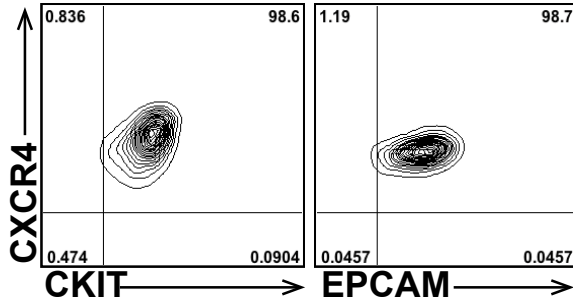
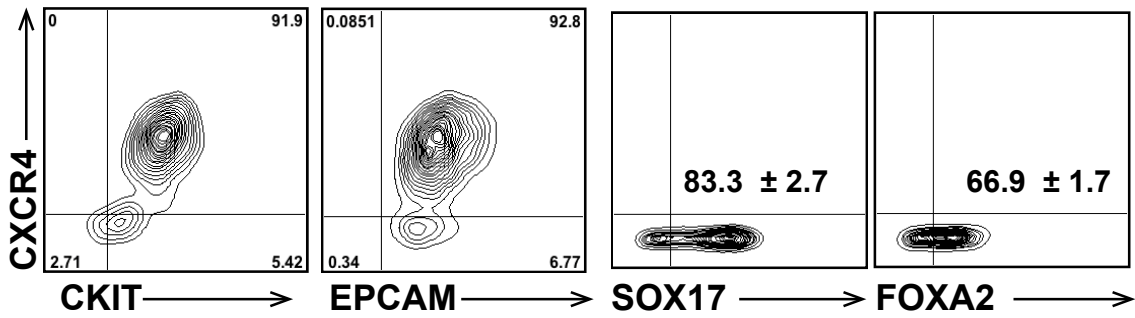
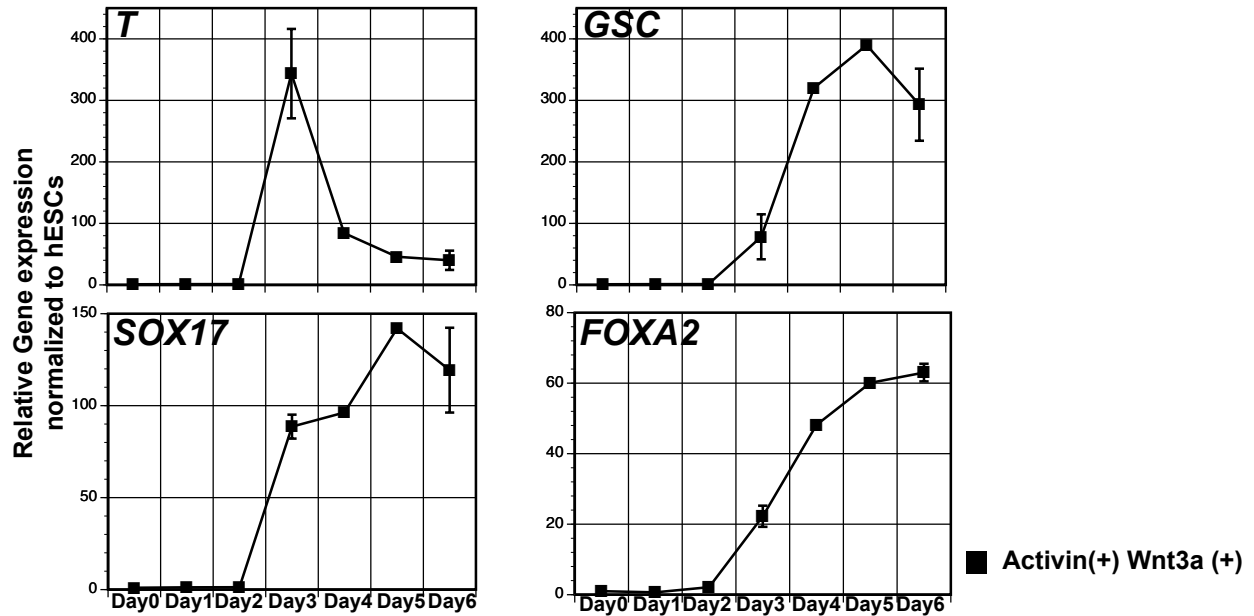
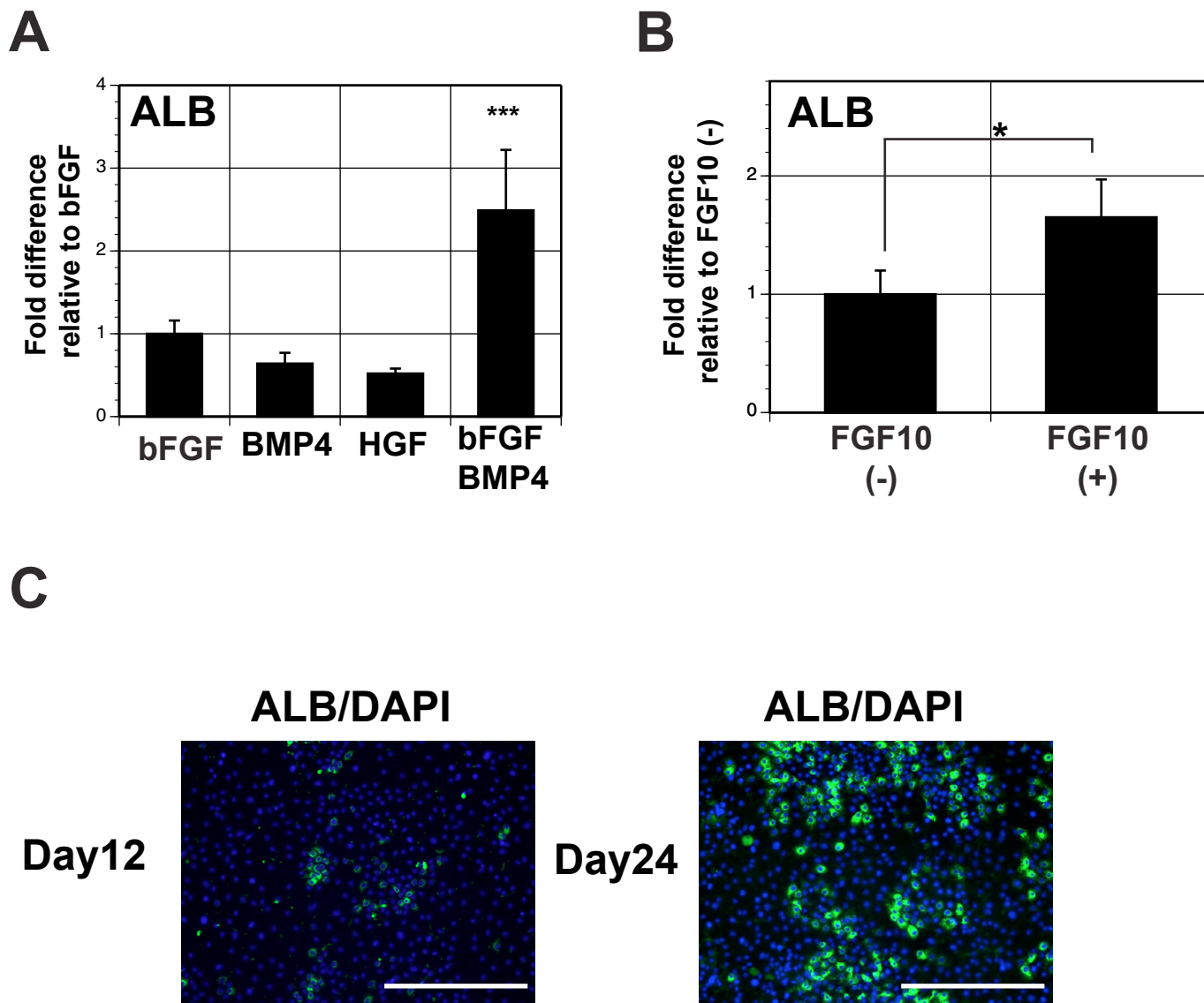
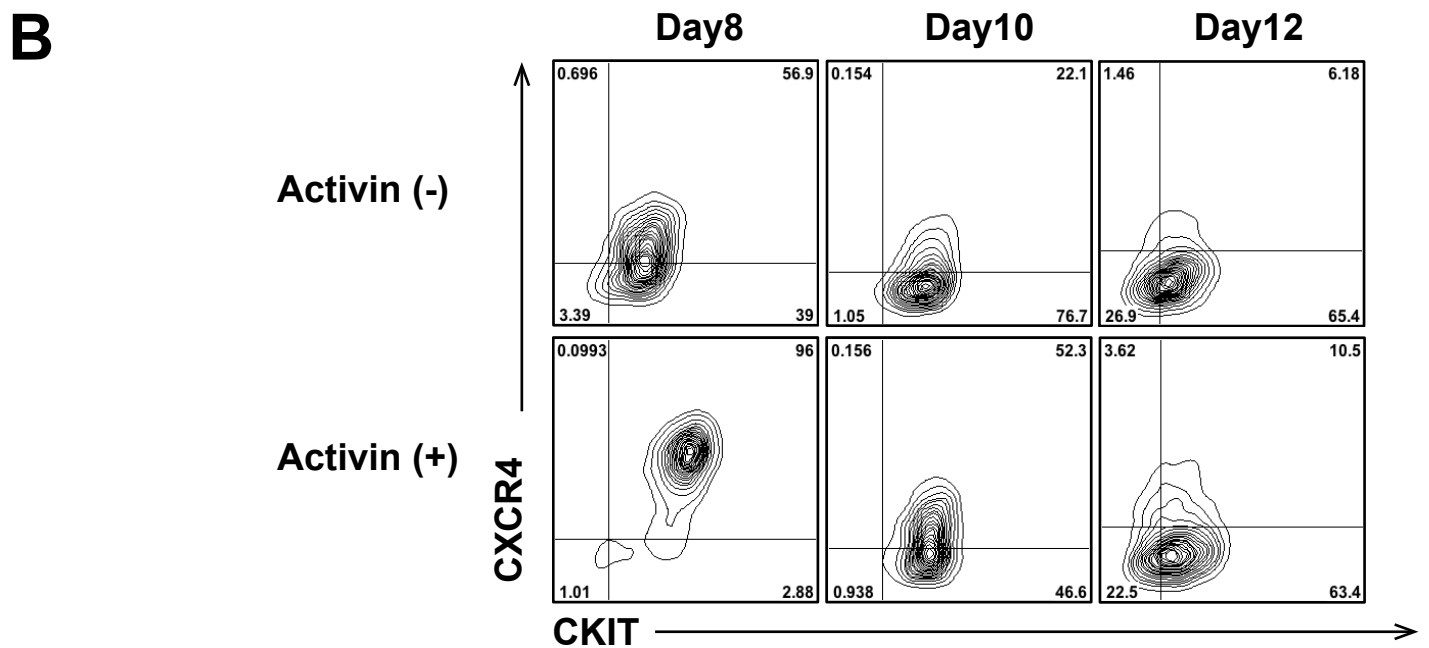
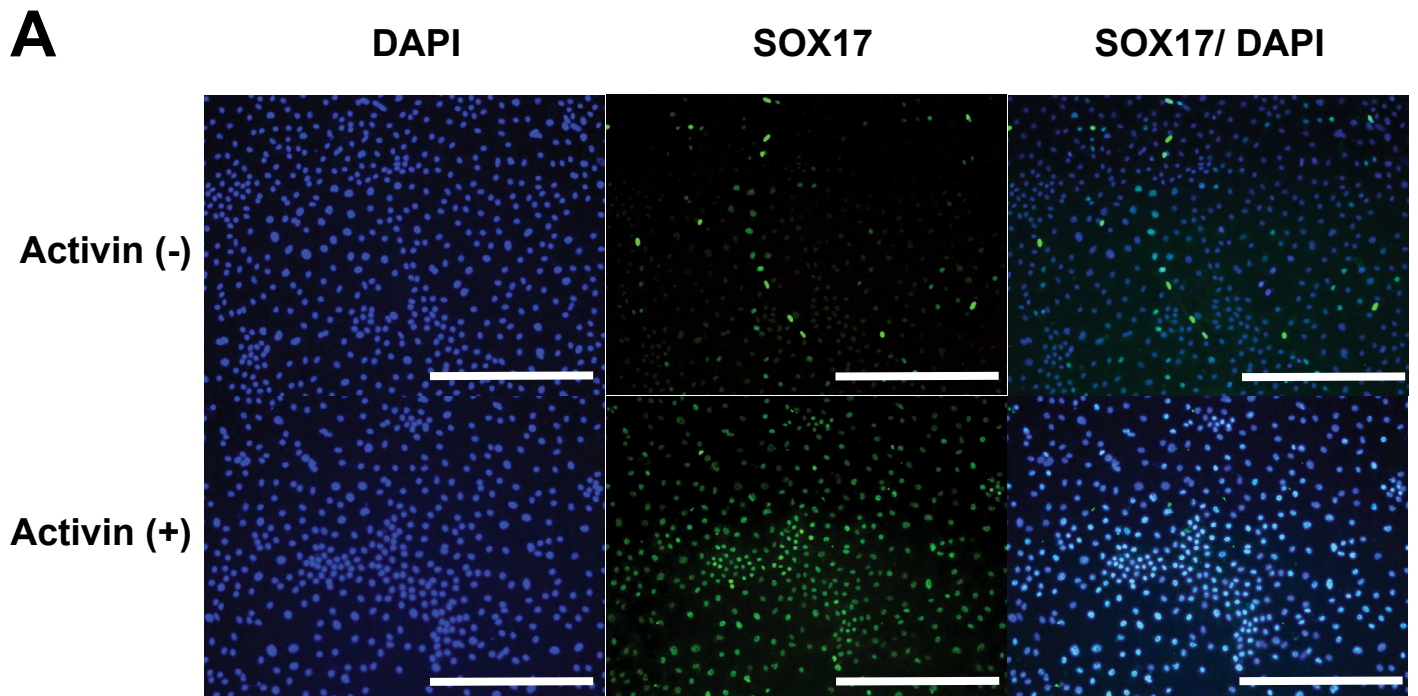


