

Hsa-miR-520d induces hepatoma cells to form normal liver tissues via a stemness-mediated process

Satoshi Tsuno¹, Xinhui Wang¹, Kohei Shomori², Junichi Hasegawa¹, Norimasa Miura¹

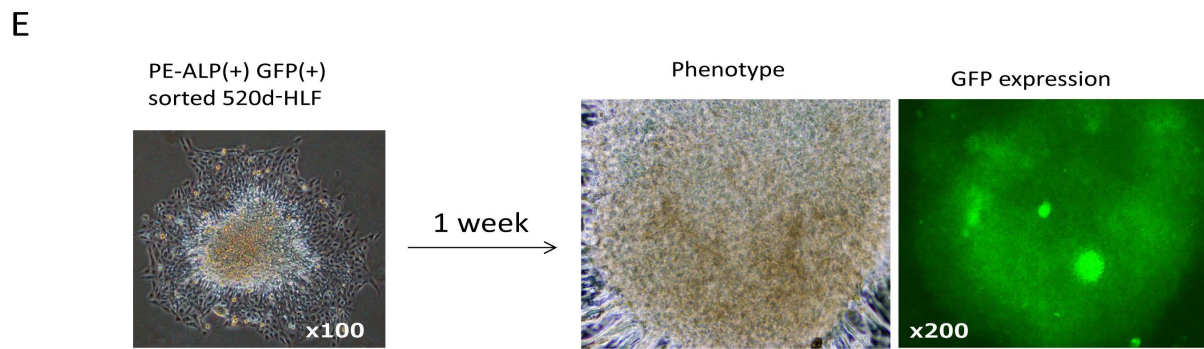
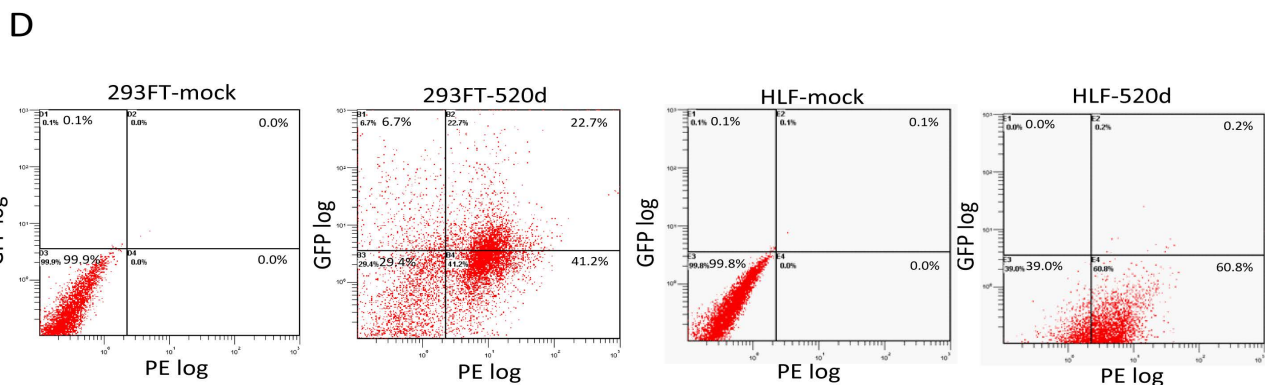
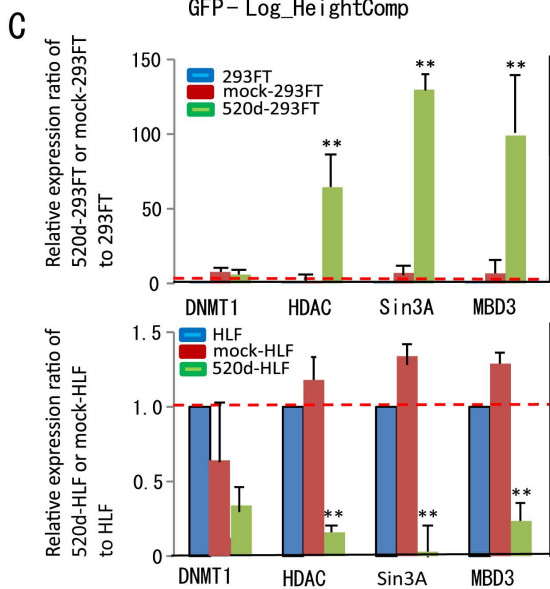
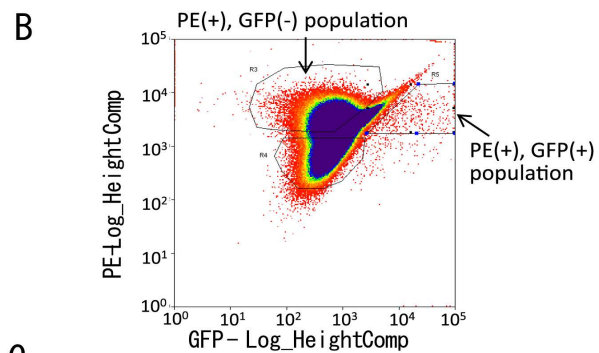
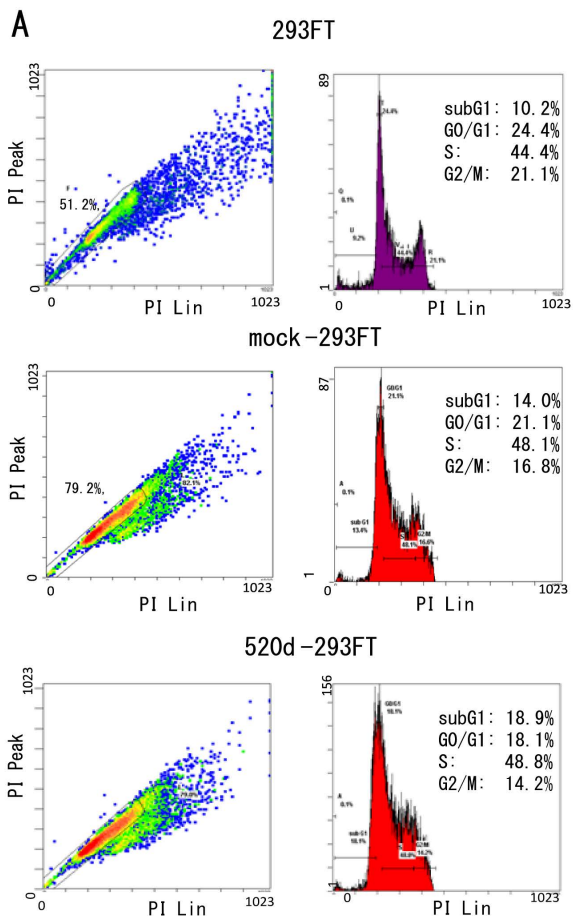
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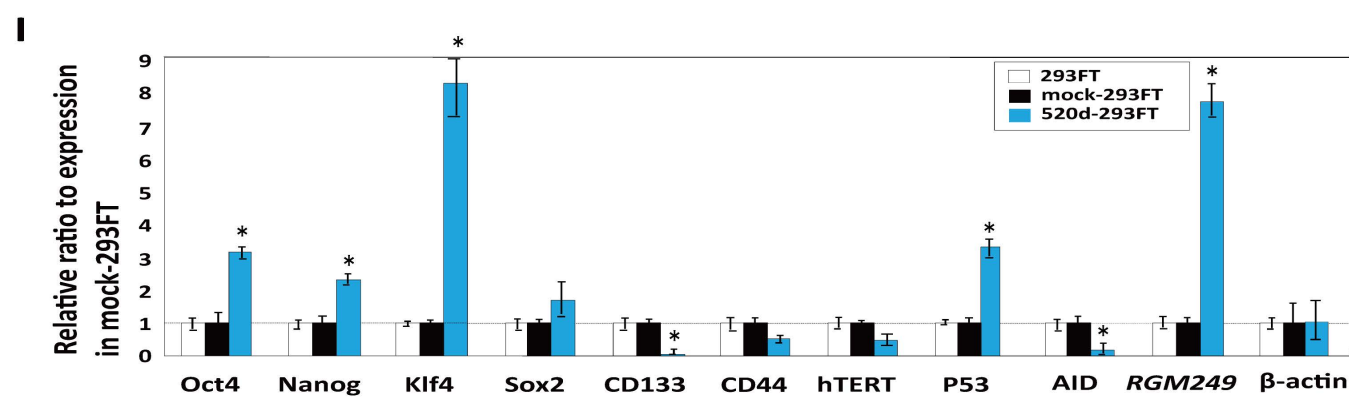
