DESCRIPTION

METHOD OF EFFICIENTLY ESTABLISHING INDUCED PLURIPOTENT STEM CELLS

Technical Field of the Invention

The present invention relates to a method of improving the efficiency of establishment of induced pluripotent stem cells (hereinafter referred to as iPS cells) and a reagent therefor, more specifically to a factor [gene or protein] that improves the efficiency of establishment of iPS cells from a somatic cell and a method of improving the efficiency of establishment of iPS cells using the factor.

Background of the Invention

In recent years, mouse and human iPS cells have been established one after another. Yamanaka et al. induced iPS cells by transferring the Oct3/4, Sox2, Klf4 and c-Myc genes into mouse and human fibroblasts, and forcing the cells to express the genes [1-3]. Thomson et al. produced human iPS cells using Nanog and Lin28 in place of Klf4 and c-Myc [4, 5]. However, the efficiency of iPS cell establishment was low at less than 1%.

Various efforts to improve the efficiency of iPS cell establishment have been made. For example, the present inventors reported that the inhibition of p53-p21 pathway remarkably increased the efficiency of iPS cell establishment [6, 7]. Maekawa et al. reported that the efficiency of iPS cell establishment was remarkably improved by transferring Glis1 along with Oct3/4, Sox2 and Klf4 into a somatic cell [8, 9]. In addition, it was found that Glis1 inhibits the proliferation of cells with imperfect reprogramming but only proliferates completely reprogrammed ones. They found that Glis1 was able to facilitate reprogramming by increasing the expressions of several genes that are reported to be involved in reprogramming.

Cited references:

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Summary of the Invention

It is an object of the present invention to provide a means of improving the efficiency of establishment of iPS cells, and a method of efficiently producing iPS cells using the means.

It is important to understand the process of direct reprogramming to facilitate induction of pluripotency. However, large numbers of non-reprogrammed cells during iPS cell generation inhibit accurate analyses of the reprogramming process. To overcome this issue, we used a pluripotent cell-specific surface antigen, TRA-1-60 to capture nascent reprogrammed cells. Comprehensive gene expression analyses revealed that TRA-1-60 (+) nascent human reprogrammed cells share the common gene expression signatures with primitive streak (PrS).

Another set of evidence connecting reprogramming and PrS arose from Glis1, which the present inventors previously reported as a maternal transcription factor enhancing iPSC generation. We found that Glis1 is highly expressed in PrS and mesoendoderm derived from human ES/iPS cells, but that it is barely expressed in undifferentiated human pluripotent stem cells. We also found that forced expression of Glis1 in human ES cells markedly increases expression of not only pluripotency-related genes but also PrS-related genes.

From these findings, the present inventors hypothesized

that genes that play important roles in PrS formation during development may facilitate iPSC generation. To confirm this hypothesis, the present inventors focused on Forkhead box H1 (Foxh1), since knockout mouse experiments have shown that the transcription factor is essential for PrS formation.

Transduction of Foxh1 along with Oct3/4, Sox2, Klf4 and c-Myc markedly increased the number of iPSC colonies. The effect of Foxh1 was stronger than p53 shRNA and Glis1, two of the strongest known enhancers of reprogramming. Foxh1 and p53 shRNA showed synergistic effects, suggesting that Foxh1 enhances reprogramming independently of p53 inhibition. Stage-specific activation of Foxh1 demonstrated that Foxh1 facilitates reprogramming efficiency in late stages in contrast to Glis1 that facilitates reprogramming in earlier stages.

The present inventors conducted further investigations based on these findings, and have developed the present invention.

Accordingly, the present invention provides:

[1] A method of improving iPS cell establishment efficiency, comprising contacting a protein involved in primitive streak (PrS) formation or a nucleic acid that encodes the same with a somatic cell in a nuclear reprogramming step.

[2] The method according to [1] above, wherein the protein is selected from the group consisting of Foxh1, brachyury, goosecoid, Foxa2, eomesodermin, LHX1, Sox17, MIXL1, Lefty2, Nodal1, Hand1, Wnt3, noggin, CER1, Foxf1, GATA4, GATA6, GSC, HESX1, HNF1A, HNF4A, OTX2, RNF111, Sox7, SP5, TBX6, Foxb1, Foxf2 and Foxg1.

[3] The method according to [1] above, wherein the protein is selected from the group consisting of Foxh1, brachyury, Foxa2, LHX1, Foxf1, Foxb1, Foxf2 and Foxg1.

[4] The method according to [1] above, wherein the protein is Foxh1.

[5] The method according to any one of [1] to [4] above,

wherein the somatic cell is further contacted with Glis1 or a nucleic acid that encodes the same and/or a p53 inhibitor in a nuclear reprogramming step.

[6] An agent for improving iPS cell establishment efficiency comprising a protein involved in primitive streak (PrS) formation or a nucleic acid that encodes the same.

[7] The agent according to [6] above, wherein the protein is selected from the group consisting of Foxh1, brachyury, goosecoid, Foxa2, eomesodermin, LHX1, Sox17, MIXL1, GDF3, Lefty2, Nodal1, Hand1, Wnt3, noggin, CER1, Foxf1, GATA4, GATA6, HESX1, HNF1A, HNF4A, OTX2, RNF111, Sox7, SP5, TBX6, Foxb1, Foxf2 and Foxg1.

[8] The agent according to [6] above, wherein the protein is selected from the group consisting of Foxh1, brachyury, Foxa2, LHX1, Foxf1, Foxb1, Foxf2 and Foxg1.

[9] The agent according to [6] above, wherein the protein is Foxh1.

[10] The agent according to any one of [6] to [9] above, further comprising Glis1 or a nucleic acid that encodes the same and/or a p53 inhibitor.

[11] A method of producing an iPS cell, comprising contacting a protein involved in primitive streak (PrS) formation or a nucleic acid that encodes the same, and nuclear reprogramming substance(s) with a somatic cell.

[12] The method according to [11] above, wherein the nuclear reprogramming substance(s) is(are) selected from the group consisting of members of the Oct family, members of the Sox family, members of the Klf family, members of the Myc family, members of the Lin family and the Nanog, as well as nucleic acids that encode the same.

[13] The method according to [11] above, wherein the nuclear reprogramming substances are Oct3/4, Sox2 and Klf4, or nucleic acids that encode the same.

[14] The method according to [11] above, wherein the nuclear reprogramming substances are Oct3/4, Sox2, Klf4 and L-Myc or c-

Myc, or nucleic acids that encode the same.

[15] The method according to any one of [11] to [14] above, wherein the protein involved in primitive streak (PrS) formation is selected from the group consisting of a Fox family member, brachyury, goosecoid, eomesodermin, LHX1, Sox17, MIXL1, Lefty2, Nodal, Hand1, Wnt3, noggin, CER1, GATA4, GATA6, GSC, HESX1, HNF1A, HNF4A, OTX2, RNF111, Sox7, SP5 and TBX6.

[16] The method according to [15] above, wherein the Fox family member is selected from the group consisting of Foxa1, Foxa2, Foxa3, Foxb1, Foxc1, Foxc2, Foxd1, Foxd3, Foxd5, Foxe3, Foxf1, Foxf2, Foxg1, Foxh1, Foxi1, Foxi2, Foxj1, Foxj2, Foxj3, Foxk1, Foxk2, Foxl2, Foxm1, Foxn1, Foxan2, Foxn3, Foxn4, Foxo3, Foxo4, Foxp1, Foxp3, Foxp4, Foxr1, Foxr2 and Foxs1.

[17] The method according to any one of [11] to [14] above, wherein the protein is selected from the group consisting of Foxh1, brachyury, Foxa2, LHX1, Foxf1, Foxb1, Foxf2 and Foxg1.

[18] The method according to any one of [11] to [14] above, wherein the protein involved in primitive streak (PrS) formation is Foxh1.

[19] The method according to any one of [11] to [18] above, wherein the somatic cell is further contacted with Glis1 or a nucleic acid that encodes the same and/or a p53 inhibitor.

[20] An agent for inducing an iPS cell from a somatic cell, comprising a protein involved in primitive streak (PrS) formation or a nucleic acid that encodes the same, and nuclear reprogramming substance(s).

[21] The agent according to [20] above, wherein the nuclear reprogramming substance(s) is(are) selected from the group consisting of members of the Oct family, members of the Sox family, members of the Klf family, members of the Myc family, members of the Lin family and the Nanog, as well as nucleic acids that encode the same.

[22] The agent according to [20] above, wherein the nuclear reprogramming substances are Oct3/4, Sox2 and Klf4, or nucleic acids that encode the same.

[23] The agent according to [20] above, wherein the nuclear reprogramming substances are Oct3/4, Sox2, Klf4 and L-Myc or c-Myc, or nucleic acids that encode the same.

[24] The agent of any one of [20] to [23] above, wherein the protein involved in primitive streak (PrS) formation is selected from the group consisting of a Fox family member, brachyury, goosecoid, eomesodermin, LHX1, Sox17, MIXL1, GDF3, Lefty2, Nodal, Hand1, Wnt3, noggin, CER1, GATA4, GATA6, GSC, HESX1, HNF1A, HNF4A, OTX2, RNF111, Sox7, SP5 and TBX6.

[25] The method according to [24] above, wherein the Fox family member is selected from the group consisting of Foxa1, Foxa2, Foxa3, Foxb1, Foxc1, Foxc2, Foxd1, Foxd3, Foxd5, Foxe3, Foxf1, Foxf2, Foxg1, Foxh1, Foxi1, Foxi2, Foxj1, Foxj2, Foxj3, Foxk1, Foxk2, Foxl2, Foxm1, Foxn1, Foxan2, Foxn3, Foxn4, Foxo3, Foxo4, Foxp1, Foxp3, Foxp4, Foxr1, Foxr2 and Foxs1.

[26] The agent according to any one of [20] to [23] above, wherein the protein is selected from the group consisting of Foxh1, brachyury, Foxa2, LHX1, Foxf1, Foxb1, Foxf2 and Foxg1.

[27] The agent of any one of [20] to [23] above, wherein the protein involved in primitive streak (PrS) formation is Foxh1.

[28] The agent of any one of [20] to [27] above, further comprising Glis1 or a nucleic acid that encodes the same and/or a p53 inhibitor.

[29] An iPS cell containing an exogenous nucleic acid that encodes Foxh1.

[30] The iPS cell according to [29] above, wherein the exogenous nucleic acid is integrated in the genome.

[31] A method of producing a somatic cell, comprising performing a differentiation induction treatment on the iPS cell according to [29] or [30] above to cause the iPS cell to differentiate into a somatic cell.

[32] A method of producing a somatic cell, comprising the steps of:

(1) producing an iPS cell by the method according to any one of [11] to [19] above, and

(2) performing a differentiation induction treatment on the iPS cell obtained through the step (1) to cause the iPS cell to differentiate into a somatic cell.

[33] A use of a protein involved in primitive streak (PrS) formation or a nucleic acid that encodes the same for improving the efficiency of establishment of iPS cells.

[34] The use according to [33] above, wherein the protein is selected from the group consisting of Foxh1, brachyury, goosecoid, Foxa2, eomesodermin, LHX1, Sox17, MIXL1, Lefty2, Nodal, Hand1, Wnt3, noggin, CER1, GATA4, GATA6, GSC, HESX1, HNF1A, HNF4A, OTX2, RNF111, Sox7, SP5 and TBX6, Foxb1, Foxf2 and Foxg1.

[35] The use according to [33] above, wherein the protein is selected from the group consisting of Foxh1, brachyury, Foxa2, LHX1, Foxf1, Foxb1, Foxf2 and Foxg1.

[36] The use according to [33] above, wherein the protein is Foxh1.

[37] A use of a protein involved in primitive streak (PrS) formation or a nucleic acid that encodes the same in combination with nuclear reprogramming substance(s) for producing an iPS cell.

[38] The use according to [37] above, wherein the nuclear reprogramming substance(s) is(are) selected from the group consisting of members of the Oct family, members of the Sox family, members of the Klf family, members of the Myc family, members of the Lin28 family, and the Nanog, as well as nucleic acids that encode the same.