**A****B****C**

**Fig. S1. Endoderm induction in hESC-derived embryoid bodies.** (A) Flow cytometric analysis showing co-expression EPCAM and CXCR4 on day 6 EBs. (B) Flow cytometric analysis showing the proportion of CXCR4<sup>+</sup>, KIT<sup>+</sup>, EPCAM<sup>+</sup>, SOX17<sup>+</sup> and FOXA2<sup>+</sup> cells in day 6 EBs induced with activin in neural-based medium. (C) RT-qPCR based analyses of *T*, *SOX17*, *GSC* and *FOXA2* expression in activin/Wnt3a-induced EBs. EBs were analyzed at the indicated time points. Bars represent s.d. of the mean of three independent experiments.

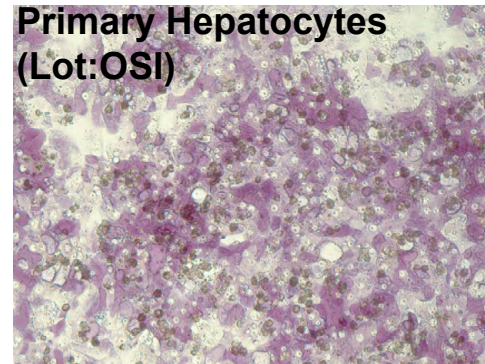
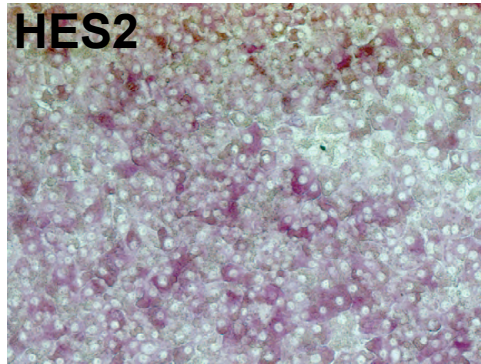


**Fig. S2. RT-qPCR analysis of albumin expression in monolayer cultures specified with the indicated cytokines.** (A) Cells were treated with the different factors (bFGF 10 ng/ml; BMP4 50 ng/ml; HGF 20 ng/ml; or bFGF 20 ng/ml plus BMP4 50 ng/ml) from 6 days to day 12 and then cultured with DEX, HGF and OSM, and analyzed at day 24. Bars represent the s.d. of the mean of three independent experiments. Values are determined relative to *TBP* and presented relative to expression in bFGF (20 ng/ml) culture, which is set to 1. \*\*\* $P < 0.001$  when compared with the culture treated with bFGF. Student's *t*-test,  $n = 3$ . (B) RT-qPCR analysis of albumin expression in populations specified in the presence and absence of FGF10. Cultures were treated (or not) with FGF10 (50 ng/ml) plus BMP4 (50 ng/ml) between days 6 and 8. At this stage, the FGF10 was removed and the cells cultured in bFGF/BMP4 between 8 and 12. Bars represent the s.d. of the mean of three independent experiments. Values are determined relative to *TBP* and presented relative to expression in FGF10 (-) culture, which is set to 1. \* $P < 0.05$ , Student's *t*-test,  $n = 3$ . (C) Immunostaining analyses showing the presence of ALB<sup>+</sup> cells at days 12 and 24 of culture. ALB is visualized with Alexa 488 (green). DAPI (blue) staining shows the nuclei. Scale bar, 200  $\mu\text{m}$ .

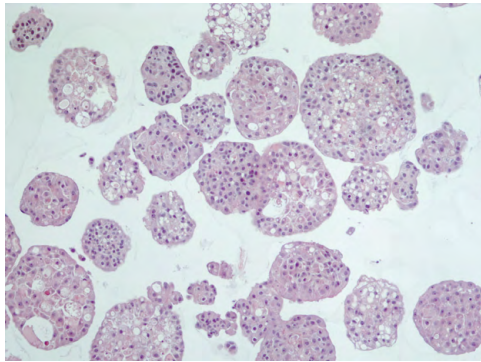


**Fig. S3. Duration of nodal/activin signaling impacts hepatic development.** (A) Immunostaining analyses showing the proportion of SOX17-positive cells in populations generated from non-treated (day 10) and activin-treated (day 12) endoderm. Sox17 is visualized with Alexa 488 (green), nuclei are stained with DAPI (blue). Scale bar: 200  $\mu$ m. (B) Flow cytometric analysis showing the proportion of CXCR4- and KIT-positive cells in populations at days 8, 10 and 12 of culture generated from non-treated cell and activin-treated endoderm

