

cytometer. (C) A representative fluorescence histogram of EGFP. (D) The median fluorescence intensities of the EGFP-expressing populations. Error bars represent the standard error of 3 independent analyses. **, $P < 0.01$ (Student's *t* test). Scale bar, 200 μm . doi:10.1371/journal.pone.0066274.g003

C-terminus (tTA-2A) and Bsd. tTA-2A binds to the TRE-tight in the absence of Dox, a tet derivative, and activates transcription of EGFP to a very high level. In the presence of Dox, tTA-2A is unable to bind the TRE-Tight in a tet-responsive promoter, and the system is inactive.

To investigate the usefulness of these lentiviral vectors, hADMPCs were transduced with pTRE-EGFP-CMV- tTA-2A-Bsd or pTRE-EGFP-EF- tTA-2A-Bsd at a m.o.i. of 250. As shown in Figure 2C, expression of EGFP was observed in the absence of Dox, whereas addition of Dox (1 $\mu\text{g}/\text{mL}$) was enough to suppress the expression. Flow cytometry analysis revealed that the transduction efficiency was relatively low (EGFP-positive cells were 7.5–10%) compared with that of CSII-CMV-EGFP or CSII-EF-EGFP (EGFP-positive cells were 45% or 77% at a m.o.i. of 250, respectively; Figure 1A), and the tet-off system completely abolished gene expression in the presence of Dox (Figure 2D). Flow cytometry analysis also revealed that fluorescent intensity was relatively uniform in hADMPCs transduced with pTRE-EGFP-EF- tTA-2A-Bsd , but a wide range of fluorescent intensities was observed in hADMPCs infected with pTRE-EGFP-CMV- tTA-2A-Bsd . These data suggest that tTA-2A functions properly in this system. Moreover, western blot analysis against tTA showed the efficient cleavage (>95%) of tTA-2A-Bsd proteins into tTA-2A and Bsd (Figure 2E).

To further determine that Bsd cleaved from tTA-2A-Bsd was effective in this system, 4 $\mu\text{g}/\text{mL}$ blasticidin was administered to hADMPCs. Within 1 week after the selection, control hADMPCs were completely killed (data not shown), whereas hADMPCs that were successfully transduced with either pTRE-EGFP-CMV- tTA-2A-Bsd or pTRE-EGFP-EF- tTA-2A-Bsd could survive and proliferate, demonstrating that Bsd from tTA-2A-Bsd is sufficient to confer blasticidin resistance to the cells. The surviving cells were kept in culture medium with blasticidin and then divided into 2 populations, either with Dox (1 $\mu\text{g}/\text{mL}$) or without Dox. As shown in Figure 3A and 3B, almost all (>90%) the cells transduced with pTRE-EGFP-EF- tTA-2A-Bsd strongly expressed EGFP in the absence of Dox. In hADMPCs transduced with pTRE-EGFP-CMV- tTA-2A-Bsd , however, >50% of the cells were EGFP negative regardless of their blasticidin resistance. Moreover, fluorescent intensities were quite variable; some cells expressed very high levels of EGFP, while others expressed very low levels (Figure 3A and 3B). This might be due to “promoter suppression,” transcript repression of an upstream transcriptional unit by a downstream unit when 2 transcriptional units lie adjacent in head-to-tail tandem on a chromosome [28,29]. Studies have revealed that the suppression by adjacent units is epigenetic and involves modification of the chromatin structure, including DNA methylation at CpG sites within the promoter, histone deacetylation, histone methylation at specific residues (e.g., H3K9, H3K27), and densely packed nucleosomes that create a closed chromatin structure. In order to determine if inhibiting histone deacetylases or DNA methylation would re-induce EGFP expression, pTRE-EGFP-CMV- tTA-2A-Bsd cells were treated with histone deacetylase inhibitor trichostatin A (TSA) and/or DNA methylation inhibitor 5-aza-2'-deoxycytidine (5-aza-dC). TSA treatment significantly increased the number of EGFP-positive cells and strengthened the fluorescent intensities of EGFP, whereas 5-aza-dC had no effect, suggesting that EGFP expression was repressed by histone deacetylation when stably transduced with pTRE-EGFP-CMV- tTA-2A-Bsd (Figure 3C and 3D). These inhibitors

had no effect on hADMPCs transduced with pTRE-EGFP-EF- tTA-2A-Bsd . These data suggest that the dual-promoter lentiviral vector using the EF promoter is more resistant to gene silencing than that using the CMV promoter.

Blasticidin-selected hADMPCs Maintain the Properties of Their Parental hADMPCs

hADMPCs are an attractive material for cell therapy because of their ability to secrete various cytokines and growth factors. These cells also have the ability to differentiate into various types of cells, including adipocytes, chondrocytes, osteocytes, hepatocytes, cardiomyoblasts, and neuronal cells. Gene manipulation of hADMPCs may thus generate great possibilities for cell therapy and tissue engineering. From this point of view, the development of an efficient and stable Dox-responsive gene transfer system to achieve high levels of transgene expression in hADMPCs, without affecting the phenotype, is of special interest for the field. We therefore studied the cell properties of hADMPCs transduced with the single tet-off lentiviral vector after blasticidin selection. Flow cytometry analysis revealed no changes in the expression of the main surface markers (positive for CD13, CD29, CD44, CD73, CD90, CD105, and CD166, and negative for CD34) either in the absence or presence of Dox (Figure 4). To further confirm the properties of hADMPCs, the cells were differentiated into adipocytes, osteocytes, chondrocytes, and neuronal cells. As shown in Figure 5, blasticidin-selected hADMPCs maintained their ability to differentiate into adipocytes, osteocytes, chondrocytes, and neuronal cells. Moreover, EGFP was stably expressed in the differentiated cells only in the absence of Dox (Figure 5).

Discussion

In recent years, there is growing interest in the use of MSCs for cell therapy and tissue engineering because of their differentiation potential and ability to secrete growth factors [7–11]. Furthermore, because of their hypo-immunogenicity and immune modulatory effects, MSCs are good candidates for gene delivery vehicles for therapeutic purposes [12,14]. In addition to primary MSCs, genetically modified MSCs have been applied to bone regeneration, muscle repair, diabetes, Parkinson's disease, and myocardial infarction recovery [14,30–35]. Duan et al. reported that the angiogenic effect of MSCs could be enhanced by adenovirus-mediated HGF overexpression in the treatment of cardiac ischemia injury [14]. Karnieli et al. and Li et al. both reported the reversal of hyperglycemia in streptozotocin-induced diabetic mice after transplantation of insulin-producing cells originating from genetically modified Pdx-1 expressing MSCs [32,33].

While significant progress has been made in the use of genetically modified MSCs for basic and applied research, the current methods for gene manipulation are still insufficient for some applications. Adenoviral vectors are commonly used for transient expression because they remain epichromosomal in the host cells, and their ability to transiently infect target cells minimizes the risk of insertional mutagenesis [36]. However, relatively brief transgene expression may limit the utility of this approach to tissue repair applications. On the other hand, lentiviral vectors, which are promising vectors for gene delivery in primary human cells, integrate into the host cell genome, which may be an appropriate strategy for tissue repair applications

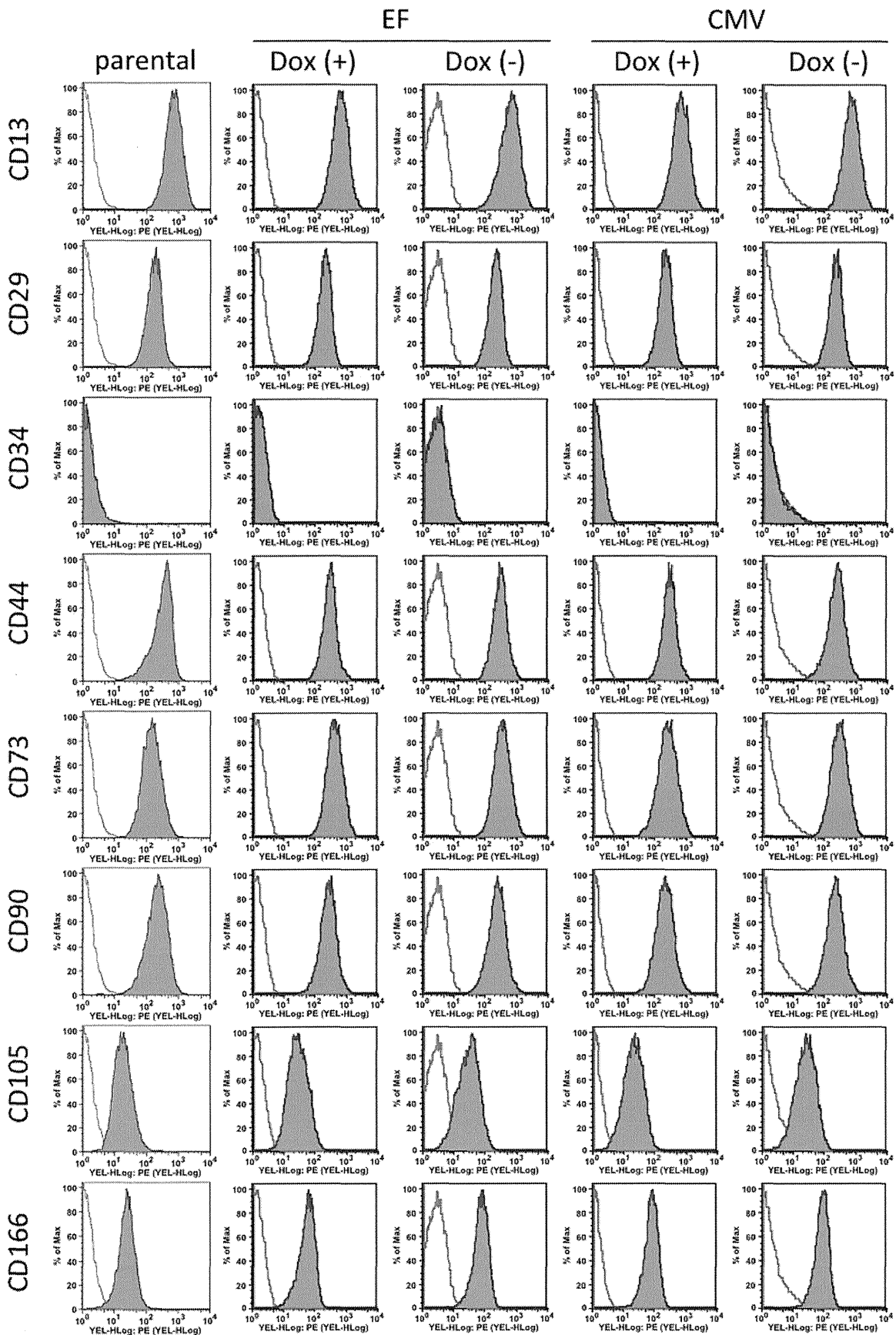


Figure 4. Expression pattern of surface cell markers on Dox-responsive hADMPs. Dox-responsive hADMPs after selection by blasticidin were cultured in the absence (Dox(-)) or presence (Dox(+)) of 1 μ g/mL Dox for 4 days. Expression of the different surface markers were analyzed by flow cytometry and compared to the expression by a parental hADMPs. They were stained with PE-coupled antibodies against CD13, CD29, CD34, CD44, CD73, CD90, CD105, and CD166. Histogram of a PE-coupled mouse IgG1 κ isotype control is shown in gray. CMV; hADMPs transduced with pTRE-EGFP-CMV-tTA-2A-Bsd, EF; hADMPs transduced with pTRE-EGFP-EF-tTA-2A-Bsd. doi:10.1371/journal.pone.0066274.g004

