

Supporting Information Materials and Methods

Culture of mouse embryonic stem cell (mES) and iPS cells without feeder cells.

mES and iPS cells were maintained as undifferentiated cells on gelatin coated plates as a feeder free culture as described in [31] with some modifications. Specifically, cells were cultured in mESC media containing 10% FBS supplemented with 6-bromoindirubin-3'-oxime (BIO), a specific inhibitor of glycogen synthase kinase-3 (GSK-3).

Purification of mES and iPS cells from feeder by MACS and FACS.

Ten million of mESC and iPSC with feeder cells were resuspended in 100 μ l of MACS buffer (0.5% BSA and 2mM EDTA in PBS) containing 2 μ g of mouse Fc block (BD Biosciences, San Jose, CA). The cells were incubated with 5 μ l of anti-SSEA-1 conjugated with Phycoerythrin (PE, Santa Cruz Biotechnology, Santa Cruz, CA) for 15 min on ice, followed by incubation with 100 μ l of MACS buffer containing PE-microbeads for 15 min on ice and MACS purification (Miltenyi Biotec, Auburn, CA). The purity of SSEA1-positive cells was analyzed by FACS using FACSCalibur (BD Biosciences, San Jose, CA) and the CellQuest program (BD Biosciences, San Jose, CA). Mouse IgM-PE (Santa Cruz) was used as an isotype control.

Supporting Information Table S1. Primer sequences used in quantitative PCR analysis

Gene		Primer sequences for QPCR	Annealing temperatures
Nanog	F	5'-ATGCCTGCAGTTTTTCATCC-3'	60
	R	5'-GAGCTTTTGTGGGACTGG-3'	
Sox2	F	5'-CAACTCGGAGATCAGCAAGC-3'	60
	R	5'-CGGGAAGCGTGTACTTATCC-3'	
Oct4	F	5'-GAGGAGTCCCAGGACATGAA-3'	60
	R	5'-AGATGGTGGTCTGGCTGAAC-3'	
HNF4a	F	5'-TGACGGGACCAAGTACAACC-3'	60
	R	5'-GTCTGCTTCTGACCCTCTCC-3'	
AFP	F	5'-CCAGGAAGTCTGTTTCACAGAAG-3'	60
	R	5'-CAAAAGGCTCACACCAAAGAG-3'	
Albumin	F	5'-ACACAAGCCCAAGGCTAC-3'	60
	R	5'-TGCATCTAGTGACAAGTTTGG-3'	
CK18	F	5'-GACTGGGGCCACTACTTCAA-3'	60
	R	5'-CATCTACCACCTTGCGGAGT-3'	
G6P	F	5'-TCTGTCCCGGATCTACCTTG-3'	60
	R	5'-GTCCACCCCTAGCCCTTTTA-3'	
Lman2l	F	5'-ACGGGAGCACTCGCTGTCTCGA-3'	57
	R	5'-GCACCCGGTTCCACAAGGCA-3'	
Irf1	F	5'-TCTGTTCCGGAGCTGGGCCA-3'	57
	R	5'-CGCACAGCAGAGCTGCCCTT-3'	
Maml1	F	5'-CAGCAGGGCTTGCCTGGCTT-3'	57
	R	5'-GGCTGCCCGCTGTAGGCAA-3'	
Smarca2	F	5'-ACAGGAGGTGGTGGCCTGCA-3'	57
	R	5'-CCTGGTGTCTGCGGCGT-3'	
Rbm15	F	5'-AGCAATGGGAGCAGCAGCGG-3'	57
	R	5'-TCGCCCCCGCCTGAGGAATT-3'	
Rnf135	F	5'-TCTGCGCCCCAGGTGACAGT-3'	57
	R	5'-ATCCGTGGGTGGGTGCCTT-3'	
GAPDH	F	5'-CATGGCCTCCAAGGAGTAAG-3'	57
	R	5'-TGTGAGGGAGATGCTCAGTG-3'	

Supporting Information Table S2. HB-iPSC gene signature.

Up-regulated genes (109)

Gene	Average Expression Value			BT-ANOVA P-value	Contrast P-value (iPSC)		Log2 Fold Changes
	AH-iPSC	HB-iPSC	MEF-iPSC		AH vs HB	HB vs MEF	
1110002N22Rik	605.59	1198.96	763.77	< 2e-16	< 2e-16	< 2e-16	0.81
1810009N02Rik	41.62	79.06	48.46	0.0203	0.0087	0.0271	0.81
2610019A05Rik	109.72	168.88	100.97	0.0150	0.0148	0.0075	0.68
5730596K20Rik	105.86	169.78	109.02	0.0177	0.0112	0.0135	0.66
Adamts4	47.76	99.01	55.97	0.0048	0.0023	0.0086	0.93
Ak3l1	615.51	1014.04	524.51	0.0001	0.0001	< 2e-16	0.83
Alkbh5	192.77	297.22	189.91	0.0368	0.0258	0.0247	0.64
Anxa3	172.38	463.17	286.12	0.0054	0.0021	0.0299	1.01
Axin2	106.73	737.15	282.37	< 2e-16	< 2e-16	< 2e-16	1.92
Bag2	27.08	72.37	45.83	0.0122	0.0058	0.0318	0.99
BC005682	58.13	112.17	73.09	0.0100	0.0035	0.0237	0.77
BC023829	47.63	139.83	81.16	< 2e-16	< 2e-16	0.0007	1.12
Bmp7	51.75	111.34	65.80	0.0100	0.0039	0.0180	0.92
Ccno	39.00	178.18	85.02	0.0002	0.0001	0.0008	1.52
Cdc37	97.73	160.82	92.03	0.0305	0.0241	0.0174	0.76
Cfl1	189.84	377.79	186.54	< 2e-16	< 2e-16	< 2e-16	1.01
Chrd	84.39	224.22	47.95	0.0001	0.0002	0.0001	1.76
Chst1	114.29	592.13	213.61	< 2e-16	< 2e-16	< 2e-16	1.85
Chst7	36.03	83.56	47.07	0.0010	0.0003	0.0012	1.01
Col16a1	113.28	460.45	130.48	0.0321	0.0204	0.0247	1.92
Creb3l2	37.43	62.71	41.57	0.0126	0.0074	0.0188	0.67
Cyp7b1	50.97	137.49	70.64	0.0008	0.0005	0.0009	1.18
Cyr61	21.21	165.42	104.60	< 2e-16	< 2e-16	0.0002	1.39
Disp1	65.79	99.86	65.84	0.0020	0.0019	0.0023	0.60
Dlk1	38.70	94.25	32.03	0.0011	0.0010	0.0004	1.41
Egr1	4392.67	7155.06	1848.30	0.0002	0.0023	0.0001	1.20
Eomes	17.81	180.21	79.03	0.0004	0.0002	0.0010	1.90
Evx1	28.44	83.35	31.73	0.0008	0.0003	0.0008	1.47
Fam169b	148.57	265.18	171.29	0.0002	0.0001	0.0004	0.73
Flrt3	147.98	245.89	150.10	< 2e-16	0.0001	0.0001	0.72
Foxq1	22.09	109.44	45.97	0.0144	0.0065	0.0188	1.69
Gad1	26.95	163.68	66.09	< 2e-16	0.0001	< 2e-16	1.81
Gps1	682.41	1117.34	710.67	0.0002	0.0001	0.0003	0.68
Hist1h2ab	42.91	96.42	60.11	0.0007	0.0002	0.0008	0.90
Hist1h3a	224.19	877.85	488.09	< 2e-16	< 2e-16	0.0002	1.30
Hist1h3c	24.29	126.89	76.79	< 2e-16	< 2e-16	0.0006	1.33