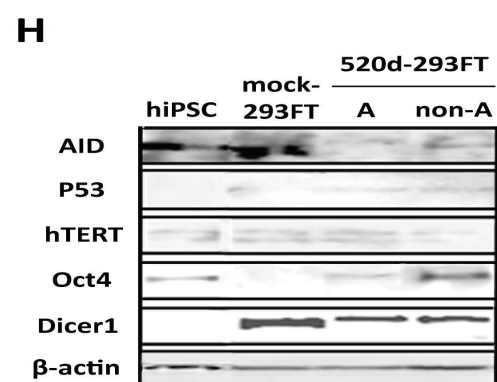
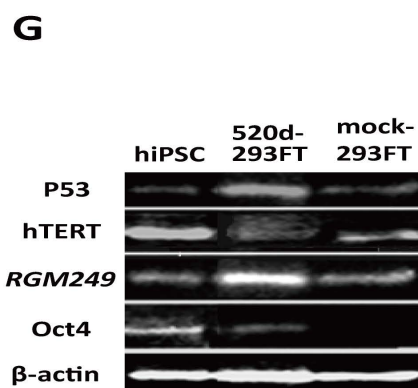
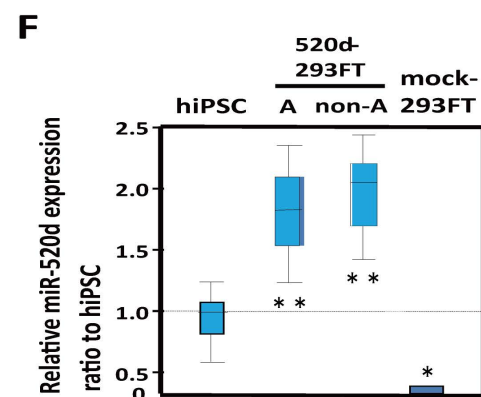
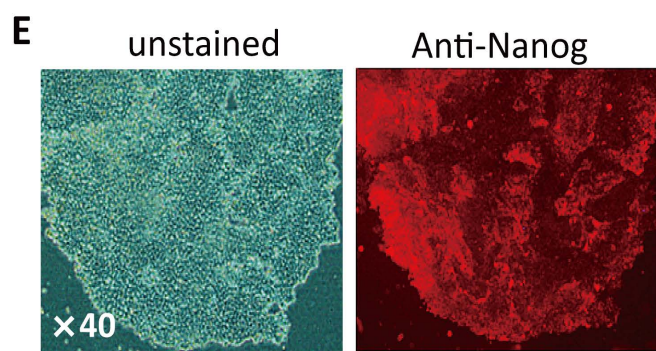
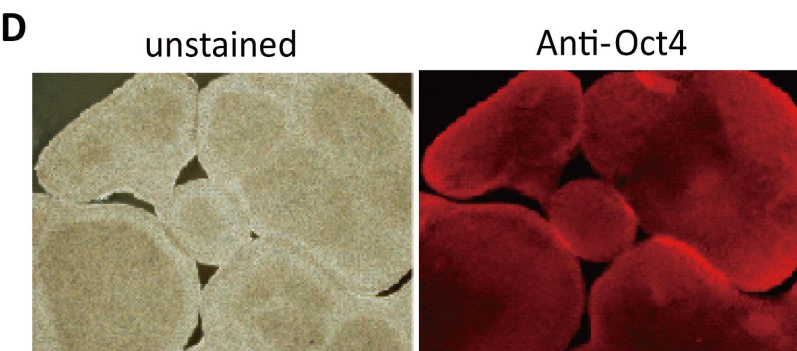
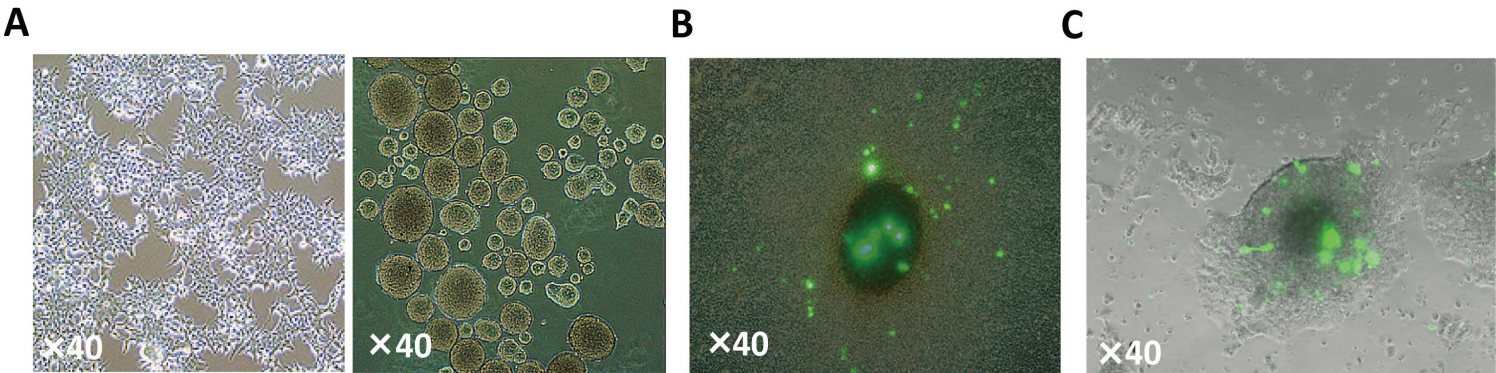
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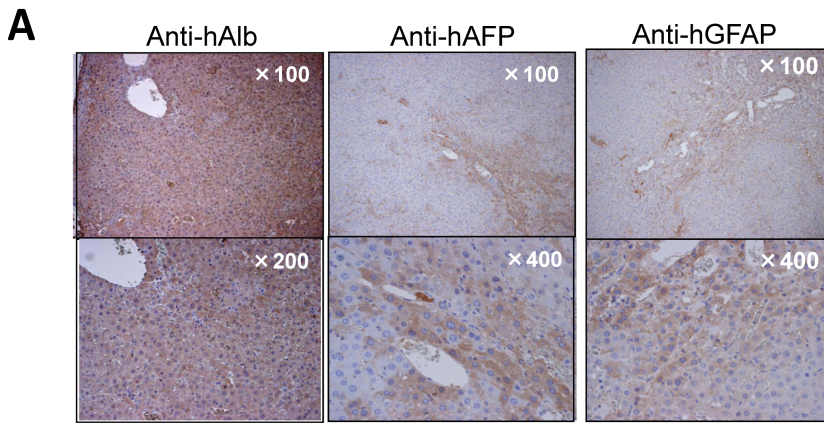
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Keywords: cancer, stemness, miRNA, differentiation, iPSC