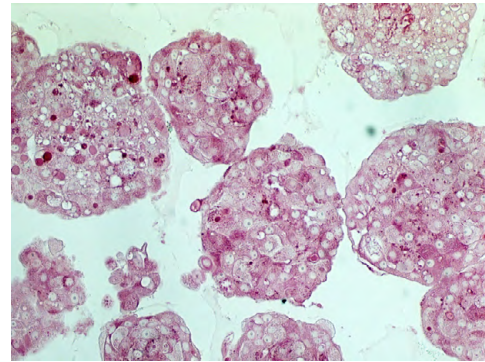
**A**



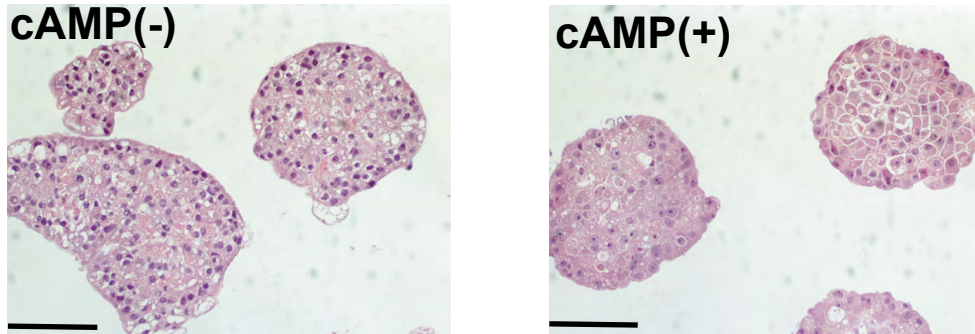
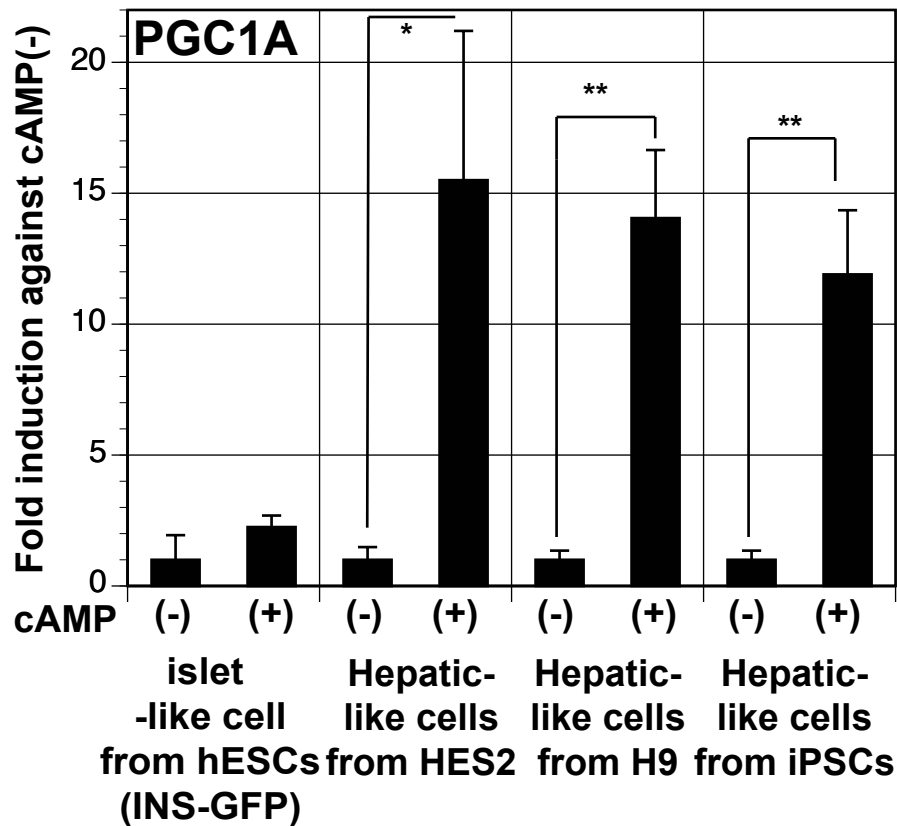
**B**



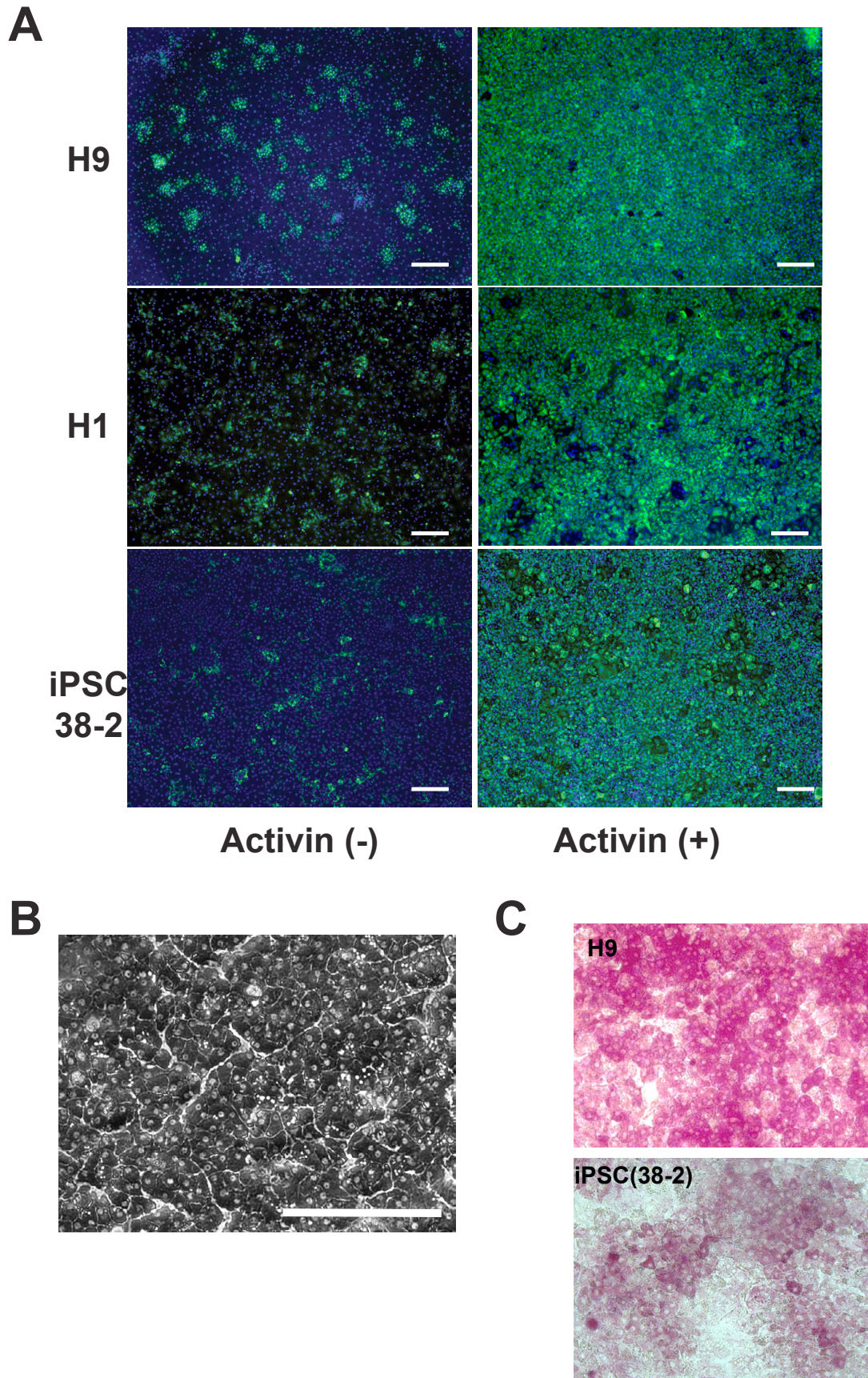
**C**



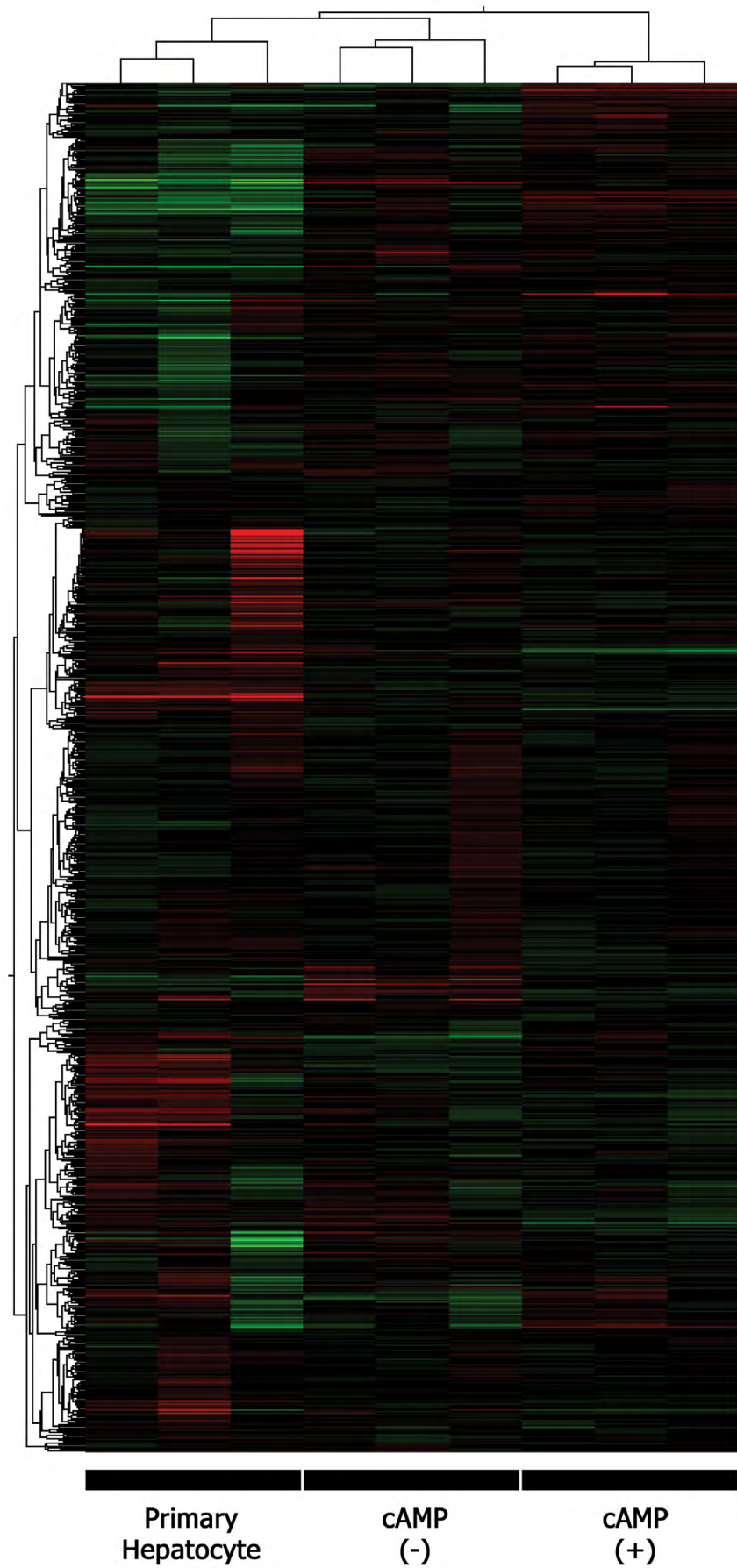
**Fig. S4. Periodic acid-Schiff (PAS) staining showing the intracellular storage of glycogen. (A) Left: HES2-derived hepatic cells at day 26 of monolayer culture. Right: cryopreserved human hepatocytes (lot OSI) (B) Hematoxylin and Eosin staining of HES2-derived aggregates at day 32. (C) PAS staining of HES2-derived aggregates at day 32.**