[39] The use according to [37] above, wherein the nuclear reprogramming substances are Oct3/4, Sox2 and Klf4, or nucleic acids that encode the same.

[40] The use according to [37] above, wherein the nuclear reprogramming substances are Oct3/4, Sox2, Klf4 and L-Myc or c-Myc, or nucleic acids that encode the same.

[41] The use according to any one of [37] to [40] above, wherein the protein involved in primitive streak (PrS) formation is

selected from the group consisting of a Fox family member, brachyury, goosecoid, eomesodermin, LHX1, Sox17, MIXL1, Lefty2, Nodal1, Hand1, Wnt3, noggin, CER1, GATA4, GATA6, GSC, HESX1, HNF1A, HNF4A, OTX2, RNF111, Sox7, SP5 and TBX6.

[42] The method according to [41] above, wherein the Fox family member is selected from the group consisting of Foxa1, Foxa2, Foxa3, Foxb1, Foxc1, Foxc2, Foxd1, Foxd3, Foxd5, Foxe3, Foxf1, Foxf2, Foxg1, Foxh1, Foxi1, Foxi2, Foxj1, Foxj2, Foxj3, Foxk1, Foxk2, Foxl2, Foxm1, Foxn1, Foxan2, Foxn3, Foxn4, Foxo3, Foxo4, Foxp1, Foxp3, Foxp4, Foxr1, Foxr2 and Foxs1.

[43] The use according to any one of [37] to [40] above, wherein the protein is selected from the group consisting of Foxh1, brachyury, Foxa2, LHX1, Foxf1, Foxb1, Foxf2 and Foxg1.

[44] The use according to any one of [37] to [40] above, wherein the protein is Foxh1.

[45] A use of the iPS cell according to [29] or [30] above in producing a somatic cell.

[46] The iPS cell according to [29] or [30] above as a source of cells for producing a somatic cell.

Because the iPS cell establishment efficiency improving factor of the present invention can more efficiently establish iPS cells by means of 3 factors except c-Myc, compared to the strongest known enhancers of reprogramming, p53 shRNA and Glis1, as stated above, it is useful in, for example, applying iPS cells to regenerative medicine (e.g., preparation of safe human differentiated cells for transplantation).

Brief Description of the Drawings

Fig. 1 shows that TRA-1-60 (+) cells are origins of human iPSC.

a. Scheme drawing of TRA-1-60 (+) intermediate cells throughout the human cellular reprogramming.

b. Percentage of TRA-1-60 (+) cells in post-transduction of Oct3/4, Sox2, Klf4 and c-Myc (OSKM) into human dermal fibroblasts (HDF).

c. The efficiencies of iPSC generation from single TRA-1-60 (+) cell in each time point. Colony forming efficiencies were estimated by the number of iPSC colony-formed wells in single TRA-1-60 (+) cell-sorted 96-well plates. N=3. Error bars indicate standard deviation.

d. The number of iPSC colonies at day 28 derived from 1 x 10^5 of TRA-1-60 (+) and (-) cells at day 7 post-transduction. N=3.

e. The expression of pluripotency-associated genes in TRA-1-60 (+) cells. Mean expression of three microarray data for each time point normalized by those of ESC are shown.

Fig. 2 shows chracteristics of TRA-1-60 (+) intermediate cells.

a. PCA (principle component analysis) of nascent reprogrammed cells, parental HDF and ES/iPS cells (ESC/iPSC). All entities of microarray data were laid out with component 1 and 2. The arrow indicates the direction of reprogramming progression.

b. Classification of fluctuating genes during human cellular reprogramming. Gene ontology analyses of unidirectional (green) and transiently-fluctuated (red) gene clusters. We choose the top 10 biological terms with statistically significances.

c. Two categories of gene expression changes during reprogramming. The comparison of gene expression included in component 1 (unidirectional) and component 2 (transiently-fluctuated) with three germ layers such as PrS, ME, NE and EN.

d. PCA of nascent reprogrammed cells, parental HDF, ESC/iPSC and tri-lineage cells. All entities of microarray data were laid out with component 2 and 3. The arrow indicates the direction of reprogramming progression.

e. PCA of microarray expression data from TRA-1-60 (+) cells at each time point (d3-49), parental HDF and ESC/iPSC. Three microarray data are shown as each sample. The green arrow indicates a putative direction of the reprogramming

progression. Both the PCA and hierarchical clustering were generated for the cell samples from averaged data in triplicate.

f. Classification of the fluctuating genes during human cellular reprogramming. Genes highly contributed for principal component 1 (Absolute contribution rate > 0.6) were classified by gene ontology analyses. Green and red bars indicate top 10 categories of transiently-suppressed and activated genes, respectively. Shown are top 10 categories.

g. Comparison of global gene expression between TRA-1-60 (+) cells and various human tissues. Shown are the hierarchical clustering of global gene expression in parental HDF, TRA-1-60 (+) cells at indicated point, ESC/iPSC and ESC/iPSC-derived differentiated cells such as neuroectoderm (NE), endoderm (EN), mesoderm (ME) and primitive streak (PrS) and human tissues and tissue-derived cells such as peripheral blood mononuclear cell (PBMC), neural projenitor cell (NPC), epidermis (EDM), prostate epithelial cell (PrEC), normal bronchial epithelium (NHBE) adipose-tissue derived stem cell (ASC), astrocyte (HA) and dermal fibroblast (HDF).

h. The expression of mesenchymal and epithelial markers. Shown are the expression of representative mesenchymal and epithelial markers from microarray data.

Fig. 3 shows transient PrS-like status in nascent reprogrammed cells in the late stage of reprogramming.

a. Comparison of global gene expression between TRA-1-60 (+) cells and germ layers. Shown are the hierarchical clustering and heat map of global gene expression in parental HDF, TRA-1-60 (+) cells at indicated point, ESC/iPSC and differentiated cells such as EDM, PrS, EN, ME, and NE.

b. PrS-enriched genes transiently upregulated in TRA-1-60 (+) cells. Shown are percentages of ever-upregulated (black), ever-downregulated (blue), transiently-upregulated (red) and transiently downregulated (green) genes in enriched genes of endoderm (EN), mesoderm (ME), neuroectoderm (NE) or primitive

streak (PrS).

c. The expression of representative primitive streak marker genes during human cellular reprogramming. Shown are the relative expression of selected primitive streak marker genes in TRA-1-60 (+) cells compared to parental HDF. In these analyses, the averages of three microarray data of each sample were used.

d. The expression and active histone marks of T gene during reprogramming. Blue circles indicate the relative expression of T compared to HDF. Red diamonds indicate the occupancy of H3K4me3 at the promoter region of T gene. N=3. Error bars indicate standard deviation.

e. Single cell expression of T. The expression of NANOG and T in single HDF, TRA-1-60 (+) cells on day 20 post-transduction and ESC. Each dot indicates one cell sample. The relative expressions were shown as ΔCt of qPCR.

f. Immunocytochemistry of T gene. The expression of NANOG (red) and T (green) in HDF, TRA-1-60 (+) cells on day 20, ESC and ESC-derived PrS were analyzed by immunocutochemistry. Nucleuses were visualized by staining with Hoechst 33342 (blue). Bars indicate 100 μm.

g. PCA of microarray expression data from TRA-1-60 (+) cells at each time point, parental cell lines (HDF, HA, ASC, NHBE and PrEC), ESC/iPSC and differentiated cells such as EN, NE, PrS and ME. Each arrow indicates a putative direction of the reprogramming progression. HA, astrocytes; NHBE, bronchial epithelium; PrEC, prostate epithelial cells; HDF, human dermal fibroblast; NE, neuroectoderm; ME, mesoderm; PrS, primitive streak; EN, endoderm.

Fig. 4 shows that nascent reprogrammed cells transiently express PrS-related genes.

a. Early-responding PrS-related genes in TRA-1-60 (+) cells during reprogramming.

b. Late-responding genes in TRA-1-60 (+) cells during reprogramming.

c. The signatures of TRA-1-60 (+) cells derived from various origins shifted to PrS. PCA of origins (closed circles), TRA-1-60 (+) cells (open circles) and PrS derived from human ESC/iPSC (square). All entities of microarray data were laid out with component 1 and 2. The arrow indicates the direction of reprogramming progression.

Fig. 5 shows that GLIS1 accelerates reprogramming with cell fate sifting to PrS and mesoderm.

a. Wild-type embryos at E5.5-6.5 were dissected and performed whole mount in situ hybridization with *Glis1* cDNA probe as described previously (*Genes Dev 15*, 1242-1256, doi:10.1101/gad. 883901 (2001); *J Biol Chem 277*, 30901-30913, doi:10.1074/jbc.M203563200 [pii] (2002)).

b. The expression of T and GLIS1 in PrS differentiated from human ESC/iPSC. We used the results of G3PDH expression for normalization and adjusted ESC to 1.

c. Phase contrast images of undifferentiated human ESC/iPSC and PrS.

d. The expression of reprogramming-related genes in GLIS1-transgenic ESC. ESC introduced with empty vector (Mock), GLIS1 or NANOG were maintained in mTeSR1 medium on Matrigel-coated plates. The expression of reprogramming-related genes was quantified by qRT-PCR. We used the results of G3PDH expression for normalization and adjusted Mock to 1.

e. The expression of mesendodermal genes in GLIS1-transgenic ESC. The expression of PrS and mesoderm-related genes in the cells showen in Fig. 3d were quantified by qRT-PCR. We used the results of G3PDH expression for normalization and adjusted Mock to 1.

f. The scatter plots of microarray gene expression data. Colored dots indicate highly (red) or lowly (blue) expressed genes in indicated cell types.

g. GLIS1 induces biased differentiation potentials of ESC. The relative cell number of differentiated ESC into indicated lineages introduced with empty vector (Mock), GLIS1 or NANOG.

N=3.

Fig. 6 shows that FOXH1 facilitates reprogramming efficiency.

a. FOXH1 is essential for PrS differentiation of ESC/iPSC. We performed PrS differentiation of ESC/iPSC transfected with non-targeted siRNA (nc) or FOXH1 siRNA (F), and then quantified the expression of pluripotent stem cell markers and PrS markers by qRT-PCR. We used the results of G3PDH expression for normalization and adjusted PrS derived from non-transfected ESC (-) to 1.

b. FOXH1 facilitates iPSC generation. We introduced each PrS-related genes along with OSKM into HDF. On day 24 post-transduction, the number of iPSC colonies was counted. N=3. Error bars indicate standard deviation. Asterisks indicate $P < 0.05$ compared to Mock.

c. The action of FOXH1 is independent from that of p53. We introduced OSKM along with various combinations of p53 shRNA, FOXH1 and GLIS1 as indicated by + and - into HDF. The relative number of iPSC colonies on day 24 post-transduction is shown. N=3. Error bars indicate standard deviation. Asterisks indicate $P < 0.05$.

d. The expression of endogenous FOXH1 in TRA-1-60 (+) cells. Shown are the relative expression of endogenous FOXH1 (vs. iPSC (left) or HDF(right)) evaluated by qRT-PCR. N=3. Error bars indicate standard deviation.

e. FOXH1 affects the reprogramming efficiency in the late stage. We introduced OSKM alone (Mock), or along with FOXH1 into HDF. Then, we added 100 nM of Dex into the medium from the timing indicated by open circles to those by closed circles. Shown are relative numbers of iPSC colonies on day 24 post-transduction compared to OSKM alone. N=3. Error bars indicate standard deviation. Asterisks indicate $P < 0.05$.

f. GLIS1 affects the reprogramming efficiency in the early stage. We introduced OSKM alone, or along with GLIS1 into HDF. Then, we added 100 nM of Dex into the medium from

the timing indicated by open circles to those by closed circles. Shown are relative numbers of iPSC colonies on day 24 post-transduction compared to OSKM alone. N=3. Error bars indicate standard deviation. Asterisks indicate $P < 0.05$.