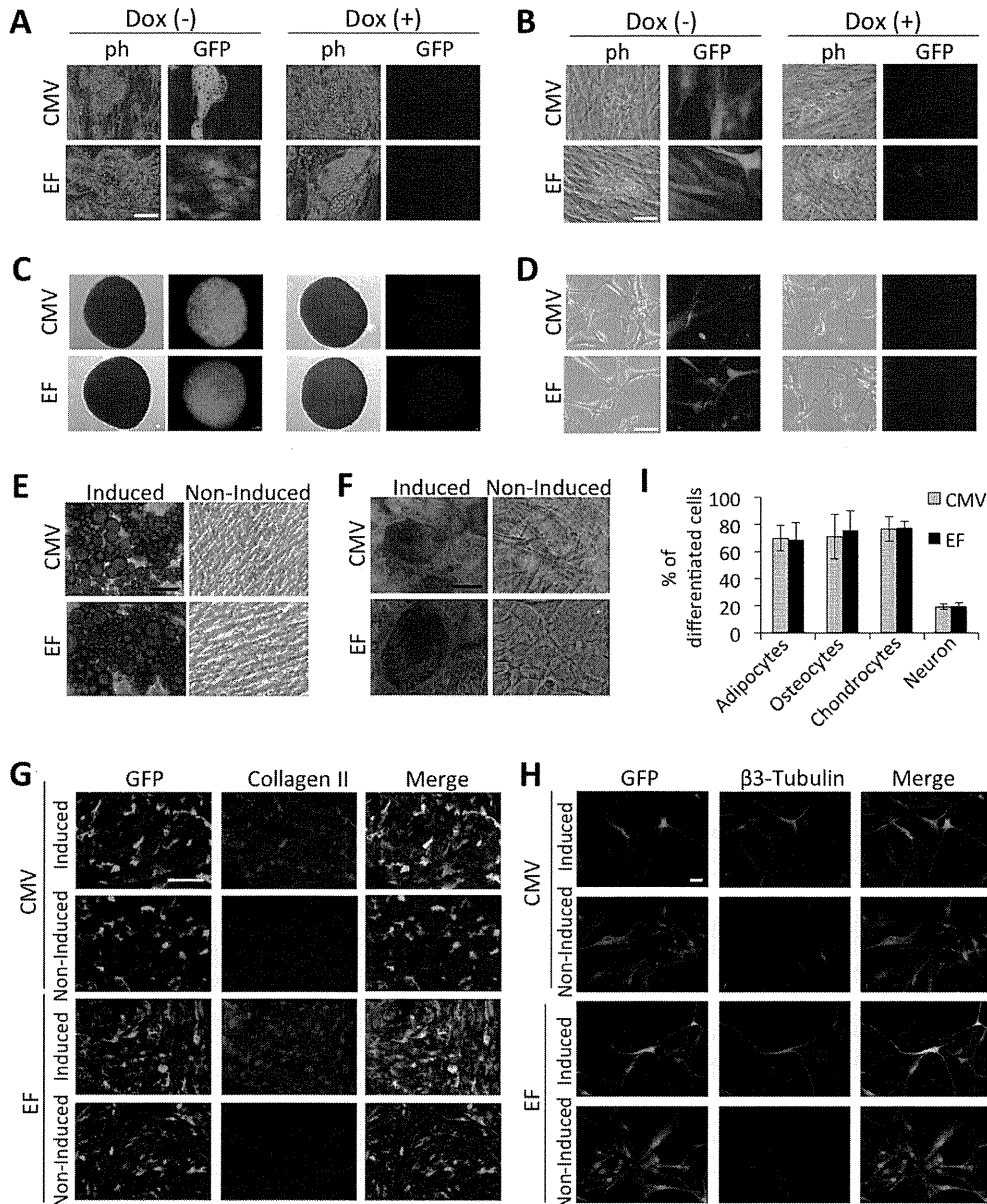


Figure 5. Differentiation potential of Dox-responsive hADMPs. Dox-responsive hADMPs were differentiated into adipocytes (A, E), osteocytes (B, F), chondrocytes (C, G), and neuronal cells (D, H). (A–D) Phase contrast (ph) and fluorescent (GFP) images. Dox-responsive hADMPs were differentiated in the absence of Dox (Dox(-)) or in the presence of 1 μ g/mL Dox (Dox(+)) as described in the material and methods section. (E–I) Confirmation of differentiated cells by oil red O staining for adipocytes (E), alizarin red staining for osteocytes (F), immunohistochemical staining against collagen II for chondrocytes (G), and immunohistochemical staining against β -tubulin for neuronal cells (H). The percentages of differentiated cells to each cell type were calculated by the computerized image analysis (I). Cells that were not induced to differentiate (non-induced) were used as a negative control. CMV; hADMPs transduced with pTRE-EGFP-CMV-tTA-2A-Bsd, EF; hADMPs transduced with pTRE-EGFP-EF-tTA-2A-Bsd. Scale bar, 50 μ m. doi:10.1371/journal.pone.0066274.g005

requiring sustained, long-term expression of therapeutic proteins. In this study, we generated novel lentiviral vectors with a tet-off system, and demonstrated that our lentiviral vector systems were significantly effective and strictly regulated in hADMPCs, without affecting their stem cell properties.

Gene silencing is of considerable importance where stable, long-term expression is required. Researchers have reported that transgene silencing occurred when the CMV promoter was used in some cell types, especially in embryonic stem cells [15–17]. Since Kawabata et al. also demonstrated that virus-derived promoters inefficiently functioned in embryonic stem cells in gene transfer experiments [37], down-regulation and unsuitability of promoters in stem cells should be considered. Therefore, transduction efficacy and durability of transgene expression in hADMPCs is also an important issue to be determined. Qin et al. reported that the human EF-1 α promoter and the TRE promoter are more efficient than the CMV promoter to drive lentiviral mediated transgene expression in rat bone marrow-derived MSCs [18]. McGinley et al. also showed that EF-1 α and human phosphoglycerate kinase-1 (PGK) promoters have a clear advantage over the CMV promoter in transducing rat bone marrow-derived MSC transduction with lentivirus [19]. Consistent with their findings, our data also demonstrated that the EF-1 α promoter was more efficient than the CMV promoter to drive EGFP expression in hADMPCs (Figure 1A, B). Moreover, a significant decrease in fluorescent intensity was observed by 28 days after transduction with lentiviral vector CSII-CMV-EGFP (Figure 1C), suggesting that the CMV promoter might be silenced in hADMPCs. We also demonstrated the intriguing finding that most (>90%) of the hADMPCs transduced with pTRE-EGFP-EF-tTA-2A-Bsd strongly expressed EGFP in the absence of Dox, whereas >50% of the cells transduced with pTRE-EGFP-CMV-tTA-2A-Bsd were EGFP negative, regardless of their blasticidin resistance (Figure 3A, B). Our data demonstrated that the inhibitor of histone deacetylation trichostatin A (TSA) re-induced the expression of EGFP (Figure 3C, D), suggesting that “promoter suppression” might occur by histone deacetylation, not by DNA methylation of CpG sites within the TRE tight promoter. “Promoter suppression” is a transcript repression of a 5' transcriptional unit by a 3' unit when 2 transcriptional units lie adjacent in head-to-tail tandem on a chromosome [28,29]. In this study, it is possible that the downstream unit of CMV-tTA-2A-Bsd repressed the upstream unit of TRE-EGFP because (1) resistance to blasticidin implies the transcriptional unit of CMV-tTA-2A-Bsd is active, and (2) reactivation of EGFP expression by TSA implies the transcriptional unit of TRE-EGFP is epigenetically silenced. In order to eliminate the promoter suppression or transcriptional interference between 2 transcriptional units, some researchers have been trying to separate the 2 units by polyadenylation, terminator, and insulator sequences [28,38]. However, these sequences extend the lentiviral vector size, which may affect the lentiviral titers produced from the vector. From this point of view, our finding that the transcriptional unit driven from the TRE tight promoter is resistant to gene silencing when arranged in tandem with the EF-tTA-2A-Bsd transcriptional unit (Figure 3) is of interest in the fields of both basic and clinical research, although the underlying mechanism remains elusive.

In general, large numbers of cells displaying the appropriate phenotypes are required for tissue engineering. Moreover, fully differentiated cells do not proliferate [39]. Therefore, in order to obtain enough cells to perform a transplant from genetically modified MSCs, it is important to develop a system in which the gene of interest is tightly regulated and inducible, and in which stably expressing transgenic cell lines can be obtained without

affecting their stem cell properties. Using the system, MSCs transduced with lentiviral vectors can be selected and increased in numbers from a limited number of MSCs, before the target genes are induced. After obtaining an adequate number of gene-manipulated MSCs, the target genes could be induced in order to start differentiation. According to our data, hADMPCs transduced with pTRE-EGFP-EF-tTA-2A-Bsd were successfully selected by blasticidin, could proliferate, maintain their stem cell properties, and regulate EGFP expression tightly by Dox (Figure 4, 5), demonstrating that this all-in-one lentiviral vector is a promising gene delivery system for generating the material for artificial organs.

A major advantage of using the 2A cleavage factor in the construction of multi-cistronic vectors is its small size compared to internal promoter entry site (IRES) sequences. Because the titer of the lentivirus decreases with increasing size of the lentiviral vector, it is important to minimize the length of the sequences. In addition, linkage of 2 genes by 2A peptide resulted in efficient co-expression of the genes, whereas a gene placed downstream of an IRES is expressed at 2- to 3-fold lower levels than a gene placed upstream [40,41]. In this study, tTA-2A-Bsd cassette driven from CMV or EF-1 α promoter showed ~90% cleavage (Figure 3). However, the point that should be considered is the effect of residual 2A peptide on the protein. As the processing occurred at the end of the 2A peptide, the 2A tag remains attached at the tTA C-terminus. Our data demonstrated that the presence of this extra 2A peptide did not seem to interfere with the activity of tTA since Dox strictly regulated the expression of EGFP under the control of TRE-tight promoter (Figure 2D, 3A, 3B and 5). Moreover, when Bsd is cleaved, an additional proline is attached at the N-terminus. We demonstrated that this did not affect a function of Bsd because hADMPCs transduced with either pTRE-EGFP-CMV-tTA-2A-Bsd or pTRE-EGFP-EF-tTA-2A-Bsd could survive and proliferate in medium containing blasticidin at a concentration at which all of the parental hADMPCs died.

Another advantage of our lentiviral system is the availability of a restriction enzyme treatment/ligation independent cloning system, called the Gateway system (Invitrogen). In general, the construction of lentiviral vectors using a conventional restriction enzyme/ligation cloning method has poor efficiency due to the large sizes and the lack of proper cloning sites. In our hands, cloning efficiency into our new lentiviral vectors pTRE-RfA-CMV-tTA-2A-Bsd or pTRE-RfA-EF-tTA-2A-Bsd using LR recombination reaches nearly 100%, saving time and effort in construction of the vectors. In addition, there are several resources available that take advantage of the Gateway vector. For example, CCSSB Human ORFeome Collection (Dana-Farber Cancer Institute, Center for Cancer Systems Biology) represents almost 12,000 fully-sequenced cloned human ORFs which can be readily transferred to Gateway compatible destination vectors for various functional proteomics studies [42]. Block-iT pol II miR RNAi system from Invitrogen, which is designed to express artificial miRNAs, also enables compatibility with Gateway destination vectors for gene knock-down experiments [43].