Hist1h3d	432.71	1508.40	930.62	< 2e-16	< 2e-16	< 2e-16	1.15
Hist1h3e	449.45	1709.00	1054.37	< 2e-16	< 2e-16	0.0002	1.18
Hist1h3h	22.61	110.40	42.62	< 2e-16	< 2e-16	< 2e-16	1.76
Hist1h4j	169.15	347.71	215.57	0.0001	0.0001	0.0003	0.85
Hoxa5	22.74	85.43	32.00	0.0008	0.0007	0.0025	1.64
Id3	53.97	137.35	72.22	0.0002	0.0002	0.0008	1.12
Igfbp3	21.40	243.69	126.18	0.0009	0.0005	0.0060	1.72
Irf1	689.84	1316.51	871.70	< 2e-16	< 2e-16	0.0001	0.75
Irx3	21.81	89.64	38.74	0.0331	0.0156	0.0434	1.57
Itga1	26.23	63.26	29.80	0.0027	0.0021	0.0048	1.18
Klhl25	46.55	81.57	41.14	0.0045	0.0060	0.0025	0.90
Krt18	47.38	164.79	102.22	0.0041	0.0014	0.0291	1.14
Krt8	268.31	1053.84	327.74	0.0007	0.0002	0.0004	1.82
Ldhc	23.49	92.36	28.52	< 2e-16	< 2e-16	< 2e-16	1.83
Leprel2	57.48	139.91	79.06	0.0095	0.0037	0.0179	1.04
Lman2l	316.62	522.10	348.05	< 2e-16	< 2e-16	< 2e-16	0.65
LOC100044190	79.71	166.30	84.65	< 2e-16	< 2e-16	< 2e-16	1.02
LOC100047028	74.04	142.40	77.17	0.0053	0.0030	0.0055	0.91
Ltb	33.04	134.24	35.82	0.0001	0.0001	0.0001	1.96
Ltbp3	91.96	174.81	89.72	0.0288	0.0220	0.0194	0.94
Magmas	37.34	71.89	42.51	0.0066	0.0033	0.0118	0.85
Mam1l	64.93	125.22	79.90	0.0026	0.0012	0.0053	0.79
Meis2	33.52	57.23	34.82	0.0098	0.0063	0.0098	0.74
Mgp	22.77	733.06	142.21	0.0037	0.0033	0.0029	3.15
Mpp1	502.06	763.47	498.97	0.0003	0.0004	< 2e-16	0.61
Mrgprf	30.71	51.14	27.61	0.0080	0.0093	0.0070	0.81
Msx1	21.53	56.36	28.68	0.0006	0.0002	0.0006	1.17
Mtvr2	107.95	213.08	131.11	0.0006	0.0002	0.0014	0.83
Nedd9	32.25	62.55	40.13	0.0046	0.0021	0.0084	0.79
Nod1	384.92	623.06	389.09	< 2e-16	< 2e-16	0.0001	0.69
Notum	167.67	350.97	66.06	< 2e-16	< 2e-16	< 2e-16	1.59
Nrp1	29.27	204.82	63.79	0.0018	0.0006	0.0045	2.14
Osm	16.85	77.58	12.76	< 2e-16	0.0001	< 2e-16	2.39
Osmr	30.88	109.96	44.49	0.0448	0.0297	0.0444	1.55
Pdia6	123.48	206.61	116.71	0.0048	0.0043	0.0023	0.78
Pemt	30.21	87.76	45.08	0.0039	0.0009	0.0085	1.22
Pes1	490.68	1113.93	473.31	< 2e-16	< 2e-16	< 2e-16	1.21
Pou6f1	31.31	116.30	37.75	0.0001	0.0001	0.0001	1.75
Prkg2	37.05	60.59	36.78	0.0031	0.0023	0.0019	0.71
Prrc1	597.48	1507.75	711.56	< 2e-16	< 2e-16	< 2e-16	1.20
Pscd2	22.29	43.73	25.27	0.0003	0.0001	0.0012	0.88
Psors1c2	21.38	101.95	39.07	0.0003	< 2e-16	0.0003	1.75
Rab38	16.97	43.53	21.48	0.0042	0.0020	0.0046	1.18

Rac3	175.41	409.46	271.86	< 2e-16	< 2e-16	0.0019	0.87
Rbm15	105.81	258.28	161.94	0.0001	0.0001	0.0004	0.95
Rhoj	22.14	50.62	22.53	0.0002	0.0001	0.0004	1.18
Rnf135	93.26	275.33	141.38	< 2e-16	< 2e-16	< 2e-16	1.23
Rps15a	300.20	523.53	334.89	0.0042	0.0021	0.0057	0.72
Rspo3	26.81	58.86	29.05	0.0198	0.0178	0.0168	1.08
S100a4	20.05	47.97	26.72	0.0210	0.0105	0.0423	1.04
Scap	76.89	119.29	73.07	0.0014	0.0015	0.0006	0.67
Scarf2	148.73	513.34	222.35	0.0234	0.0106	0.0378	1.47
Serpinf1	247.97	853.30	397.52	0.0305	0.0126	0.0496	1.40
Setd7	15.43	36.74	22.74	0.0219	0.0088	0.0288	0.94
Sf3a2	44.80	76.03	49.32	0.0135	0.0066	0.0151	0.69
Sh3pxd2b	54.06	88.47	45.93	0.0016	0.0021	0.0006	0.82
Shf	53.15	204.84	133.89	< 2e-16	< 2e-16	0.0002	1.13
Slc30a1	86.12	212.83	114.32	0.0001	< 2e-16	0.0001	1.09
Slit2	92.82	285.07	122.99	< 2e-16	0.0002	0.0001	1.40
Smarca2	69.57	129.69	78.50	0.0008	0.0003	0.0011	0.81
Socs7	17.06	35.21	22.15	0.0025	0.0018	0.0148	0.84
Sp5	35.61	2231.24	445.80	< 2e-16	< 2e-16	< 2e-16	3.21
Spink3	159.82	776.55	114.32	0.0019	0.0018	0.0009	2.50
St6galnac2	181.35	422.75	204.05	< 2e-16	< 2e-16	< 2e-16	1.13
Tap2	43.81	90.54	48.54	0.0080	0.0050	0.0083	0.97
Tex19.1	1248.43	1970.28	1240.37	0.0011	0.0008	0.0004	0.66
Thbs2	90.66	318.81	88.17	0.0382	0.0240	0.0247	1.83
Tinagl	21.05	39.36	22.29	0.0019	0.0012	0.0013	0.86
Tmem176b	41.77	71.52	32.37	0.0017	0.0022	0.0006	0.95
Tmem97	968.24	1817.11	1181.06	< 2e-16	< 2e-16	< 2e-16	0.76
Trib2	119.36	325.28	202.87	< 2e-16	< 2e-16	< 2e-16	1.01
Tubd1	45.63	85.33	46.77	0.0050	0.0034	0.0041	0.89
Zp3	56.34	183.50	97.09	0.0005	0.0001	0.0022	1.26

Down-regulated genes (115)