g. FOXH1 increases the proportion of TRA-1-60 (+) cells in the late stage. Shown are the relative proportion of TRA-1-60 (+) cells induced by OSKM along with GLIS1 (closed bars) or FOXH1 (opened bars) on day 7, 11 and 15 post-transduction compared to those of OSKM alone at each time point. N=3. Error bars indicate standard deviation.

h. FOHX1 does not increase the proportion of TRA-1-60(+) cells at day 7. We introduced OSKM along with FOXH1, p53 shRNA or GLIS1. The relative cell number of TRA-1-60 (+) cells at day 7 post transduction was shown. Mock=1. N=3. Asterisks indicate $p < 0.05$.

i. FOXH1 promotes the epithelialization of TRA-1-60 (+) cells. The proportion of CD13 (+) or EpCAM (+) cells in TRA-1-60 (+) cells carrying OSKM with (opened bars) or without (closed bars) FOXH1 were analyzed by flow cytometry on day 7, 11 and 15 post-transduction. N=3. Error bars indicate standard deviation. Asterisks indicate $P < 0.05$.

j. FOXH1 enhances the expression of late reprogramming markers. Shown are the relative expression of indicated genes in TRA-1-60 (+) cells induced by OSKMF on day 7, 11 and 15 compared to those of OSKM. N=3. Error bars indicate standard deviation.

k. FOXH1 is required normal PrS-differentiation from ESC/iPSC. We performed PrS-differentiation of ESC/iPSC transfected with negative control (nc) or FOXH1 siRNA. The marker gene expression evaluated by qPCR was normalized by G3PDH expression of each sample. Shown are the relative expression compared to PrS derived from non-transfected ESC/iPSC. N=3. Error bars indicate standard deviation.

l. Endogenous FOXH1 is required for iPSC generation. We first introduced OSKM along with shRNA expression vector

encoding scramble shRNA (Scr) or three different sequences of shRNAs against human FOXH1 gene (FOXH1 shRNA 1, 3 and 6) into human ESC. Next day, the knockdown efficiencies in transduced ESCs were evaluated by qRT-PCR (closed bars). Next, we introduced pMKO.1-puro encoding scramble shRNA (Scr), FOXH1 shRNA1, 3 or 6 with OSKM into HDF. Shown are the relative numbers of iPSC colonies on day 24 compared to Mock (opened bars). N=3. Error bars indicate standard deviation. Asterisks indicate $P < 0.05$.

m. Endogenous FOXH1 does not affect HDF proliferation. Shown are relative cell numbers of HDF transduced with OSKM along with pMKO.1-puro encoding scramble shRNA (Scr), FOXH1 shRNA1, 3 or 6. N=3. Error bars indicate standard deviation.

Fig. 7 shows characterization of OSKMF-iPSC lines.

a. Phase contrast images of OSKMF-iPSC (1082A1) on SNL feeders at passage number 5. Bar indicates 100 μm.

b. The expression analyses of *OCT3/4*, *SOX2* and *NANOG* in OSKMF-iPSC, H1 (ESC), 201B7 (OSKM-iPSC) and HDF. We used the results of G3PDH expression for normalization and adjusted ES cells to 1.

c. DNA methylation statuses of *OCT3/4* promoter (CR1, CR2, 5′ UTR) and *NANOG* promoter (CR1). White and black indicate the percentage of unmethylated and methylated CpG, respectively.

d. Karyotype analysis of OSKMF-iPSC.

e. The expression of surface markers such as SSEA-4, TRA-1-60 and TRA-2-49/6E in OSKMF-iPSC. Ten thousand of stained cells (closed histograms) were analyzed by flow cytometry. Open histogram indicates unstained control.

f. In vitro differentiation potentials of OSKMF-iPSC. OSKMF-iPSC were spontaneously differentiated by embryoid body-mediated protocol. A upper-left panel shows phase contrast of floating-cultured cells at day 8. After 16-days differentiation, the cells were stained with indicated antibodies (green or red) and Hoechst 33342 (blue). Bar indicates 100 μm.

g. In vivo differentiation potentials of OSKMF-iPSC. Sections of teratoma derived from OSKMF-iPSC were stained with hematoxylin and eosin.

Fig. 8 shows the effects of FOX family genes on reprogramming. We introduced OSKM along with each FOX family gene as indicated into HDF by retroviral transduction. The numbers of iPSC colonies were counted on day 24 post-transduction. N=3. Error bars indicate standard deviation. Asterisks indicate $P < 0.05$ compared to Mock. Left part of the figure shows the result of multiple protein sequence alignment as rooted phylogenetic tree.

Fig. 9 shows the overlapping effects of FOX genes on reprogramming. We introduced OSKM or OSKMF along with Mock, FOXA2, FOXB1, FOXF1, FOXG1 into HDF by retroviral transduction. Shown are the numbers of iPSC colonies from 1×10^5 transduced HDF on day 24. N=3. Error bars indicate standard deviation.

Detailed Description of the Invention

The present invention provides a method of improving the efficiency of iPS cell establishment by bringing a protein involved in PrS formation or a nucleic acid that encodes the same (hereinafter also referred to as the establishment efficiency improving factor of the present invention) into contact with a somatic cell in the step of nuclear reprogramming of the somatic cell. Here, the nuclear reprogramming of the somatic cell is achieved by transferring nuclear reprogramming substance(s) to the somatic cell; therefore, the present invention also provides a method of producing an iPS cell by bringing the establishment efficiency improving factor and nuclear reprogramming substance(s) into contact with a somatic cell. Herein, cases where iPS cells cannot be established by merely transferring nuclear reprogramming substance(s) alone to a somatic cell, but can be established by bringing nuclear reprogramming substance(s) along with the establishment efficiency improving factor of the present invention into

contact with a somatic cell, are also deemed as corresponding to "an improvement of establishment efficiency."

(a) Source of somatic cells

In the present invention, any cells other than germ cells of mammalian origin (e.g., humans, mice, monkeys, pigs, rats etc.) can be used as starting material for the production of iPS cells. Examples include keratinizing epithelial cells (e.g., keratinized epidermal cells), mucosal epithelial cells (e.g., epithelial cells of the superficial layer of tongue), exocrine gland epithelial cells (e.g., mammary gland cells), hormone-secreting cells (e.g., adrenomedullary cells), cells for metabolism or storage (e.g., liver cells), intimal epithelial cells constituting interfaces (e.g., type I alveolar cells), intimal epithelial cells of the obturator canal (e.g., vascular endothelial cells), cells having cilia with transporting capability (e.g., airway epithelial cells), cells for extracellular matrix secretion (e.g., fibroblasts), contractile cells (e.g., smooth muscle cells), cells of the blood and the immune system (e.g., T lymphocytes), sense-related cells (e.g., rod cells), autonomic nervous system neurons (e.g., cholinergic neurons), sustentacular cells of sensory organs and peripheral neurons (e.g., satellite cells), nerve cells and glia cells of the central nervous system (e.g., astroglia cells), pigment cells (e.g., retinal pigment epithelial cells), progenitor cells thereof (tissue progenitor cells) and the like. There is no limitation on the degree of cell differentiation, the age of the animal from which cells are collected and the like; even undifferentiated progenitor cells (including somatic stem cells) and finally differentiated mature cells can be used alike as sources of somatic cells in the present invention. Examples of undifferentiated progenitor cells include tissue stem cells (somatic stem cells) such as neural stem cells, hematopoietic stem cells, mesenchymal stem cells, and dental pulp stem cells.

The choice of mammal individual as a source of somatic

cells is not particularly limited; however, when the iPS cells obtained are to be used for the regenerative medicine in humans, it is preferable, from the viewpoint of prevention of graft rejection to collect the somatic cells from the patient or another person with the same or substantially the same HLA type as that of the patient. "Substantially the same HLA type" as used herein means that the HLA type of donor matches with that of patient to the extent that the transplanted cells, which have been obtained by inducing differentiation of iPS cells derived from the donor's somatic cells, can be engrafted when they are transplanted to the patient with use of immunosuppressant and the like. For example, it includes an HLA type wherein major HLAs (e.g., the three major loci of HLA-A, HLA-B and HLA-DR) are identical and the like (hereinafter the same meaning shall apply). When the iPS cells obtained are not to be administered (transplanted) to a human, but used as, for example, a source of cells for screening for evaluating a patient's drug susceptibility or adverse reactions, it is likewise desirable to collect the somatic cells from the patient or another person with the same genetic polymorphism correlating with the drug susceptibility or adverse reactions.

Before being subjected to the step of nuclear reprogramming, somatic cells separated from a mammal can be pre-cultured using a medium known per se suitable for the cultivation thereof, depending on the kind of the cells. Examples of such media include, but are not limited to, a minimal essential medium (MEM) containing about 5 to 20% fetal calf serum, Dulbecco's modified Eagle medium (DMEM), RPMI1640 medium, 199 medium, F12 medium and the like. When using, for example, a transfection reagent such as a cationic liposome in contacting the cell with the establishment efficiency improving factors of the present invention and nuclear reprogramming substance(s) (and another iPS cell establishment efficiency improver as required), it is sometimes preferable

that the medium be previously replaced with a serum-free medium to prevent a reduction in the transfer efficiency.

(b) The establishment efficiency improving factor of the present invention

The establishment efficiency improving factor of the present invention is a protein involved in PrS formation, or a nucleic acid that encodes the same. The proteins involved in PrS formation include, but are not limited to, Foxh1, brachyury (T), goosecoid (GSC), Foxa2, eomesodermin (EOMES), LHX1, Sox17, MIXL1, GDF3, Lefty2, Nodal, Hand1, Wnt3, noggin (NOG), CER1, Foxf1, GATA4, GATA6, HESX1, HNF1A, HNF4A, OTX2, RNF111, Sox7, SP5 and TBX6. Preferably, the protein involved in PrS formation is Foxh1, brachyury (T), Foxa2, LHX1 or Foxf1, more preferably Foxh1.

Alternatively, each of the above factors may be substituted by any of other members of a family to which it belongs. For example, Foxh1 or Foxa2 may be substituted by other Fox family members including, but are not limited to, Foxa1, Foxa3, Foxb1, Foxc1, Foxc2, Foxd1, Foxd3, Foxd5, Foxe3, Foxf1, Foxf2, Foxg1, Foxi1, Foxi2, Foxj1, Foxj2, Foxj3, Foxk1, Foxk2, Foxl2, Foxm1, Foxn1, Foxan2, Foxn3, Foxn4, Foxo3, Foxo4, Foxp1, Foxp3, Foxp4, Foxr1, Foxr2 and Foxs1. Preferably, the Fox family member used as the establishment efficiency improving factor of the present invention is Foxh1, Foxa2, Foxb1, Foxf1, Foxf2 or Foxg1, more preferably Foxh1.

Although the establishment efficiency improving factor of the present invention may be proteins derived from optionally chosen mammals (e.g., humans, mice, rats, monkeys, bovines, horses, pigs, dogs and the like) or nucleic acids that encode the same, proteins or nucleic acids of human or mouse origin are preferred. Information on the amino acid sequences and cDNA sequences of Foxh1, brachyury (T), goosecoid (GSC), Foxa2, eomesodermin (EOMES), LHX1, Sox17, MIXL1, GDF3, Lefty2, Nodal, Hand1, Wnt3, noggin (NOG), CER1, Foxf1, GATA4, GATA6, HESX1, HNF1A, HNF4A, OTX2, RNF111, Sox7, SP5 and TBX6 of human or

mouse origin can be acquired by referring to the NCBI accession numbers shown in Table 1; and information on the amino acid sequences and cDNA sequences of Foxa1, Foxa2, Foxa3, Foxb1, Foxc1, Foxc2, Foxd1, Foxd3, Foxd5, Foxe3, Foxf1, Foxf2, Foxg1, Foxh1, Foxi1, Foxi2, Foxj1, Foxj2, Foxj3, Foxk1, Foxk2, Foxl2, Foxm1, Foxn1, Foxan2, Foxn3, Foxn4, Foxo3, Foxo4, Foxp1, Foxp3, Foxp4, Foxr1, Foxr2 and Foxs1 of human or mouse origin can be acquired by referring to the NCBI accession numbers shown in Table 2. Those skilled in the art are easily able to isolate nucleic acids that encode the respective proteins on the basis of the cDNA sequence information, and to produce recombinant proteins as required.