In conclusion, our new single tet-off lentiviral vector system provides powerful tools not only for applied research on hADMPCs and other stem cells, but also basic research on a variety of cell lines and primary cells.

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Author Contributions

Conceived and designed the experiments: HM MM. Performed the experiments: HM MM KS HO AM. Analyzed the data: HM MM KS.

Contributed reagents/materials/analysis tools: HM MM HO AI AM. Wrote the paper: HM MM TH.

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Long-Term Self-Renewal of Human ES/iPS-Derived Hepatoblast-like Cells on Human Laminin III-Coated Dishes

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SUMMARY

The establishment of self-renewing hepatoblast-like cells (HBCs) from human pluripotent stem cells (PSCs) would realize a stable supply of hepatocyte-like cells for medical applications. However, the functional characterization of human PSC-derived HBCs was not enough. To purify and expand human PSC-derived HBCs, human PSC-derived HBCs were cultured on dishes coated with various types of human recombinant laminins (LN). Human PSC-derived HBCs attached to human laminin-111 (LN111)-coated dish via integrin alpha 6 and beta 1 and were purified and expanded by culturing on the LN111-coated dish, but not by culturing on dishes coated with other laminin isoforms. By culturing on the LN111-coated dish, human PSC-derived HBCs were maintained for more than 3 months and had the ability to differentiate into both hepatocyte-like cells and cholangiocyte-like cells. These expandable human PSC-derived HBCs would be manageable tools for drug screening, experimental platforms to elucidate mechanisms of hepatoblasts, and cell sources for hepatic regenerative therapy.

INTRODUCTION

Human embryonic stem cells (hESCs) and human induced pluripotent stem cells (hiPSCs) have the ability to self-replicate and to differentiate into all types of body cells including hepatoblasts and hepatocytes. Although cryopreserved primary human hepatocytes are useful in drug screening and liver cell transplantation, they rapidly lose their functions (such as drug metabolism capacity) and hardly proliferate in *in vitro* culture systems. On the other hand, human hepatic stem cells from fetal and postnatal human liver are able to self-replicate and able to differentiate into hepatocytes (Schmelzer et al., 2007; Zhang et al., 2008). However, the source of human hepatic stem cells is limited, and these cells are not available commercially. Therefore, the human pluripotent stem cell (hPSC)-derived hepatoblast-like cells (HBCs), which have potential to differentiate into the hepatocyte-like cells, would be an attractive cell source to provide abundant hepatocyte-like cells for drug screening and liver cell transplantation.

Because expandable and multipotent hepatoblasts or hepatic stem cells are of value, suitable culture conditions for the maintenance of hepatoblasts or hepatic stem cells obtained from fetal or adult mouse liver were developed (Kamiya et al., 2009; Tanimizu et al., 2004). Soluble factors, such as hepatocyte growth factor (HGF) and epidermal growth factor (EGF), are known to support the proliferation

of mouse hepatic stem cells and hepatoblast (Kamiya et al., 2009; Tanimizu et al., 2004). Extracellular matrix (ECM) also affects the maintenance of hepatoblasts or hepatic stem cells. Laminin can maintain the character of mouse hepatoblasts (Dlk1-positive cells) (Tanimizu et al., 2004). However, the methodology for maintaining HBCs differentiated from hPSCs has not been well investigated. Zhao et al. (2009) have reported that hESC-derived hepatoblast-like cells (sorted N-cadherin-positive cells were used) could be maintained on STO feeder cells. Although a culture system using STO feeder cells for the maintenance of hepatoblast-like cells might be useful, there are two problems. The first problem is that N-cadherin is not a specific marker for human hepatoblasts. N-cadherin is also expressed in hESC-derived mesendoderm cells and definitive endoderm (DE) cells (Sumi et al., 2008). The second problem is that residual undifferentiated cells could be maintained on STO feeder cells. Therefore, their culture condition cannot rule out the possibility of the proliferation of residual undifferentiated cells. Because it is known that hPSC-derived cells have the potential to form teratomas in the host, the production of safer hepatocyte-like cells or hepatoblast-like cells has been required. Therefore, we decided to purify hPSC-derived HBCs, which can differentiate into mature hepatocyte-like cells, and then expand these cells.

In this study, we attempt to determine a suitable culture condition for the extensive expansion of HBCs derived



from hPSCs. We found that the HBCs derived from hPSCs can be maintained and proliferated on human laminin-111 (LN111)-coated dishes. To demonstrate that expandable, multipotent, and safe (i.e., devoid of residual undifferentiated cells) hPSC-derived HBCs could be maintained under our culture condition, the hPSC-derived HBCs were used for hepatic and biliary differentiation, colony assay, and transplantation into immunodeficient mice.

RESULTS

Human PSC-Derived Hepatoblast-like Cells Could Adhere onto Human LN111 via Integrin $\alpha 6$ and $\beta 1$

The HBCs were generated from hPSCs (hESCs and hiPSCs) as described in Figure 1A (details of the characterization of hPSC-derived HBCs are described in Figure 3). Definitive endoderm differentiation of hPSCs was promoted by stage-specific transient transduction of FOXA2 in addition to the treatment with appropriate soluble factors (such as Activin A). Overexpression of FOXA2 is not necessary for establishing the hPSC-derived HBCs, but it is helpful for efficient generation of the hPSC-derived HBCs. On day 9, these hESC-derived populations contained two cell populations with distinct morphology (Figure 1B). One population resembled human hepatic stem cells that were isolated from human fetal liver (shown in red) (Schmelzer et al., 2007), whereas the other population resembled definitive endoderm cells (shown in green) (Hay et al., 2008). The population that resembled human hepatic stem cells was alpha-1-fetoprotein (AFP) positive, whereas the other population was AFP negative (Figure 1C, left). On day 9, the percentage of AFP-positive cells was approximately 80% (Figure 1C, right). To characterize these two cell populations (hESC-derived HBC and non-HBC [NHBC] populations), the colonies were manually isolated by using a pipette, and then the gene expression analysis was performed. The gene expression levels of *AFP*, *CD133*, *EpCAM*, *CK8*, and *CK18* in the hESC-derived HBCs were higher than those in the bulk population containing both hESC-derived HBCs and NHBCs (*CD133*, *EpCAM*, *CK8*, and *CK18* were named as pan-hepatoblast markers and are known to be strongly expressed in both human hepatic stem cells and hepatoblasts [Schmelzer et al., 2007; Zhang et al., 2008]) (Figure 1D). On the other hand, the gene expressions of *AFP*, *CD133*, *EpCAM*, *CK8*, and *CK18* in the hESC-derived NHBCs were hardly detected. The gene expression levels of DE, mesendoderm, and pluripotent markers in the hESC-derived NHBCs were higher than those in the hESC-derived HBCs, indicating that the hESC-derived NHBCs could remain in a more undifferentiated state than the hESC-derived HBCs (Figures S1A–S1C available online). These results suggest

that hepatoblast-like cells could be differentiated from hPSCs.

To purify the hESC-derived HBCs, these cells were plated onto dishes coated with various laminins. There are 15 different laminin isoforms in human tissues. Although laminin is known to be useful to sustain mouse hepatoblasts (Tanimizu et al., 2004), it remains unknown which human laminin isoform has the potential to purify and expand the HBCs. To identify a human laminin isoform that would be useful for purifying hESC-HBCs, the hESC-HBCs and -NHBCs were plated onto dishes coated with various types of commercially available human laminins (Figure 1E). The hESC-derived HBCs could more efficiently adhere onto the human LN111-coated dish compared with hESC-derived NHBCs or unseparated populations (containing both HBCs and NHBCs). These data suggest that a hESC-derived HBC population can be purified from the unseparated populations by culturing on human LN111-coated dishes. Because integrins are known to be important molecules for cell adhesion to the ECM including laminins, we expected that certain types of integrins would allow selective adhesion of the hESC-derived HBCs to human LN111-coated dish. The gene expression levels of various integrins were examined (Figure 1F). Among the integrin α subunits, the gene expression level of *integrin $\alpha 6$* in the hESC-derived HBCs was significantly higher than that in the hESC-derived NHBCs. In contrast, among the integrin β subunits, the gene expression level of *integrin $\beta 1$* was higher than those of *integrin $\beta 2$* and *$\beta 3$* in all cell populations. The hESC-derived HBCs, but not NHBCs, expressed both *integrin $\alpha 6$* and *$\beta 1$* (Figure S1D). Almost all adhesion of the hESC-derived HBCs to a human LN111-coated dish was inhibited by both function-blocking antibodies to *integrin $\alpha 6$* and *$\beta 1$* (Figure 1G). These results indicated that the hESC-derived HBCs could attach to a human LN111-coated dish via *integrin $\alpha 6$* and *$\beta 1$* .

The hPSC-Derived HBCs Could Be Proliferated and Maintained on a Human LN111-Coated Dish

To obtain the purified hESC-derived HBC population, the hESC-derived cells (day 9) were plated onto a human LN111-coated dish, and then unattached cells were removed at 15 min after plating (Figure 2A). Among various laminins, only human LN111 could proliferate (Figure 2B) and purify (Figure 2C) the AFP-positive population in the presence of HGF and EGF. During culture on the human LN111-coated dish, the morphology of the hESC-derived HBCs gradually changed into that of human hepatoblasts (Figure S1E) (Schmelzer et al., 2007). Therefore, the characteristics of hESC-derived HBCs might be changed by culturing on a human LN111-coated dish (details of the characterization of the hESC-derived HBCs are described in Figure 3). After culturing on a human LN111-coated