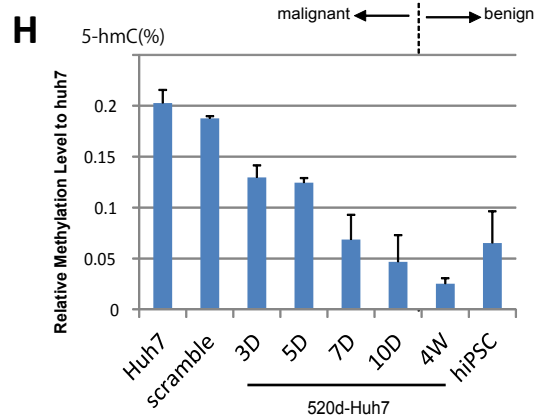
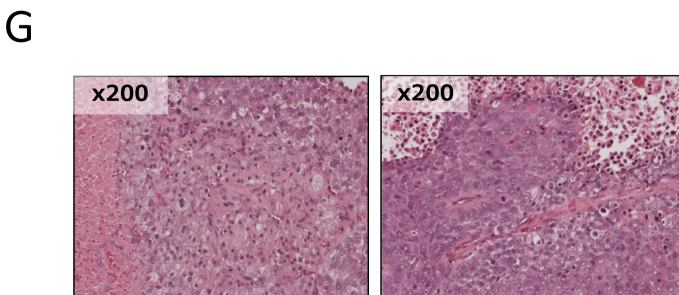
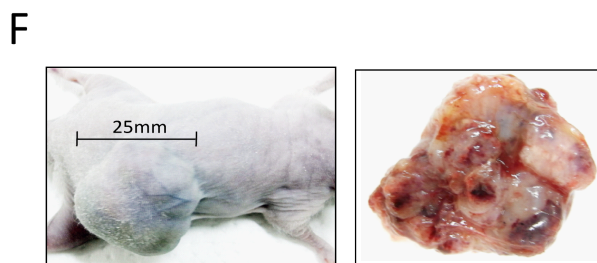
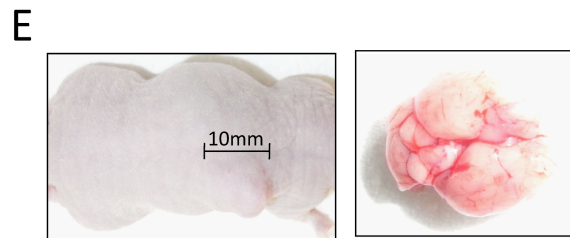
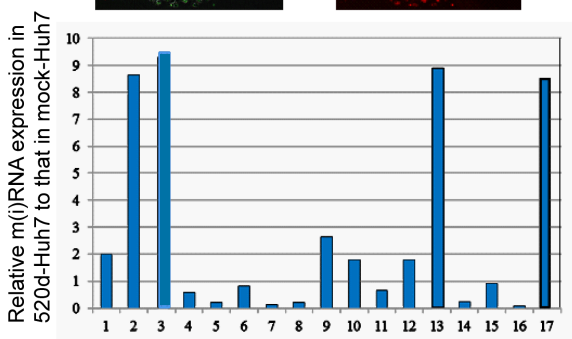
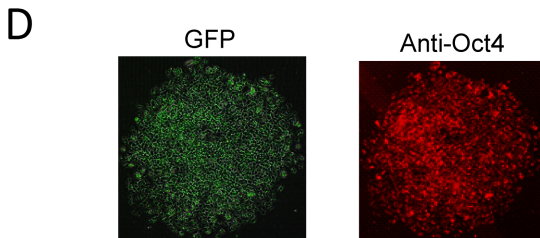
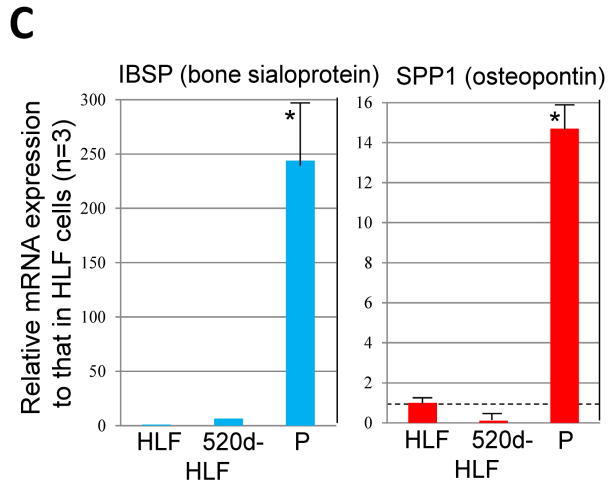
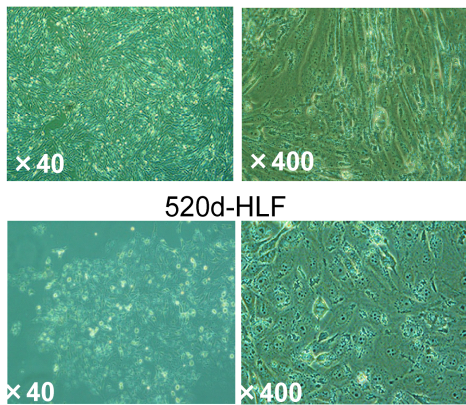
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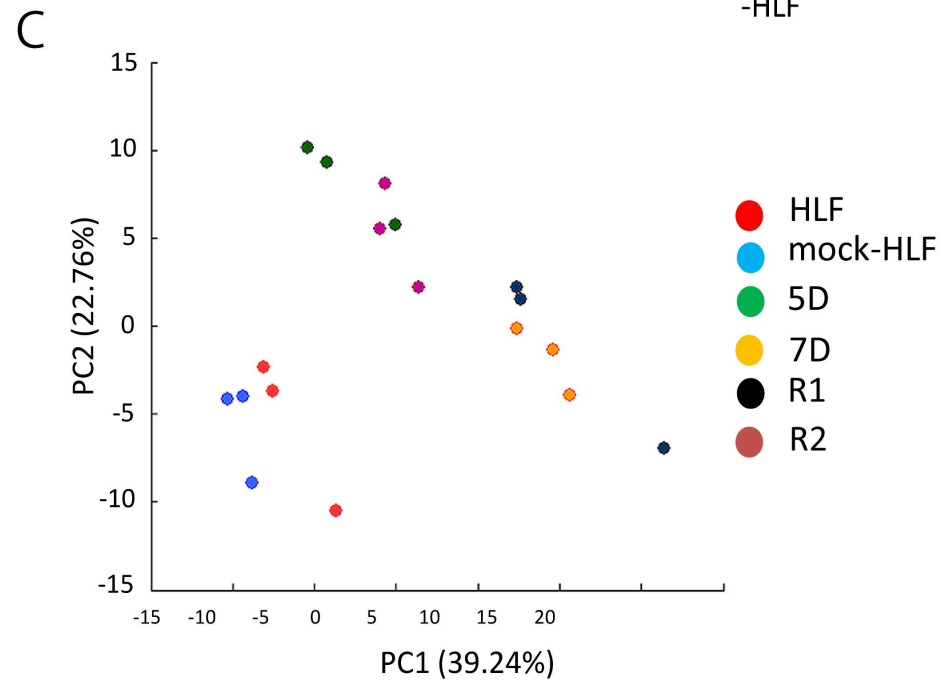
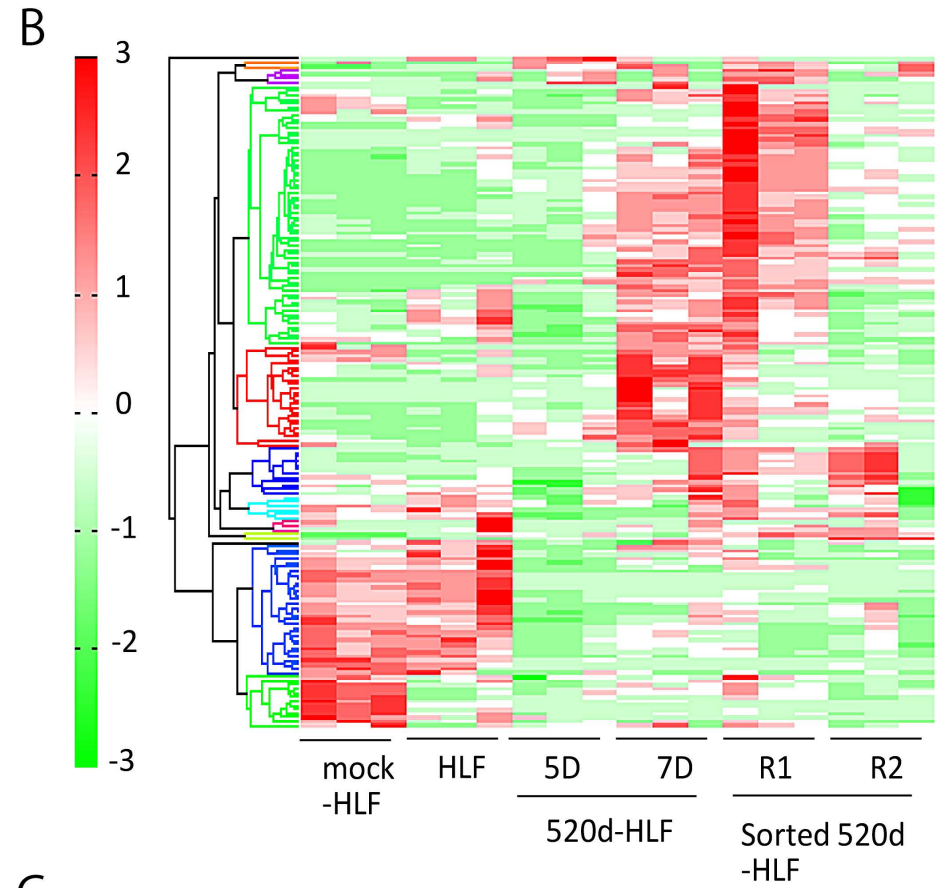
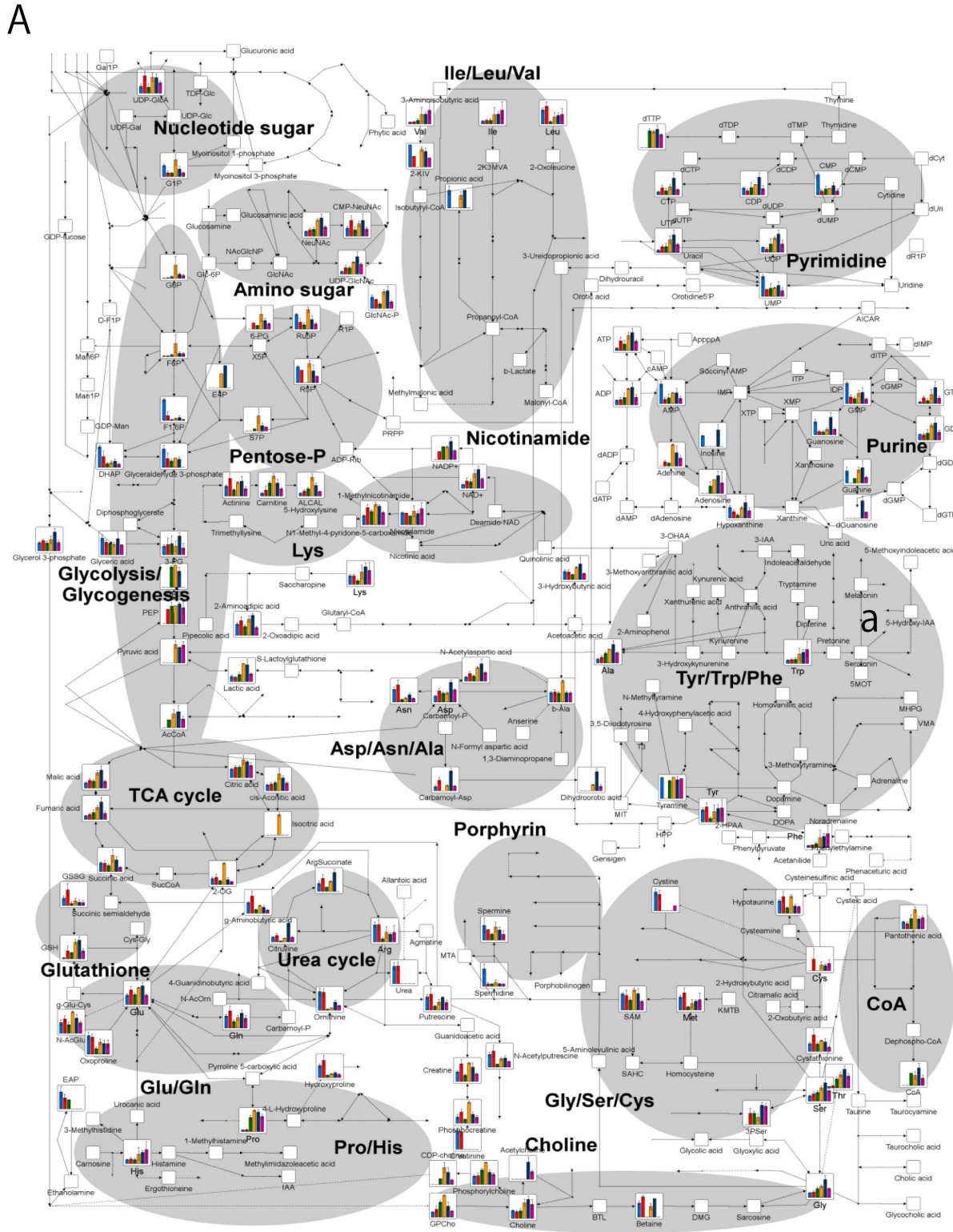