Table 1

Protein name (Gene name)	Human		Mouse	
	cDNA	Protein	cDNA	Protein
Foxh1	NM_003923	NP_003914	NM_007989	NP_032015
brachyury (T)	NM_003181	NP_003172	NM_009309	NP_033335
goosecoid (GSC)	NM_173849	NP_776248	NM_010351	NP_034481
Foxa2	NM_021784	NP_068556	NM_010446	NP_034576
eomesodermin (EOMES)	NM_005442	NP_005433	NM_010136	NP_034266
LHX1	NM_005568	NP_005559	NM_008498	NP_032524
Sox17	NM_022454	NP_071899	NM_011441	NP_035571
MIXL1	NM_031944	NP_114150	NM_013729	NP_038757
GDF3	NM_020634	NP_065685	NM_008108	NP_032134
Lefty2	NM_003240	NP_003231	NM_177099	NP_796073
Nodal	NM_018055	NP_060525	NM_013611	NP_038639
Hand1	NM_004821	NP_004812	NM_008213	NP_032239
Wnt3	NM_030753	NP_110380	NM_009521	NP_033547
noggin (NOG)	NM_005450	NP_005441	NM_008711	NP_032737
CER1	NM_005454	NP_005445	NM_009887	NP_034017
Foxf1	NM_001451	NP_001442	NM_010426	NP_034556
GATA4	NM_002052	NP_002043	NM_008092	NP_032118

Table 1 (continued)

GATA6	NM_005257	NP_005248	NM_010258	NP_034388
GSC	NM_173849	NP_776248	NM_010351	NP_034481
HESX1	NM_003865	NP_003856	NM_010420	NP_034550
HNF1A	NM_000545	NP_000536	NM_009327	NP_033353
HNF4A	NM_178849	NP_000448	NM_008261	NP_032287
OTX2	NM_021728	NP_068374	NM_144841	NP_659090
RNF111	NM_001270528	NP_060080	NM_033604	NP_291082
Sox7	NM_031439	NP_113627	NM_011446	NP_035576
SP5	NM_001003845	NP_001003845	NM_022435	NP_071880
TBX6	NM_004608	NP_004599	NM_011538	NP_035668

Table 2

Protein name	Human		Mouse	
(Gene name)	cDNA	Protein	cDNA	Protein
Foxa1	NM_004496	NP_004487	NM_008259	NP_032285
Foxa2	NM_021784	NP_068556	NM_010446	NP_034576
Foxa3	NM_004497	NP_004488	NM_008260	NP_032286
Foxb1	NM_012182	NP_036314	NM_022378	NP_071773
Foxc1	NM_001453	NP_001444	NM_008592	NP_032618
Foxc2	NM_005251	NP_005242	NM_013519	NP_038547
Foxd1	NM_205192	NP_004463	NM_008242	NP_004463
Foxd3	NM_012183	NP_036315	NM_010425	NP_034555
Foxd5	NM_012184	NP_036316	NM_008022	NP_032048
Foxe3	NM_012186	NP_036318	NM_015758	NP_056573
Foxf1	NM_001451	NP_001442	NM_010426	NP_034556
Foxf2	NM_001452	NP_001443	NM_010225	NP_034355
Foxg1	NM_005249	NP_005240	NM_008241	NP_001153584
Foxh1	NM_003923	NP_003914	NM_007989	NP_032015
Foxi1	NM_012188	NP_036320	NM_023907	NP_076396
Foxi2	NM_207426	NP_997309	NM_183193	NP_899016
Foxj1	NM_001454	NP_001445	NM_008240	NP_032266
Foxj2	NM_018416	NP_060886	NM_021899	NP_068699

Table 2 (continued)

Foxj3	NM_014947	NP_001185781	NM_172699	NP_766287
Foxk1	NM_001037165	NP_001032242	NM_199068	NP_951031
Foxk2	NM_004514	NP_004505	NM_001080932	NP_001074401
Foxl2	NM_023067	NP_075555	NM_012020	NP_036150
Foxm1	NM_202002	NP_973732	NM_008021	NP_032047
Foxn1	NM_003593	NP_003584	NM_008238	NP_032264
Foxn2	NM_002158	NP_002149	NM_180974	NP_851305
Foxn3	NM_001085471	NP_001078940	NM_183186	NP_899009
Foxn4	NM_213596	NP_998761	NM_148935	NP_683737
Foxo3	NM_001455	NP_001446	NM_019740	NP_062714
Foxo4	NM_005938	NP_005929	NM_018789	NP_061259
Foxp1	NM_032682	NP_116071	NM_053202	NP_444432
Foxp3	NM_014009	NP_054728	NM_001199347	NP_001186276
Foxp4	NM_001012426	NP_001012426	NM_001110824	NP_001104294
Foxr1	NM_181721	NP_859072	NM_001033469	NP_001028641
Foxr2	NM_198451	NP_940853	NM_001034894	NP_001030066
Foxs1	NM_004118	NP_004109	NM_010226	NP_034356

A natural or artificial mutant protein having an identity of 80% or more, preferably 90% or more, more preferably 95% or more, particularly preferably 97% or more, to each amino acid sequence shown above, and possessing a potential for improving iPS cell establishment efficiency equivalent to or greater than that of the wild-type protein and a nucleic acid that encodes the same, can also be utilized as the establishment efficiency improving factors of the present invention.

Out of the proteins involved in PrS formation (including nucleic acids that encode the same), any one kind alone may be used, and two kinds or more may be used in combination.

The establishment efficiency improving factor of the present invention may also be used as "a nuclear reprogramming substance" as stated below, in combination with any other nuclear reprogramming substance(s) in producing an iPS cell.

Transfer of the protein involved in PrS formation to a somatic cell can be achieved using a method known per se for protein transfer into a cell, provided that the substance is a proteinous factor. Such methods include, for example, the method using a protein transfer reagent, the method using a protein transfer domain (PTD)- or cell penetrating peptide (CPP)-fusion protein, the microinjection method and the like. Protein transfer reagents are commercially available, including those based on a cationic lipid, such as BioPOTER Protein Delivery Reagent (Gene Therapy Systems), Pro-Ject™ Protein Transfection Reagent (PIERCE) and ProVectin (IMGENEX); those based on a lipid, such as Profect-1 (Targeting Systems); those based on a membrane-permeable peptide, such as Penetrain Peptide (Q biogene) and Chariot Kit (Active Motif), GenomONE (ISHIHARA SANGYO KAISHA, LTD.) utilizing HVJ envelope (inactivated hemagglutinating virus of Japan) and the like. The transfer can be achieved per the protocols attached to these reagents, a common procedure being as described below. The protein involved in PrS formation is diluted in an appropriate solvent (e.g., a buffer solution such as PBS or HEPES), a transfer reagent is added, the mixture is incubated at room temperature for about 5 to 15 minutes to form a complex, this complex is added to cells after exchanging the medium with a serum-free medium, and the cells are incubated at 37°C for one to several hours. Thereafter, the medium is removed and replaced with a serum-containing medium.

Alternatively, a reverse transfection may be used, wherein the protein is immobilized onto a solid phase such as a well plate, culture dish and the like followed by the addition of somatic cells to the solid phase.

Developed PTDs include those using transcellular domains of proteins such as drosophila-derived AntP, HIV-derived TAT (Frankel, A. et al, *Cell 55*, 1189-93 (1988) or Green, M. & Loewenstein, P. M. *Cell 55*, 1179-88 (1988)), Penetratin (Derossi, D. et al, *J. Biol. Chem. 269*, 10444-50 (1994)),

Buforin II (Park, C. B. et al. *Proc. Natl Acad. Sci. USA 97*, 8245-50 (2000)), Transportan (Pooga, M. et al. *FASEB J. 12*, 67-77 (1998)), MAP (model amphipathic peptide) (Oehlke, J. et al. *Biochim. Biophys. Acta. 1414*, 127-39 (1998)), K-FGF (Lin, Y. Z. et al. *J. Biol. Chem. 270*, 14255-14258 (1995)), Ku70 (Sawada, M. et al. *Nature Cell Biol. 5*, 352-7 (2003)), Prion (Lundberg, P. et al. *Biochem. Biophys. Res. Commun. 299*, 85-90 (2002)), pVEC (Elmquist, A. et al. *Exp. Cell Res. 269*, 237-44 (2001)), Pep-1 (Morris, M. C. et al. *Nature Biotechnol. 19*, 1173-6 (2001)), Pep-7 (Gao, C. et al. *Bioorg. Med. Chem. 10*, 4057-65 (2002)), SynB1 (Rousselle, C. et al. *Mol. Pharmacol. 57*, 679-86 (2000)), HN-I (Hong, F. D. & Clayman, G L. *Cancer Res. 60*, 6551-6 (2000)), and HSV-derived VP22. CPPs derived from the PTDs include polyarginines such as 11R (*Cell Stem Cell, 4*,381-384 (2009)) and 9R (*Cell Stem Cell, 4*, 472-476 (2009)).

A fusion protein expression vector incorporating a cDNA encoding the protein involved in PrS formation and a PTD or CPP sequence is prepared to allow the recombinant expression of the fusion protein, and the fusion protein is recovered for use for transfer. This transfer can be achieved as described above, except that no protein transfer reagent is added.

Microinjection, a method of placing a protein solution in a glass needle having a tip diameter of about 1 μm, and injecting the solution into a cell, ensures the transfer of the protein into the cell.

Other useful methods of protein transfer include electroporation, the semi-intact cell method [Kano, F. et al. Methods in Molecular Biology, Vol. 322, 357-365(2006)], transfer using the Wr-t peptide [Kondo, E. et al., Mol. Cancer Ther. 3(12), 1623-1630(2004)] and the like.

The protein transferring operation can be performed one or more optionally chosen times (e.g., once or more to 10 times or less, or once or more to 5 times or less and the like). Preferably, the transferring operation can be performed

twice or more (e.g., 3 times or 4 times) repeatedly. The time interval for repeated transferring operation is, for example, 6 to 48 hours, preferably 12 to 24 hours.

The choice of a nucleic acid that encodes a protein involved in PrS formation is not particularly limited. The nucleic acid may be a DNA or an RNA, or a DNA/RNA chimera, and is preferably a DNA. The nucleic acid may be double-stranded or single-stranded. In the case of double strands, the nucleic acid may be a double-stranded DNA, a double-stranded RNA or a DNA:RNA hybrid.

A nucleic acid encoding a protein involved in PrS formation can, for example, be cloned from a cell or tissue [e.g., cells and tissues of thymus, bone marrow, spleen, brain, spinal cord, heart, skeletal muscle, kidney, lung, liver, pancreas or prostate, progenitor cells, stem cells or cancer cells of these cells, and the like] of a human or another mammal (e.g., mouse, rat, monkey, pig, dog and the like) by a conventional method.

Transfer of a nucleic acid encoding a protein involved in PrS formation to a somatic cell can be achieved using a method of gene transfer to cells known per se. A nucleic acid that encodes a protein involved in PrS formation is inserted into an appropriate expression vector containing a promoter capable of functioning in the host somatic cell. Useful expression vectors include, for example, viral vectors such as retrovirus, lentivirus, adenovirus, adeno-associated virus, herpes virus and Sendai virus, plasmids for the expression in animal cells (e.g., pA1-11, pXT1, pRc/CMV, pRc/RSV, pcDNAI/Neo) and the like.

A vector for this purpose can be chosen as appropriate according to the intended use of the iPS cell to be obtained. Useful vectors include adenovirus vector, plasmid vector, adeno-associated virus vector, retrovirus vector, lentivirus vector, Sendai virus vector, episomal vector and the like.

Examples of promoters used in expression vectors include

the EF1α promoter, the CAG promoter, the SRα promoter, the SV40 promoter, the LTR promoter, the CMV (cytomegalovirus) promoter, the RSV (Rous sarcoma virus) promoter, the MoMuLV (Moloney mouse leukemia virus) LTR, the HSV-TK (herpes simplex virus thymidine kinase) promoter and the like, with preference given to the EF1α promoter, the CAG promoter, the MoMuLV LTR, the CMV promoter, the SRα promoter and the like.