Gene	Average Expression Value			BT-ANOVA P-value	Contrast P-value (iPSC)		Log2 Fold Changes
	AH-iPSC	HB-iPSC	MEF-iPSC		AH vs HB	HB vs MEF	
1500003O03Rik	38.45	21.45	37.17	0.0034	0.0019	0.0027	-0.82
1700019D03Rik	1528.93	815.07	1983.87	0.0001	0.0001	< 2e-16	-1.11
2610318N02Rik	194.84	77.90	164.52	0.0015	0.0004	0.002	-1.21
4632404H12Rik	19.97	8.93	20.19	0.0304	0.0219	0.0192	-1.17
4930424G05Rik	61.25	30.67	54.14	0.0438	0.0137	0.0416	-0.91
A230107C01Rik	88.10	57.53	103.07	0.0141	0.0309	0.0058	-0.73
A930024E05Rik	38.24	18.06	34.76	0.0134	0.0065	0.0184	-1.02
Acss1	990.41	478.15	940.50	0.0001	0.0001	0.0001	-1.01
Adam32	35.14	18.99	38.45	0.0412	0.0309	0.0148	-0.95
Ahnak2	242.22	139.62	223.09	0.0260	0.0122	0.0317	-0.74
Aldh3b1	53.93	16.67	29.50	< 2e-16	< 2e-16	0.0074	-1.32
Ankrd12	98.51	55.86	151.36	0.0005	0.0112	0.0001	-1.16
Ankrd35	396.16	122.00	183.23	< 2e-16	< 2e-16	0.0162	-1.25
Ankrd56	99.18	36.40	73.24	< 2e-16	< 2e-16	< 2e-16	-1.24
Apoe	6596.25	3776.76	5736.12	0.0007	0.0002	0.0028	-0.71
Aqp3	301.17	144.20	561.31	0.0001	0.0007	< 2e-16	-1.58
Arhgap9	163.70	47.48	78.98	0.000	< 2e-16	0.0112	-1.35
Arhgef19	160.07	65.81	106.07	0.0008	0.0003	0.0255	-1.02
AU023871	72.00	41.54	71.12	0.0014	0.0012	0.0012	-0.78
B230219D22Rik	937.72	516.22	777.80	0.0020	0.0004	0.0096	-0.73
B230373P09Rik	216.89	68.47	140.19	< 2e-16	< 2e-16	0.0004	-1.38
B930041F14Rik	977.31	336.76	624.97	< 2e-16	< 2e-16	0.0015	-1.25
BC016495	126.52	79.41	138.26	0.0119	0.0139	0.0054	-0.74
Bdh2	639.28	299.66	530.22	0.0002	< 2e-16	0.0010	-0.96
Btbd11	492.81	221.09	377.59	< 2e-16	< 2e-16	< 2e-16	-0.98
C80008	52.16	27.56	49.78	0.0004	0.0003	0.0003	-0.89
Camk1	134.70	76.50	120.59	0.0209	0.0092	0.0331	-0.74
Cbr3	697.33	368.59	662.47	0.0017	0.0005	0.0017	-0.88
Cds2	50.65	29.31	48.27	0.0194	0.0099	0.0150	-0.75
Chrna4	34.70	14.88	24.04	0.0048	0.0024	0.0187	-0.98
Col9a2	246.58	163.70	277.40	< 2e-16	0.0004	< 2e-16	-0.68
Cox6b2	802.35	304.01	585.13	< 2e-16	< 2e-16	0.0003	-1.19
Cplx1	159.66	29.15	57.34	< 2e-16	< 2e-16	0.0077	-1.90
Cpt1b	47.17	16.61	36.35	0.0137	0.0090	0.0338	-1.33
Ctsa	385.85	152.54	258.13	0.0001	< 2e-16	0.0027	-1.08
Cyp27a1	34.50	13.75	29.12	0.0144	0.005	0.029	-1.21
D630023F18Rik	140.73	80.89	132.31	0.0088	0.0051	0.0123	-0.76
Dak	147.12	79.66	128.41	0.0250	0.0087	0.0475	-0.79

Depdc6	247.18	134.59	223.34	0.0094	0.0042	0.0156	-0.81
Dnaic1	59.85	16.51	39.89	0.0013	0.0004	0.0088	-1.59
Dnase2a	130.27	70.80	115.09	0.0008	0.0003	0.0008	-0.79
Dpp7	2651.27	1665.48	3327.40	< 2e-16	0.0001	< 2e-16	-0.84
Entpd2	123.08	49.40	97.59	0.0084	0.0028	0.0229	-1.16
Faah	52.73	13.68	27.79	0.0001	< 2e-16	0.012	-1.56
Fahd1	442.64	187.51	296.02	0.0001	< 2e-16	0.0086	-0.98
Fam129a	150.09	58.29	106.89	0.0010	0.0003	0.0071	-1.14
Fbxo2	807.34	233.50	520.12	< 2e-16	< 2e-16	< 2e-16	-1.51
Fbxo44	112.36	54.41	100.56	0.0018	0.0009	0.0022	-0.97
Fgf15	154.97	62.91	162.65	< 2e-16	< 2e-16	< 2e-16	-1.34
Flywch2	556.69	348.66	539.06	0.0002	0.0002	0.0002	-0.65
Frs3	125.19	59.96	120.34	0.0026	0.0013	0.0014	-1.03
Fxyd6	2917.97	1486.11	3385.23	< 2e-16	< 2e-16	< 2e-16	-1.08
Garnl3	512.24	233.32	355.52	0.0001	< 2e-16	0.0060	-0.89
Gdf15	195.38	55.82	107.81	< 2e-16	< 2e-16	0.0038	-1.44
Gpt2	461.04	259.01	407.18	0.0005	0.0001	0.0018	-0.75
Grasp	893.78	405.97	614.11	< 2e-16	< 2e-16	0.0001	-0.89
Gsta4	2872.56	1786.92	2718.22	0.0048	0.0025	0.0063	-0.65
Gys1	72.19	30.24	67.16	0.0348	0.015	0.033	-1.20
H2afj	249.15	95.29	156.91	0.0005	0.0001	0.0296	-1.09
Hcn3	32.24	19.25	35.00	0.0164	0.0217	0.0082	-0.80
Hebp2	61.06	35.30	75.52	0.0003	0.0008	0.0001	-0.95
Hpcal1	102.93	50.68	76.94	0.0012	0.0005	0.0219	-0.83
Htatif2	491.66	243.03	455.67	0.0001	< 2e-16	< 2e-16	-0.96
Ifi30	605.02	267.36	522.88	0.001	0.0010	0.0030	-1.08
Ifitm5	57.61	28.66	48.68	0.0009	0.0003	0.0020	-0.89
Insl6	249.00	126.32	222.70	0.0012	0.0004	0.0024	-0.90
Iqgap2	411.43	214.61	339.23	0.0005	< 2e-16	0.0028	-0.81
Itga6	183.04	107.31	164.16	0.0040	0.0014	0.0088	-0.69
Letmd1	69.64	43.96	67.46	0.0157	0.0091	0.0154	-0.64
LOC100045403	222.37	90.42	147.98	< 2e-16	< 2e-16	0.0044	-1.03
Lsm14b	148.16	96.51	146.95	0.0292	0.0194	0.0184	-0.61
Mdk	3077.42	1311.97	2210.83	< 2e-16	< 2e-16	< 2e-16	-1.01
Mef2b	104.80	57.57	118.44	0.0014	0.0027	0.0008	-0.96
Mical1	148.15	51.05	102.73	0.0001	0.0001	0.0105	-1.30
Mocos	173.19	78.27	143.86	< 2e-16	< 2e-16	< 2e-16	-1.02
Mreg	3456.98	1791.30	2728.44	< 2e-16	< 2e-16	0.0001	-0.79
Muc1	29.73	18.13	27.36	0.0139	0.0057	0.0171	-0.66
Myo6	588.79	266.20	509.41	< 2e-16	< 2e-16	< 2e-16	-1.04
Nagk	184.52	71.42	110.34	< 2e-16	< 2e-16	0.0030	-1.05
Nek8	107.42	62.58	103.46	0.0048	0.0021	0.0039	-0.75
Nupr1	583.04	251.68	810.41	0.0007	0.0045	0.0002	-1.47

Pdgfc	262.42	71.18	143.91	< 2e-16	< 2e-16	0.002	-1.51
Pfkfb2	111.80	65.29	132.20	0.0053	0.0124	0.0022	-0.90
Pkn1	57.91	30.98	56.58	0.0068	0.0043	0.0041	-0.89
Plcd1	579.95	320.61	505.49	0.0011	0.0004	0.0032	-0.76
Plk2	168.28	86.43	137.83	0.0132	0.0058	0.0323	-0.82
Ppapdc2	76.39	21.64	39.23	0.0001	< 2e-16	0.0210	-1.42
Ppfibp2	135.51	77.87	117.33	0.0008	0.0003	0.0024	-0.70
Ptprk	731.22	418.95	738.05	< 2e-16	< 2e-16	< 2e-16	-0.81
Rad9b	297.55	120.89	222.79	0.0001	< 2e-16	0.0002	-1.11
Raet1b	248.52	135.05	240.43	< 2e-16	< 2e-16	0.0001	-0.86
Rassf4	104.47	12.93	22.33	< 2e-16	< 2e-16	0.0087	-2.29
Rgs9bp	184.29	88.55	173.62	0.0001	0.0001	0.0002	-1.01
Rims3	312.10	194.80	319.29	0.0010	0.0008	0.0003	-0.70
Sct	199.46	43.80	99.51	< 2e-16	< 2e-16	0.0047	-1.77
Serpinb6c	1386.59	238.33	423.16	< 2e-16	< 2e-16	0.0278	-1.92
Slc25a33	1338.05	786.66	1259.34	0.0006	0.0003	0.0003	-0.72
Slc25a37	171.73	88.26	152.85	0.0022	0.0011	0.0033	-0.88
Slc29a4	408.40	202.47	324.06	0.0002	0.0002	0.0015	-0.86
Smox	262.91	148.77	245.05	0.0002	< 2e-16	< 2e-16	-0.77
Spock2	59.40	31.46	52.68	0.0225	0.0082	0.0326	-0.83
Spsb1	306.20	71.60	182.83	< 2e-16	< 2e-16	0.0009	-1.77
Sv2a	81.29	44.80	84.61	0.0010	0.0010	0.0007	-0.89
Syt9	532.25	318.33	498.37	< 2e-16	< 2e-16	0.0001	-0.69
Tcl1	1446.14	462.51	840.29	< 2e-16	< 2e-16	0.0001	-1.31
Tmem118	201.18	75.82	166.79	0.0010	0.0004	0.0015	-1.28
Tmem16j	1876.78	564.33	893.97	< 2e-16	< 2e-16	0.0084	-1.30
Trp53i11	52.01	16.82	42.83	0.0002	0.0001	0.0003	-1.49
Usp2	151.57	70.57	126.63	0.0011	0.0002	0.0051	-0.98
Whrn	230.48	101.37	215.47	0.0003	< 2e-16	0.0003	-1.14
Wscd1	94.98	43.22	112.08	0.0189	0.0285	0.0077	-1.26
Zcwpw1	93.09	55.88	90.31	0.0011	0.0012	0.0017	-0.71
Zfp385c	71.38	21.28	46.67	0.0017	0.0004	0.0159	-1.47
Zfp655	1712.77	1104.37	1736.11	< 2e-16	< 2e-16	< 2e-16	-0.64
Zmat4	225.59	38.94	80.81	< 2e-16	< 2e-16	0.0402	-1.98