B 520d-HLF treated with $2\mu\text{M}$ Purmorphamine

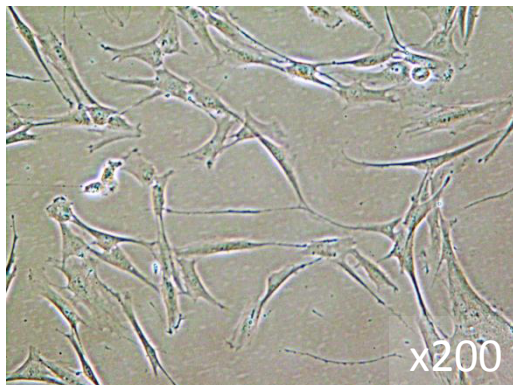




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 CC
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A

NHDF-Neo

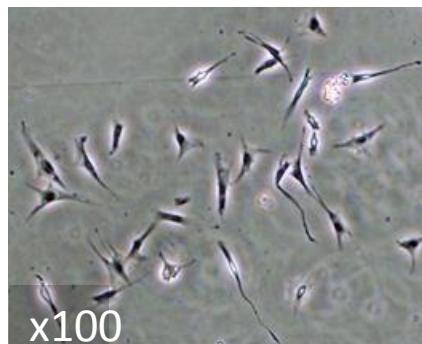


NHDF-Ad

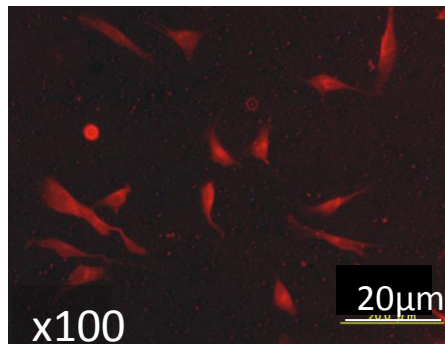


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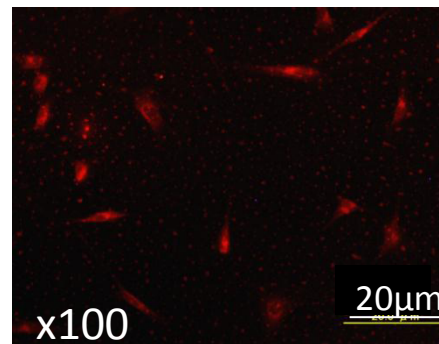
520d-NHDF-Neo