The expression vector may contain as desired, in addition to a promoter, an enhancer, a polyadenylation signal, a selectable marker gene, a SV40 replication origin and the like. Examples of selectable marker genes include the dihydrofolate reductase gene, the neomycin resistant gene, the puromycin resistant gene and the like.

A nucleic acid that encodes a protein involved in PrS formation may be integrated alone into an expression vector, or along with one or more reprogramming genes into an expression vector. Preference is sometimes given to the former case when using a retrovirus or lentivirus vector, which offer high gene transfer efficiency, and to the latter case when using a plasmid, adenovirus, or episomal vector and the like, but there are no particular limitations.

In the context above, when a nucleic acid that encodes a protein involved in PrS formation and one or more reprogramming genes are integrated in one expression vector, these genes can preferably be integrated into the expression vector via a sequence enabling polycistronic expression. By using a sequence enabling polycistronic expression, it is possible to more efficiently express a plurality of genes integrated in one expression vector. Useful sequences enabling polycistronic expression include, for example, the 2A sequence of foot-and-mouth disease virus (PLoS ONE3, e2532, 2008, Stem Cells 25, 1707, 2007), the IRES sequence (U.S. Patent No. 4,937,190) and the like, with preference given to the 2A sequence.

An expression vector harboring a nucleic acid that encodes a protein involved in PrS formation can be introduced into a

cell by a technique known per se according to the choice of the vector. In the case of a viral vector, for example, a plasmid containing the nucleic acid is introduced into an appropriate packaging cell (e.g., Plat-E cells) or a complementary cell line (e.g., 293-cells), the viral vector produced in the culture supernatant is recovered, and the vector is infected to the cell by a method suitable for each viral vector. For example, specific means using a retroviral vector are disclosed in WO2007/69666, *Cell, 126*, 663-676 (2006) and *Cell, 131*, 861-872 (2007); when a lentivirus vector is used, a disclosure is available in *Science, 318*, 1917-1920 (2007). When iPS cells are utilized as a source of cells for regenerative medicine, the expression (reactivation) of a protein involved in PrS formation or the activation of an endogenous gene present in the vicinity of the site where the exogenous gene is integrated potentially increases the risk of carcinogenesis in tissues regenerated from differentiated cells of iPS cell derivation; therefore, a nucleic acid that encodes a protein involved in PrS formation is preferably expressed transiently, without being integrated into the chromosome of the cells. From this viewpoint, use of an adenoviral vector, whose integration into chromosome is rare, is preferred. Specific means using an adenoviral vector is described in *Science, 322*, 945-949 (2008). Because an adeno-associated viral vector is also low in the frequency of integration into chromosome, and is lower than adenoviral vectors in terms of cytotoxicity and inflammation-inducibility, it can be mentioned as another preferred vector. Because Sendai viral vector is capable of being stably present outside the chromosome, and can be degraded and removed using an siRNA as required, it is preferably utilized as well. Regarding a Sendai viral vector, one described in *J. Biol. Chem., 282*, 27383-27391 (2007) and JP-3602058 B can be used.

When a retroviral vector or a lentiviral vector is used, even if silencing of the transgene has occurred, it possibly

becomes reactivated later; therefore, for example, a method can be used preferably wherein a nucleic acid that encodes a protein involved in PrS formation is cut out using the Cre/loxP system, when becoming unnecessary. That is, with loxP sequences arranged on both ends of the nucleic acid in advance, after iPS cells are induced, the Cre recombinase is allowed to act on the cells using a plasmid vector or adenoviral vector, and the region sandwiched by the loxP sequences can be cut out. Because the enhancer-promoter sequence of the LTR U3 region possibly upregulates a host gene in the vicinity thereof by insertion mutation, it is more preferable to avoid the expression regulation of the endogenous gene by the LTR outside of the loxP sequence remaining in the genome without being cut out, using a 3'-self-inactivating (SIN) LTR prepared by deleting the sequence, or substituting the sequence with a polyadenylation sequence such as of SV40. Specific means using the Cre-loxP system and SIN LTR is disclosed in Soldner et al., *Cell, 136*: 964-977 (2009), Chang et al., *Stem Cells, 27*: 1042-1049 (2009) and the like.

Meanwhile, being a non-viral vector, a plasmid vector can be transferred into a cell using the lipofection method, liposome method, electroporation method, calcium phosphate co-precipitation method, DEAE dextran method, microinjection method, gene gun method and the like. Specific means using a plasmid as a vector are described in, for example, *Science, 322*, 949-953 (2008) and the like.

When a plasmid vector, an adenovirus vector and the like are used, the transfection can be performed once or more optionally chosen times (e.g., once to 10 times, once to 5 times or the like). When two or more kinds of expression vectors are introduced into a somatic cell, it is preferable that these all kinds of expression vectors be concurrently introduced into a somatic cell; however, even in this case, the transfection can be performed once or more optionally chosen times (e.g., once to 10 times, once to 5 times or the

like), preferably the transfection can be repeatedly performed twice or more (e.g., 3 times or 4 times).

Also when an adenovirus or a plasmid is used, the transgene can get integrated into chromosome; therefore, it is eventually necessary to confirm the absence of insertion of the gene into chromosome by Southern blotting or PCR. For this reason, like the aforementioned Cre-loxP system, it can be advantageous to use a means wherein the transgene is integrated into chromosome, thereafter the gene is removed. In another preferred mode of embodiment, a method can be used wherein the transgene is integrated into chromosome using a transposon, thereafter a transposase is allowed to act on the cell using a plasmid vector or adenoviral vector so as to completely eliminate the transgene from the chromosome. As examples of preferable transposons, piggyBac, a transposon derived from a lepidopterous insect, and the like can be mentioned. Specific means using the piggyBac transposon is disclosed in Kaji, K. et al., *Nature, 458*: 771-775 (2009), Woltjen et al., *Nature, 458*: 766-770 (2009).

Another preferable non-integration type vector is an episomal vector, which is autonomously replicable outside the chromosome. Specific means with the use of an episomal vector is described by Yu et al. in *Science, 324*, 797-801 (2009). As appropriate, an expression vector in which a nucleic acid that encodes a protein involved in PrS formation is inserted into an episomal vector having loxP sequences placed in the same orientation on the 5′ and 3′ sides of the vector constituent essential for the replication of the episomal vector can be constructed and introduced into a somatic cell.

Examples of the episomal vector include a vector comprising, as a vector component, a sequence derived from EBV, SV40 and the like necessary for self-replication. The vector component necessary for self-replication is specifically exemplified by a replication origin and a gene that encodes a protein that binds to the replication origin to control the

replication; examples include the replication origin oriP and the EBNA-1 gene for EBV, and the replication origin ori and the SV40 large T antigen gene for SV40.

The episomal expression vector harbors a promoter that controls the transcription of a nucleic acid that encodes a protein involved in PrS formation. Useful promoters include those mentioned above. The episomal expression vector, like the aforementioned vectors, may further contain as desired an enhancer, a polyA addition signal, a selection marker gene and the like. Examples of useful selection marker genes include the dihydrofolate reductase gene, the neomycin resistance gene and the like.

The loxP sequences useful in the present invention include, in addition to the bacteriophage P1-derived wild type loxP sequence, optionally chosen mutant loxP sequences capable of deleting the sequence flanked by the loxP sequence by recombination when placed in the same orientation at positions flanking a vector component necessary for the replication of the introduced gene. Examples of such mutant loxP sequences include lox71, mutated in 5′ repeat, lox66, mutated in 3′ repeat, and lox2272 and lox511, mutated in spacer portion. Although the two loxP sequences placed on the 5′ and 3′ sides of the vector component may be identical or not, the two mutant loxP sequences mutated in spacer portion must be identical (e.g., a pair of lox2272 sequences, a pair of lox511 sequences). Preference is given to a combination of a mutant loxP sequence mutated in 5′ repeat (e.g., lox71) and a mutant loxP sequence mutated in 3′ repeat (e.g., lox66). In this case, the loxP sequences remaining on the chromosome have double mutations in the repeats on the 5′ side and 3′ side as a result of recombination, and are therefore unlikely to be recognized by Cre recombinase, thus reducing the risk of causing a deletion mutation in the chromosome due to unwanted recombination. When the mutant loxP sequences lox71 and lox66 are used in combination, each may be placed on any of the 5′

and 3′ sides of the aforementioned vector component, but it is necessary that the mutant loxP sequences be inserted in an orientation such that the mutated sites would be located at the outer ends of the respective loxP sequences. Although a preferred episomal vector of the present invention is a self-removal vector early shedding from the cell even without being acted on by Cre recombinase, there are possibly exceptional cases where longer time is taken for the episomal vector to be shed from the cell. It is preferable, therefore, that the loxP sequences be designed in preparation for risks such as unwanted recombination due to Cre recombinase treatment.

Each of the two loxP sequences is placed in the same orientation on the 5′ and 3′ sides of a vector constituent essential for the replication of the introduced gene (i.e., a replication origin, or a gene sequence that encodes a protein that binds to the replication origin to control the replication). The vector constituent flanked by the loxP sequences may be either the replication origin or a gene sequence that encodes a protein that binds to a replication origin to control the replication, or both.

The episomal vector allows the vector to be introduced into the cell using, for example, the lipofection method, liposome method, electroporation method, calcium phosphate co-precipitation method, DEAE dextran method, microinjection method, gene gun method and the like. Specifically, for example, methods described in *Science, 324*: 797-801 (2009) and elsewhere can be used.

Whether or not the vector component necessary for the replication of the introduced gene has been removed from the iPS cell can be confirmed by performing a Southern blot analysis or PCR analysis using a nucleic acid comprising a nucleotide sequence in the vector component as a probe or primer, with the episome fraction isolated from the iPS cell as a template, and determining the presence or absence of a band or the length of the band detected. The episome fraction

can be prepared by a method well known in the art; for example, methods described in *Science, 324*: 797-801 (2009) and elsewhere can be used.

(c) Nuclear reprogramming substances

As used herein, "a nuclear reprogramming substance" can include a proteinous factor, a nucleic acid that encodes the same (including a form integrated in a vector) or a low molecular weight compound, as long as it can induce an iPS cell from a somatic cell upon its contact with the somatic cell together with the iPS cell establishment efficiency improving factors of the present invention. When the nuclear reprogramming substance is a proteinous factor or a nucleic acid that encodes the same, the following combinations, for example, are preferable (hereinafter, only the names for proteinous factors are shown).

(1) Oct3/4, Klf4, c-Myc

(2) Oct3/4, Klf4, c-Myc, Sox2 (Sox2 is replaceable with Sox1, Sox3, Sox15, Sox17 or Sox18; Klf4 is replaceable with Klf1, Klf2 or Klf5; c-Myc is replaceable with T58A (active mutant), N-Myc, or L-Myc)

(3) Oct3/4, Klf4, c-Myc, Sox2, Fbx15, Nanog, Eras, ECAT15-2, TclI, β-catenin (active mutant S33Y)

(4) Oct3/4, Klf4, c-Myc, Sox2, TERT, SV40 Large T antigen (hereinafter SV40LT)

(5) Oct3/4, Klf4, c-Myc, Sox2, TERT, HPV16 E6

(6) Oct3/4, Klf4, c-Myc, Sox2, TERT, HPV16 E7

(7) Oct3/4, Klf4, c-Myc, Sox2, TERT, HPV6 E6, HPV16 E7

(8) Oct3/4, Klf4, c-Myc, Sox2, TERT, Bmil

[For more information on the factors shown above, see WO 2007/069666 (for information on replacement of Sox2 with Sox18 and replacement of Klf4 with Klf1 or Klf5 in the combination (2) above, see *Nature Biotechnology, 26*, 101-106 (2008)); for the combination "Oct3/4, Klf4, c-Myc, Sox2", see also *Cell, 126*, 663-676 (2006), *Cell, 131*, 861-872 (2007) and the like; for the combination "Oct3/4, Klf2 (or Klf5), c-Myc, Sox2", see

also *Nat. Cell Biol., 11*, 197-203 (2009); for the combination "Oct3/4, Klf4, c-Myc, Sox2, hTERT, SV40 LT", see also *Nature, 451*, 141-146 (2008).]