Supporting Information Table S3. Unique donor memory genes in HB-iPSC.

Up-regulated genes (62)

Gene	Average Expression Value			BT-ANOVA P-value	Contrast P-value		Log2 Fold Changes
	HB-iPSC	HB	mESC		HB-iPSC vs mESC	HB vs mESC	
1700019H03Rik	492.43	471.50	232.35	0.0002	0.0002	0.0003	1.05
2610207I05Rik	1342.01	1419.50	598.09	0.0002	0.0001	0.0001	1.21
4930432O21Rik	113.08	226.13	54.90	0.0005	0.0187	0.0001	1.63
5830427D03Rik	55.30	65.11	26.48	0.0132	0.0196	0.0048	1.18
5930434B04Rik	85.66	263.45	38.74	0.0001	0.0099	0.0001	2.17
Acsf3	172.07	370.86	78.82	< 2e-16	0.0006	< 2e-16	1.78
Agpat3	188.86	293.11	86.93	0.0006	0.0179	< 2e-16	1.47
Angptl2	43.49	50.55	18.57	0.0017	0.0009	0.0016	1.34
Car14	266.46	1532.90	34.56	< 2e-16	0.0180	< 2e-16	4.70
Ccdc28b	152.15	235.91	73.91	< 2e-16	< 2e-16	< 2e-16	1.39
Cebpb	1206.88	7241.52	574.67	< 2e-16	0.0449	< 2e-16	2.88
Cldn3	155.26	191.65	49.22	0.0055	0.0132	0.0021	1.82
Cnksr3	70.56	118.73	33.93	0.0014	0.0312	0.0006	1.48
D5Wsu178e	400.40	715.31	185.94	0.0002	0.0156	< 2e-16	1.59
D930015E06Rik	292.77	334.33	143.48	< 2e-16	0.0001	< 2e-16	1.13
Dab2	76.00	112.99	31.45	0.0019	0.0135	0.0007	1.59
Emilin1	86.12	218.62	41.17	< 2e-16	0.0143	< 2e-16	1.89
Epha1	216.31	324.76	40.67	< 2e-16	0.0002	< 2e-16	2.73
Ephb4	50.93	51.92	25.07	0.0059	0.0046	0.0035	1.04
Esd	332.49	718.05	160.90	< 2e-16	0.0016	< 2e-16	1.71
Espn	252.46	225.45	74.27	< 2e-16	< 2e-16	< 2e-16	1.69
Fbxo21	1657.86	1738.04	747.62	0.0002	0.0001	0.0001	1.18
Ghr	117.43	1701.12	24.47	< 2e-16	0.0346	< 2e-16	5.22
Glipr2	716.77	1136.61	262.67	< 2e-16	0.0011	< 2e-16	1.82
H13	220.47	743.43	55.31	< 2e-16	0.0023	< 2e-16	3.12
H47	1608.24	6008.10	783.69	< 2e-16	0.0066	< 2e-16	2.28
Hgsnat	1252.93	2890.95	575.42	< 2e-16	0.0006	< 2e-16	1.85
Inpp5e	135.62	160.49	62.10	0.0014	0.0024	0.0004	1.25
Irf1	1316.51	2394.52	516.81	< 2e-16	< 2e-16	< 2e-16	1.84
Lars2	500.22	552.29	247.86	0.0003	0.0006	0.0003	1.09
Lman2l	522.10	577.99	245.25	< 2e-16	< 2e-16	< 2e-16	1.17
LOC100044170	185.19	210.19	79.77	0.0006	0.0006	0.0003	1.31
LOC100044190	166.30	543.89	60.02	< 2e-16	0.0005	< 2e-16	2.56
LOC100046056	305.31	398.84	149.84	0.0007	0.0062	0.0001	1.23
Lrig1	425.82	947.17	190.86	< 2e-16	0.0094	< 2e-16	1.85
Mad1l1	168.31	178.29	78.25	0.0011	0.0011	0.0007	1.15

Maml1	125.22	141.60	43.93	0.0016	0.0028	0.0004	1.60
Mgat4b	581.16	742.42	269.96	0.0003	0.0023	< 2e-16	1.29
Mmp15	90.19	83.01	27.89	0.0290	0.0097	0.0178	1.63
Nt5e	194.12	1241.85	54.42	< 2e-16	0.0248	< 2e-16	3.72
Pcsk4	42.68	97.53	20.13	< 2e-16	0.0131	< 2e-16	1.80
Ppp4r4	145.12	123.93	29.06	0.0003	0.0001	0.0002	2.21
Prss8	247.22	1457.00	111.27	< 2e-16	0.0004	< 2e-16	2.94
Pycrl	1118.44	1510.55	547.68	0.0013	0.0039	0.0005	1.26
Rbm15	258.28	341.13	91.66	0.0004	0.0026	0.0001	1.71
Reep3	656.69	1623.42	309.86	0.0001	0.0090	< 2e-16	1.88
Rffl	205.40	123.54	54.26	< 2e-16	< 2e-16	0.0009	1.60
Rnf135	275.33	241.69	103.70	< 2e-16	< 2e-16	0.0004	1.32
Rrbp1	605.02	4842.92	256.06	< 2e-16	0.0006	< 2e-16	3.41
Scd2	486.58	801.48	196.60	< 2e-16	0.0007	< 2e-16	1.71
Slc12a7	224.28	237.11	107.74	0.0035	0.0034	0.0021	1.10
Slc27a2	720.55	4665.82	110.52	< 2e-16	< 2e-16	< 2e-16	4.61
Slc4a2	720.83	1075.54	278.57	0.0002	0.0015	0.0001	1.69
Smarca2	129.69	350.24	48.38	< 2e-16	0.0005	< 2e-16	2.31
Snx9	125.80	244.31	52.56	0.0002	0.0256	0.0001	1.82
Srpr	1191.48	1443.19	569.42	0.0001	0.0003	< 2e-16	1.21
Tgfb1	211.23	373.56	69.77	0.0014	0.0318	0.0008	2.07
Trappc5	36.32	37.56	10.98	0.0196	0.0117	0.0113	1.75
Trub1	565.70	349.70	169.36	< 2e-16	< 2e-16	< 2e-16	1.43
Tsc22d4	149.80	192.48	67.21	0.0082	0.0242	0.0024	1.35
Ttyh3	130.81	271.96	24.75	< 2e-16	0.0084	< 2e-16	3.02
Vldlr	119.60	328.95	35.33	< 2e-16	0.0003	< 2e-16	2.67

Down-regulated genes (142)