**A****B**

**Fig. S5. cAMP signaling induces maturation of hESC-derived hepatocyte-like cells.** (A) Hematoxylin and eosin staining of 8-Br-cAMP-treated and non-treated HES2-derived aggregates at day 44. (B) RT-qPCR analysis of *PGC1- $\alpha$*  expression in cAMP-treated pancreatic aggregates and hepatic aggregates generated from HES2, H9 and 38-2 cells. Values are determined relative to *TBP* and presented as fold change relative to expression in non-treated cells, which is set as 1. Bars represent the s.d. of the mean of three independent experiments, \* $P < 0.05$ , \*\* $P < 0.01$ , \*\*\* $P < 0.001$ , Student's *t*-test.



**Fig. S6. Hepatic specification and maturation from other hPSC lines.** (A) Immunostaining analyses showing proportion of ALB-positive cells in cultures generated from activin-treated (day 26-28) and non-treated (day 24) endoderm derived from H9 hESCs, H1 hESCs and 38-2 hiPSCs. ALB is visualized with Alexa 488 (green), nuclei are stained with DAPI (blue). Scale bar: 200  $\mu$ m. (B) Phase-contrast image showing morphology of H9-derived hepatic cells at day 26 of culture. Scale bar: 200  $\mu$ m. (C) PAS staining of H9 hESC- and 38-2 iPSC-derived hepatic cells at day 26.



**Fig. S7. Heat map summarizing expression of 23038 filtered transcripts, showing the results of a two-way unsupervised hierarchical cluster analysis.** Degree of intensity for red and green colors represents the relative amounts of over or underexpression, respectively, compared with median (black) for each transcript.

**Table S1. Hepatic specification and maturation from other hPSC cell lines****Hepatic specification and maturation of H9 cells**

Culture periods	Based medium	Growth factors and cytokines
Day 8-day 14	H16 DMEM	bFGF (40 ng/ml), BMP4 (50 ng/ml)
Day 14-day 20	H16 DMEM plus 25% Ham's F12 and 0.1% BSA	HGF (20 ng/ml), Dex (40 ng/ml), OSM (20ng/ml)
Day 20-day 32	H21 DMEM plus 25% Ham's F12 and 0.1% BSA	HGF (20 ng/ml), Dex (40 ng/ml), OSM (20 ng/ml)
Day 32-day 44	Hepatocyte culture medium (HCM) (Lonza: CC-4182)	$\pm$ 1 mM 8-bromo-cAMP (Biolab:B007)

**Hepatic specification and maturation of H1 and iPS (38-2) cells**

Culture periods	Based medium	Growth factors and cytokines
Day 10-day 16	H16 DMEM	bFGF (40 ng/ml), BMP4 (50 ng/ml)
Day 16-day 22	H16 DMEM plus 25% Ham's F12 and 0.1% BSA	HGF (20 ng/ml), Dex (40 ng/ml), OSM (20 ng/ml)
Day 22-day 32	H21 DMEM plus 25% Ham's F12 and 0.1% BSA	HGF (20 ng/ml), Dex (40 ng/ml), OSM (20 ng/ml)
Day 32-day 44	Hepatocyte culture medium (HCM) (Lonza: CC-4182)	$\pm$ 1 mM 8-bromo-cAMP (Biolab:B007)



**Table S2. Gene Ontology (GO) analysis**  
Significantly enriched Gene Ontology (GO) terms upregulated in cAMP(+) lines

GO ID	GO ACCESSION	GO Term	p-value	corrected p-value	Count in Selection	% Count in Selection	Count in Total	% Count in Total
3962	GO:0005737	cytoplasm	6.558086E-5	0.018937081	48	88.88885	7926	44.38844
7176	GO:0009987(GO:0008151)(GO:0050875)	cellular process	3.710204E-4	0.06418881	24	44.44443	10864	60.842293
20307	GO:0044444	cytoplasmic part	5.3280417E-7	3.769804E-4	23	42.92584	5338	29.894712
3963	GO:0005739	mitochondrion	1.137161E-8	7.151987E-4	20	37.037037	1157	6.4796147
20156	GO:0044237	cellular metabolic process	3.742244E-4	0.06418881	20	37.037037	8902	38.09364
4255	GO:0006082	organic acid metabolic process	2.2573053E-19	8.518051E-16	19	35.185184	621	3.4778225
11694	GO:0019752	carboxylic acid metabolic process	1.6723905E-19	8.518051E-16	19	35.185184	614	3.43862
18201	GO:0034180	cellular ketone metabolic process	3.0354533E-16	8.5903236E-16	19	35.185184	523	3.5170225
19372	GO:0043436	oxoacid metabolic process	1.6723905E-19	8.518051E-16	19	35.185184	614	3.43862
20200	GO:0044281	small molecule metabolic process	9.6049245E-12	1.8122323E-8	19	35.185184	2093	11.72155
2603	GO:0003824	catalytic activity	1.0261457E-4	0.02662119	17	31.481482	5422	30.365143
4696	GO:0006629	lipid metabolic process	2.2636404E-9	2.8473262E-6	17	31.481482	879	4.922715
15224	GO:0032787	monocarboxylic acid metabolic process	2.4227023E-15	6.489315E-12	15	27.777778	322	1.8033154
4697	GO:0006631	fatty acid metabolic process	4.5773118E-11	7.402598E-8	11	20.37037	209	1.1704749
20174	GO:0044255	cellular lipid metabolic process	6.67601E-10	9.4470914E-7	11	20.37037	581	3.2538083
26607	GO:0055114	oxidation reduction	1.2482255E-4	0.030065356	11	20.37037	658	3.685036
3997	GO:0005777(GO:0019818)	peroxisome	1.3808894E-6	7.8162795E-4	7	12.962963	109	0.1043906
18575	GO:0042370	microbody	1.3808894E-6	7.825E-4	7	12.962963	109	0.1043906
3980	GO:0005759	mitochondrial matrix	2.3700214E-4	0.043983888	6	11.111111	242	1.352867
4181	GO:0006006	glycine metabolic process	1.5651867E-4	0.031640932	6	11.111111	158	0.8848564
6371	GO:0009056	catabolic process	1.984098E-4	0.03941785	6	11.111111	1919	10.7407785
9242	GO:0016042(GO:0006874)	lipid catabolic process	4.8472257E-6	0.02429426	6	11.111111	186	1.0416666
11287	GO:0019318	hexose metabolic process	5.255418E-4	0.08008407	6	11.111111	198	1.108871
14422	GO:0031980	mitochondrial lumen	2.3700214E-4	0.043983888	6	11.111111	242	1.352867
20292	GO:0044429	mitochondrial part	6.0606044E-6	0.002928196	6	11.111111	661	3.7018388
11362	GO:0019396	fatty acid oxidation	7.766657E-8	6.763351E-5	5	9.259259	43	0.24081542
12938	GO:0032259	lipid modification	1.6807688E-5	0.0097954065	5	9.259259	106	0.593638
16857	GO:0034440	lipid oxidation	7.766657E-8	6.763351E-5	5	9.259259	43	0.24081542
20202	GO:0044283	small molecule biosynthetic process	1.8157081E-5	0.008851662	5	9.259259	451	2.5257816
4261	GO:0006900(GO:0006087)	pyruvate metabolic process	6.891167E-5	0.018937081	4	7.4074073	43	0.24081542
4262	GO:0006901	generation of precursor metabolites and energy	1.2851076E-5	0.005595479	4	7.4074073	280	1.5681003
4263	GO:0006900	glucogenesis	6.203296E-6	0.002928196	4	7.4074073	24	0.13440861
4589	GO:0006519	cellular amino acid and derivative metabolic process	2.7302689E-5	0.009658876	4	7.4074073	308	1.7249104
4590	GO:0006520	cellular amino acid metabolic process	5.5848763E-5	0.017087676	4	7.4074073	261	1.4616935
4700	GO:0006635	fatty acid beta-oxidation	1.7875504E-5	0.008851662	4	7.4074073	31	0.1736111
4911	GO:0008387(GO:0016194)(GO:0016195)	axocytosis	4.8270303E-4	0.07591444	4	7.4074073	126	0.70564514
6377	GO:0009062	fatty acid catabolic process	1.7855429E-6	9.479923E-4	4	7.4074073	40	0.2241434
6379	GO:0009064	glutamine family amino acid metabolic process	1.0452608E-5	0.004733211	4	7.4074073	57	0.31922042
9254	GO:0016054	organic acid catabolic process	1.565747E-8	1.6113878E-5	4	7.4074073	126	0.70564514
11288	GO:0019319	hexose biosynthetic process	1.5629736E-5	0.006553285	4	7.4074073	30	0.16801076
11052	GO:0034637	cellular carbohydrate biosynthetic process	4.4716681E-4	0.074542749	4	7.4074073	70	0.39220508
20025	GO:0044106	cellular amine metabolic process	4.3171964E-4	0.072945446	4	7.4074073	352	1.9713261
20161	GO:0044242	cellular lipid catabolic process	7.3200616E-5	0.020211663	4	7.4074073	85	0.47603047
20167	GO:0044248	cellular catabolic process	8.693695E-5	0.02343283	4	7.4074073	1882	9.419903
21400	GO:0046165	alcohol biosynthetic process	1.034687E-4	0.02662119	4	7.4074073	48	0.26881722
21568	GO:0046364	monosaccharide biosynthetic process	3.2819313E-5	0.01125686	4	7.4074073	38	0.2018129
21596	GO:0046395	carboxylic acid catabolic process	1.565747E-8	1.6113878E-5	4	7.4074073	126	0.70564514
30	GO:0000038	very long-chain fatty acid metabolic process	2.1062282E-4	0.040413324	3	5.5555553	23	0.12880825
3799	GO:0005496	steroid binding	4.7255788E-4	0.07642371	3	5.5555553	71	0.39762545
4611	GO:0006444	glutamine metabolic process	1.3708798E-4	0.031514384	3	5.5555553	20	0.11200717
4702	GO:0006637	acyl-CoA metabolic process	4.4752804E-5	0.01447516	3	5.5555553	14	0.078405015
4791	GO:0006732(GO:0006752)	coenzyme metabolic process	1.2436652E-7	9.386061E-5	3	5.5555553	160	0.89605737
9441	GO:0016289	CoA hydrolase activity	5.5734665E-5	0.017087676	3	5.5555553	15	0.08405038
9443	GO:0016291(GO:0008778)(GO:0016292)	acyl-CoA thioesterase activity	2.0512542E-5	0.007490813	3	5.5555553	11	0.06160394
15931	GO:0033500	steroid catabolic process	1.5271563E-4	0.031514384	3	5.5555553	53	0.296819
17785	GO:0035833	thioester metabolic process	4.4752804E-5	0.01447516	3	5.5555553	14	0.078405015
18588	GO:0042593	glucose homeostasis	1.5271563E-4	0.031514384	3	5.5555553	53	0.296819
25157	GO:0051186	cofactor metabolic process	1.00181786E-7	8.1008744E-5	3	5.5555553	207	1.1592742
4606	GO:0006536	glutamate metabolic process	1.3708798E-4	0.031514384	2	3.7037036	20	0.11200717
4768	GO:0006708	steroid catabolic process	1.962282E-4	0.040413324	2	3.7037036	23	0.12880825
9196	GO:0015980	energy derivation by oxidation of organic compounds	6.395557E-7	4.293311E-4	2	3.7037036	142	0.7925209
9442	GO:0016290(GO:0016293)	palmitoyl-CoA hydrolase activity	5.3056213E-4	0.08008407	2	3.7037036	7	0.039202508
15370	GO:0032934(GO:0005498)	steroid binding	2.7152587E-4	0.048791237	2	3.7037036	25	0.14000896
15971	GO:0033540	fatty acid beta-oxidation using acyl-CoA oxidase	5.3056213E-4	0.08008407	2	3.7037036	7	0.039202508
16120	GO:0033695	oxalotransferase activity, acting on CH or CH2 groups, quinone or similar compound as acceptor	1.5310886E-4	0.031514384	2	3.7037036	4	0.02241433
17290	GO:0034875	caffeine oxidation	1.5310886E-4	0.031514384	2	3.7037036	4	0.02241433
20612	GO:0045333	cellular respiration	1.18166370E-4	0.02908086	2	3.7037036	94	0.5264337