(9) Oct3/4, Klf4, Sox2 (see *Nature Biotechnology, 26*, 101-106 (2008))

(10) Oct3/4, Sox2, Nanog, Lin28 (see *Science, 318*, 1917-1920 (2007))

(11) Oct3/4, Sox2, Nanog, Lin28, hTERT, SV40LT (see *Stem Cells, 26*, 1998-2005 (2008))

(12) Oct3/4, Klf4, c-Myc, Sox2, Nanog, Lin28 (see *Cell Research* (2008) 600-603)

(13) Oct3/4, Klf4, c-Myc, Sox2, SV40LT (see also *Stem Cells, 26*, 1998-2005 (2008))

(14) Oct3/4, Klf4 (see *Nature 454*:646-650 (2008), Cell Stem Cell, 2:525-528 (2008))

(15) Oct3/4, c-Myc (see *Nature 454*:646-650 (2008))

(16) Oct3/4, Sox2 (see Nature, 451, 141-146 (2008), WO2008/118820)

(17) Oct3/4, Sox2, Nanog (see WO2008/118820)

(18) Oct3/4, Sox2, Lin28 (see WO2008/118820)

(19) Oct3/4, Sox2, c-Myc, Esrrb (Here, Essrrb can be substituted by Esrrg, see *Nat. Cell Biol., 11*, 197-203 (2009))

(20) Oct3/4, Sox2, Esrrb (see *Nat. Cell Biol., 11*, 197-203 (2009))

(21) Oct3/4, Klf4, L-Myc (see *Proc. Natl. Acad. Sci. U S A., 107*, 14152-14157 (2010))

(22) Oct3/4, Nanog

(23) Oct3/4 (*Cell 136*: 411-419 (2009); *Nature*, 08436, doi:10.1038 published online(2009))

(24) Oct3/4, Klf4, c-Myc, Sox2, Nanog, Lin28, SV40LT (see *Science, 324*: 797-801 (2009))

(25) Oct3/4, Sox2, Klf4, L-Myc, Lin28, Glis1

In (1)-(25) above, Oct3/4 may be replaced with another member of the Oct family, for example, Oct1A, Oct6 or the like. Sox2 (or Sox1, Sox3, Sox15, Sox17, Sox18) may be replaced with

another member of the Sox family, for example, Sox7 or the like. Furthermore, in (1) to (25) above, when c-Myc or Lin28 is included as a nuclear reprogramming factor, L-Myc or Lin28B can be used in place of c-Myc or Lin28, respectively.

Any combination that does not fall in (1) to (25) above but comprises all the constituents of any one of (1) to (25) above and further comprises an optionally chosen other substance can also be included in the scope of "nuclear reprogramming substances" in the present invention. Provided that the somatic cell to undergo nuclear reprogramming is endogenously expressing one or more of the constituents of any one of (1) to (25) above at a level sufficient to cause nuclear reprogramming, a combination of only the remaining constituents excluding the one or more constituents can also be included in the scope of "nuclear reprogramming substances" in the present invention.

Of these combinations, a combination of at least one, preferably two or more, more preferably three or more, selected from among Oct3/4, Sox2, Klf4, c-Myc or L-Myc, Nanog, Lin28 or Lin28B, Glis1 and SV40LT, is a preferable nuclear reprogramming substance.

Particularly, when the iPS cells obtained are to be used for therapeutic purposes, a combination of the three factors Oct3/4, Sox2 and Klf4 [combination (9) above] or a combination of the four factors Oct3/4, Sox2, Klf4 and L-Myc [combination (2) above] are preferably used. In addition, Lin28 or Lin28B and/or Glis1 can further be used. When the iPS cells obtained are not to be used for therapeutic purposes (e.g., used as an investigational tool for drug discovery screening and the like), in addition to the three factors consisting of Oct3/4, Sox2 and Klf4 and the four factors consisting of Oct3/4, Sox2,Klf4 and L-Myc, four factors consisting of Oct3/4, Sox2, Klf4 and c-Myc, five to seven factors consisting of Oct3/4, Sox2, Klf4 and c-Myc/L-Myc as well as Nanog and/or Lin28/Lin28b and/or Glis1, or six to eight factors consisting

of the above five to seven factors and additional SV40 Large T antigen are exemplified.

Information on the mouse and human cDNA sequences of the aforementioned nuclear reprogramming substances is available with reference to the NCBI accession numbers mentioned in WO 2007/069666 (in the publication, Nanog is described as ECAT4. Mouse and human cDNA sequence information on Lin28, Lin28b, Esrrb, Esrrg, L-Myc can be acquired by referring to the following NCBI accession numbers, respectively); those skilled in the art are easily able to isolate these cDNAs.

Name of gene	Mouse	Human
Lin28	NM_145833	NM_024674
Lin28b	NM_001031772	NM_001004317
Esrrb	NM_011934	NM_004452
Esrrg	NM_011935	NM_001438
L-Myc	NM_008506	NM_001033081
Glis1	NM_147221	NM_147193

A proteinous factor for use as a nuclear reprogramming substance can be prepared by inserting the cDNA obtained into an appropriate expression vector, introducing the vector into a host cell, and recovering the recombinant proteinous factor from the cultured cell or its conditioned medium. Meanwhile, when the nuclear reprogramming substance used is a nucleic acid that encodes a proteinous factor, the cDNA obtained is inserted into a viral vector, episomal vector, or plasmid vector to construct an expression vector, and the vector is subjected to the step of nuclear reprogramming. As appropriate, the above-mentioned Cre-loxP system or piggyBac transposon system can be utilized. When two or more nucleic acids encoding proteinous factors are introduced into a cell, respective nucleic acids can be carried in separate vectors. Alternatively, a polycistronic vector can be constructed by ligating a plurality of nucleic acids in tandem. In latter, it is preferable that 2A self-cleaving peptide from a foot-and-mouth disease virus (*Science*, *322*, 949-953, 2008) is ligated

between the nucleic acids to allow for an efficient polycistronic expression.

Contact of a nuclear reprogramming substance with a somatic cell can be achieved as with a protein involved in PrS formation (a) when the substance is a proteinous factor; as with the aforementioned nucleic acid that encodes a protein involved in PrS formation (b) when the substance is a nucleic acid that encodes the proteinous factor of (a).

(d) Other iPS cell establishment efficiency improvers

In recent years, various substances that improve the efficiency of establishment of iPS cells, which has traditionally been low, have been proposed one after another. When brought into contact with a somatic cell together with the aforementioned iPS cell establishment efficiency improving factors of the present invention, these other establishment efficiency improvers are expected to further raise the efficiency of establishment of iPS cells.

Examples of other iPS cell establishment efficiency improvers include, but are not limited to, histone deacetylase (HDAC) inhibitors [e.g., valproic acid (VPA) (*Nat. Biotechnol.*, *26*(7): 795-797 (2008)], low-molecular inhibitors such as trichostatin A, sodium butyrate, MC 1293, and M344, nucleic acid-based expression inhibitors such as siRNAs and shRNAs against HDAC (e.g., HDAC1 siRNA Smartpool® (Millipore), HuSH 29mer shRNA Constructs against HDAC1 (OriGene) and the like), and the like], DNA methyltransferase inhibitors (e.g., 5'-azacytidine) [*Nat. Biotechnol.*, *26*(7): 795-797 (2008)], G9a histone methyltransferase inhibitors [e.g., low-molecular inhibitors such as BIX-01294 (*Cell Stem Cell*, *2*: 525-528 (2008)], nucleic acid-based expression inhibitors such as siRNAs and shRNAs against G9a [e.g., G9a siRNA (human) (Santa Cruz Biotechnology) and the like) and the like], L-channel calcium agonists (e.g., Bayk8644) [*Cell Stem Cell*, *3*, 568-574 (2008)], p53 inhibitors [e.g., siRNA, shRNA, dominant negative mutant and the like against p53 (*Cell Stem Cell*, *3*, 475-479

(2008); Nature 460, 1132-1135 (2009))], UTF1 [*Cell Stem Cell, 3*, 475-479 (2008)], Wnt Signaling (e.g., soluble Wnt3a) [*Cell Stem Cell, 3*, 132-135 (2008)], 2i/LIF [2i is an inhibitor of mitogen-activated protein kinase signaling and glycogen synthase kinase-3, *PloS Biology, 6*(10), 2237-2247 (2008)], ES cell-specific miRNA (for example, miR-302-367 cluster (*Mol. Cell. Biol.* doi:10.1128/MCB.00398-08)、miR-302 (*RNA* (2008) 14: 1-10), miR-291-3p, miR-294 and miR-295 (*Nat. Biotechnol. 27*: 459-461 (2009)) and the like. As mentioned above, the nucleic acid-based expression inhibitors may be in the form of expression vectors harboring a DNA that encodes an siRNA or shRNA.

Preferably, a p53 inhibitor such as p53 shRNA, p53 siRNA or dominant negative mutant of p53, or a nucleic acid that encodes the same is used as an additional iPS cell establishment efficiency improver, since a protein involved in PrS formation and p53 inhibitor independently enhance reprogramming each other and they can exert synergetic effects in combination.

Among the constituents of the aforementioned nuclear reprogramming substances, SV40 large T and the like, for example, can also be included in the scope of iPS cell establishment efficiency improvers because they are deemed not essential, but auxiliary, factors for somatic cell nuclear reprogramming. In the situation of the mechanisms for nuclear reprogramming remaining unclear, the auxiliary factors, which are not essential for nuclear reprogramming, may be conveniently considered as nuclear reprogramming substances or iPS cell establishment efficiency improvers. Hence, because the somatic cell nuclear reprogramming process is understood as an overall event resulting from contact of nuclear reprogramming substance(s) and iPS cell establishment efficiency improver(s) with a somatic cell, it seems unnecessary for those skilled in the art to always distinguish between the nuclear reprogramming substance and the iPS cell

establishment efficiency improver.

Contact of an iPS cell establishment efficiency improver with a somatic cell can be achieved as with a protein involved in PrS formation (a) when the improver is a proteinous factor; as with the aforementioned nucleic acid that encodes a protein involved in PrS formation (b) when the improver is a nucleic acid that encodes the proteinous factor of (a).

An iPS cell establishment efficiency improver including a protein involved in PrS formation or a nucleic acid encoding the same may be brought into contact with a somatic cell simultaneously with a nuclear reprogramming substance, or either one may be contacted in advance, as far as the efficiency of establishment of iPS cells from the somatic cell is significantly improved, compared with the absence of the improver. In an embodiment, for example, when the nuclear reprogramming substance is a nucleic acid that encodes a proteinous factor and the iPS cell establishment efficiency improver is a chemical inhibitor, the iPS cell establishment efficiency improver can be added to the medium after the cell is cultured for a given length of time after the gene transfer treatment, because the nuclear reprogramming substance involves a given length of time lag from the gene transfer treatment to the mass-expression of the proteinous factor, whereas the iPS cell establishment efficiency improver is capable of rapidly acting on the cell. In another embodiment, when a nuclear reprogramming substance and an iPS cell establishment efficiency improver are both used in the form of a viral or plasmid vector, for example, both may be simultaneously introduced into the cell.