520d-NHDF-Neo Oct4

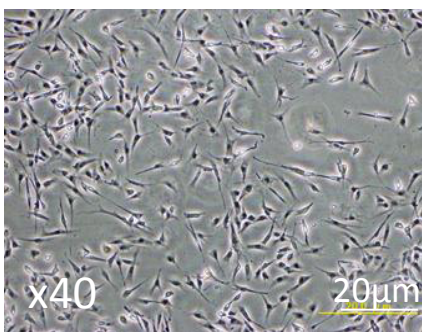


520d-NHDF-Neo Nanog

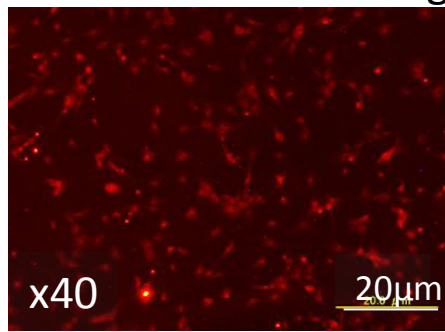


C

520d-NHDF-Ad



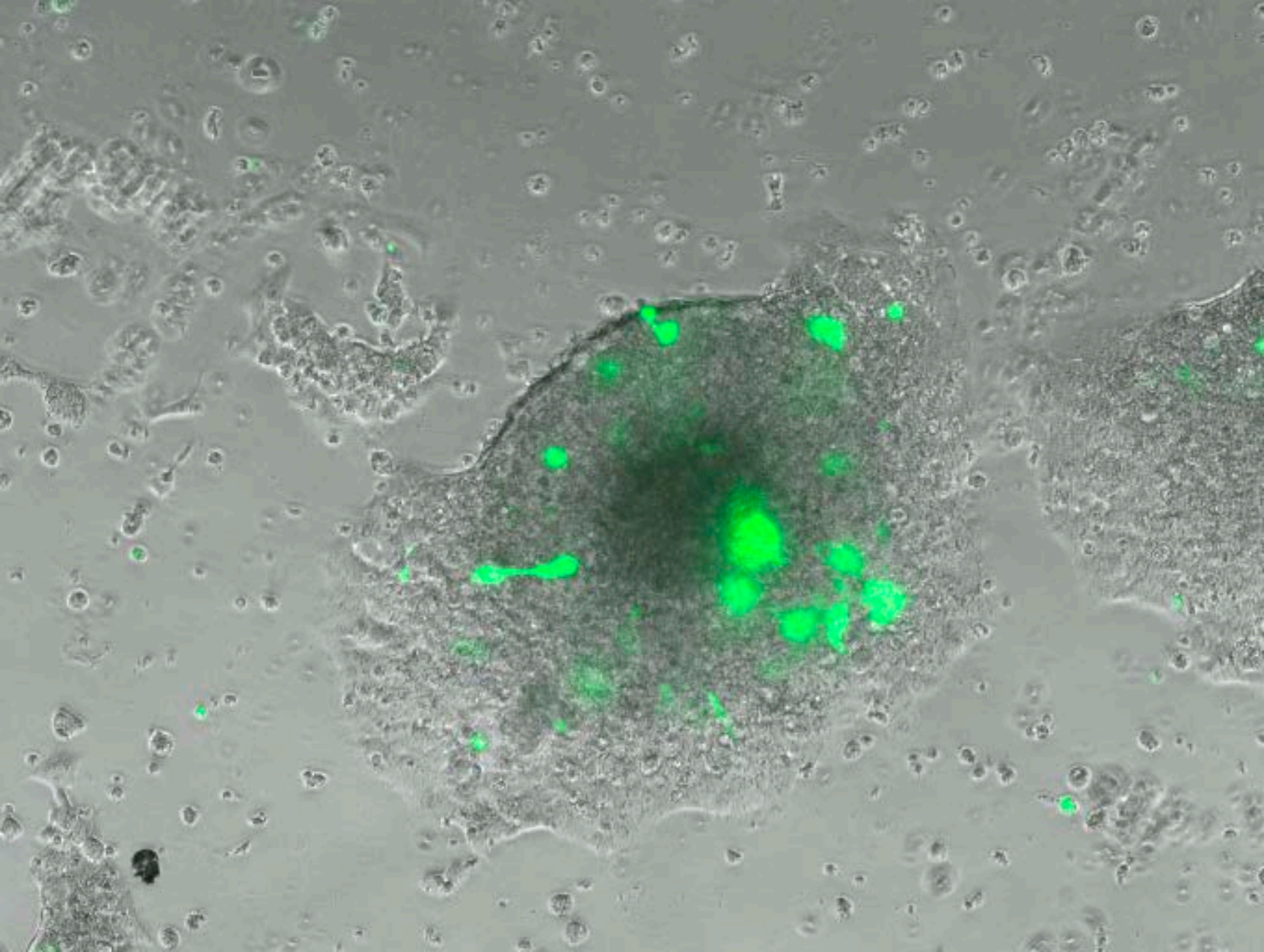
520d-NHDF-Ad Nanog



D



tumor formation 0/6

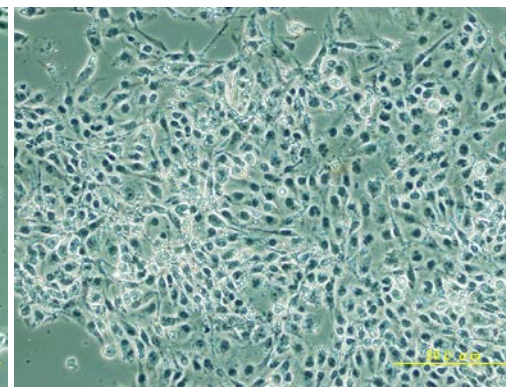
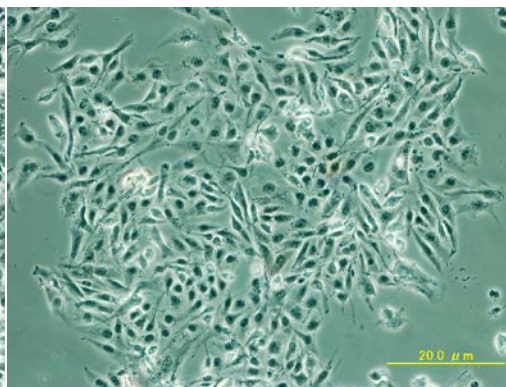
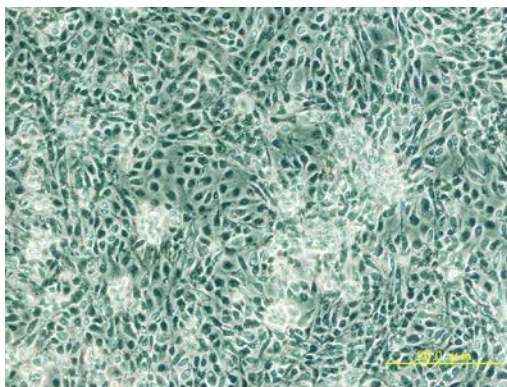


HLF

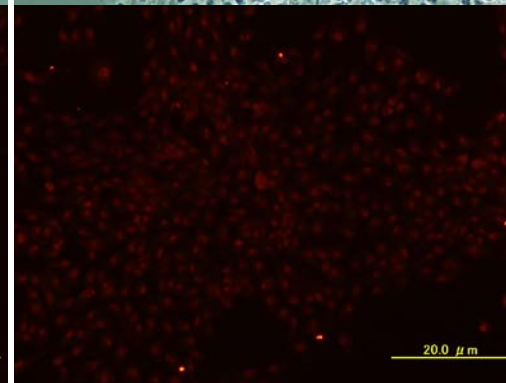
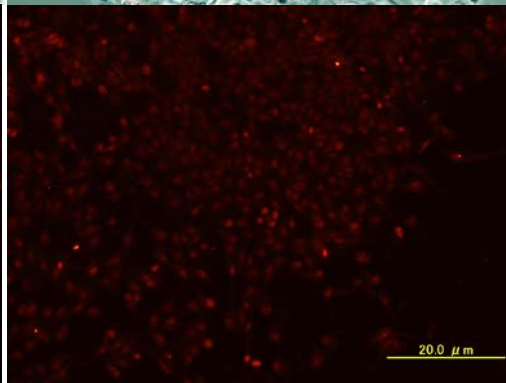
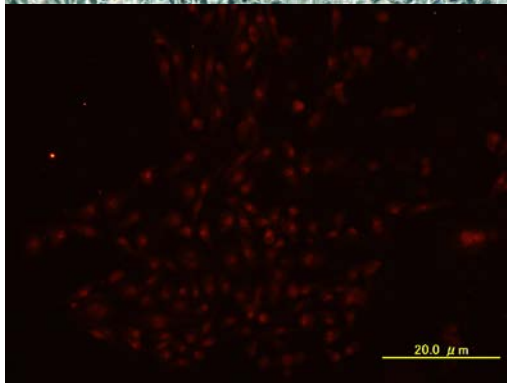
pCDH (mock)-HLF

psiLV (scramble)-HLF

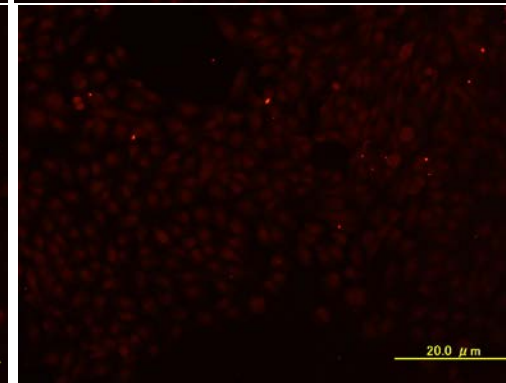
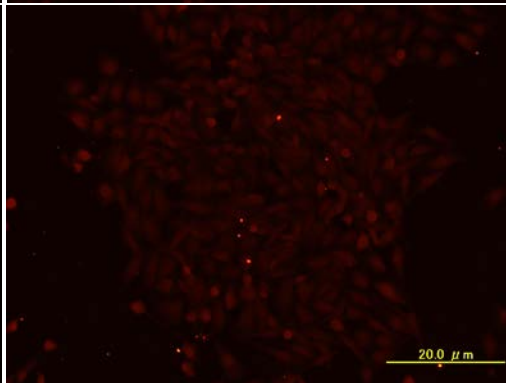
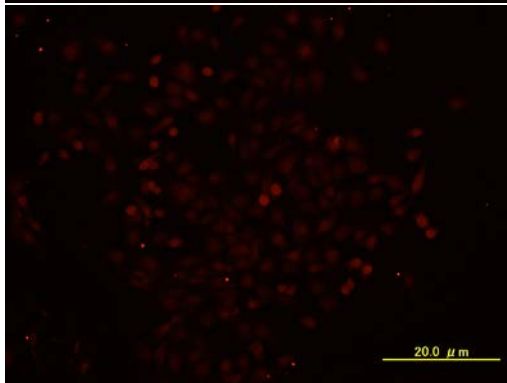
unstained