Significantly enriched Gene Ontology (GO) terms up-regulated in the hepatocytes

GO ID	GO ACCESSION	GO Term	p-value	corrected p-value	Count in Selection	% Count in Selection	Count in Total	% Count in Total
1562	GO:0002376	immune system process	3.677121E-12	6.5012102E-9	28	68.29269	1034	5.7907705
4964	GO:0006955	immune response	1.4757004E-12	3.0651428E-9	28	68.29269	670	3.7522402
4080	GO:0005887	integral to plasma membrane	1.14432696E-4	0.08318992	22	53.658535	1257	7.0396504
20282	GO:0044419	interspecies interaction between organisms	7.3517453E-10	1.1876774E-6	17	41.463413	348	1.9489248
25661	GO:0051704(GO:0051706)	multi-organism process	1.3370409E-7	1.9439956E-4	17	41.463413	781	4.37388
4961	GO:0006952(GO:0002217)(GO:0042829)	defense response	1.1787167E-6	0.02326235	12	29.268293	644	3.6063308
11793	GO:0019882(GO:0030333)	antigen processing and presentation	1.033701E-15	3.7573833E-12	12	29.268293	73	0.40882617
1660	GO:0002474	antigen processing and presentation of peptide antigen via MHC class I	1.875959E-20	2.7275575E-16	11	26.829268	28	0.15681003
18603	GO:0042611	MHC protein complex	2.2178988E-15	6.449443E-12	11	26.829268	46	0.2576165
18604	GO:0042612	MHC class I protein complex	4.479748E-16	2.171153E-12	11	26.829268	30	0.1680176
23156	GO:0048002	antigen processing and presentation of peptide antigen	1.6743372E-18	1.2127044E-14	11	26.829268	37	0.20721327
14832	GO:0032393	MHC class I receptor activity	3.54134E-15	8.581574E-12	10	24.390244	25	0.14000896
14345	GO:0031901	early endosome membrane	8.606433E-5	0.07360797	5	12.195122	54	0.30241936
1439	GO:0002253	activation of immune response	2.4822812E-5	0.027752476	4	9.756098	103	0.57683694
1641	GO:0002455	humoral immune response mediated by circulating immunoglobulin	1.2295373E-4	0.085128106	4	9.756098	31	0.1736111
1712	GO:0002526	acute inflammatory response	8.180872E-6	0.009912174	4	9.756098	87	0.482312
4967	GO:0006958	complement activation, classical pathway	9.402098E-5	0.07594564	4	9.756098	29	0.1624104
24757	GO:0050778	positive regulation of immune response	4.3423148E-5	0.045096606	4	9.756098	153	0.85685486
24045	GO:0005051	leukotriene-B4 20-monooxygenase activity	6.91678E-5	0.06285423	2	4.878049	2	0.011200717

Gene Ontology (GO) analysis showing the gene transcripts in cAMP-induced cells (green) and primary hepatocyte (purple) from Table S9 (Fig. 7A). The cluster showing enhanced expression in the cAMP(+) treated cells is enriched for genes related to liver function. The cluster expressed at the highest level in the primary hepatocytes contains immune system, inflammatory and MHC genes.

# Table S3. Phase I drug metabolism enzyme

## cAMP(+) versus primary hepatocyte

Gene Symbol	Affymetrix ID	Fold Change	cAMP(+) versus hepatocyte	Direction of fold change	Corrected p-value	p-value	Significant in post-hoc Tukey (P<0.1)
CYP1A1	7990391	46.071194	up	up	0.012067234	0.00334378	*
CYP3A7	8141342	21.097319	up	up	0.017114632	0.0059243	*
CYP2C8 CYP2C19	7935169	16.09552	up	up	0.012067234	0.00241581	*
CYP2E1	7931643	9.311104	down	down	0.012067234	0.00289097	*
CYP7A1	8150920	9.042042	up	up	0.012067234	0.00305444	*
FMO3	7907249	5.937933	down	down	0.012067234	0.003713	*
CYP1A2	7984862	5.2238216	up	up	0.012067234	9.765099E-4	*
CYP3A4	8141317	3.6115234	up	up	0.012067234	0.00104858	*
CYP8B1	8086457	2.8518157	up	up	0.012067234	0.0037024	*
CYP2C19	7929478	2.6333666	up	up	0.5220973	0.48193598	
CYP3A5	8141328	2.5988102	up	up	0.110070765	0.06350236	
CYP2C18	7929466	2.417497	up	up	0.20925228	0.15291514	
CYP1B1	8051583	2.1679187	up	up	0.1742982	0.12066799	
FMO5	7919314	2.101705	up	up	0.121317275	0.07465679	
ADH4	8101852	1.9780805	down	down	0.01808588	0.00695611	*
CYP7B1	8151056	1.4362873	up	up	0.08954843	0.04477422	*
CYP2B6	8028963	1.4358941	up	up	0.071706966	0.03309552	*
ADH6	8101862	1.3970135	up	up	0.095975235	0.05167897	*
CYP2C9	7929487	1.3147879	up	up	0.4188202	0.35438633	
ALDH2	7958784	1.1899356	down	down	0.06618735	0.02800234	*
CYP2D6	8076424	1.1894984	up	up	0.34041327	0.2749492	
ADH1B	8101881	1.176147	up	up	0.1742982	0.11466285	*
ADH1C	8101893	1.1680543	down	down	0.6280842	0.6039271	
CYP2A13 CYP2A6 CYP2A7	8028973	1.0301366	down	down	0.2404887	0.1849913	*
ADH1A	8101874	1.0277959	down	down	0.4814003	0.42585412	
FMO4	7907297	1.0077161	down	down	0.8514573	0.8514573	