Gene	Average Expression Value			BT-ANOVA P-value	Contrast P-value		Log2 Fold Changes
	HB-iPSC	HB	mESC		HB-iPSC vs mESC	HB vs mESC	
1110032E23Rik	97.56	55.76	287.55	< 2e-16	< 2e-16	< 2e-16	-1.91
1700025K23Rik	76.54	32.49	156.35	0.0008	0.0011	0.0002	-1.52
2200001I15Rik	127.27	48.78	4278.50	0.0002	0.0001	0.0002	-5.60
2210016L21Rik	67.95	40.71	166.11	0.0008	0.0007	0.0002	-1.61
2410137M14Rik	152.28	26.84	638.95	< 2e-16	< 2e-16	< 2e-16	-2.83
2610318N02Rik	77.90	31.33	165.04	0.0005	0.0004	0.0002	-1.60
2610524H06Rik	174.11	41.43	442.89	0.0001	0.0004	< 2e-16	-2.04
4632417K18Rik	210.67	130.19	583.81	0.0002	0.0002	0.0001	-1.78
A330080J22Rik	65.19	35.46	135.72	0.0051	0.0105	0.0018	-1.43
Adprh	2710.74	2268.96	6632.62	< 2e-16	< 2e-16	< 2e-16	-1.41
Agpat4	606.94	92.70	1563.85	< 2e-16	< 2e-16	< 2e-16	-2.16
Amd2	73.13	65.56	185.04	0.0005	0.0005	0.0003	-1.42
Amhr2	84.19	19.96	210.11	0.0003	0.0002	0.0003	-2.01
Ankrd12	55.86	45.72	154.39	0.0015	0.0014	0.0010	-1.60
Apob48r	23.12	21.92	65.47	0.0001	0.0001	< 2e-16	-1.54
Apobec1	46.06	64.69	257.46	0.0001	0.0001	0.0001	-2.22
Aqp3	144.20	131.39	478.46	0.0030	0.0020	0.0023	-1.80
Arhgap30	134.80	66.23	348.36	0.0001	0.0002	0.0001	-1.79
Arhgap8	238.51	27.95	520.30	0.0028	0.0090	0.0016	-1.97
B930041F14Rik	336.76	35.71	1331.64	< 2e-16	< 2e-16	< 2e-16	-2.84
Bbx	50.67	51.74	152.50	0.0064	0.0051	0.0048	-1.57
BC004701	108.48	66.13	224.20	0.0002	0.0002	< 2e-16	-1.36
BC031575	38.44	29.70	94.07	0.0026	0.0025	0.0026	-1.47
Calca	114.86	24.40	464.75	0.0051	0.0041	0.0037	-2.74
Camk2b	302.00	101.65	702.58	< 2e-16	< 2e-16	< 2e-16	-1.80
Car13	187.83	37.08	512.72	< 2e-16	< 2e-16	< 2e-16	-2.19
Cbr3	368.59	21.98	1044.03	< 2e-16	< 2e-16	< 2e-16	-2.42
Cd55	24.11	37.47	80.32	0.0310	0.0170	0.0472	-1.38
Cd68	223.62	100.80	497.61	0.0004	0.0032	0.0001	-1.62
Cdkn1a	458.91	507.86	1102.11	< 2e-16	< 2e-16	< 2e-16	-1.19
Cecr5	123.90	104.70	275.14	0.0001	0.0003	< 2e-16	-1.27
Cep63	37.06	37.89	84.99	0.0015	0.0009	0.0017	-1.18
Chd5	27.70	26.76	70.17	0.0135	0.0102	0.0096	-1.37
Cib2	30.92	23.89	73.46	0.0273	0.0349	0.0122	-1.42
Cmtm7	242.85	108.62	815.82	0.0007	0.0006	0.0005	-2.21
Col9a2	163.70	39.70	345.38	0.0003	0.0010	0.0002	-1.76
Coro2b	23.94	18.56	63.21	0.0014	0.0011	0.0008	-1.57
Cox6b2	304.01	49.77	915.10	< 2e-16	< 2e-16	< 2e-16	-2.37

Crtac1	123.39	24.32	448.92	0.0019	0.0011	0.0016	-2.60
Ctsa	152.54	135.94	319.96	0.0017	0.0016	0.0009	-1.15
Cxcl16	42.62	47.04	121.60	0.0137	0.0083	0.0103	-1.44
D12Ertd647e	234.52	153.25	7174.47	< 2e-16	< 2e-16	< 2e-16	-5.21
D9Ertd392e	347.55	396.77	960.44	0.0001	< 2e-16	0.0001	-1.37
Ddit4l	215.80	83.91	813.58	< 2e-16	< 2e-16	< 2e-16	-2.44
Def6	189.30	35.62	421.68	< 2e-16	0.0001	< 2e-16	-1.91
Des	70.17	34.60	161.45	0.0117	0.0132	0.0080	-1.62
Dnajb13	37.65	29.71	77.95	0.0020	0.0011	0.0016	-1.21
Dscr1l2	402.33	105.59	953.52	< 2e-16	< 2e-16	< 2e-16	-1.91
Eda2r	35.17	30.35	79.49	0.0204	0.0170	0.0104	-1.28
Efr3a	154.90	102.83	374.90	< 2e-16	< 2e-16	< 2e-16	-1.54
Eif2ak2	222.12	277.73	748.20	0.0005	0.0003	0.0003	-1.58
Elk3	67.00	24.87	201.92	< 2e-16	< 2e-16	< 2e-16	-2.14
Eng	120.26	45.70	337.41	0.0001	0.0004	0.0001	-2.02
Ephx1	310.02	344.34	1129.18	0.0006	0.0004	0.0004	-1.79
Ercc5	573.79	395.56	1553.77	< 2e-16	< 2e-16	< 2e-16	-1.68
Evi5l	37.59	36.01	91.84	0.0002	0.0003	0.0004	-1.32
Exoc4	519.82	184.48	1308.11	< 2e-16	0.0001	< 2e-16	-1.89
Fcho1	353.23	31.30	973.05	< 2e-16	< 2e-16	< 2e-16	-2.34
Flywch2	348.66	36.79	815.44	0.0017	0.0008	0.0014	-2.08
Frs3	59.96	36.20	227.90	< 2e-16	< 2e-16	< 2e-16	-2.24
Gab3	14.02	11.27	56.82	0.0018	0.0007	0.0021	-2.17
Gna12	53.86	55.95	122.07	0.0458	0.0344	0.0276	-1.15
Gspt2	555.42	45.20	1148.65	< 2e-16	0.0002	< 2e-16	-1.94
H2-Ab1	28.22	66.37	189.29	0.0065	0.0021	0.0135	-2.00
Hdac8	55.47	27.82	133.28	< 2e-16	< 2e-16	< 2e-16	-1.68
Hist1h2ag	802.22	642.10	2317.06	0.0003	0.0004	0.0001	-1.68
Hist2h2ac	14718.02	10738.18	31560.69	< 2e-16	< 2e-16	< 2e-16	-1.31
Hnrnp3	47.23	54.81	144.94	0.0020	0.0014	0.0018	-1.51
Hyal1	35.34	33.69	175.83	0.0001	0.0002	0.0002	-2.35
Inpp5d	41.28	27.34	131.07	0.0002	0.0002	0.0001	-1.93
Irak1	36.01	33.59	75.17	0.0097	0.0062	0.0084	-1.11
Kat2b	29.38	32.92	71.30	0.0018	0.0008	0.0016	-1.19
Kdelr3	176.64	38.10	886.42	0.0001	0.0002	0.0001	-3.05
Laptm5	4041.65	1296.86	16911.72	< 2e-16	< 2e-16	< 2e-16	-2.66
Lgals3	728.86	402.76	2930.73	< 2e-16	< 2e-16	< 2e-16	-2.37
LOC100038882	51.93	53.84	164.64	0.0020	0.0012	0.0023	-1.64
LOC100048056	21.96	20.34	45.50	0.0026	0.0035	0.0016	-1.11
LOC677317	155.49	170.85	382.67	< 2e-16	< 2e-16	< 2e-16	-1.23
Max	51.53	33.45	146.95	0.0002	0.0002	0.0001	-1.79
Mgmt	121.45	84.35	271.39	0.0002	0.0001	0.0001	-1.40
Napsa	28.20	46.13	1010.64	0.0005	0.0003	0.0010	-4.77