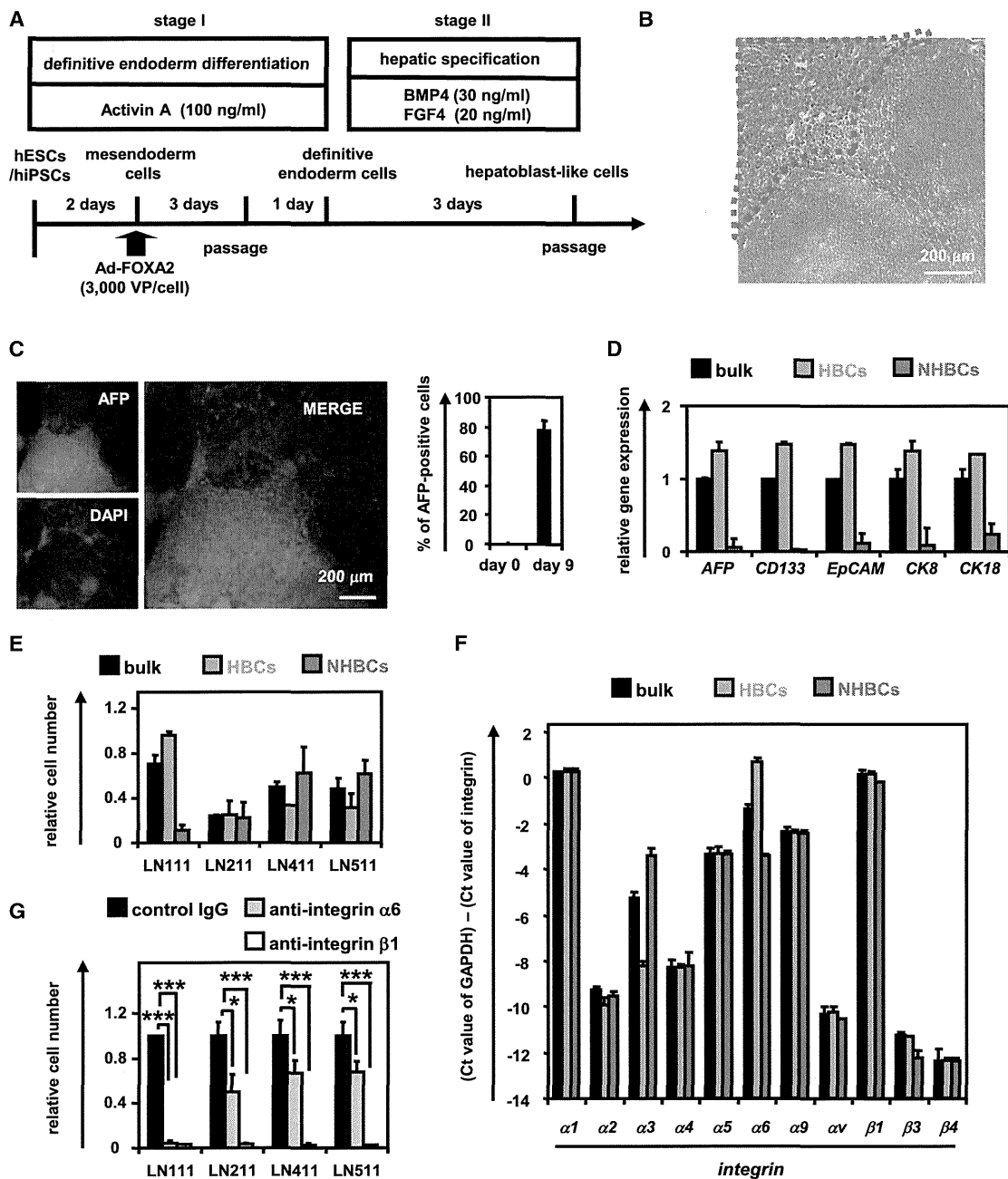


Figure 1. The Human ESC-Derived HBCs Selectively Attached to a Human LN111-Coated Dish via Integrin $\alpha 6$ and $\beta 1$

(A) The procedure for the differentiation of hESCs (H9) into hepatoblast-like cells (HBCs) is presented schematically. Details are described in the Experimental Procedures.

(B) Phase-contrast micrographs of the hESC-derived HBCs (red) and non-HBCs (NHBCs) (green) are shown.

(C) The hESC-derived cells (day 9) were subjected to immunostaining with anti-AFP (red) antibodies. The percentage of AFP-positive cells was examined on day 0 or 9 by using FACS analysis. Data represent the mean \pm SD from ten independent experiments. Cells on "day 0" and "day 9" were compared using Student's t test ($p < 0.01$).

(D) On day 9, the hESC-derived HBCs and NHBCs were manually picked, and the gene expression levels of AFP and pan-hepatoblast markers (CD133, EpCAM, CK8, and CK18) were measured by real-time RT-PCR. The gene expression levels of AFP and pan-hepatoblast markers in the hESC-derived cells (day 9; bulk) were taken as 1.0. Data represent the mean \pm SD from four independent experiments. The gene expression levels in the HBCs were significantly different among the three groups (bulk, HBCs, and NHBCs) based on analysis with one-way ANOVA followed by Bonferroni post hoc tests ($p < 0.05$).

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dish for a week, almost all of the cells were still AFP positive (Figures 2C and 2D). To characterize the cells cultured on various types of human laminins for 7 days, the gene expression levels of *AFP* and pan-hepatoblast (*CD133*, *CK8*, *CK18*, and *EpCAM*) markers were examined on day 16 (Figure 2E). The gene expression levels of *AFP* and pan-hepatoblast markers in the hESC-derived HBCs P1 (HBCs passaged once) did not change as compared with those of the hESC-derived HBCs (day 9; HBC P0) (the definitions of HBC P0, P1, P10, and clone in the present study are shown in Figure S3). The gene expression levels of mature hepatocyte and cholangiocyte markers in the hESC-derived HBC P1 did not change as compared with those of the hESC-derived HBC P0 (day 9) (Figure S1F). These results suggest that the characteristics of the hESC-derived HBC P1 are similar to those of the hESC-derived HBC P0, although their morphologies are quite different from each other. Interestingly, the gene expression levels of mature cholangiocyte markers in the cells cultured on human LN411- or 511-coated dishes were upregulated as compared with those of the hESC-derived HBC P0 (day 9) (Figure S1F), suggesting that human LN411 and 511 might promote biliary differentiation. Importantly, both hESC-derived HBCs and hiPSC-derived HBCs could extensively proliferate on a human LN111-coated dish for more than 15 passages (Figure 2F) in the presence of HGF and EGF. Doubling times of hESC (H9)-derived HBCs and hiPSC (Dotcom)-derived HBCs were approximately 78 and 67 hr, respectively. Almost all of the populations cultured on a human LN111-coated dish were AFP positive (Figure 2G). Taken together, these results suggested that the hPSC-derived HBCs would proliferate and be maintained on a human LN111-coated dish.

Characterization of the hESC-Derived HBCs

To characterize the hESC-derived HBCs, the gene expression profiles in the hESC-derived purified HBCs (HBC P0), short-term cultured HBCs (HBCs passaged once [HBC P1]), and long-term cultured HBC (HBCs passaged ten times [HBC P10]) were examined. The hESC-derived HBCs were AFP positive (Figure 3A). Although the hESC-

derived HBC P0 were negative for *ALB*, *CK7*, and *CK19*, the hESC-derived HBC P1 and P10 were positive for these genes (Figure 3A). Both integrin $\alpha 6$ and $\beta 1$ (receptors of LN111) were strongly expressed in the hESC-derived HBC P0, P1, and P10 (Figure 3B). The gene expression levels of human hepatic stem cell markers (*N-CAM* and *Claudin 3* [Schmelzer et al., 2007]; these are not expressed in human hepatoblasts) in the hESC-derived HBC P0 were higher than those of the hESC-derived HBC P1 and P10 (Figure 3C). However, the gene expression level of *CK19* in the hESC-derived HBC P0 was lower than that of the hESC-derived HBC P1 and P10. The gene expression levels of pan-hepatoblast markers in the hESC-derived HBC P0 were similar to those of the hESC-derived HBC P1 and P10 (Figure 3D). The gene expression levels of human hepatoblast markers (*ALB*, *CYP3A7*, and *I-CAM* [Schmelzer et al., 2007], none of which were expressed in human hepatic stem cells) in the hESC-derived HBC P1 and P10 were higher than those of the hESC-derived HBC P0 (Figure 3E). However, the AFP expression level in the hESC-derived HBC P0 was similar to that of the hESC-derived HBC P1 and P10. Because the gene expression levels of mature hepatocyte and cholangiocyte markers in the hESC-derived HBC P1 and P10 were not increased as compared with those in the hESC-derived HBC P0 (Figure 3F), the hESC-derived HBC P1 and P10 were not segregated into either of the hepatic and biliary lineages. We also examined the gene expression levels of hepatoblast markers, which have been reported only in mice and not in humans (Figure 3G). The characteristics of the hPSC-derived HBCs are summarized in Figure S3. In addition, hESC-derived HBC P0 and HBC P10 showed normal karyotypes (Figure S2A). Therefore, the genetic stability of the HBCs was confirmed throughout the maintenance period. Taken together, these results suggest that the hESC-derived HBC P0 resemble human hepatic stem cells and the hESC-derived HBC P1 and P10 resemble human hepatoblasts, although some gene expression patterns in the hESC-derived HBCs differ from those in human hepatic stem cells and human hepatoblasts, respectively.

(E) The hESC-derived cells (day 9; bulk), HBCs, and NHBCs were plated onto human LN111-, 211-, 411-, or 511-coated dishes, and the attached cells were counted at 60 min after plating. The cell number that was initially plated was taken as 1.0. Data represent the mean \pm SD from four independent experiments. The number of attached HBCs on LN111-coated dishes were significantly different among three groups (bulk, HBCs, and NHBCs) based on analysis with one-way ANOVA followed by Bonferroni post hoc tests ($p < 0.05$).

(F) The gene expression levels of the indicated integrins were measured in the hESC-derived cells (day 9; bulk), HBCs, and NHBCs by real-time RT-PCR. Data represent the mean \pm SD from four independent experiments. The gene expression levels of *integrin $\alpha 3$* and *$\alpha 6$* in the HBCs were significantly different among three groups (bulk, HBCs, and NHBCs) based on analysis with one-way ANOVA followed by Bonferroni post hoc tests ($p < 0.05$).

(G) The adhesion of the hESC-derived HBCs to human LN111-, 211-, 411-, or 511-coated dishes was examined by using the indicated integrin antibodies. IgG antibodies were used as a control for uninhibited cell adhesion. The number of attached cells was estimated at 60 min after plating. The cell number in the control IgG-treated group was taken as 1.0. Data represent the mean \pm SD from three independent experiments. "Control IgG" and "anti-integrin $\alpha 6$ or integrin $\beta 1$ " were compared using Student's *t* test. * $p < 0.05$; *** $p < 0.001$. See also Figure S1 and Tables S2–S5.