(e) Improving establishment efficiency by culture conditions

iPS cell establishment efficiency can further be improved by culturing the cells under hypoxic conditions in the nuclear reprogramming process for somatic cells (*Cell Stem Cell*, *5*(3): 237-241 (2009); WO 2010/013845). As mentioned herein, the term "hypoxic conditions" means that the ambient oxygen

concentration as of the time of cell culture is significantly lower than that in the atmosphere. Specifically, conditions involving lower oxygen concentrations than the ambient oxygen concentrations in the 5-10% CO_2/95-90% air atmosphere, which is commonly used for ordinary cell culture, can be mentioned; examples include conditions involving an ambient oxygen concentration of 18% or less. Preferably, the ambient oxygen concentration is 15% or less (e.g., 14% or less, 13% or less, 12% or less, 11% or less and the like), 10% or less (e.g., 9% or less, 8% or less, 7% or less, 6% or less and the like), or 5% or less (e.g., 4% or less, 3% or less, 2% or less and the like). The ambient oxygen concentration is preferably 0.1% or more (e.g., 0.2% or more, 0.3% or more, 0.4% or more and the like), 0.5% or more (e.g., 0.6% or more, 0.7% or more, 0.8% or more, 0.9% or more and the like), or 1% or more (e.g., 1.1% or more, 1.2% or more, 1.3% or more, 1.4% or more and the like).

Although any method of creating a hypoxic state in a cellular environment can be used, the easiest way is to culture cells in a CO_2 incubator permitting adjustments of oxygen concentration, and this represents a suitable case. CO_2 incubators permitting adjustment of oxygen concentration are commercially available from various manufacturers (e.g., CO_2 incubators for hypoxic culture manufactured by Thermo scientific, Ikemoto Scientific Technology, Juji Field, Wakenyaku etc.).

The time of starting cell culture under hypoxic conditions is not particularly limited, as far as iPS cell establishment efficiency is not prevented from being improved compared with the normal oxygen concentration (20%). Although the culture may be started before the somatic cell is contacted with a protein involved in PrS formation or a nucleic acid encoding the same and nuclear reprogramming substance(s), or at the same time as the contact, or after the contact, it is preferable, for example, that the culture under hypoxic conditions be started just after the somatic cell is

contacted with the protein involved in PrS formation or the nucleic acid encoding the same and the nuclear reprogramming substance(s), or at a given time interval after the contact [e.g., 1 to 10 (e.g., 2, 3, 4, 5, 6, 7, 8 or 9) days].

The duration of cultivation of cells under hypoxic conditions is not particularly limited, as far as iPS cell establishment efficiency is not prevented from being improved compared with the normal oxygen concentration (20%); examples include, but are not limited to, periods of 3 days or more, 5 days or more, 7 days or more or 10 days or more, and 50 days or less, 40 days or less, 35 days or less or 30 days or less and the like. Preferred duration of cultivation under hypoxic conditions varies depending on ambient oxygen concentration; those skilled in the art can adjust as appropriate the duration of cultivation according to the oxygen concentration used. In an embodiment of the present invention, if iPS cell candidate colonies are selected with drug resistance as an index, it is preferable that a normal oxygen concentration be restored from hypoxic conditions before starting drug selection.

Furthermore, preferred starting time and preferred duration of cultivation for cell culture under hypoxic conditions also vary depending on the choice of nuclear reprogramming substance used, iPS cell establishment efficiency under normal oxygen concentration conditions and the like.

(f) Selection and confirmation of iPS cell

After being contacted with nuclear reprogramming substance(s) and the iPS cell establishment efficiency improving factors of the present invention (and other iPS cell establishment efficiency improving factors), the cell can be cultured under conditions suitable for the cultivation of, for example, ES cells. In the case of mouse cells, the cultivation is carried out with the addition of Leukemia Inhibitory Factor (LIF) as a differentiation suppressor to an ordinary medium.

Meanwhile, in the case of human cells, it is desirable that basic fibroblast growth factor (bFGF) and/or stem cell factor (SCF) be added in place of LIF. Usually, the cells are cultured in the co-presence of mouse embryo-derived fibroblasts (MEF) treated with radiation or an antibiotic to terminate the cell division thereof, as feeder cells. MEF in common use as feeders include the STO cell and the like; for induction of an iPS cell, the SNL cell [McMahon, A. P. & Bradley, A. Cell 62, 1073-1085 (1990)] and the like are commonly used. Co-culture with these feeder cells may be started before contact of the nuclear reprogramming substance(s) and the iPS cell establishment efficiency improving factors of the present invention, at the time of the contact, or after the contact (e.g., 1-10 days later).

A candidate colony of iPS cells can be selected by a method with drug resistance and reporter activity as indicators, and also by a method based on visual examination of morphology. As an example of the former, a colony positive for drug resistance and/or reporter activity is selected using a recombinant somatic cell wherein a drug resistance gene and/or a reporter gene is targeted to the locus of a gene highly expressed specifically in pluripotent cells (e.g., Fbx15, Nanog, Oct3/4 and the like, preferably Nanog or Oct3/4). Examples of such recombinant somatic cells include MEFs or TTFs from a mouse having the βgeo (which encodes a fusion protein of β-galactosidase and neomycin phosphotransferase) gene knocked-in to the Fbx15 locus [Takahashi & Yamanaka, *Cell, 126,* 663-676 (2006)], MEFs or TTFs from a transgenic mouse having the green fluorescent protein (GFP) gene and the puromycin resistance gene integrated in the Nanog locus [Okita et al., *Nature, 448,* 313-317 (2007)] and the like. Meanwhile, examples of the method of selecting candidate colonies based on visual examination of morphology include the method described by Takahashi et al. in *Cell, 131,* 861-872 (2007). Although the method using reporter cells is convenient and

efficient, it is desirable from the viewpoint of safety that colonies be selected by visual examination when iPS cells are prepared for the purpose of human treatment.

The identity of the cells of a selected colony as iPS cells can be confirmed by positive responses to a Nanog (or Oct3/4) reporter (puromycin resistance, GFP positivity and the like) as well as by the formation of a visible ES cell-like colony, as described above. However, to ensure higher accuracy, it is possible to perform tests such as alkaline phosphatase staining, analyzing the expression of various ES-cell-specific genes, and transplanting the cells selected to a mouse to confirm the formation of teratomas.

When a nucleic acid that encodes a protein involved in PrS formation such as Foxh1 is introduced into a somatic cell, the iPS cell obtained is a novel cell distinct from conventionally known iPS cells because of the containment of the exogenous nucleic acid. In particular, when the exogenous nucleic acid is introduced into the somatic cell using a retrovirus, lentivirus or the like, the exogenous nucleic acid is usually integrated in the genome of the iPS cell obtained, so that the phenotype of containing the exogenous nucleic acid is stably retained.

(g) Use of iPS cell

The iPS cells thus established can be used for various purposes. For example, by utilizing a method of differentiation induction reported with respect to ES cells (for example, see JP 2002-291469 as a method for inducing differentiation into nerve stem cells, JP 2004-121165 as a method for inducing differentiation into pancreatic stem-like cells, JP 2003-505006 as a method for inducing differentiation into hematopoietic cells, JP 2003-523766 as a differentiation induction method via embryonic body formation), differentiation into various cells (e.g., myocardial cells, blood cells, nerve cells, vascular endothelial cells, insulin-secreting cells and the like) from iPS cells can be induced. Therefore, inducing iPS cells using a somatic cell collected from a patient or

another person of the same or substantially the same HLA type would enable stem cell therapy by autogeneic or allogeneic transplantation, wherein the iPS cells are differentiated into desired cells (that is, cells of an affected organ of the patient, cells that have a therapeutic effect on disease, and the like), which are transplanted to the patient. Furthermore, because functional cells (e.g., hepatocytes) differentiated from iPS cells are thought to better reflect the actual state of the functional cells *in vivo* than do corresponding existing cell lines, they can also be suitably used for *in vitro* screening for the effectiveness and toxicity of pharmaceutical candidate compounds and the like.

The present invention is hereinafter described in further detail by means of the following examples, to which, however, the invention is never limited.

Examples

MATERIALS & METHODS

The policy of statistical analyses

All quantitative experiments were conducted at least biological triplicates. We evaluated data by paired t-test by using Kaleida graph software, and P-values less than 0.05 were considered significant indicated as asterisks. Error bars indicate standard deviation.

Cell culture

We obtained HDF from the Japanese Collection of Research Bioresources. HDF, PLAT-E and PLAT-GP were maintained in Dulbecco's modified eagle medium (DMEM, Nacalai tesque) containing 10% fetal bovine serum (FBS, Thermo) and 0.5% penicillin and streptomycin (Pen/Strep, Invitrogen).

H1 and H9 ESCs were obtained from WiCELL, and maintained in Primate ESC medium (ReproCELL) supplemented with 4 ng/ml recombinant human basic fibroblast growth factor (bFGF, Wako) on mitomycin C (MMC) -inactivated SNL feeders, or in mTeSR1

(Veritas) on Matrigel-coated plates(BD biosciences) as described previously. Normal human epidermal keratinocytes (NHEK, Lonza), human astrocytes (HA, Cell applications), normal human bronchial epitheliums (NHBE, Lonza), adipose tissue-derived stem cell (ASC, Invitrogen) and prostate epithelium (PrE, Lonza) were maintained in manufacturer's recommended conditions.

Reprogramming

Reprogramming experiments were performed as described previously (*Cell* **131**, 861-872 (2007)). To generate retroviral particles, we introduced retroviral vectors into PLAT-E or PLAT-GP by using FuGENE 6 transfection reagent (Roche) as manufacturer's protocol. Next day, the medium was replaced with fresh one and incubate them for another 24 hours. The virus-containing supernatant was collected, filtrated through a 0.45 μm pore size cellulose acetate filter (Whatman) and was added 4 μg/ml Polybrene (Nacalai Tesque). Then, we mixed appropriate combination and exposed to HDF carrying mouse *Slc7a1* gene overnight. This point was designated as day 0. For transduction of retroviruses to cell lines except HDF, we performed spinfection at 700 *x g* for an hour with VSVG-pseudotyped pantropic viruses produced by PLAT-GP. We harvested the cells at day 7 post-transduction, and re-plated them onto MMC-inactivated SNL feeders for generation of iPSC. Next day, the medium was replaced with Primate ESC medium supplemented with 4 ng/ml bFGF, and changed every other day.

Gene silencing

For short-term gene silencing, Stealth siRNA for FOXH1 (equal amount mixture of HSS189664, HSS113216 and HSS113217) or Negative control Mid GC (Invitrogen) were transfected into human ESC/iPSC by using Lipofectamine RNAi Max (Invitrogen) according to manufacturer's protocol on day 0 of PrS differentiation protocol. For stable knockdown during

reprogramming, we introduced pMKO.1-puro retroviral vector (#8452, Addgene) encoding shRNA against genes of interest, at the same timing of OSKM transduction. The target sequences of FOXH1 shRNA 1, 3 and 6 are 5′-CACCTCCTACTTGCCTATCTA-3′ (SEQ ID NO:1), 5′-GCCTATCTACACTCCCAATGT-3′ (SEQ ID NO:2) and 5′-TGCAGCCTGTGAGGCTCTTAA-3′ (SEQ ID NO:3), respectively.

Flow cytometry and fluorescence activated cell sorting (FACS)

We harvested the cells at indicated time points by treatment with 0.25% trypsin/1 mM EDTA (Invitrogen) or Accutase (Invitrogen). Fixation and permeabilization were performed before antibody staining with 4% paraformaldehyde and 0.2% TritonX-100, respectively. At least, 5 x 10^4 cells were analyzed for quantification in all experiments by using FACS Aria II (BD biosciences). Cell sorting was also performed by using FACS Aria II. We used following antibodies; Alexa 488-conjugated TRA-1-60 (1:20, 560173, BD biosciences), Alexa 488-conjugated SSEA-4 (1:20, 506348, BD biosciences), fluorescein isothiocyanate (FITC) -conjugated TRA-1-2-49/6E (1:5, FCMAB133, Millipore), allophycocyanin (APC) -labeled TRA-1-85 (1:5, FAB3195A, R&D systems), APC-labeled anti- C-X-C chemokine receptor type 4 (CXCR4) mouse monoclonal antibody (1:5, FAB170A, R&D systems), PE-labeled anti- platelet-derived growth factor receptor alpha (PDGFRA) mouse monoclonal antibody (1:5, 556002, BD Pharmingen), APC-conjugated anti-BRACHYURY (1:5, IC20851A, R&D systems), anti-polysialylated neuronal cell adhesion molecule (PSA-NCAM) antibody (MAB5324, Millipore) and Alexa 647-conjugated anti-mouse IgM antibody (1:500, A-21238, Invitogen).