Nos3	26.96	27.66	79.27	0.0004	0.0001	0.0009	-1.54
Nptx2	487.63	63.99	1027.90	0.0005	0.0018	0.0004	-1.90
Nr5a2	99.20	127.32	285.64	0.0093	0.0056	0.0076	-1.33
Nup54	20.02	29.00	84.77	0.0038	0.0023	0.0035	-1.79
P2ry6	24.16	29.79	106.86	0.0012	0.0008	0.0007	-1.99
Phlda2	2426.40	2084.53	4871.05	0.0001	< 2e-16	0.0001	-1.11
Pitpnc1	112.64	155.71	312.66	0.0059	0.0031	0.0094	-1.22
Piwil1	31.99	29.90	94.52	0.0029	0.0021	0.0015	-1.61
Plek2	36.45	33.21	82.05	0.0267	0.0158	0.0341	-1.24
Plekhb1	74.84	53.14	416.25	< 2e-16	< 2e-16	< 2e-16	-2.70
Plekhb2	217.72	106.73	639.26	0.0004	0.0015	0.0001	-1.98
Plekhf1	81.64	27.65	178.23	0.0007	0.0006	0.0006	-1.71
Pltp	108.74	39.02	273.58	0.0016	0.0014	0.0011	-1.89
Pmaip1	142.73	27.86	291.49	0.0017	0.0013	0.0013	-1.77
Polh	76.67	60.87	194.23	0.0007	0.0006	0.0003	-1.50
Ppp2r5c	900.58	352.23	1998.72	0.0032	0.0048	0.0015	-1.67
Prei3	50.81	44.12	123.90	0.0027	0.0027	0.0017	-1.38
Prkcb	24.50	31.67	106.81	0.0125	0.0172	0.0090	-1.93
Pros1	449.05	545.42	1414.25	< 2e-16	< 2e-16	0.0002	-1.51
Prosc	74.15	40.82	166.56	< 2e-16	0.0001	< 2e-16	-1.53
Pstpip1	38.67	23.14	86.19	0.0040	0.0055	0.0032	-1.48
Ptp4a3	139.40	127.80	373.50	0.0001	< 2e-16	0.0001	-1.48
Rab11fip5	121.33	38.51	436.36	0.0015	0.0012	0.0010	-2.45
Rab12	102.12	75.63	292.72	< 2e-16	< 2e-16	< 2e-16	-1.72
Rab23	85.05	27.16	186.50	0.0002	0.0014	< 2e-16	-1.73
Rad9b	120.89	35.58	309.58	< 2e-16	< 2e-16	< 2e-16	-1.98
Rassf4	12.93	18.43	63.47	0.0069	0.0055	0.0080	-2.02
Rec8	215.77	34.28	516.63	0.0013	0.0048	0.0006	-2.05
Ribc1	122.76	44.33	290.70	< 2e-16	< 2e-16	< 2e-16	-1.80
Rpl3l	45.55	35.91	142.44	0.0030	0.0021	0.0030	-1.81
Rsad2	27.17	45.22	226.24	0.0017	0.0009	0.0035	-2.64
S100a13	332.36	226.95	791.02	0.0004	0.0003	0.0002	-1.50
Senp1	62.65	36.62	147.01	< 2e-16	0.0001	< 2e-16	-1.57
Shisa2	97.45	35.82	347.31	0.0002	0.0001	0.0001	-2.38
Si	84.04	21.44	299.95	0.0027	0.0030	0.0016	-2.51
Slc25a30	38.19	29.70	77.66	0.0014	0.0022	0.0006	-1.19
Slc29a3	120.28	68.46	258.24	< 2e-16	0.0001	< 2e-16	-1.45
Slc38a5	78.40	181.17	1019.97	0.0001	0.0001	< 2e-16	-2.97
Slc6a8	696.73	280.30	3118.09	< 2e-16	< 2e-16	< 2e-16	-2.67
Slco4a1	142.84	56.99	290.22	0.0002	0.0001	0.0002	-1.54
Sntb2	85.87	55.92	175.60	< 2e-16	< 2e-16	< 2e-16	-1.31
Spock2	31.46	22.92	66.88	0.0389	0.0457	0.0296	-1.30
Spsb1	71.60	59.95	671.71	0.0006	0.0002	0.0005	-3.35

Srp54	55.27	136.08	349.56	0.0002	0.0001	0.0005	-1.87
Ssbp4	134.69	31.47	272.44	< 2e-16	< 2e-16	< 2e-16	-1.71
Susd4	51.94	28.67	192.69	0.0014	0.0021	0.0012	-2.26
Tgs1	133.67	125.04	326.84	0.0001	0.0001	0.0001	-1.34
Tmem118	75.82	29.88	250.11	0.0001	0.0001	< 2e-16	-2.24
Tmem16j	564.33	106.64	2234.50	0.0006	0.0004	0.0003	-2.74
Tmem39a	2970.29	1915.43	5966.47	0.0020	0.0043	0.0005	-1.29
Tnpo2	42.34	39.39	113.69	< 2e-16	< 2e-16	< 2e-16	-1.48
Tpd52l1	112.31	17.45	229.03	< 2e-16	< 2e-16	< 2e-16	-1.82
Tpmt	23.00	67.45	171.19	0.0009	0.0003	0.0018	-1.92
Trit1	142.02	146.28	297.63	0.0005	0.0003	0.0004	-1.05
Trp53inp1	1259.04	713.18	3071.38	< 2e-16	< 2e-16	< 2e-16	-1.64
Trps1	33.62	38.73	90.72	0.0015	0.0009	0.0012	-1.33
Ube2e1	84.69	43.26	179.35	0.0006	0.0025	0.0001	-1.49
Vax2	27.74	29.40	103.73	0.0107	0.0068	0.0146	-1.86
Whrn	101.37	52.92	219.27	0.0002	0.0003	0.0001	-1.51
Wipi1	108.12	100.84	265.09	0.0036	0.0040	0.0027	-1.34
Zfp691	87.89	44.52	195.30	0.0005	0.0011	0.0001	-1.56

SC-11-1037-R1

Supporting Information Figure Legends

Fig. S1. Loss of GFP expression after reprogramming. Hepatic lineage cells (AH and HB) and MEF were transduced with pLentG-KOSM vector containing fusion of 4 genes, including KLF, Oct4, Sox2, Myc and GFP. The infected cells were cultured on feeder cells until appearance of ES-like cells which expressed GFP (P0). At passage 1 (P1), the reprogrammed cells lost GFP expression. Images were taken with original magnification, $\times 100$. iPS, induced pluripotent stem cells; HB-iPSC, hepatoblast-derived iPSC; AH-iPSC, adult hepatocyte-derived iPSC; MEF-iPSC, mouse embryonic fibroblast-derived iPSC.

Fig. S2. Protocol development for induced differentiation of mES cells towards hepatocytes in monolayer without feeder cells. (A) Schematic representation of the key factors required for differentiation of mES cells towards hepatic lineage cells. (B) The morphology and immunofluorescence staining of mESC with antibodies against pluripotency markers at passage 4. The cells were cultured on collagen-coated plates in mESC media containing a GSK3 inhibitor BIO (1 μ M). Scale bar, 20 μ M. (C) Phase-contrast micrograph ($\times 200$). By day 25, the cells acquired a hepatocyte-like cells morphology and sporadic binuclearity (arrow). (D) Double immunofluorescence staining with AFP and Albumin at day 25. Scale bar, 20 μ M. (E) Quantitative reverse transcription polymerase chain reaction analysis with primers specific to AFP, Albumin, HNF4 α , and G6P. The data are shown as means expression values \pm SEM relative to GAPDH of triplicate measurements. EB, embryoid body, Mono, monolayer culture.

Fig. S3. Purification of mES and iPSC cells from feeder cells for microarray analysis. (A) Ten million of the bulk mES or iPSC and feeder cells were isolated and stained with PE-SSEA1, a cell surface-specific marker of mESC. SSEA1-positive cells were separated from feeder cells using MACS PE-conjugated MicroBeads followed by FACS analysis of purity. (A) Representative FACS plots of mES cells stained with isotope control (top) and PE-SSEA1 before after MACS separation demonstrate a high purity of MACS-isolated mES cells. (B) Fractions of cells expressing SSEA1 (red histograms) after MACS separation as shown by FACS analysis. Black histograms, isotype control. iPSC, induced pluripotent stem cells; HB-iPSC, hepatoblast-derived iPSC; AH-iPSC, adult hepatocyte-derived iPSC; MEF-iPSC, mouse embryonic fibroblast-derived iPSC.