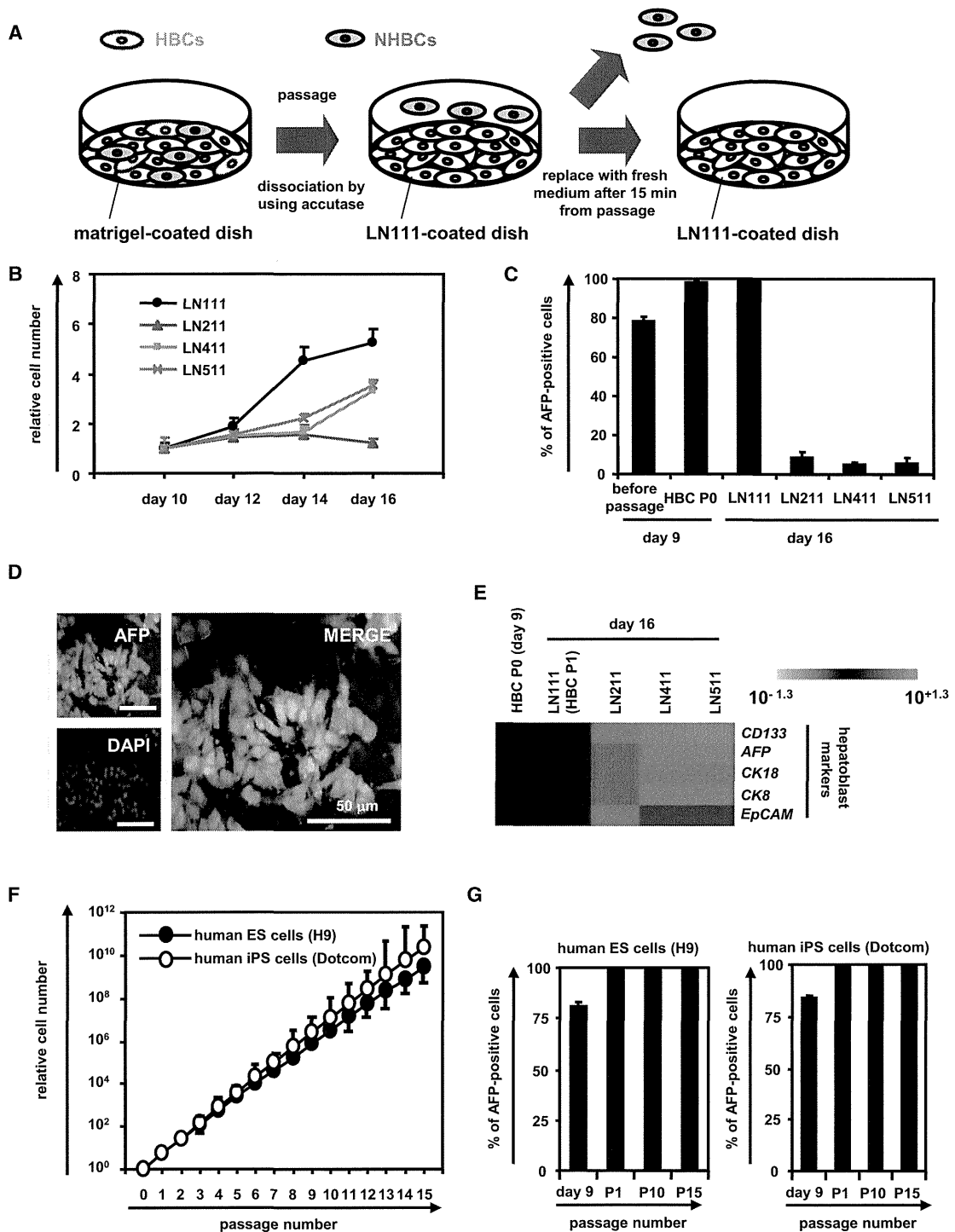


Figure 2. The hESC-Derived HBCs Could Be Proliferated and Maintained on a Human LN111-Coated Dish

(A) The hESC (H9)-derived cells (day 9) were plated onto a human LN111-coated dish. At 15 min after plating, the unattached cells were removed.

(B) The hESC (H9)-derived cells (day 9) were plated onto a human LN111, 211, 411, or 511-coated dish, and then the cell number were counted on days 10, 12, 14, and 16. The cell number on day 10 was taken as 1.0. Data represent the mean \pm SD from three independent experiments. "LN111" was significantly different among four groups (LN111, 211, 411, and 511) on day 14 and 16 based on analysis with one-way ANOVA followed by Bonferroni post hoc tests ($p < 0.05$).

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In order to examine whether the hESC-derived HBC P0 have the potential to proliferate clonally on various types of human laminins, single HBCs were plated on separate wells of a human LN111-coated 96-well plate at a low density (one cell per one well) (Table S1). Single cells that attached to the human LN111-coated dish were AFP positive and HNF4 α positive (Figure S2B). At 7 days after plating, the hESC-derived HBC colonies (albumin [ALB]- and cytokeratin 7 [CK7] double positive) (a representative colony is shown in Figure S2C) were efficiently generated from the hESC-derived HBC P0 on a LN111-coated dish. Taken together, these results showed that the hESC-derived HBCs could be generated from both the hESC-derived HBC P0 population and the single hESC-derived HBC P0.

The hPSC-Derived HBCs Could Differentiate into Both Hepatic and Biliary Lineages In Vitro

To examine whether the hESC-derived HBCs have the potential to differentiate into both hepatic and biliary lineages, first, these cells were differentiated into hepatocyte-like cells as described in Figure 4A. After 2 weeks of hepatic differentiation, almost all of the cells were polygonal in shape (Figure 4B) and were CYP3A4, α AT, and ALB positive (Figure 4C). The gene expression levels of mature hepatocyte markers in the HBC P0-, HBC P10-, or HBC clone-derived hepatocyte-like cells were higher than those in the cells that had not undergone hepatic differentiation (Figure 4D), although the gene expression levels of mature cholangiocyte markers in these cells did not change (Figure 4E). The ASGR1-positive cells in the HBC P0-, HBC P10-, and HBC clone-derived population accounted for approximately 60%, 90%, and 90% of the total, respectively (Figure 4F). The HBC P0-, HBC P10-, or HBC clone-derived hepatocyte-like cells had the ability to produce ALB (Figure 4G, left) and urea (Figure 4G, right). Next, the hESC-derived HBCs were differentiated into cholangiocyte-like cells as described in Figure 4H. After 2 weeks of biliary differentiation, tubular structures (Fig-

ure 4I) that were CK7 positive (Figure 4J) were observed. Although the gene expression levels of mature hepatocyte markers (Figure 4K) in the HBC P0-, HBC P10-, or HBC clone-derived cholangiocyte-like cells did not change, the gene expression levels of mature cholangiocyte markers (Figure 4L) in these cells were higher than those in the cells that had not undergone differentiation. Similar results were obtained by using another hESC line (H1) and hiPSC line (Dotcom) (Figure S4). Moreover, HBC-derived hepatocyte-like cells exhibited CYP metabolism capacity (Figure S5A) and a functional urea cycle that could respond to ammonia (Figure S5B) and were considered to have potential to be applied in the prediction of drug-induced hepatotoxicity (Figure S5C). Taken together, these results indicated that the hPSC-derived HBCs have the ability to differentiate into both hepatic and biliary lineages in vitro.

In Vivo Cell Transplantation Assays of the hPSC-Derived HBCs

To examine whether the hESC-derived HBCs could be used for hepatocyte transplantation, these cells were transplanted into CCl₄-treated immunodeficient mice as shown in Figure 5A. The hepatocyte functionality of the hESC-derived HBC P0 or HBC P10 was assessed by measuring secreted human ALB levels in the recipient mice (Figure 5B). Although human ALB was detected in the mice that were transplanted with the hESC-derived HBC P0 or HBC P10, it was not detected in the mice that were not transplanted with these cells. The ALB-positive cells were observed in mice transplanted with the hESC-derived HBC P0 or HBC P10 (Figure 5C). Most of the ALB-positive cells in mice transplanted with the hESC-derived HBC P10 were AFP negative (Figure 5D), indicating that transplanted hESC-derived HBCs were differentiated into mature hepatocyte-like cells (some of them were binuclear [Figure 5E, white arrows]). These results demonstrated that hESC-derived HBCs have the potential to be applied for hepatocyte transplantation.

(C) The hESC-derived cells (day 9) were plated onto a human LN111, 211, 411, or 511-coated dish. The percentage of AFP-positive cells was examined by using FACS analysis on day 9 (before passage and after passage [HBC P0]) or day 16. Data represent the mean \pm SD from three independent experiments.

(D) The hESC-derived cells cultured on a human LN111-coated dish for 7 days were subjected to immunostaining with anti-AFP (green) antibodies.

(E) The hESC-derived cells (day 9) were plated onto human LN111, 211, 411, or 511-coated dishes. The gene expression levels of *AFP* and pan-hepatoblast markers (*CD133*, *EpCAM*, *CK8*, and *CK18*) were measured by real-time RT-PCR on day 16. The gene expression levels in the hESC-derived HBCs (the LN111-attached cells were collected at 15 min after plating) were taken as 1.0.

(F) The HBCs derived from hESCs (H9) or hiPSCs (Dotcom) were cultured and cell growth was analyzed by obtaining a cell count at each passage. Data represent the mean \pm SD from three independent experiments.

(G) The percentage of AFP-positive cells was examined by using FACS analysis on day 9 (before passage), P1 (HBCs passaged once), P10 (HBCs passaged ten times), and P15 (HBCs passaged 15 times). Data represent the mean \pm SD from seven independent experiments. See also Tables S2 and S3.

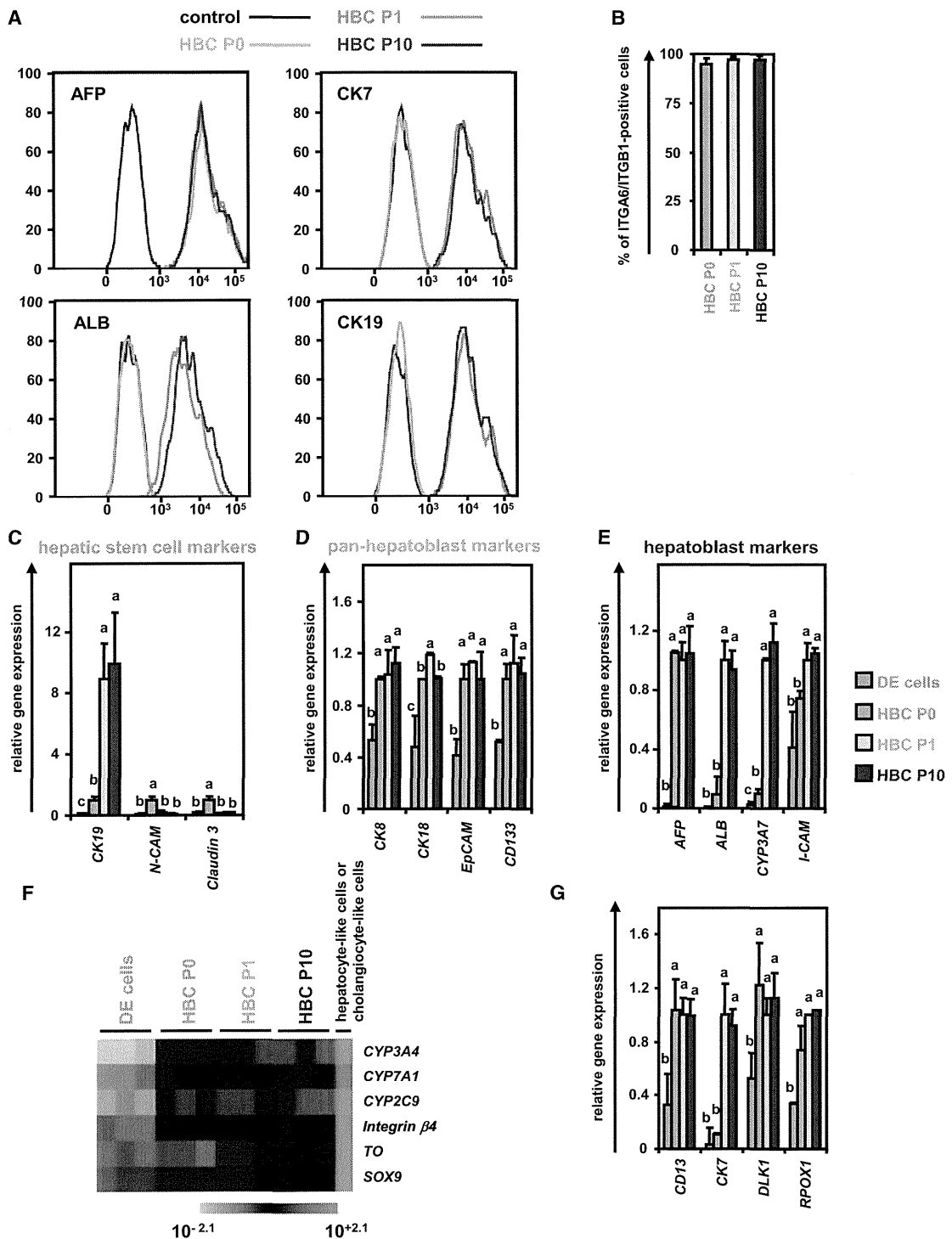


Figure 3. The hESC-Derived HBCs Were Characterized

(A and B) The hESCs (H9) were differentiated according to Figure 1A and then passaged onto a human LN111-coated dish. The attached cells (hESC-derived HBCs [HBC P0]) were collected at 15 min after plating. The percentage of AFP-positive, ALB-positive, CK7-positive, CK19-positive (A), and integrin $\alpha 6$ - and integrin $\beta 1$ -double positive (B) cells in the hESC-derived HBC P0, HBC P1 (HBCs passaged once), and HBC P10 (HBCs passaged ten times) populations was estimated by using FACS analysis. Data represent the mean \pm SD from seven independent experiments.