## cAMP(+) versus cAMP (-)

Gene Symbol	Affymetrix ID	Fold change	cAMP(+) versus	Direction of fold change	p-value	Corrected p-value	Significant in post-hoc Tukey (P<0.1)
CYP2C8 CYP2C19	7935169	17.61894	up	up	0.012067234	0.002415811	*
CYP8B1	8086457	9.690104	up	up	0.012067234	0.0037024	*
CYP7A1	8150920	8.396973	up	up	0.012067234	0.003054444	*
CYP3A4	8141317	5.700867	up	up	0.012067234	0.001048583	*
CYP1A2	7984862	5.6071825	up	up	0.012067234	9.765099E-4	*
ADH1B	8101881	4.874928	up	up	0.1742982	0.11466285	*
CYP2B6	8028963	4.513215	up	up	0.071706966	0.033095524	*
CYP1A1	7990391	3.9629219	up	up	0.012067234	0.003343782	*
CYP1B1	8051583	3.9326298	up	up	0.1742982	0.12066799	*
CYP2C9	7929487	2.832749	up	up	0.4188202	0.35438633	
CYP2C18	7929466	2.1275349	up	up	0.20925228	0.15291514	
ADH1A	8101874	2.0610342	up	up	0.4814003	0.42585412	
FMO5	7919314	1.9418982	up	up	0.121317275	0.074656785	
CYP3A7	8141342	1.670188	up	up	0.017114632	0.005924296	*
CYP3A5	8141328	1.5908221	up	up	0.110070765	0.063502364	*
CYP2D6	8076424	1.4976844	up	up	0.34041327	0.2749492	
ADH6	8101862	1.4162867	down	down	0.095975235	0.051678974	*
CYP2A13 CYP2A6 CYP2A7	8028973	1.3861729	up	up	0.2404887	0.1849913	*
ADH1C	8101893	1.3693517	up	up	0.6280842	0.6039271	
CYP2C19	7929478	1.3029042	up	up	0.5220973	0.48193598	
ALDH2	7958784	1.2843883	up	up	0.06618735	0.028002342	*
CYP7B1	8151056	1.1916578	up	up	0.08954843	0.044774216	*
ADH4	8101852	1.1621644	down	down	0.01808588	0.006956108	*
CYP2E1	7931643	1.1376745	up	up	0.012067234	0.002890972	*
FMO4	7907297	1.1074113	down	down	0.8514573	0.8514573	
FMO3	7907249	1.027153	up	up	0.012067234	0.003712995	*

A comparison of expression levels of a selected group of Phase I drug metabolism genes between cAMP-treated hepatocyte-like cells and primary hepatocytes (blue) and between cAMP-treated and non-treated hepatocyte-like cells (green).

# Table S4. Phase II drug metabolism enzyme

## cAMP(+) versus primary hepatocyte

Gene Symbol	Affymetrix ID	Fold Change	cAMP(+) VS Hepatocyte	Direction of Fold Change	Corrected p-value	p-value	Significant in Post-hoc Tukey (p<.1)
GSTA2	8127065	8.09758	up	up	0.045971643	0.0204318	*
SULT2A1	8037949	4.501422	up	up	0.008581583	0.0012713	*
EPHX1	7910111	4.0225717	up	up	0.012243672	0.0022673	*
CES1	8001457	3.9624193	down	down	7.7732874E-4	8.636986E-5	*
EPHX2	8145532	3.5328372	up	up	0.016735837	0.0050373	*
UGT2B7	8095395	3.345876	up	up	0.1260292	0.0793522	*
GSTA1	8127072	2.7610693	up	up	0.47513044	0.4223382	*
UGT2B7	8100758	2.7340186	up	up	0.23812853	0.1763915	*
UGT2A3	8100760	2.3408983	up	up	0.1260292	0.0792332	*
GSTM2 GSTM4	7903753	2.218478	up	up	0.016735837	0.0061985	*
UGT3A1	8111512	1.8036636	down	down	0.10196026	0.0566446	*
NAT2	8144866	1.7318547	down	down	9.925069E-6	8759516E-	*
SULT1E1	8100808	1.4051794	up	up	8.63045E-5	.3929256E-	*
SULT1A3 GIYD1 GIYD2 SULT1A2 SULT1A4	7994582	1.4016013	up	up	0.22789103	0.1603678	*
UGT1A1 UGT1A6 UGT1A10 UGT1A9 UGT1A4 UGT1A3 UGT1A5 UGT1A7 UGT1A8	8049349	1.4001894	up	up	0.016735837	0.0050807	*
UGT2B4	8100784	1.3852446	up	up	0.016735837	0.0059566	*
SULT1A2	8000582	1.3303971	down	down	0.59399104	0.5499917	*
UGT2B28	8095404	1.3045363	down	down	0.07000782	0.0337075	*
GSTA3	8127087	1.2955159	up	up	0.0954211	0.0494776	*
SULT1A1	8000590	1.2795404	down	down	0.43535653	0.3708593	*
GSTK1	8136849	1.2583706	up	up	0.03604819	0.0146863	*
CES2	7996345	1.1977214	up	up	0.016735837	0.0052718	*
UGT2B17	8100734	1.1170508	up	up	0.3367106	0.2743568	*
GSTM2	7919578	1.1149895	up	up	0.22247058	0.1483137	*
GSTO1	7930304	1.0659491	up	up	0.9567845	0.9567845	*
UGT2A1 UGT2A2	8100791	1.0262581	up	up	0.3367106	0.2642122	*

## cAMP(+) versus cAMP (-)

Gene Symbol	Affymetrix ID	Fold Change	cAMP(+) VS cAMP(-)	Direction of Fold Change	p-value	Corrected p-value	Significant in Post-hoc Tukey (p<.1)
UGT1A1 UGT1A6 UGT1A10 UGT1A9 UGT1A4 UGT1A3 UGT1A5 UGT1A7 UGT1A8	8049349	9.1351	up	up	0.016735837	0.005080654	*
SULT2A1	8037949	4.9485445	up	up	0.008581583	0.001271346	*
EPHX1	7910111	4.8572507	up	up	0.012243672	0.002267347	*
CES1	8001457	4.7324866	down	down	7.7732874E-4	8.636986E-5	*
SULT1E1	8100808	4.077046	down	down	8.63045E-5	6.3929256E-6	*
GSTA1	8127072	3.6004374	up	up	0.47513044	0.42233816	*
GSTA2	8127065	3.5906198	up	up	0.045971643	0.02043184	*
UGT2B7	8095395	3.5550961	up	up	0.1260292	0.0793522	*
UGT2B4	8100784	3.4201937	up	up	0.016735837	0.005595609	*
CES2	7996345	3.3923113	up	up	0.016735837	0.005271834	*
UGT2B7	8100758	2.0410874	up	up	0.23812853	0.1763915	*
EPHX2	8145532	2.0409768	up	up	0.016735837	0.005037259	*
UGT2A3	8100760	1.3768438	down	down	0.1260292	0.07923323	*
GSTA3	8127087	1.3496046	up	up	0.0954211	0.049477607	*
SULT1A3 GIYD1 GIYD2 SULT1A2 SULT1A4	7994582	1.2940637	up	up	0.22789103	0.16036776	*
GSTK1	8136849	1.227205	up	up	0.03604819	0.0146863	*
SULT1A2	8000582	1.1342998	down	down	0.59399104	0.5499917	*
GSTO1	7930304	1.064542	up	up	0.9567845	0.9567845	*
UGT2A1 UGT2A2	8100791	1.0529388	up	up	0.3367106	0.2642122	*
NAT2	8144866	1.0509216	down	down	9.925069E-6	3.6759516E-7	*
UGT2B28	8095404	1.0417112	down	down	0.07000782	0.03370747	*
NAT1	8144857	1.0342079	down	down	0.7743908	0.74570966	*
UGT2B17	8100734	1.0268425	down	down	0.3367106	0.27435678	*
GSTM2 GSTM4	7903753	1.0195614	down	down	0.016735837	0.006198458	*
SULT1A1	8000590	1.0132033	down	down	0.43535653	0.37085927	*
UGT3A1	8111512	1.0086902	up	up	0.10196026	0.056644585	*
GSTM2	7919578	1.0031872	up	up	0.22247058	0.14831372	*

# Transporters

## cAMP(+) versus primary hepatocyte

Gene Symbol	Affymetrix ID	Fold Change	cAMP(+) VS Hepatocyte	Direction of Fold Change	Corrected p-value	p-value	Significant in post-hoc Tukey (P<0.1)
ABCB1	8140782	5.399585	down	down	0.074096315	0.03554574	*
ABCB4	8140752	4.592113	down	down	0.01389056	0.00231509	*
ABCB11	8056583	3.9600024	up	up	0.01389056	0.00126014	*
SLCO1B1	7954356	3.4501076	up	up	0.036024522	0.00900613	*
SLC10A1	7979878	1.8501159	down	down	0.39103138	0.3258595	*
SLCO2B1	7942569	1.7992761	up	up	0.47115463	0.43488163	*
ABCC3	8008454	1.562891	down	down	0.074096315	0.03704816	*
ABCC2	7929779	1.5118597	up	up	0.07192941	0.02397647	*
SLC22A10	7940737	1.436169	down	down	0.47115463	0.47115463	*
SLCO1B3	7954344	1.2984133	down	down	0.12872237	0.07508805	*
SLC22A7	8119782	1.2072212	up	up	0.13624907	0.09083271	*
SLCO1A2	7961626	1.082006	up	up	0.16357224	0.12267918	*

## cAMP(+) versus cAMP (-)

Gene Symbol	Affymetrix ID	Fold change	cAMP(+) VS cAMP(-)	Direction of Fold Change	p-value	Corrected p-value	Significant in post-hoc Tukey (P<0.1)
SLCO1B1	7954356	10.375665	up	up	0.0360245	0.009006131	*
ABCC2	7929779	3.5463655	up	up	0.0719294	0.023976471	*
ABCB11	8056583	2.6618686	up	up	0.0138906	0.001260135	*
SLCO2B1	7942569	1.8878269	up	up	0.4711546	0.43488163	*
SLC22A7	8119782	1.8327168	up	up	0.1362491	0.09083271	*
SLC10A1	7979878	1.3948876	up	up	0.3910314	0.3258595	*
ABCB4	8140752	1.1143088	down	down	0.0138906	0.002315093	*
ABCB1	8140782	1.0972914	down	down	0.0740963	0.035545744	*
ABCC3	8008454	1.0846786	up	up	0.0740963	0.037048157	*
SLCO1B3	7954344	1.052959	up	up	0.1287224	0.07508805	*
SLC22A10	7940737	1.0351869	down	down	0.4711546	0.47115463	*
SLCO1A2	7961626	1.015178	up	up	0.1635722	0.12267918	*

A comparison of expression levels of a selected group of Phase II drug metabolism and transporters genes between cAMP-treated hepatocyte-like cells and primary hepatocytes (blue) and between cAMP-treated and non-treated hepatocyte-like cells (green).