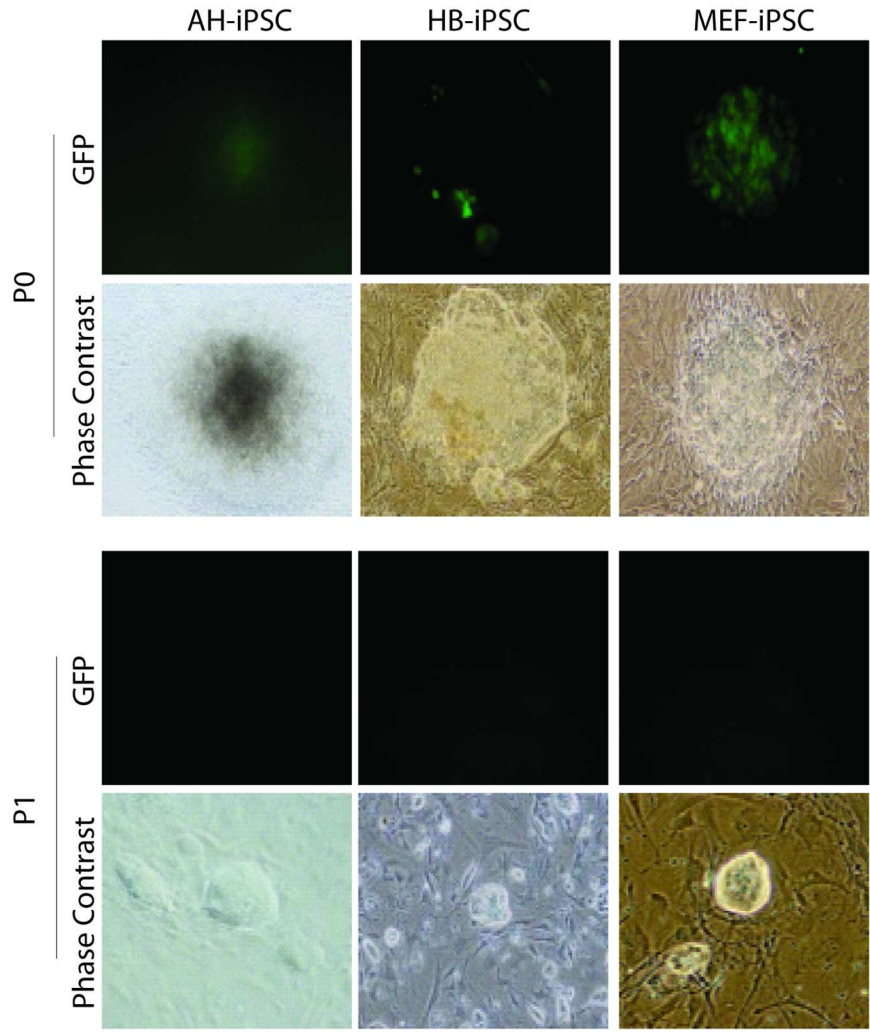
Fig. S4. Venn diagram analysis of donor memory genes in AH-iPSC, HB-iPSC and MEF-iPSC. The numbers in the Venn diagrams indicate both unique and commonly dysregulated donor memory genes in AH-iPSC, HB-iPSC, and MEF-iPSC. The unique donor memory genes in HB-iPSC comprise of 62 up-regulated genes (red) and 142 down-regulated genes (blue). iPSC, induced pluripotent stem cells; HB-iPSC, hepatoblast-derived iPSC; AH-iPSC, adult hepatocyte-derived iPSC; MEF-iPSC, mouse embryonic fibroblast-derived iPSC.

Fig. S5. Upregulation of DNMT1 and DNMT3b in iPSC cells generated in hepatic lineage cells. (A) The expression levels of DNMT1 and (B) DNMT3b based on the analysis of microarray. The data represent the mean expression levels \pm SEM (n=4). iPSC, induced pluripotent stem cells; HB-iPSC, hepatoblast-derived iPSC; AH-iPSC, adult hepatocyte-derived

iPSC; MEF-iPSC, mouse embryonic fibroblast-derived iPSC; mESC, mouse embryonic stem cells.

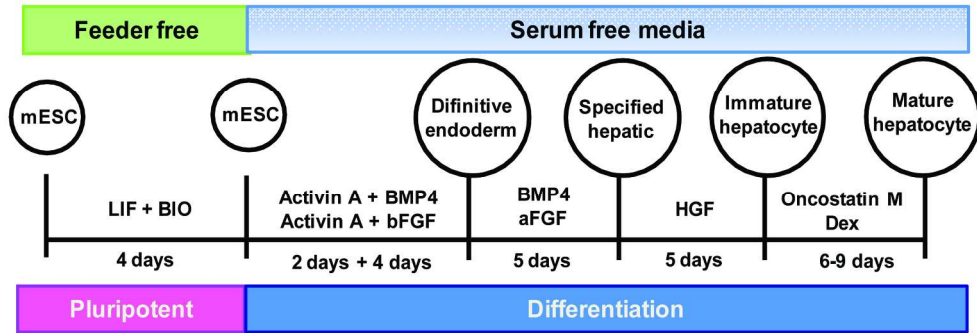
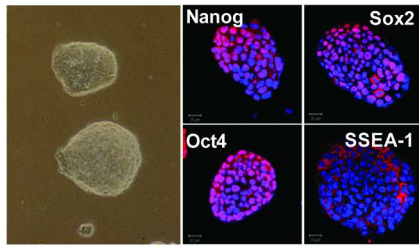
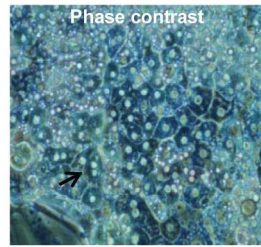
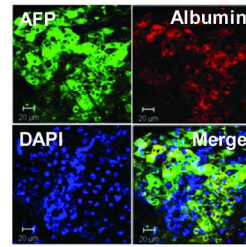
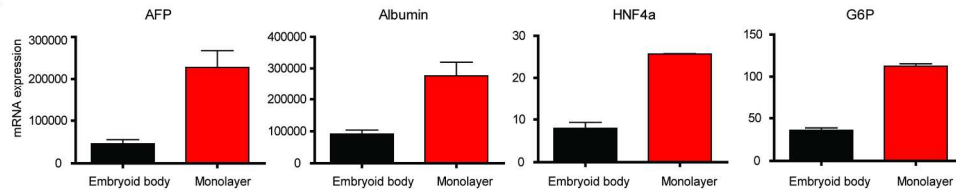
Fig. S6. HB-iPSC specific donor memory genes. (A, B) Expression pattern of up-regulated HB-iPSC specific donor memory genes in the parental (A) and corresponding iPSC cells (B). The data are shown as means of \log_2 fold changes relative to mES cells \pm SEM ($n=4$). (C, D) Expression pattern of down-regulated HB-iPSC specific donor memory genes in parental (C) and corresponding iPSC (D) cells. The data are shown as means of \log_2 fold changes relative to mES cells \pm SEM ($n=4$). iPS, induced pluripotent stem cells; HB, hepatoblast; AH, adult hepatocyte; MEF, mouse embryonic fibroblast; HB-iPSC, hepatoblast-derived iPSC; AH-iPSC, adult hepatocyte-derived iPSC; MEF-iPSC, mouse embryonic fibroblast-derived iPSC. Red line indicates a two-fold expression differences as compared to mESC.