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DISCUSSION

The main purpose of this study was to establish and characterize expandable HBCs from hPSCs. First, we identified that human LN111 could support self-renewal and proliferation of hPSC-derived HBCs in the presence of HGF and EGF. Second, we showed that the hPSC-derived HBCs have the potential to segregate into both hepatic and biliary lineages, and to integrate into the mouse liver parenchyma.

We have demonstrated that the hPSC-derived HBCs could be maintained on a human LN111-coated dish in an integrin $\alpha 6$ - and $\beta 1$ -dependent manner (Figure 1). It is known that undifferentiated hPSCs could be maintained on a human LN511-coated dish but not on a human LN111-coated dish (Rodin et al., 2010). This might suggest that human LN111 has the potential not only to selectively maintain HBCs, but also to eliminate residual undifferentiated cells. Our hepatoblast-like cells could efficiently proliferate for more than 3 months on a human LN111-coated dish (Figure 2). In the human liver development (during 5–10 weeks gestation), laminin is observed in both the perisinusoidal space and portal tracts (Couvelard et al., 1998). The expression of laminin is localized around the periportal biliary trees during the later stage of liver development (Couvelard et al., 1998). Hepatic stem cells reside around the hepatic portal area (Clément et al., 1988). It is also known that laminin is accumulated around oval cells although laminin is not expressed around quiescent mature hepatocytes (Paku et al., 2001). These facts suggest that laminin plays an important role in the maintenance and proliferation of hepatoblasts.

The hPSC-derived HBC P10 and clone were positive for hepatoblast markers (AFP, ALB, CYP3A7, and I-CAM), but negative for hepatic stem cell markers (N-CAM and Claudin 3) (Figure 3) (Schmelzer et al., 2007). Although the hPSC-derived HBCs were able to expand on human LN111-coated dish, Schmelzer et al. showed that human hepatoblasts do not proliferate under a monolayer culture condition, but human hepatic stem cells could self-replicate for more than 6 months (Schmelzer et al., 2007). Although further investigations of the hepatoblast characteristics in the hPSC-derived HBCs will be needed in the future, the results in the present study suggest that the characteristics of hPSC-derived HBCs expanded on human LN111-coated

dishes were similar to those in human hepatoblasts isolated from the human liver (Schmelzer et al., 2007; Zhang et al., 2008).

The hPSC-derived HBCs had the ability to integrate into the mouse liver parenchyma (Figure 5), in the manner of human hepatic stem cells or hepatoblasts (Schmelzer et al., 2007). The human ALB serum levels (approximately 20–70 ng/ml) in mice transplanted with the hESC-derived HBC P0 or HBC P10 were comparable to those in the previous paper in which the hESC-derived definitive endoderm cells, hepatoblasts, and hepatocyte-like cells were transplanted into mice (Liu et al., 2011), but were lower than those of human liver chimeric mice (Tateno et al., 2004). Human ALB serum levels would increase if more suitable host mice, such as urokinase plasminogen activator-SCID mice were used (Tateno et al., 2004).

In this study, we have developed a technology for the maintenance and proliferation of hPSC-derived HBCs by using human LN111. To transplant these cells for purposes of regenerative medicine, a xeno-free culture condition for hPSC-derived HBCs must be developed in the future. It is hoped that the hPSC-derived HBCs and their derivatives will be helpful in various medical applications, such as drug screening and regenerative medicine.

EXPERIMENTAL PROCEDURES

hESC and hiPSC Culture

The hESC lines (H1 [WA01] and H9 [WA09] [WiCell Research Institute]) and the hiPSC line, Dotcom (JCRB number: JCRB1327) (Makino et al., 2009; Nagata et al., 2009), were maintained on a feeder layer of mitomycin-C-treated mouse embryonic fibroblasts (Millipore) with ReproStem medium (ReproCELL) supplemented with 5 and 10 ng/ml fibroblast growth factor 2 (FGF2) (Katayama Kagaku Kogyo), respectively. H1 and H9 were used following the Guidelines for Derivation and Utilization of Human Embryonic Stem Cells of the Ministry of Education, Culture, Sports, Science and Technology of Japan, and, furthermore, the study was approved by an independent ethics committee.

In Vitro Hepatoblast Differentiation

The differentiation protocol for the induction of definitive endoderm cells and hepatoblasts was based on our previous report with some modifications (Inamura et al., 2011; Takayama et al., 2012a, 2012b, 2013). In mesendoderm differentiation, hESCs/iPSCs were

(C–F) The gene expression levels of hepatic stem cell markers (C), pan-hepatoblast markers (D), hepatoblast markers (E), and mature hepatocyte (*CYP3A4*, *7A1*, *2C9*, and *T0*) or cholangiocyte markers (*integrin $\beta 4$* and *SOX9*) (F) were measured in the definitive endoderm cells, HBC P0, HBC P1, or HBC P10 by real-time RT-PCR.

(G) The gene expression levels of *CD13*, *CK7*, *DLK1*, and *PROX1* were measured in the hESC-derived definitive endoderm cells, HBC P0, HBC P1, or HBC P10 by real-time RT-PCR. Data represent the mean \pm SD from three independent experiments. Statistical significance was evaluated by ANOVA followed by Bonferroni post hoc tests to compare four groups (DE cells, HBC P0, HBC P1, and HBC P10). Groups that do not share the same letter are significantly different from each other ($p < 0.05$). DE, definitive endoderm cells.

See also Figures S2 and S3 and Tables S2–S4.

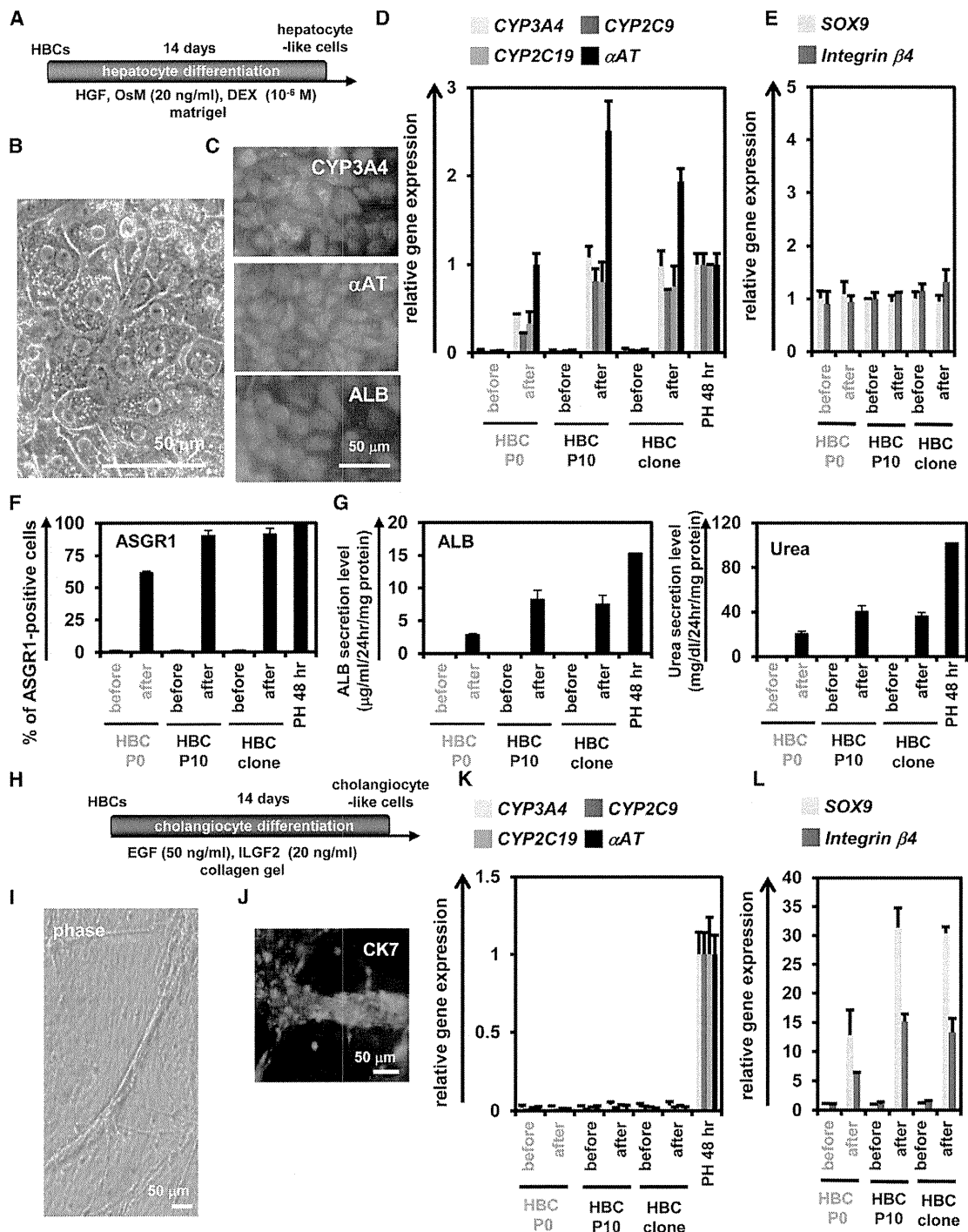


Figure 4. The hESC-Derived HBCs Could Differentiate into Both Hepatic and Biliary Lineages

(A) The procedure for differentiation of the hESC (H9)-derived HBC P0, HBC P10, or HBC clone into the hepatocyte-like cells is presented schematically. Details are described in Experimental Procedures.

(B) Phase-contrast micrographs of the HBC P10-derived hepatocyte-like cells are shown.

(C) The HBC P10-derived hepatocyte-like cells were subjected to immunostaining with anti-CYP3A4 (green), anti- α AT (red), and anti-ALB (red) antibodies.