# Table S5. Expression levels of coagulation factors and apolipoproteins

## Coagulation factors

### cAMP(+) VS Primary Hepatocyte

Gene Symbol	Affymetrix ID	Fold Change	cAMP(+) VS Hepatocyte	Direction of	Fold Change	Corrected p-value	p-value	Significant in Post-hoc Tukey (p<.1)
F11	8098671	5.6883545		up		0.004182067	5.576089E-4	*
PLG	8123259	3.113888		up		0.002581835	1.7212232E-4	*
F13A1	8123744	2.233513		down		0.54852325	0.40225038	
F10	7970241	1.7014513		up		0.4975024	0.269627	
FGB	8097910	1.6944155		down		0.015524478	0.003104896	*
F13B	7923073	1.6196274		down		0.4975024	0.24436827	
SERPINC1	7922420	1.5490543		down		0.54852325	0.37034133	
VWF	7960464	1.5394		down		0.4975024	0.29850143	
F12	8116033	1.3436115		up		0.6435278	0.60062593	
PROC	8045018	1.245822		down		0.6435278	0.5670104	
PROS1	8089015	1.1732916		down		0.11162717	0.037209056	
F2	7939706	1.117765		down		0.92382735	0.92382735	
PROS1	8089011	1.095369		up		0.5775279	0.4620223	
F7	7970232	1.0684249		down		0.45363718	0.18145487	
F9	8170215	1.0481349		down		0.10211771	0.02723139	

### cAMP(+) VS cAMP (-)

Gene Symbol	Affymetrix ID	Fold Change	cAMP(+) VS cAMP(-)	Direction of	Fold Change	Corrected p-value	p-value	Significant in Post-hoc Tukey (p<.1)
F9	8170215	3.0743692		up		0.10211771	0.02723139	
F11	8098671	2.358331		up		0.004182067	5.576089E-4	*
FGB	8097910	1.4688783		down		0.015524478	0.003104896	*
F7	7970232	1.4170613		down		0.45363718	0.18145487	
PROS1	8089015	1.2703807		down		0.11162717	0.037209056	
F12	8116033	1.1323404		up		0.6435278	0.60062593	
PROS1	8089011	1.1102681		down		0.5775279	0.4620223	
F13B	7923073	1.1000786		down		0.4975024	0.24436827	
F10	7970241	1.0886061		down		0.4975024	0.269627	
F2	7939706	1.0793462		down		0.92382735	0.92382735	
VWF	7960464	1.0779397		down		0.4975024	0.29850143	
SERPINC1	7922420	1.0443034		up		0.54852325	0.37034133	
F13A1	8123744	1.0372078		up		0.54852325	0.40225038	
PROC	8045018	1.0074449		down		0.6435278	0.5670104	
PLG	8123259	1.0009212		up		0.002581835	1.7212232E-4	

## Apolipoproteins

### cAMP(+) VS Primary Hepatocyte

Gene Symbol	Affymetrix ID	Fold Change	cAMP(+) VS Hepatocyte	Direction of	Fold Change	Corrected p-value	p-value	Significant in Post-hoc Tukey (p<.1)
APOA1	8077185	5.7201715		up		0.006371556	0.001820445	*
APOC3	7944035	2.7706282		up		0.08003705	0.045735456	*
APOB	8050619	1.7165838		up		0.006371556	0.001291146	*
APOA2	7921834	1.5493222		up		0.15048462	0.11079896	
APOC2	8029551	1.4680355		up		0.056342013	0.024146577	
APOC1	8029536	1.1765927		up		0.31744564	0.31744564	
APOC4	8029541	1.1487213		down		0.15048462	0.12898682	

### cAMP(+) VS cAMP (-)

Gene Symbol	Affymetrix ID	Fold Change	cAMP(+) VS cAMP(-)	Direction of	Fold Change	Corrected p-value	p-value	Significant in Post-hoc Tukey (p<.1)
APOC2	8029551	2.429501		up		0.056342013	0.024146577	*
APOA1	8077185	1.8780366		up		0.006371556	0.001820445	
APOC1	8029536	1.5829909		up		0.31744564	0.31744564	
APOC3	7944035	1.4547877		up		0.08003705	0.045735456	
APOB	8050619	1.1659406		down		0.006371556	0.001291146	
APOA2	7921834	1.1425041		up		0.15048462	0.11079896	
APOC4	8029541	1.0462136		up		0.15048462	0.12898682	

A comparison of expression levels of a selected group of coagulation factor and apolipoprotein genes between cAMP-treated hepatocyte-like cells and primary hepatocytes (blue) and between cAMP-treated and non-treated hepatocyte-like cells (green).

# Table S6. Expression levels of liver related genes, nuclear receptors and transcriptional factors

## Liver genes of interest

### cAMP(+) VS Primary Hepatocyte

Gene Symbol	Affymetrix ID	Fold Change	cAMP(+) VS Hepatocyte	Direction of	Fold Change	Corrected p-value	p-value	Significant in	Post-hoc Tukey (p<.1)
AFP	8095646	65.93792		up		1.00699835E-4	4.378254E-6	*	*
AGXT	8049737	4.618539		up		0.013570489	0.006858653	*	*
AKR1C4	7925939	1.1564364		up		0.028816327	0.021172486	*	*
AKR1D1	8136459	4.816972		up		0.010609764	0.003690352	*	*
ALB	8095628	2.048784		up		0.047936797	0.039599963	*	*
ALDOB	8162884	2.979772		up		0.013570489	0.007301067	*	*
ARG1	8122058	4.721421		up		0.013570489	0.007670276	*	*
ASGR1	8012043	2.2643049		up		0.011706066	0.005089594	*	*
ASGR2	8012028	1.2812967		up		0.47513378	0.4544758	*	*
BAAT	8162870	4.6314807		up		0.020830221	0.013584927	*	*
CPS1	8048026	5.977915		up		0.038876355	0.030424973	*	*
CPT1A	7949971	6.476342		up		5.8171514E-4	1.01167854E-4	*	*
CTPS	7900510	1.7996519		up		0.004022882	0.001224356	*	*
FAH	7985268	2.0180252		up		0.06254039	0.05710209	*	*
G6PC	8007429	22.897436		up		0.001131729	2.5702044E-4	*	*
HMGCS2	7919055	34.45101		up		0.001131729	2.9523356E-4	*	*
HP	7997188	3.59377		down		0.01160576	0.004541385	*	*
OTC	8166769	3.481216		up		0.058319274	0.050712414	*	*
PCK1	8063590	30.076572		up		3.0852502E-4	2.6828262E-5	*	*
PCK2	7973530	1.0236868		up		0.9756709	0.9756709	*	*
POR	8133670	4.5288434		up		5.665288E-4	7.389506E-5	*	*
TAT	8002556	6.752994		up		0.01819622	0.01107596	*	*
TDO2	8097991	5.6013775		up		0.028816327	0.021299025	*	*

### cAMP(+) VS cAMP (-)

Gene Symbol	Affymetrix ID	Fold Change	cAMP(+) VS cAMP(-)	Direction of	Fold Change	Corrected p-value	p-value	Significant in	Post-hoc Tukey (p<.1)
PCK1	8063590	33.72393		up		3.0852502E-4	2.6828262E-5	*	*
TAT	8002556	17.730682		up		0.01819622	0.01107596	*	*
G6PC	8007429	14.40543		up		0.001131729	2.5702044E-4	*	*
ARG1	8122058	9.107302		up		0.013570489	0.007670276	*	*
ALDOB	8162884	5.797745		up		0.013570489	0.007301067	*	*
CPT1A	7949971	5.121549		up		5.8171514E-4	1.01167854E-4	*	*
BAAT	8162870	5.0343623		up		0.020830221	0.013584927	*	*
POR	8133670	4.5395484		up		5.665288E-4	7.389506E-5	*	*
CPS1	8048026	3.4659047		up		0.038876355	0.030424973	*	*
AGXT	8049737	3.361046		up		0.013570489	0.006858653	*	*
HMGCS2	7919055	3.0780334		up		0.001131729	2.9523356E-4	*	*
CTPS	7900510	3.069189		up		0.004022882	0.001224356	*	*
TDO2	8097991	3.0548642		up		0.028816327	0.021299025	*	*
OTC	8166769	2.8020606		up		0.058319274	0.050712414	*	*
FAH	7985268	2.1173558		up		0.06254039	0.05710209	*	*
AKR1C4	7925939	1.9009632		up		0.028816327	0.021172486	*	*
ASGR1	8012043	1.5339662		up		0.011706066	0.005089594	*	*
HP	7997188	1.353287		down		0.01160576	0.004541385	*	*
AFP	8095646	1.3416045		down		1.00699835E-4	4.378254E-6	*	*
AKR1D1	8136459	1.2814606		down		0.010609764	0.003690352	*	*
ASGR2	8012028	1.0487944		up		0.47513378	0.4544758	*	*
PCK2	7973530	1.0429556		up		0.9756709	0.9756709	*	*
ALB	8095628	1.0322695		up		0.047936797	0.039599963	*	*