ICC: Nanog

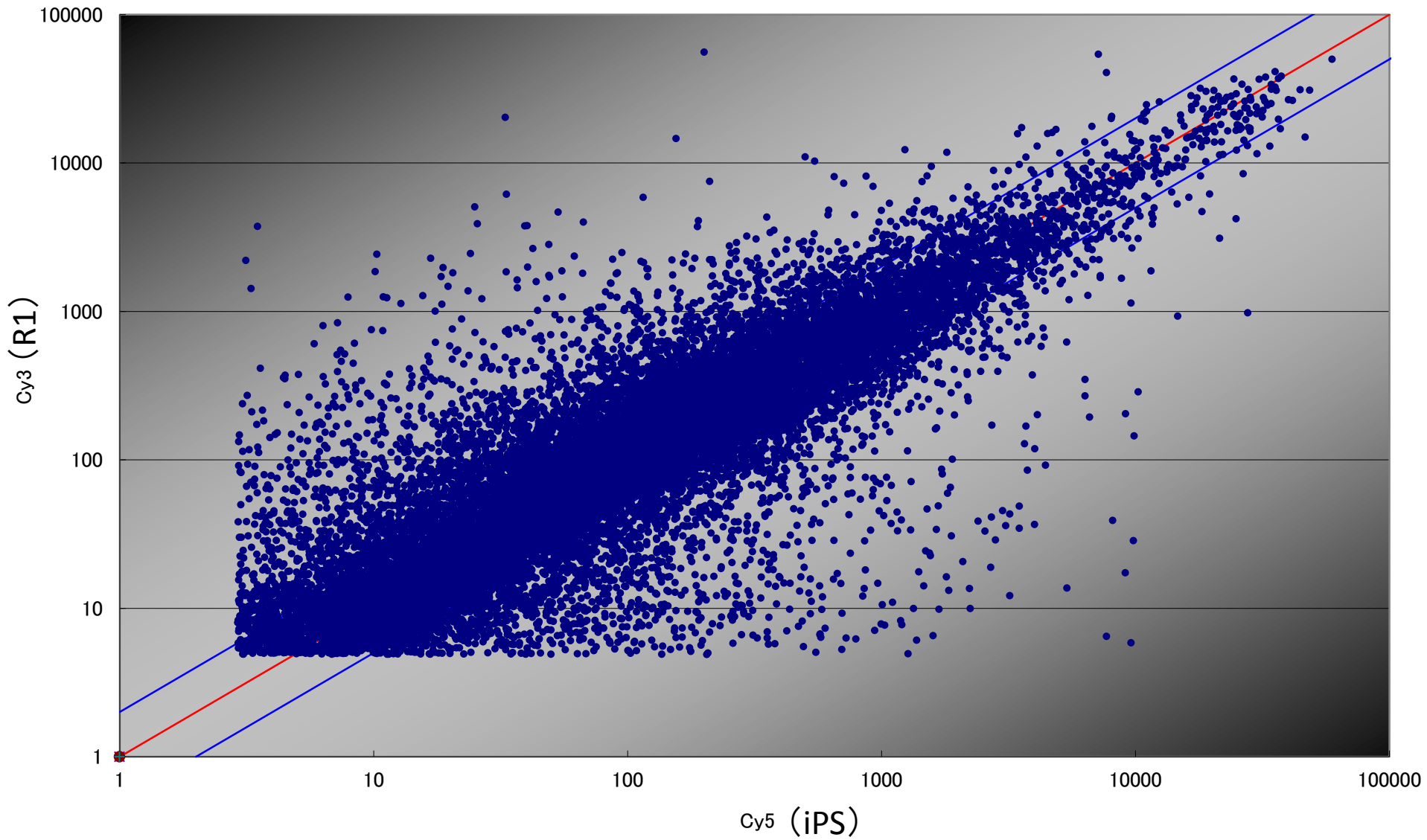


ICC: Oct4



bar 20μm

Normalized_Data



symbol	description	LOG2[ratio(R1/iPS)]
SEMA3C	Semaphorin-3C Precursor (Semaphorin-E)(Sema E)	10.06
MAGEC2	Melanoma-associated antigen C2 (MAGE-C2 antigen)(MAGE-E1 antigen)(Hepatocellular carcinoma-associated antigen 587)(Cancer/testis antigen 10)(CT10)	9.45
TM4SF1	Transmembrane 4 L6 family member 1 (Tumor-associated antigen L6)(Membrane component surface marker 1)(M3S1)	9.26
RP13-36C9.3	Cancer/testis antigen 45-3 (CT45-3)	8.75
IGFBP7	Insulin-like growth factor-binding protein 7 Precursor (IGF-binding protein 7)(IGFBP-7)(IBP-7)(MAC25 protein)(Prostacyclin-stimulating factor)(PGI2-stimulating factor)(IGFBP-rP1)	8.12
NT5E	5'-nucleotidase Precursor (EC 3.1.3.5)(Ecto-5'-nucleotidase)(5'-NT)(CD73 antigen)	7.87
MMP1	Interstitial collagenase Precursor (EC 3.4.24.7)(Matrix metalloproteinase-1)(MMP-1)(Fibroblast collagenase) [Contains 22 kDa interstitial collagenase;27 kDa interstitial collagenase]	7.65
PAGE2	G antigen family E member 2 (Prostate-associated gene 2 protein)(PAGE-2)	7.52
FILIP1	Filamin-A-interacting protein 1 (FILIP)	7.51
ALPK2	Alpha-protein kinase 2 (EC 2.7.11.-)(Heart alpha-protein kinase)	7.29
CCL2	C-C motif chemokine 2 Precursor (Small-inducible cytokine A2)(Monocyte chemoattractant protein 1)(Monocyte chemotactic protein 1)(MCP-1)(Monocyte chemotactic and activating factor)(MCAF)(Monocyte secretory protein JE)(HC11)	7.24
PRAME	Melanoma antigen preferentially expressed in tumors (Preferentially expressed antigen of melanoma)(OPA-interacting protein 4)(OIP4)	7.08
IL18	Interleukin-18 Precursor (IL-18)(Interferon-gamma-inducing factor)(IFN-gamma-inducing factor)(Interleukin-1 gamma)(IL-1 gamma)(Iboctadekin)	6.98
AC069282.6	Putative uncharacterized protein FLJ21075 Precursor	6.85
FGB	Fibrinogen beta chain Precursor [Contains Fibrinopeptide B]	6.84
IFI44	Interferon-induced protein 44 (p44)(Microtubule-associated protein 44)	6.84
MVP	Major vault protein (MVP)(Lung resistance-related protein)	6.76
SPANXD	Sperm protein associated with the nucleus on the X chromosome D (SPANX-D)(SPANX family member D)(Nuclear-associated protein SPAN-Xd)(Cancer/testis antigen 11.4)(CT11.4)	6.71
IFI44L	Interferon-induced protein 44-like	6.69
CXCL2	C-X-C motif chemokine 2 Precursor (Macrophage inflammatory protein 2-alpha)(MIP2-alpha)(Growth-regulated protein beta)(Gro-beta) [Contains GRO-beta(5-73)(GRO-beta-T)(SB-251353)(Hematopoietic synergistic factor)(HSF)]	6.66