(D and E) The gene expression levels of hepatocyte (D) or cholangiocyte (E) markers in HBC P0-, HBC P10-, or HBC clone-derived hepatocyte-like cells were measured by real-time RT-PCR after 14 days of hepatocyte differentiation. In (D), the gene expression levels in

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cultured for 2 days on Matrigel (BD Biosciences) in differentiation hESF-DIF medium that contains 100 ng/ml Activin A (R&D Systems) (hESF-DIF medium was purchased from Cell Science & Technology Institute; differentiation hESF-DIF medium was supplemented with 10 μ g/ml human recombinant insulin, 5 μ g/ml human apotransferrin, 10 μ M 2-mercaptoethanol, 10 μ M ethanolamine, 10 μ M sodium selenite, and 0.5 mg/ml bovine fatty acid free serum albumin [all from Sigma]). To generate definitive endoderm cells, the mesendoderm cells (day 2) were transduced with 3,000 vector particle (VP)/cell of FOXA2-expressing adenovirus vectors (Ad-FOXA2) for 1.5 hr and cultured until day 6 on Matrigel in differentiation hESF-DIF medium supplemented with 100 ng/ml Activin A. For induction of hepatoblasts, the definitive endoderm cells were cultured for 3 days on a Matrigel in differentiation hESF-DIF medium supplemented with 30 ng/ml bone morphogenetic protein 4 (BMP4) (R&D Systems) and 20 ng/ml FGF4 (R&D Systems).

Establishment and Maintenance of the hPSC-Derived HBCs

The hPSC-derived HBCs were first purified from the hPSC-derived cells (day 9) by selecting attached cells on a human recombinant LN111 (BioLamina)-coated dish at 15 min after plating. The hPSC-derived HBCs were cultured on a human LN111-coated dish (2.0×10^4 cells/cm²) in maintenance DMEM/F12 medium (DMEM/F12 medium [Invitrogen] was supplemented with 10% FBS, 1 \times insulin/transferrin/selenium, 10 mM nicotinamide, 10^{-7} M dexamethasone (DEX) (Sigma), 20 mM HEPES, 25 mM NaHCO₃, 2 mM L-glutamine, penicillin/streptomycin, 40 ng/ml hepatocyte growth factor [HGF] [R&D Systems] and 20 ng/ml epidermal growth factors [EGF] [R&D Systems]). The medium was refreshed every day. The hPSC-derived HBCs were dissociated with Accutase (Millipore) into single cells and subcultured every 6 or 7 days.

Establishment and Maintenance of a Single hPSC-Derived HBC

For single-cell culture, the single HBC was plated to separate well of human LN111-coated 96-well plate in maintenance DMEM/F12

medium supplemented with 25 μ M Y-27632 (ROCK inhibitor) (Millipore), and then colonies derived from a single cell were manually picked up and cultured as well as HBCs (these cells were designated the HBC clone).

In Vitro Hepatocyte and Cholangiocyte Differentiation

To induce hepatocyte differentiation, the hPSC-derived HBC P0, HBC P10, and HBC clone were cultured for 14 days on a Matrigel-coated dish (7.5×10^4 cells/cm²) in HCM (Lonza) supplemented with 20 ng/ml HGF, 20 ng/ml Oncostatin M (OsM) (R&D Systems), and 10^{-6} M DEX. To induce cholangiocyte differentiation, the hPSC-derived HBC P0, HBC P10, and HBC clone were cultured in collagen gel for 14 days. To establish collagen gel plates, 500 μ l collagen gel solution (consisting of 400 μ l type I-A Collagen (Nitta gelatin), 50 μ l $10 \times$ DMEM, and 50 μ l of 200 mM HEPES buffer containing 2.2% NaHCO₃ and 0.05 M NaOH) was added to each well, and then the plates were incubated at 37°C for 30 min. The hPSC-derived HBC P0, HBC P10, and HBC clone (5×10^4 cells) were resuspended in 500 μ l differentiation DMEM/F12 medium (differentiation DMEM/F12 medium was supplemented with 20 mM HEPES, 2 mM L-glutamine, 100 ng/ml EGF, and 40 ng/ml insulin-like growth factor 2 [ILGF2]), and then mixed with 500 μ l of the collagen gel solution and plated onto the basal layer of collagen. After 30 min, 2 ml of differentiation DMEM/F12 medium was added to the well.

Ad Vectors

Ad vectors were constructed by an improved in vitro ligation method. The human EF-1 α promoter-driven FOXA2-expressing Ad vectors (Ad-FOXA2) were constructed previously (Takayama et al., 2012b). All of Ad vectors contain a stretch of lysine residue (K7) peptides in the C-terminal region of the fiber knob for more efficient transduction of hESCs, hiPSCs, mesendoderm cells, and definitive endoderm cells, in which transfection efficiency was almost 100%, and purified as described previously (Inamura

PH 48 hr were taken as 1.0. In (E), the gene expression levels in HBC P10 (before differentiation) were taken as 1.0. Data represent the mean \pm SD from three independent experiments. Student's t test indicated that gene expression levels of the hepatocyte markers in "after" were significantly higher than those in "before" ($p < 0.01$).

(F) The efficiency of hepatocyte differentiation was measured by estimating the percentage of ASGR1-positive cells using FACS analysis.

(G) The amounts of ALB (left) and urea (right) secretion were examined. Data represent the mean \pm SD from three independent experiments. Student's t test indicated that the percentage of ASGR1-positive cells, the ALB secretion level, and urea secretion level in "after" were significantly higher than those in "before" ($p < 0.01$).

(H) The procedure for the differentiation of the hESC-derived HBC P0, HBC P10, or HBC clone into cholangiocyte-like cells is presented schematically. Details are described in Experimental Procedures.

(I) Phase-contrast micrographs of the HBC P10-derived cholangiocyte-like cells are shown.

(J) The HBC P10-derived cholangiocyte-like cells were subjected to immunostaining with anti-CK7 (red) antibodies.

(K and L) The gene expression levels of hepatocyte (K) or cholangiocyte (L) markers in the HBC P0-, HBC P10-, or HBC clone-derived cholangiocyte-like cells were measured by real-time RT-PCR after 14 days of cholangiocyte differentiation. In (K), the gene expression levels in PH 48 hr were taken as 1.0. In (L), the gene expression levels in HBC P10 (before cholangiocyte differentiation) were taken as 1.0. Data represent the mean \pm SD from three independent experiments. Student's t test indicated that the gene expression levels of cholangiocyte markers in "after" were significantly higher than those in "before" ($p < 0.01$). "Before" indicates the HBCs before hepatocyte or cholangiocyte differentiation; "After" indicates the HBCs after hepatocyte or cholangiocyte differentiation.

See also Figures S4 and S5 and Tables S1–S4.

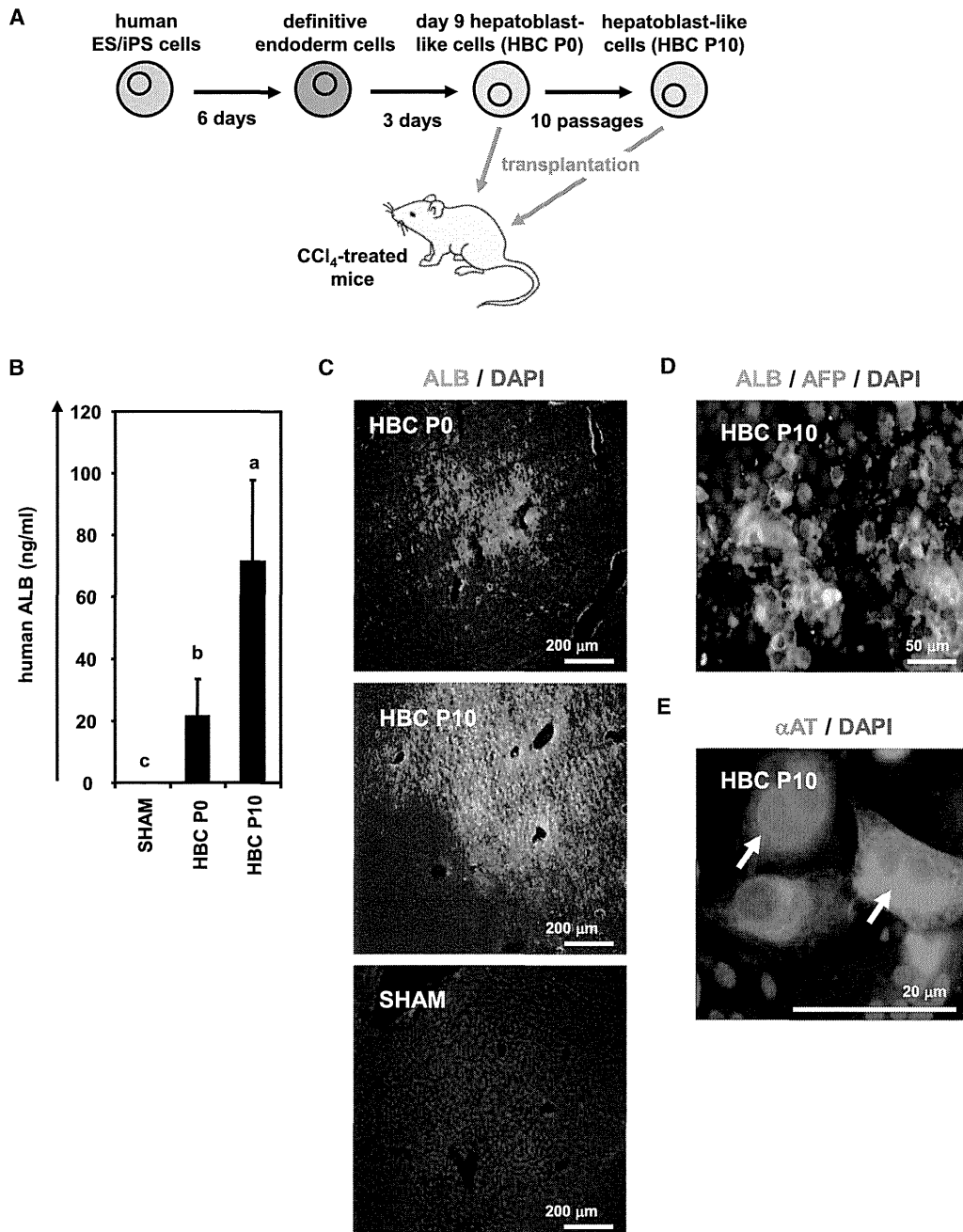


Figure 5. The hESC-Derived HBCs Were Integrated into the Mouse Liver Parenchyma

(A) The procedure for transplantation of the hESC (H9)-derived HBC P0 and HBC P10 into CCl₄ (4 ml/kg)-treated Rag2/IL2 receptor gamma double-knockout mice is presented schematically.

(B) The human ALB level in recipient mouse serum was measured at 2 weeks after transplantation. Data represent the mean ± SD from six to eight mice in each group. Statistical significance was evaluated by ANOVA followed by Bonferroni post hoc tests to compare all groups. Groups that do not share the same letter are significantly different from each other ($p < 0.05$).

(C) Expressions of the ALB (green) in the liver of transplanted mice were examined by immunohistochemistry at 2 weeks after transplantation.

(D and E) The expressions of AFP (red), ALB (green) (D), and αAT (red) (E) were examined by immunohistochemistry at 2 weeks after hESC-derived HBC P10 transplantation. White arrows show transplanted cells, which have double nuclei.

See also Tables S2 and S3.



Stem Cell Reports

Self-Renewing Human ESC/iPSC-Derived HBCs

et al., 2011; Takayama et al., 2011; Tashiro et al., 2010). The VP titer was determined by using a spectrophotometric method.