## Nuclear Receptors and Transcriptional Factors

### cAMP(+) VS Primary Hepatocyte

Gene Symbol	Affymetrix ID	Fold Change	cAMP(+) VS Hepatocyte	Direction of	Fold Change	Corrected p-value	p-value	Significant in	Post-hoc Tukey (p<.1)
PPARGC1A	8099633	8.664994		up		6.924728E-4	6.924728E-5	*	*
PPARA	8073826	4.299654		up		0.006155438	0.001846631	*	*
RXRA	8159127	3.0369213		up		0.060834873	0.038636036	*	*
HNF4A	8062823	2.534574		up		0.006155438	0.001739987	*	*
NR1I3	7921840	2.3120933		up		0.05959569	0.023838276	*	*
NR1H4	7957835	1.6012238		up		0.5780357	0.52023214	*	*
HNF4G	8146986	1.5168575		up		0.060834873	0.04258441	*	*
NR1I2	8081925	1.5157825		down		0.117566794	0.09405343	*	*
AHR	8131614	1.4667602		up		0.060834873	0.032607585	*	*
RARA	8007084	1.119617		down		0.6022417	0.6022417	*	*

### cAMP(+) VS cAMP (-)

Gene Symbol	Affymetrix ID	Fold Change	cAMP(+) VS cAMP(-)	Direction of	Fold Change	Corrected p-value	p-value	Significant in	Post-hoc Tukey (p<.1)
PPARGC1A	8099633	5.670558		up		6.924728E-4	6.924728E-5	*	*
RXRA	8159127	2.6896641		up		0.060834873	0.038636036	*	*
PPARA	8073826	2.247845		up		0.006155438	0.001846631	*	*
NR1I3	7921840	1.9786081		up		0.05959569	0.023838276	*	*
HNF4A	8062823	1.7265012		up		0.006155438	0.001739987	*	*
AHR	8131614	1.4156159		down		0.060834873	0.032607585	*	*
HNF4G	8146986	1.1821347		down		0.060834873	0.04258441	*	*
RARA	8007084	1.0773768		up		0.6022417	0.6022417	*	*
NR1I2	8081925	1.0684412		up		0.117566794	0.09405343	*	*
NR1H4	7957835	1.0335269		down		0.5780357	0.52023214	*	*

A comparison of expression levels of a selected group of liver-related genes, nuclear receptors and transcriptional factors between cAMP-treated hepatocyte-like cells and primary hepatocytes (blue) and between cAMP-treated and non-treated hepatocyte-like cells (green).

Table S7. Antibody lists

Primary Antibody List (related to Figure1-6)

Antibody	Company	Product Codes	Ig Species	Conjugate	Dilution
AFP	DAKO	A0008	Rabbit	none	1:4000(Flow), 1:2000 (Immuno)
ALB	Bethyl	A80-129A	Goat	none	1:200(Flow), 1:400(Immuno)
ALB	DAKO	A0001	Rabbit	none	1:400(Flow), 1:4000(Immuno)
E-cadherin	BD Biosciences	610181	Mouse	none	1:200 (Immuno)
HNF4 $\alpha$	Santa Cruz	sc-6556	Goat	none	1:200(Immuno)
ASGPR1	Santa Cruz	SC13467	Goat	none	1:100(Flow), 1:100(Immuno)
CD117 (c-KIT)	BD Pharmingen	BD 340529	Mouse IgG1	PE	1:50(Flow)
CD117 (c-KIT)	Invitrogen	CD11705	Mouse IgG1	APC	1:100(Flow)
CD184(CXCR4)	BD Pharmingen	BD 555974	Mouse IgG1	PE	1:100(Flow)
CD184(CXCR4)	BD Pharmingen	BD 555976	Mouse IgG1	APC	1:50(Flow)
CD31	BD Pharmingen	BD 555456	Mouse IgG1	PE	1:10 (Flow)
CD326(EPCAM)	eBioscience	12-9326-73	Mouse IgG1	PE	1:20(Flow)
CD90	BioLegend	328110	Mouse IgG1	PE	1:400(Flow)
FOXA2	Abcam	Ab40874	Rabbit	none	1:50 (Flow)
SOX17	R&D	AF1924	Goat	none	1:40(Flow), 1:100(Immuno)

IgG control List

IgG Control	Company	Product Code	Concentration (Stock)
Goat IgG	Sigma	Sigma I5256	1mg/ml
Rabbit IgG	Jackson ImmunoResearch	001-000-003	11mg/ml

Secondary Antibody List

Antibody	Company	Product Code	Dilution
IgG goat anti-Mouse cy3	Jackson ImmunoResearch	115-166-071	1:300
IgG Donkey anti Rabbit Cy3	Jackson ImmunoResearch	711-165-152	1:300
IgG F(ab') <sub>2</sub> Donkey anti- Rabbit (PE)	Jackson ImmunoResearch	711-116-152	1:300
IgG Donkey anti-Goat Alexa 488	Invitrogen	A11055	1:400
IgG goat anti-Rabbit Alexa 488	Invitrogen	A11008	1:400

Primary antibody list for flow cytometry and immunofluorescence analysis.

IgG control for flow cytometry and immunofluorescence analysis.

Secondary antibody list for flow cytometry and immunofluorescence analysis.

Table S8. Quantitative PCR primer and RNA RNA lists  
qPCR primer list (=related to Figs 1-6)

Gene	Sequences (Forward)	Sequences (Reverse)
AFP	5'- ACAGAGGAACAACCTTGAGGCTGTC-3'	5'- AGCAAAGCAGACTTCCTGTTCTG-3'
ALB	5'- GTGAAACACAAGCCCAAGGCAACA-3'	5'- TCAGCCTTGCAGCACTTCTCTACA -3'
BRY (T)	5'- TGTCCCAGGTGGCTTACAGAT GAA -3'	5'- GGTGTGCCAAAGTTGCCAATACAC -3'
CD31	5'- TTCCTGACAGTGTCTTGAGTGGGT-3'	5'- TTTGGCTAGGCGTGGTTCTCATCT-3'
CD90	5'- ATACCAGCAGTTCACCCATTCAGT-3'	5'- AATTGCTGGTGAAGTTGGTTCGGG-3'
CPS1	5'- AATCTCGCAAGGTGGACTCCAAGA-3'	5'- GGTGTCTGCATCTCTATGCTGCTT-3'
CYP1A2	5'- ATGATGCTGTTTGGCATGGGCAAC-3'	5'- GAACTCCAGTTGCTGTAGCAGGAT-3'
CYP2B6	5'- TCTTCCAGTCCATTACCGCCAACA-3'	5'- GCCGAATACAGAGCTGATGAGTGA-3'
CYP3A4	5'- TTGAGTCAAGGGATGGCACCGTAA-3'	5'- TCTCTGGTGTCTCAGGCACAGAT-3'
CYP3A7	5'- GCACATCATTTGGAGTGAGCATCG-3'	5'- TGAGAGAACGAATGGATCTAATGGA-3'
CYP7A1	5'- TTACAGGACTGCAGAACACCCTCA-3'	5'- GCACTGGTGAACAACATTGGACCT -3'
FOXA2	5'- GCATTCCCAATCTTGACACGGTGA-3'	5'- GCCCTTGCAGCCAGAATACACATT-3'
G6P	5'- CTGTCAGGCATTGCTGTTGCAGAA-3'	5'- ATGGCGAAGCTGAACAGGAAGAAG-3'
GSC	5'- ACGATGCTACTTTCTTGACACGC-3'	5'- ACCCTCCCGCTCTGTACACTATTTA-3'
HEX	5'- TGGATAGCTCTCAATGTTCCGCCT-3'	5'- TATCGCCCTCAATGTCCACTTCCT-3'
HNF4 $\alpha$	5'- TTCTCCAAAGGCTCCCTGTGTTCT-3'	5'- AACGAGTCTGGTTTCTGAGGCTGT-3'
MEOX1	5'- TGAGGACTGATGCCAAAGAGCAT-3'	5'- ATCCAAACTCACGTTGACCTCCCT-3'
MESP1	5'- AGCCCAAGTGACAAGGGACAAC-3'	5'- AAGGAACCACTTCGAAGGTGCTGA-3'
OCT4	5'- ATGCATTCAAACCTGAGGTGCCTGC-3'	5'- CCACCCTTTGTGTTCCCAATTCCT-3'
PGC1 $\alpha$	5'- GACACTGTGGGTAGCCCATCAA-3'	5'- ACTTACCACGGCATGAAGGCAATG-3'
SOX17	5'- AGGAAATCCTCAGACTCCTGGGTT-3'	5'- CCCAAACTGTTCAAGTGGCAGACA-3'
TAT	5'- ACCCGAATTTTCATCCGAGTGGTCA-3'	5'- AGCACAATGGTAGTGCTGCTCACA -3'
TDO	5'- GTGATAGCTCCTACTTCAGCAGTG-3'	5'- ATCAGAGCATCGTGGTGTGTAACA-3'
UGT1A1	5'- GAGAGAGGTGACTGTCCAGGAC-3'	5'- CAAATTCCTGGGATAGTGGATTTT-3'
TBP	5'- TGAGTTGCTCATACCCTGCTGCTA-3'	5'- CCCTCAAACCAACTTGTCAACAGC-3'
TBP (for UGT1A1)	5'- TGTGCACAGGAGCCAAGAGT-3'	5'- ATTTTCTTGCTGCCAGTCTGG-3'

## RNA list (related to Figs 1-7)

	RNA	Source	Sex	Lot	Company	Product number
AL1	human adult liver	51-years old	male	7030173	Clontech	636531
AL2	human adult liver	pooled from 30,44 and 55 years old 3 individual	male and female	603161	Agilent Technologies	540017
FL1	human fetal liver	pooled from 63 sponatneously aborted fetus, aged 22-40 weeks	male and female	7030173	Clontech	636540
FL2	human fetal liver	20 weeks fetus	female	601607	BioChain	R1244149-50
PH1	primary cultured hepatocyte	1- year-old	male	HH1892	from Stephen Strom	
PH2	primary cultured hepatocyte	14 months- old	male	HH1901	from Stephen Strom	
PH3	Human hepatocyte	48- years old	male	ZBH2199	Zenbio	RNA-L10-2

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[Download Table S10](#)

[Download Table S11](#)