symbol	description	LOG2[ratio(Cy3/Cy5)]
LIN28	Lin-28 homolog A (Zinc finger CCHC domain-containing protein 1)	-10.69
TACSTD1	Tumor-associated calcium signal transducer 1 Precursor (Major gastrointestinal tumor-associated protein GA733-2)(Epithelial cell surface antigen)(Epithelial glycoprotein)(EGP)(Adenocarcinoma-associated antigen)(KSA)(KS 1/4 antigen)(Cell surface glycoprotein Trop-1)(CD326 antigen)	-10.22
EPCAM	Tumor-associated calcium signal transducer 1 Precursor (Major gastrointestinal tumor-associated protein GA733-2)(Epithelial cell surface antigen)(Epithelial glycoprotein)(EGP)(Adenocarcinoma-associated antigen)(KSA)(KS 1/4 antigen)(Cell surface glycoprote	-9.05
GAL	Galanin Precursor [Contains Galanin;Galanin message-associated peptide(GMAP)]	-8.62
L1TD1	LINE-1 type transposase domain-containing protein 1 (ES cell-associated protein 11)	-8.44
SERPINB9	Serpin B9 (Cytoplasmic antiproteinase 3)(CAP-3)(CAP3)(Proteinase inhibitor 9)	-8.05
FGF13	Fibroblast growth factor 13 (FGF-13)(Fibroblast growth factor homologous factor 2)(FHF-2)	-8.02
SLC16A9	Monocarboxylate transporter 9 (MCT 9)(Solute carrier family 16 member 9)	-7.94
SLC7A3	Cationic amino acid transporter 3 (CAT-3)(Cationic amino acid transporter γ)(Solute carrier family 7 member 3)	-7.83
SALL4	Sal-like protein 4 (Zinc finger protein SALL4)	-7.82
TDGF1	Teratocarcinoma-derived growth factor 1 Precursor (Epidermal growth factor-like cripto protein CR1)(Cripto-1 growth factor)(CRGF)	-7.71
CRABP1	Cellular retinoic acid-binding protein 1 (Cellular retinoic acid-binding protein I)(CRABP-I)	-7.42
LECT1	Chondromodulin-1 Precursor (Chondromodulin-I)(ChM-I)(Leukocyte cell-derived chemotaxin 1) [Contains Chondrosurfactant protein(CH-SP)]	-7.36
ZSCAN10	Zinc finger and SCAN domain-containing protein 10 (Zinc finger protein 206)	-7.28
ZFP42	Zinc finger protein 42 homolog (Zfp-42)(Reduced expression protein 1)(REX-1)(hREX-1)(Zinc finger protein 754)	-7.18
EDNRB	Endothelin B receptor Precursor (ET-B)(Endothelin receptor non-selective type)	-7.17
FOXN3	Forkhead box protein N3 (Checkpoint suppressor 1)	-7.13
GPM6B	Neuronal membrane glycoprotein M6-b (M6b)	-7.08
RASL11B	Ras-like protein family member 11B	-7.07
PXDN	Peroxidasin homolog Precursor (EC 1.11.1.7)(Vascular peroxidase 1)(Melanoma-associated antigen MG50)(p53-responsive gene 2 protein)	-7.06

Table 1

Primers used in the study

Gene or miRNA	Sense	Antisense
β -actin	ACCTGACTGACTACCTCATG	GCAGCCGTGGCCATCTCTTG
Oct4	CGGAAAGAGAAAGCGAACCA	CGGACCACATCCTTCTCCAG
NANOG	CAGAAGGCCTCAGCACCTAC	ACTGGATGTTCTGGGTCTGG
Sox2	CAAGATGCACAACTCGGAGA	CGGGGCCGGTATTTATAATC
Klf4	AAACTGACCCTCCTCCAGGT	TGCTTTGCTCCAGGAACTTT
hTERT	GTGCACCAACATCTACAAGATCC	GTTCTTCCAACTTGCTGATG
c-Myc	GCCAGAGGAGGAACGAGCTA	TGGACGGACAGGATGTATGC
p53	GCTTCGAGATGTTCCGAGAG	TTATGGCGGGAGGTAGACTG
PROM1	TGGCAACGTAGTGACTCAGG	ACAGGAAGGGAGGGAGTCAT
CD44	AAGGTGGAGCAAACACAACC	GCTTTTTCTTCTGCCACAC
RGM249	TGGTACTTCACGAGGATGTGA	CCTGCCTCCTGAGTCTTCTG
ELAVL2	CTGCCATGGAAACACAACCTG	TTCTTCTGCCTCAATTCGCT
AICDA	CGTAGTGAAGAGGCGTGACA	TGTAGCGGAGGAAGAGCAAT
DNMT1	GCAAGAAGTGAAGCCCGTAG	TGAACGTTAGCCTCTCCAT
HDAC	GCTCAGCTGGTCATTCAACA	ACTGCCTGGTTGCTTCAGTT
Sin3A	TTTTTATGCGACTGCACCAG	CGTTCCCATTCTCTCTCTCG
MBD3	TGTCCCAGCTCCTTGAGACT	CAAACACGCCTCCAGACC
SIRT1	TCAGTGGCTGGAACAGTGAG	AGCGCCATGGAAAATGTAAC
miR-520d	TCTACAAAGGGAAGCCCTTCTG	

1 Supporting File Legends

2 **Supplementary Figure S1**

3 A. DNA content in 293FT, mock-293FT and 520d-293FT were assessed in
4 approximately 20,000 collected events. GFP-positive cells in mock-293FT and
5 520d-293FT were sorted. Cell cycle analysis of 520d-293FT showed increases and
6 decreases in the S and G0 phases, respectively, with synchronized and
7 homogeneous proliferation compared with 293FT and mock-293FT, although the
8 effect of miR-520p on G0, S phase did not appear to be significant.

9 B. Sorted immature populations were shown as PE positive cells or GFP (+) and
10 ALP-PE (+) cells as arrows indicated. The cells were maintained in an immature state
11 for two weeks after sorting. Although we found GFP (-) cells more than cells received
12 2% formaldehyde treatment due to the leakage of GFP during staining process, GFP
13 (-) cells post-sorting had a similar populations to GFP (+) cells regarding gene
14 expression and phenotype.

15 C. Transcriptional examination of methylation status to determine the 520d-293FT
16 reprogramming level. DNMT1 was not significantly expressed compared with
17 mock-293FT, although HDAC, Sin3A and MBD3 expression levels were significantly
18 upregulated ($P < 0.01$) (top). In HLF, DNMT1 was not significantly expressed
19 compared with mock-HLF, but HDAC, Sin3A and MBD3 levels were significantly
20 downregulated ($P < 0.01$), unlike those in 293FT (bottom). Significant differences
21 were not observed in expression levels between 293FT and HLF or between
22 mock-293FT and mock-HLF, but the average relative ratio of 520d-293FT to

1 520d-HLF was 261.3 (range: 11.9-2164.8). Data (n = 9) were analyzed with a Mann-
2 Whitney U test. **: P < 0.01.

3 D. FACS analysis in which mock- and 520d-293FT or mock- and 520d-HLF were
4 compared. After 3 days, GFP positive or ALP positive cell frequencies were
5 estimated. After one week under culture conditions to maintain an immature state,
6 the majority of 520d-expressing 293FT and HLF cells expressed the pluripotent
7 marker ALP (PE-labeled).

8 E. GFP (+) and ALP-PE (+) cells were selected and maintained in an immature state
9 for 2 weeks after sorting. The phenotype of these cells before sorting was similar to
10 that of iPS-like cells, and the sorted HLF continued to express GFP after sorting (left;
11 two weeks post-sorting, right; three weeks post-sorting).

12

13 **Supplementary Figure S2**

14 Result of *In vitro* study and microscopic observations in miR-520d-virus-infected
15 293FT cells (520d-293FT) were shown.

16 A. Phenotypic changes in 520d-293FT were evaluated microscopically. Changes in
17 cell morphology of 520d-293FT (right) was shown. Many non-adherent cells as well
18 as adherent cells emerged after transfection in 12-24 hours. 293FT cells (control)
19 were shown (left).

20 B. Confirmation of GFP expression in 520d-293FT that resembled a human-induced
21 pluripotent stem cell. GFP-positive non-adherent cells were cultured in feeder
22 cell-free ES cell medium.

1 C. Time-lapse observations of an induced cell with GFP expression for 12 hours (x40
2 magnification) to show morphology and proliferation. Observation of another cell in
3 video mode is provided as Supplementary video 7. 520d-293FT maintained in Repro
4 Stem medium grew up while maintaining the form of the colony unlike those cultured
5 in DMEM. Scattered spheroid colonies were interlinked through long, branched
6 groups of cells.

7 D. Immunocytochemistry in a representative round cell with an anti-Oct4 antibody
8 and a Rhodamine Red-conjugated secondary antibody. Oct4 was strongly expressed.
9 Unstained cells (left) and cells with Oct4 staining (right) were shown.

10 E. Immunocytostaining with an anti-Nanog antibody concomitantly with GFP
11 expression. Three days to one week later, the cells formed larger colonies and
12 maintained a Nanog-positive state under the same culture conditions.