Flow Cytometry

Single-cell suspensions of the hPSC-derived cells were fixed with 4% paraformaldehyde (PFA) at 4°C for 10 min and then incubated with the primary antibody (described in Table S2), followed by the secondary antibody (described in Table S3). Control cells were incubated with anti-mouse, goat, or rabbit immunoglobulin (Ig) G antibodies (Santa Cruz Biotechnology) and then incubated with the secondary antibody. Flow cytometry analysis was performed using a fluorescence-activated cell sorting (FACS) LSR Fortessa flow cytometer (BD Biosciences). Cell sorting was performed using a FACS Aria (BD Biosciences).

RNA Isolation and RT-PCR

Total RNA was isolated from hPSCs and their derivatives using ISOGENE (Nippon Gene). cDNA was synthesized using 500 ng of total RNA with a Superscript VILO cDNA synthesis kit (Invitrogen). Real-time RT-PCR was performed with SYBR green PCR Master Mix (Applied Biosystems) using an Applied Biosystems StemOnePlus real-time PCR systems. Relative quantification was performed against a standard curve, and the values were normalized against the input determined for the housekeeping gene, glyceraldehyde 3-phosphate dehydrogenase. The primer sequences used in this study are described in Table S4. In addition, we confirmed that every beta integrin primer used in this manuscript showed a similar amplification efficacy (Table S5). The amplification efficiency was calculated from the slope of the standard curve according to the following formula: $e = 10^{-(1/\text{slope})-1}$. Every beta integrin primer used in this manuscript showed a similar amplification efficacy.

Immunohistochemistry

The cells were fixed with 4% PFA for 15 min and then blocked with PBS containing 2% FBS, 2% bovine serum albumin (BSA), and 0.1% Triton X-100 (Wako Pure Chemicals Industries) for 1 hr. The cells were incubated with primary antibody (described in Table S2) at 4°C for overnight, followed by incubation with a secondary antibody (described in Table S3) at room temperature for 1 hr. Nuclei were counterstained with DAPI (blue).

ELISA

The hPSC-derived HBC P0, HBC P10, and HBC clone were differentiated into the hepatocyte-like cells as described in Figure 4A. The culture supernatants, which were incubated for 24 hr after fresh medium was added, were collected and analyzed for the amount of ALB secretion by ELISA. ELISA kits for ALB were purchased from Bethyl Laboratories. The amount of ALB secretion was calculated according to each standard followed by normalization to the protein content per well. The human ALB amount in mice serum was also examined by ELISA.

Transplantation of the hESC-Derived HBCs

The hESC-derived HBCs were dissociated using accutase and then suspended with maintenance DMEM/F12 medium without serum.

Eight- to 10-week-old Rag2/IL2Rg double-knockout mice were prepared. The hESC-derived HBCs (1×10^6 cells) were transplanted 24 hr after administration of CCl₄ (4 ml/kg) by intrasplenic injection. Recipient mouse liver and blood were harvested at 2 weeks after transplantation. The livers were fixed with 4% PFA and processed for immunohistochemistry. Human hepatocytes producing the ALB, AFP, and α AT protein were identified in mouse liver by an antibody specifically recognizing human but not mouse albumin. In addition, serum was extracted and subjected to ELISA analysis. All animal experiments were conducted in accordance with institutional guidelines.

Urea Secretion

The hPSC-derived HBC P0, HBC P10, and HBC clone were differentiated into hepatocyte-like cells as described in Figure 4A. The culture supernatants, which were incubated for 24 hr after fresh medium was added, were collected and analyzed for the amount of urea secretion. The urea measurement kits were purchased from BioAssay Systems. The amount of urea secretion was calculated according to each standard followed by normalization to the protein content per well. In Figure S5B, both the HBC-derived hepatocyte-like cells and primary human hepatocytes (PHs) (three lots of cryopreserved human hepatocytes were used), that were cultured for 48 hr after the cells were plated (PH 48 hr), were cultured in HCM (containing glutamine) or DMEM (not containing glutamine; Wako) in the presence or absence of 1 mM ammonium chloride (NH₄Cl, Wako) for 24 hr, and then the amount of urea secretion was measured.

Primary Human Hepatocytes

Three lots of cryopreserved human hepatocytes (lot Hu8072 [CellzDirect], HC2-14, and HC10-101 [Xenotech]) were used. The vials of hepatocytes were rapidly thawed in a shaking water bath at 37°C; the contents of the vial were emptied into prewarmed Cryopreserved Hepatocyte Recovery Medium (Gibco) and the suspension was centrifuged at 100 g for 10 min at room temperature. The hepatocytes were seeded at 1.25×10^5 cells/cm² in HCM (Lonza) containing 10% fetal calf serum (FCS) (Gibco) onto type I collagen-coated 12-well plates. The medium was replaced with hepatocyte culture medium containing 10% FCS 6 hr after seeding. The hepatocytes, which were cultured 48 hr after plating the cells, were used in the experiments.

Adhesion-Blocking Assay Using Integrin Antibody

Twelve-well plates were coated with human recombinant LN111, 211, 411, or 511 (all from BioLamina) and blocked by 1% heat-denatured BSA containing PBS. The hESC-derived single cells were incubated with function-blocking antibodies to integrin α 6 and β 1 (at the concentrations as recommended by the manufacturer) for 30 min, plated on a human LN111-coated 12-well dish, and allowed to adhere for 1 hr at 37°C. After unattached cells were removed, the remaining adherent cells were fixed for 20 min with 5% glutaraldehyde. The hESC-derived cells that had adhered to the wells were stained with 200 μ l of 0.3% crystal violet (Wako) solution at room temperature for 15 min. Excess crystal violet was then removed, and the wells were washed three times. Fixed crystal violet was solubilized in 200 μ l of 100% ethanol at room



temperature for 15 min. Cell viability was estimated by measuring the absorbance at 595 nm of each well using a microtiter plate reader (Sunrise, Tecan).

CYP Activity

To measure the CYP1A2, 2C9, and 3A4 activity of the cells, we performed lytic assays by using P450-Glo™ CYP1A2, 2C9, and 3A4 Assay Kits (Promega), respectively. We measured the fluorescence activity with a luminometer (Lumat LB 9507; Berthold) according to the manufacturer's instructions. The CYP activity was normalized with the protein content per well.

Karyotyping

This experiment was carried out at Chromosome Science Labo.

Cell Viability Tests

Cell viability was assessed by using a WST-8 assay kit (Dojindo), and the results are presented in Figure S5C. After treatment with test compounds, such as acetaminophen (Wako) and troglitazone (Wako) for 24 hr, the cell viability was measured. The control cells were incubated in the absence of test compounds and were considered to have 100% viability value. Controls were treated with DMSO (final concentration 0.1%).

SUPPLEMENTAL INFORMATION

Supplemental Information includes five figures and five tables and can be found with this article online at <http://dx.doi.org/10.1016/j.stemcr.2013.08.006>.

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RESEARCH ARTICLE

STEM CELLS AND REGENERATION

CCAAT/enhancer binding protein-mediated regulation of TGF β receptor 2 expression determines the hepatoblast fate decision

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ABSTRACT

Human embryonic stem cells (hESCs) and their derivatives are expected to be used in drug discovery, regenerative medicine and the study of human embryogenesis. Because hepatocyte differentiation from hESCs has the potential to recapitulate human liver development *in vivo*, we employed this differentiation method to investigate the molecular mechanisms underlying human hepatocyte differentiation. A previous study has shown that a gradient of transforming growth factor beta (TGF β) signaling is required to segregate hepatocyte and cholangiocyte lineages from hepatoblasts. Although CCAAT/enhancer binding proteins (c/EBPs) are known to be important transcription factors in liver development, the relationship between TGF β signaling and c/EBP-mediated transcriptional regulation in the hepatoblast fate decision is not well known. To clarify this relationship, we examined whether c/EBPs could determine the hepatoblast fate decision via regulation of TGF β receptor 2 (TGFBR2) expression in the hepatoblast-like cells differentiated from hESCs. We found that *TGFBR2* promoter activity was negatively regulated by c/EBP α and positively regulated by c/EBP β . Moreover, c/EBP α overexpression could promote hepatocyte differentiation by suppressing TGFBR2 expression, whereas c/EBP β overexpression could promote cholangiocyte differentiation by enhancing TGFBR2 expression. Our findings demonstrated that c/EBP α and c/EBP β determine the lineage commitment of hepatoblasts by negatively and positively regulating the expression of a common target gene, *TGFBR2*, respectively.

KEY WORDS: Hepatoblasts, c/EBP, CEBP, Human ESCs

INTRODUCTION

Many animal models, such as chick, *Xenopus*, zebrafish and mouse, have been used to investigate the molecular mechanisms of liver development. Because many functions of the key molecules in liver

development are conserved in these species, studies on liver development in these animals can be highly informative with respect that in humans. However, some functions of important molecules in liver development might differ between human and other species. Although analysis using genetically modified mice has been successfully performed, it is not of course possible to perform genetic experiments to elucidate molecular mechanisms of liver development in human. Pluripotent stem cells, such as human embryonic stem cells (hESCs), are expected to overcome some of these problems in the study of human embryogenesis, including liver development, because the gene expression profiles of this model are similar to those in normal liver development (Agarwal et al., 2008; DeLaForest et al., 2011).

During liver development, hepatoblasts differentiate into hepatocytes and cholangiocytes. A previous study has shown that a high concentration of transforming growth factor beta (TGF β) could give rise to cholangiocyte differentiation from hepatoblasts (Clotman et al., 2005). To transmit the TGF β signaling, TGF β receptor 2 (TGFBR2) has to be stimulated by TGF β 1, TGF β 2 or TGF β 3 (Kitisun et al., 2007). TGF β binding to the extracellular domain of TGFBR2 induces a conformational change, resulting in the phosphorylation and activation of TGFBR1. TGFBR1 phosphorylates SMAD2 or SMAD3, which binds to SMAD4, and then the SMAD complexes move into the nucleus and function as transcription factors to express various kinds of differentiation-related genes (Kitisun et al., 2007). Although the function of TGFBR2 in regeneration of the adult liver has been thoroughly examined (Oe et al., 2004), the function of TGFBR2 in the hepatoblast fate decision has not been elucidated.

CCAAT/enhancer binding protein (c/EBP) transcription factors play decisive roles in the differentiation of various cell types, including hepatocytes (Tomizawa et al., 1998; Yamasaki et al., 2006). The analysis of c/EBP α (*Cebpa*) knockout mice has shown that many abnormal pseudoglandular structures, which co-express antigens specific for both hepatocytes and cholangiocytes, are present in the liver parenchyma (Tomizawa et al., 1998). These data demonstrated that c/EBP α plays an important role in hepatocyte differentiation. It is also known that the suppression of c/EBP α expression in periportal hepatoblasts stimulates cholangiocyte differentiation (Yamasaki et al., 2006). Although the function of c/EBP α in liver development is well known, the relationship between TGF β signaling and c/EBP α -mediated transcriptional regulation in the hepatoblast fate decision is poorly understood. c/EBP β is also known to be an important factor for liver function (Chen et al., 2000), although the function of c/EBP β in the cell fate decision of hepatoblasts is not well known. c/EBP α and c/EBP β bind to the same DNA binding site. However, the promoter activity of hepatocyte-specific genes, such as those encoding hepatocyte nuclear factor 6 (HNF6, also known as ONECUT1) and UGT2B1,

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