.67	cell division cycle 20 homolog (S. cerevisiae)
1426601_at	4.586	solute carrier family 37 (glycerol-3-phosphate transporter), member 1
1427838_at	4.575	tubulin, beta 2
1451358_a_at	4.516	Rac GTPase-activating protein 1
1448377_at	4.496	secretory leukocyte peptidase inhibitor

1416558_at	4.49	maternal embryonic leucine zipper kinase
1419943_s_at	4.489	cyclin B1
1430617_at	4.391	Opa interacting protein 5
1426858_at	4.376	inhibin beta-B
1436791_at	4.365	wingless-related MMTV integration site 5A
1455691_at	4.364	cytochrome P450, family 21, subfamily a, polypeptide 1
1417971_at	4.344	nurim (nuclear envelope membrane protein)
1421731_a_at	4.33	flap structure specific endonuclease 1
1437094_x_at	4.309	dynein, axonemal, intermediate chain 1
1423877_at	4.307	chromatin assembly factor 1, subunit B (p60)
1423100_at	4.305	FBJ osteosarcoma oncogene
1428167_a_at	4.24	myelin protein zero-like 1
1438665_at	4.232	sphingomyelin phosphodiesterase 3, neutral
1417420_at	4.196	cyclin D1
1442339_at	4.19	stefin A2 like 1
1441835_x_at	4.185	myotubularin related protein 11
1439478_at	4.183	acyl-CoA thioesterase 2
1460550_at	4.169	myotubularin related protein 11
1452314_at	4.12	kinesin family member 11
1451306_at	4.096	cell division cycle associated 7 like
1427541_x_at	4.089	hyaluronan mediated motility receptor (RHAMM)
1417878_at	4.081	E2F transcription factor 1
1428168_at	4.078	myelin protein zero-like 1
1422694_at	4.056	tweety homolog 1 (Drosophila)
1429295_s_at	4.04	thyroid hormone receptor interactor 13
1421375_a_at	4.035	S100 calcium binding protein A6 (calcyclin)
1452534_a_at	4.024	high mobility group box 2
1450670_at	4.023	dopamine beta hydroxylase
1437785_at	4.016	ADAMTS9
1426002_a_at	4.012	cell division cycle 7 (S. cerevisiae)
1427357_at	4	cytidine deaminase
1418311_at	0.3	fructosamine 3 kinase
1428447_at	0.297	transmembrane protein 14A
1451721_a_at	0.296	histocompatibility 2, class II antigen A, beta 1
1419476_at	0.291	ADAM-like, decysin 1
1423348_at	0.29	frizzled homolog 8 (Drosophila)
1457563_at	0.29	epidermal growth factor receptor
1425918_at	0.289	EGL nine homolog 3 (C. elegans)
1452431_s_at	0.289	histocompatibility 2, class II antigen A, alpha
1457871_at	0.288	collectin liver 1
1446254_at	0.286	DEP domain containing 6 (Depdc6), mRNA
1437916_at	0.285	Kruppel-like factor 13 (Klf13), mRNA

1418600_at	0.284	Kruppel-like factor 1 (erythroid)
1437273_at	0.283	HtrA serine peptidase 4
1446844_at	0.28	coiled-coil-helix-coiled-coil-helix domain containing 7
1420342_at	0.276	ganglioside-induced differentiation-associated-protein 10
1437953_at	0.275	preimplantation protein 4
1453191_at	0.275	procollagen, type XXVII, alpha 1
1453588_at	0.272	carbonic anhydrase 3
1452944_at	0.272	synaptogyrin 2
1428885_at	0.27	synaptogyrin 2 ; arylformamidase
1418028_at	0.262	dopachrome tautomerase
1456973_at	0.254	Modulator recognition factor 2 (Mrf2)
1426850_a_at	0.253	mitogen activated protein kinase kinase 6
1448092_x_at	0.253	serine (or cysteine) peptidase inhibitor, clade A, member 4, pseudogene 1
1420549_at	0.252	guanylate nucleotide binding protein 1
1450830_a_at	0.25	phosphodiesterase 6C, cGMP specific, cone, alpha prime
1416194_at	0.248	cytochrome P450, family 4, subfamily b, polypeptide 1
1429549_at	0.246	procollagen, type XXVII, alpha 1
1430893_at	0.244	major urinary protein 1
1417600_at	0.242	solute carrier family 15 (H+/peptide transporter), member 2
1444296_a_at	0.237	serine (or cysteine) peptidase inhibitor, clade A, member 4, pseudogene 1
1431240_at	0.236	C-type lectin domain family 2, member h
1435188_at	0.235	similar to chromosome 1 open reading frame 51
1444166_at	0.227	thyroid hormone responsive SPOT14 homolog (Rattus)
1423397_at	0.22	UDP glucuronosyltransferase 2 family, polypeptide B38
1419146_a_at	0.22	glucokinase
1424673_at	0.219	C-type lectin domain family 2, member h
1449409_at	0.196	sulfotransferase family, cytosolic, 1C, member 2
1427981_a_at	0.194	cysteine sulfinic acid decarboxylase
1449816_at	0.192	sulfotransferase family 5A, member 1
1420531_at	0.175	hydroxysteroid dehydrogenase-5, delta<5>-3-beta
1424969_s_at	0.17	uridine phosphorylase 2
1437584_at	0.153	Transcribed locus
1424737_at	0.15	thyroid hormone responsive SPOT14 homolog (Rattus)
1426516_a_at	0.15	lipin 1
1418857_at	0.145	solute carrier family 13, member 2
1444297_at	0.136	serine (or cysteine) peptidase inhibitor, clade A, member 4, pseudogene 1
1451548_at	0.124	uridine phosphorylase 2
1426037_a_at	0.118	regulator of G-protein signaling 16
1415965_at	0.118	stearoyl-Coenzyme A desaturase 1
1460256_at	0.108	carbonic anhydrase 3
1460059_at	0.105	uridine phosphorylase 2
1444032_at	0.0878	Kidney expressed gene 1 (Keg1), mRNA

1455265_a_at	0.0833	regulator of G-protein signaling 16
1460258_at	0.0801	leukocyte cell derived chemotaxin 1
1422973_a_at	0.0697	thyroid hormone responsive SPOT14 homolog (Rattus)
1422100_at	0.0618	cytochrome P450, family 7, subfamily a, polypeptide 1
1449347_a_at	0.0589	X-linked lymphocyte-regulated 4B ; X-linked lymphocyte-regulated 4A
1438743_at	0.0565	cytochrome P450, family 7, subfamily a, polypeptide 1
1416193_at	0.0539	carbonic anhydrase 1
1449309_at	0.0366	cytochrome P450, family 8, subfamily b, polypeptide 1