Fig. S1



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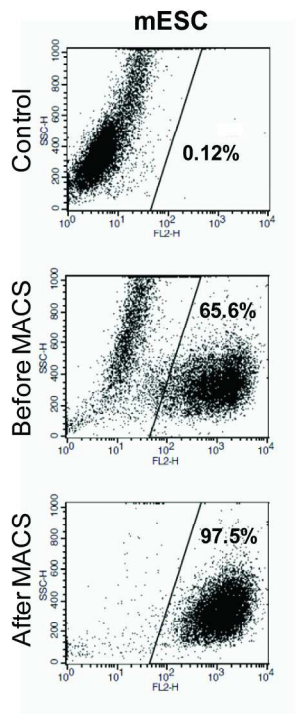
Fig. S2

A**B****C****D****E**

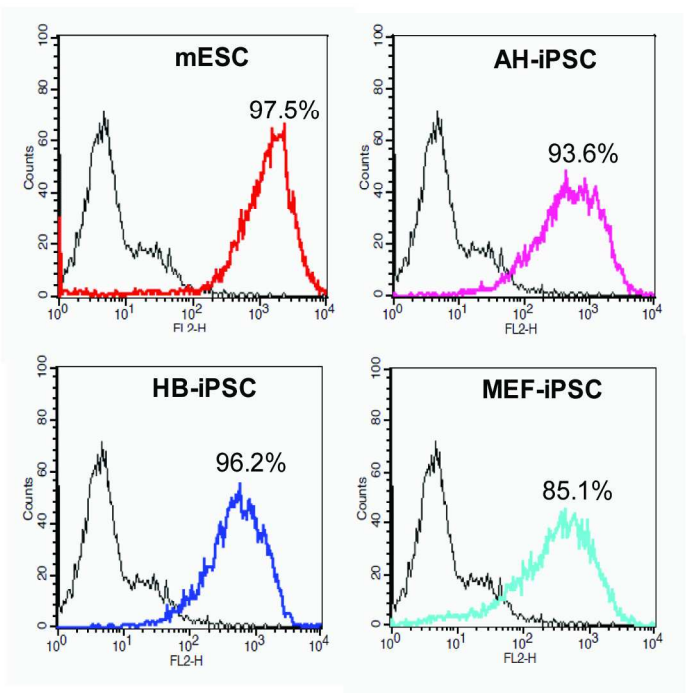
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Fig. S3

A

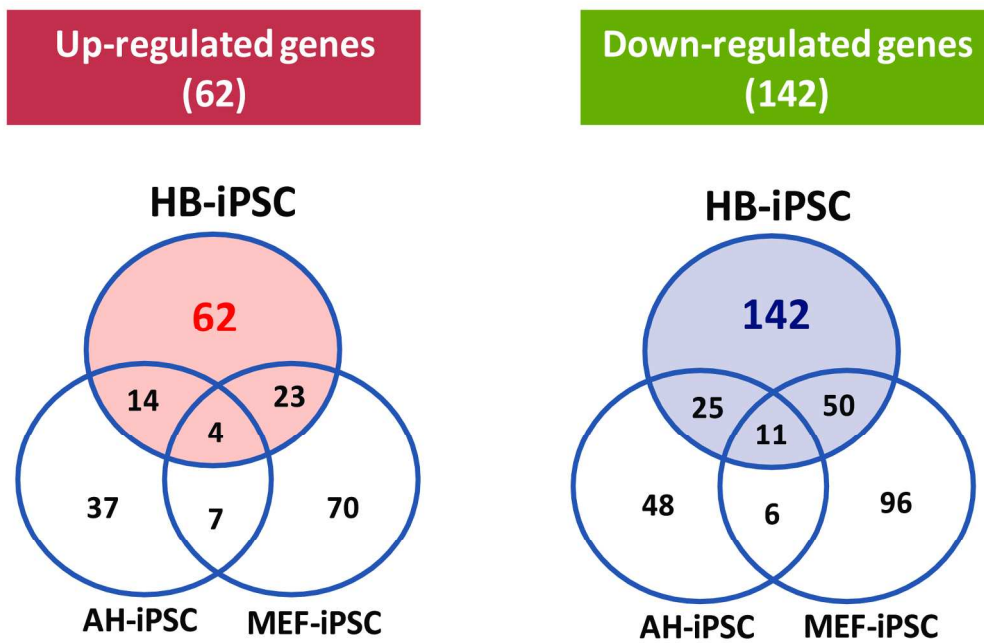


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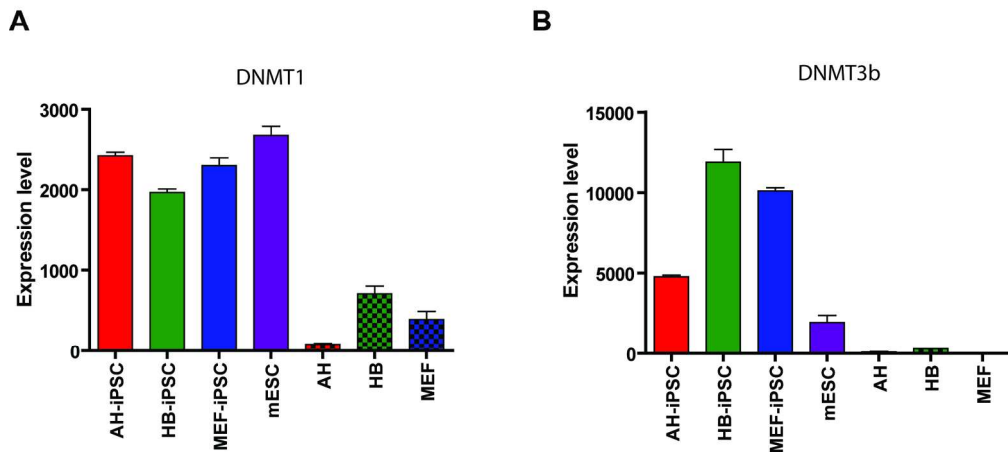
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Fig. S4



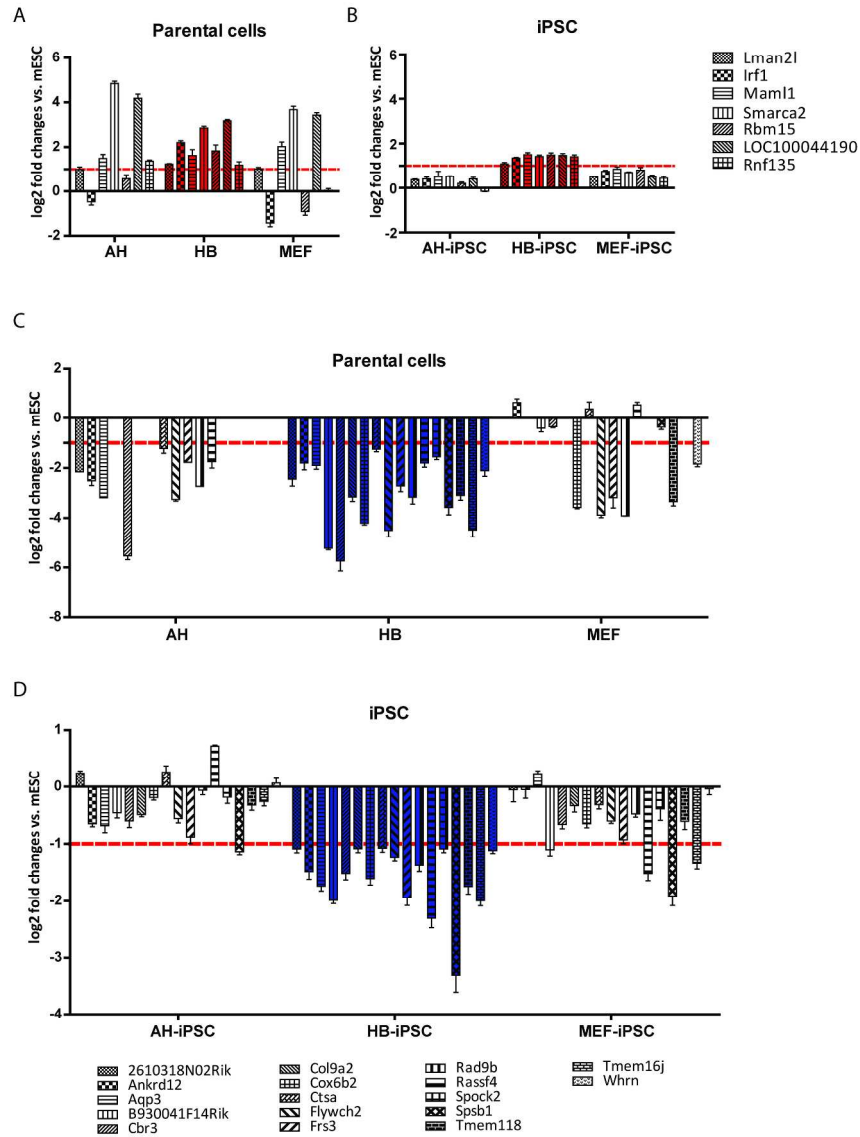
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Fig. S5



170x90mm (300 x 300 DPI)

Fig. S6



238x334mm (300 x 300 DPI)