13 F. The effects on miRNA expression were confirmed in 520d-293FT and the relative
14 ratio to hiPSCs was shown. 520d-293FT stably expressed miR-520d-5p in both the
15 adherent and non-adherent states in culture and the viral infection efficiency was
16 greater than 99.1% according to GFP-positive cell sorting. miR-520d was significantly
17 upregulated in 520d-293FT compared with hiPSCs. *: $P < 0.05$, **: $P < 0.01$. Data (n
18 = 9) were analyzed using a Mann–Whitney U test. A: adherent cells, non-A:
19 non-adherent spherical cells.

20 G. Comparison of transcriptional expression in 520d-293FT, hiPSCs or mock-293FT.
21 RT-PCR showed that 520d-293FT showed greater upregulation of P53 and *RGM249*
22 and weaker expression of Oct4 and hTERT than did hiPSCs. However, 520d-293FT

1 showed greater upregulation of Oct4 than did mock-293FT. 520d-293FT showed
2 greater upregulation of P53, *RGM249* and Oct4 expression than 293FT.

3 H. Western blotting was performed in hiPSCs, mock-293FT and 520d-293FT.
4 Western blotting showed that non-adherent cells expressed P53 and Oct4 stronger
5 than mock-293FT. *Dicer1* expression was also downregulated compared with
6 mock-293FT. The expression of AID known as one of epigenetic markers was
7 downregulated compared with hiPSC. A: adherent cells, non-A: non-adherent cells.

8 I. Relative ratio of the representative gene expression profile to that in mock-293FT
9 by RT-PCR. Data depict the average relative ratio of 520d-293FT to mock-293FT,
10 and a significant difference was shown, as *:P < 0.01 (n = 5). The pluripotent markers,
11 P53 and *RGM249* were upregulated, whereas AID was downregulated. Cancer stem
12 cell (CSC) markers (CD133 and CD44) were not upregulated.

14 **Supplementary Figure S3**

15 A. Immunohistochemical analysis of liver tissue generated from 520d-HLF cells in
16 xenograft model. (left) Human albumin was expressed strongly in hepatocytes from
17 liver tissue generated from 520d-HLF cells in a xenograft model. (middle-right)
18 Human AFP or GFAP were expressed weakly in the cytoplasm of hepatocytes.

19 B-C. Osteoblastic differentiation from 520d-HLF cells was induced morphologically
20 and transcriptionally. **B.** Morphological changes were shown in 520d-HLF that were
21 treated with 2 μ M purmorphamine (top) compared with untreated 520d-HLF cells
22 (bottom). **C.** IBSP (bone sialoprotein) and SPP1 (osteopontin) were strongly
23 expressed in 520d-HLF cells treated with 2 μ M purmorphamine (n = 4). P:

1 purmorphamine-treated 520d-HLF, **: $P < 0.01$. Tumorigenicity of well-differentiated
2 hepatoma cells (Huh7) received miR-520d-5p was examined.

3 D. Induction of pluripotency by miR-520d in Huh7. Colonies of small round cells
4 emerged within 12 days. Both GFP (left top) and Oct4 (right top) expression were
5 confirmed by immunocytochemistry. Average gene expression levels were examined
6 ($n = 5$) and pluripotent marker gene and P53 mRNA levels were upregulated
7 compared with mock-Huh7 (right column). Alb, c-Myc, AID and *RGM249* levels were
8 downregulated. 1-17: Oct4, Nanog, P53, hTERT, c-Myc, PROM1, CD44, AID, HDAC,
9 DNMT1, Sin3A, MBD3, Lin28, *RGM249*, AFP, Alb and miR-520d.

10 E. With the same viral vehicle titer used in the previous *in vivo* study with HLF, ten
11 mice inoculated mock-Huh7 formed a tumor (top). The HE stain of representative
12 tumor was shown. Well-differentiated neoplastic cells (partly squamous cell
13 carcinoma-like cells) with substantial or alveolar arrangement were shown (bottom;
14 x100).

15 F. 520d-Huh7 was cultured for one week (once per week, we infected cells with the
16 viral construct *in vitro*), tumorigenicity was confirmed one month after inoculation.

17 G. Fifty percent of inoculated mice generated less-differentiated tumors one month
18 later; the remaining mice did not generate tumors ($n = 4$). HE staining (x200
19 magnification) showed that the tumors were identical with low-differentiated
20 hepatoma (left) and poorly-differentiated hepatoma (right).

21 H. Average methylation rate of Huh7 was 0.20% and the data was standardized,
22 compared with that in Huh7. An average hmC(%) in Huh7 cells was estimated to
23 understand general methylation level during de-differentiation process by

1 miR-520d-5p. Induction of hypermethylation was not induced in this cell type, but
2 decreasing methylation level after 3D were observed, followed by the decrease less
3 than iPS level a month later (n=3).

4

5 **Supplementary Figure S4**

6 A. Summarized pathway map (original summarized scheme) from HMT analysis. The
7 result of this analysis was described in the discussion section in this text.

8 B. heat map (original data) obtained from metabolomic analysis. Mock-HLF and HLF
9 (parental cells) were prominently different from the other four types of cells that
10 expressed miR-520d-5p.

11 C. A principal component analysis (PCA). Mock-HLF and HLF were found to have
12 similar patterns, and the patterns of 7D and R1 were similar. R2 appears to possess
13 similar characteristics to those of 5D and 7D (or R1).

14

15 **Supplementary Figure S5**

16 The 10 predicted binding sites (shown in red letters) of miR-520d-5p in the 3'UTR
17 (1356-3805) of ELAVL2 (1-3805) are shown. Two sites (1853-1880 and 2235-2249 in
18 3'UTR) were investigated with a luciferase reporter expression assay. These sites
19 were predicted based on the four databases described above. Bases 1607-1626 of
20 the 3'UTR were used for a sense primer sequence.

21

22 **Supplementary Figure S6**

1 Tumorigenicity of miR-520d-expressing fibroblasts (NHDF-Neo and -Ad) in KSN/Slc
2 mice.

3 A. Parental cells [NHDF-Neo (left) and -Ad (right), x200 magnification] were infected
4 with a miR-520d-expressing lentiviral vector and inoculated into the right hindquarters
5 of KSN/Slc mice.

6 B. The fibroblast lines are represented as 520d-NHDF-Neo and 520d-NHDF-Ad. The
7 phenotype of 520d-NHDF-Neo is shown (left; x100 magnification).
8 Immunocytochemistry revealed the upregulation of Nanog (right) and Oct4 (middle)
9 in 520d-NHDF-Neo (white bar = 20 μ m).

10 C. The phenotype of 520d-NHDF-Ad is shown (left; x40 magnification).
11 Immunocytochemistry revealed the upregulation of Nanog expression (middle; white
12 bar = 20 μ m). Average mRNA expression level of 520d-NHDF-Ad to mock-NHDF-Ad
13 was shown.

14 D. The tumorigenicity of 520d-induced fibroblasts was examined in KSN/Slc mice.
15 Neither 520d-NHDF-Neo (n = 3) nor -Ad (n = 3; right) generated tumors in mice.

16

17 **Supplementary File (video) 7**

18 520d-HLF cells in video mode is provided by time-lapse image.

19

20 **Supplementary File 8**

21 Oct4 or Nanog expression in a parental HLF, pCDH-HLF or psiLV (scrambled)-HLF
22 was shown. pCDH and psiLV were used as controls for pMIR-520d-5p and siELAVL2
23 [unstained (top), ICC: Nanog (middle) and ICC: Oct4 (bottom)]. Nanog and Oct4 were

1 both weakly expressing the pluripotent markers. Approximately 8% of populations in
2 HLF cells seemed to be slightly expressing both markers stronger than other
3 populations around them. Also, Oct4 was expressed in each sample weaker than
4 Nanog. ICC: immunocytochemistry.

5 **Supplementary File 9**

6 Normalized data between R1 and hiPSC in microarray analysis is shown as a graph.

7 **Supplementary File 10**

8 Upregulated 20 genes (more than 8 fold) were representatively shown between R1
9 and hiPSC for reference (n=1). R1 was a cell population formed liver tissue *in vivo*.

10 **Supplementary File 11**

11 Downregulated 20 genes (more than 8 fold) were representatively shown between
12 R1 and hiPSC for reference (n=1).

13 **Supplementary Table S1**

14 Primers used in this study are shown.

15