Magnetic activated cell sorting (MACS)

The harvested cells by using 0.25% Trypsin/1 mM EDTA were passed through a 40 μm pore size cell strainer (BD biosciences) to remove the cell debris. The cells were incubated with PE-conjugated TRA-1-60 (1:5, 560193, BD

Pharmingen) or SSEA-1 (1:5, 560866, BD Pharmingen), and then with anti-PE microbeads (130-048-801, Miltenyibiotec). Cell separation was performed with serial two column mode of AutoMACS (Miltenyibiotec). After separation, we confirmed the purity by flow cytometry.

Plasmid construction

The open reading frames (ORF) of genes used in this study were amplified by PCR, subcloned into pENTR-D-TOPO (Invitrogen) and verified by sequencing. ORF were transferred to expression vectors such as pMXs-gw, pMXs-gw-IG, PB/CAG-gw-IP or PB/CAG-gw-IB by using Gateway LR reaction system (Invitrogen) according to manufacturer's protocol. For generation of cGR-fused construct, stop codon-lacking GLIS1 and FOXH1 were amplified by PCR and cloned into pCR2.1-TOPO (Invitrogen). An EcoRI/SpeI fragment of each gene cloned in pCR2.1 and a SpeI/NotI fragment of pPyCAG-cGR-IP were inserted into the EcoRI/NotI site of pMXs. A knockdown vector for human p53 gene (pMKO.1-puro p53 shRNA2, #10672) was purchased from Addgene.

Quantitative reverse-transcription polymerase chain reaction

Total RNA was purified from cell lysates treated with Qiazol reagent (Qiagen), and incubated with the Turbo DNA free kit (Ambion) to remove genomic DNA. The reverse transcription reaction was performed with 1 μg of DNase-treated RNA by using the Rever tra ace -α- kit (Toyobo) and oligo dT_{20} primer. Primer sequences for each gene are provided in Table 3.

Table 3

SEQ ID NO	Primer	Sequence (5' to 3')	Purpose
4	hOCT3/4-S1165	GAC AGG GGG AGG GGA GGA GCT AGG	qRT-PCR for endogenous OCT3/4
5	hOCT3/4-AS1283	CTT CCC TCC AAC CAG TTG CCC CAA AC	
6	hOCT3/4-S944	CCC CAG GGC CCC ATT TTG GTA CC	qRT-PCR for total OCT3/4
7	hOCT3/4-AS	ACC TCA GTT TGA ATG CAT GGG AGA GC	
8	hSOX2-S1430	GGG AAA TGG GAG GGG TGC AAA AGA GG	qRT-PCR for endogenous SOX2
9	hSOX2-AS1555	TTG CGT GAG TGT GGA TGG GAT TGG TG	
10	hSOX2-S875	TTC ACA TGT CCC AGC ACT ACC AGA	qRT-PCR for total SOX2
11	hSOX2-AS	TCA CAT GTG TGA GAG GGG CAG TGT GC	
12	hNANOG-S1678	TGG CTG CCG TCT CTG GCT ATA GAT	qRT-PCR for NANOG
13	hNANOG-AS1797	AAG CCT CCC AAT CCC AAA CAA TAC	
14	hKLF2-S811	ACT CAC ACC TGC AGC TAC GC	qRT-PCR for KLF2
15	hKLF2-AS951	GTC TGA GCG CGC AAA CTT CC	
16	hKLF4-S1094	CAT GCC AGA GGA GCC CAA GCC AAA GAG GGG	qRT-PCR for KLF4
17	hKLF4-AS1225	CGC AGG TGT GCC TTG AGA TGG GAA CTC TTT	
18	hKLF5-S1344	TCC AAA TTT ACC CAC CAC CCT GCC AG	qRT-PCR for KLF5
19	hKLF5-AS1536	TCC AGT CGC AGC CTT CCC AGG TAC AC	
20	hMYC-S547	GCC GCC GCC TCA GAG TGC ATC GAC	qRT-PCR for c-MYC
21	hMYC-AS947	CGA GTG GAG GGA GGC GCT GCG TAG	
22	hMYCN-S835	GTG GTC ACT GTG GAG AAG CGG CGT TC	qRT-PCR for MYCN
23	hMYCN-AS1047	GAC GTG GGG ACG CCT CGC TCT TTA TC	
24	hMYCL-S581	ACC CCC TGG ATC CCT GCA TGA AGC	qRT-PCR for MYCL1
25	hMYCL-AS724	TCC TCA TCT TCC TTT TCC CCT GCA GC	
26	hLIN28A-S229	AGT AAG CTG CAC ATG GAA GG	qRT-PCR for LIN28A
27	hLIN28A-AS414	CCT GTC TCC TTT TGA TCT GC	
28	hLIN28B-S477	AAA GGC CTT GAG TCA ATA CGG GTA AC	qRT-PCR for LIN28B
29	hLIN28B-AS581	GGC CAC CAC AGT TGT AGC ATC TAT CT	
30	hGDF3-S248	GCT ACG TAA AGG AGC TGG GCG TC	qRT-PCR for GDF3
31	hGDF3-AS372	CCC TTT CTT TGA TGG CAG ACA GG	
32	hLEFTY2-S715	AAC CGC ACC TCC CTC ATC GAC TC	qRT-PCR for LEFTY2
33	hLEFTY2-AS840	GCT CCC TCT GCA CCG ACA CCT GT	
34	hGSC-S721	CAG CTG GCC CGG AAA GTG CAC CTC	qRT-PCR for GSC
35	hGSC-AS855	TTC TCC GGT GAC GCC TTC GAC GAC	
36	hHEX-S623	ATC GAC GCG CTA AAT GGA GGA GAC	qRT-PCR for HEX
37	hHEX-AS757	GGA GGG CGA ACA TTG AGA GCT ATC	
38	hSFRP5-S698	ACC AAG ATC TGC GCC CAG TGT GAG	qRT-PCR for SFRP5
39	hSFRP5-AS806	AAT CAG CTT CCG GTC CCC ATT CTC	
40	hDKK1-S593	CGA GGA GAA ATT GAG GAA ACC ATC	qRT-PCR for DKK1
41	hDKK1-AS707	TGA CCG GAG ACA AAC AGA ACC TTC	
42	hGATA4-S2044	CGG GTG TTG GAT TTT CTC AGA TGC	qRT-PCR for GATA4
43	hGATA4-AS2179	AAA CCC ACG GTC TAG GCC ACA GTG	
44	hTBX6-S771	CTC CTT CCG CTT CCC CGA GAC CAC	qRT-PCR for TBX6
45	hTBX6-AS913	GCC CCG CAG TTT CCT CTT CAC ACG	
46	hHNF3β-qS	GGA GCG GTG AAG ATG GAA	qRT-PCR for HNF3β
47	hHNF3β-qAS	TAC GTG TTC ATG CCG TTC AT	
48	hSox17-S423	CGC TTT CAT GGT GTG GGC TAA GGA CG	qRT-PCR for SOX17
49	hSox17-AS583	TAG TTG GGG TGG TCC TGC ATG TGC TG	
50	hBrachyury-S1807	CAA GGC CCA GGT CCC GAA AGA TGC	qRT-PCR for T
51	hBrachyury-AS1939	GGT GCC GTG TGC TCC TCC ACT GC	
52	hFLK1-qS	TGA TCG GAA ATG ACA CTG GA	qRT-PCR for KDR
53	hFLK1-qAS	CAC GAC TCC ATG TTG GTC AC	
54	hPAX6-S1206	ACC CAT TAT CCA GAT GTG TTT GCC CGA G	qRT-PCR for PAX6
55	hPAX6-AS1497	ATG GTG AAG CTG GGC ATA GGC GGC AG	
56	hMIXL1-S350	CGC GCT CAC CCT GCT CCC CGA GTC	qRT-PCR for MIXL1
57	hMIXL1-AS538	TTG GTT CGG GCA GGC AGT TCA CAT C	
58	hGLIS1-S2434	CAC CTC GCC CAC CTG CTG TCG CTC	qRT-PCR for endogenous GLIS1
59	hGLIS1-AS2604	GTG CGC CCA GCT CAA GCT CGG ATG	
60	hGLIS1-S1421	TGC CCC CAT CCT CTC AGA GCC ATT C	qRT-PCR for total GLIS1
61	hGLIS1-AS1578	CAG CCA TCC GGT AGC AGT CGC CAT AG	
62	G3PDH-S	ACC ACA GTC CAT GCC ATC AC	qRT-PCR for G3PDH
63	G3PDH-AS	TCC ACC ACC CTG TTG CTG TA	
64	hFOXH1-S709	TTG GTG ATT CAG GCC GCT CCC TC	qRT-PCR for FOXH1
65	hFOXH1-AS848	GTC CTT GGG CAC CTT GCG GAA GC	
66	hLHX1-S1957	CGG TCT GCG GAG TTC GTG GTT GT	qRT-PCR for LHX1
67	hLHX1-AS2139	GAC AGC CAG TGC GCG GAT CCC AG	
68	hCER1-S553	GGA CAG TGC CCT TCA GCC AGA CTA	qRT-PCR for CER1
69	hCER1-AS659	TGG CAG GCA AAC AGT GAG AGC AGG	
70	hFOXF1-S1230	ACC CTG GAC CGG CAC AAG AAA CTG	qRT-PCR for FOXF1
71	hFOXF1-AS1338	GCC AAC CGC AGC GCT GTG TCT TTG	

Table 3 (continued)

SEQ ID NO	Primer	Sequence (5' to 3')	Purpose
72	hID3-S871	ACT TCG CCC TGC CCA CTT GAC TTC	qRT-PCR for ID3
73	hID3-AS1045	CAG CCA CTC CTT CCA CAC CTC CAC	
74	hEVX1-S1049	CCG CCT TCA CCC GAG AGC AGA TTG	qRT-PCR for EVX1
75	hEVX1-AS1179	TTG TCC TTC ATG CGC CGG TTC TGG	
76	hBMP4-S678	TAC CGG CTT CAG TCT GGG GAG GAG	qRT-PCR for BMP4
77	hBMP4-AS798	TTC ACT GGT CCC TGG GAT GTT CTC	
78	hOCT3-CR1-F1	TTT TTT GGA TGG GTG GAG GAG A	Methylome of OCT3/4 CR1
79	hOCT3-CR1-R1 (Biotinated)	CAC CAT TAC CAC CAC CAT TAA AC	
80	hOCT3-CR1-S1	ATG GGT GGA GGA GAG	
81	hOCT3-CR2-F1	GGG TGT GGA GAA AAA ATA TTT GAT TTT AGG	Methylome of OCT3/4 CR2
82	hOCT3-CR2-R1 (Biotinated)	CCA AAC CCA TTC AAA AAT TAA ACA CTT A	
83	hOCT3-CR2-S1	GGG GGT AGG ATA ATG	
84	hNANOG-CR1-F1	TTT GTA TTA TAA TGG TTT TGG TGA GAT TG	Methylome of NANOG CR1
85	hNANOG-CR1-R1 (Biotinated)	CCT ACT AAC CCA CCC TTA TAA ATT	
86	hNANOG-CR1-S1	GTT TTG GTG AGA TTG G	
87	h-OCT3/4-DMR pyro-F1	GTG GGA TTG GGG AGG GAG A	Methylome of OCT3/4 5' UTR
88	h-OCT3/4-DMR pyro-R1 (Biotinated)	CCC CTA ACC CAT CAC CTC C	
89	h-OCT3/4-DMR pyro-S1	GTA AGT TTT TAT TTT ATT AGG TTT	
90	hGLIS1 ChIP S1	ACA CAG AAC GTT GCA GGA GGG TAT C	ChIP-PCR for GLIS1 locus
91	hGLIS1 ChIP AS1	AAA TGC CTG CTG AGT GTT ATT GCT G	
92	hGLIS1 ChIP S2	AGG GCC TGA GAC AGA ACA GCA CTG G	
93	hGLIS1 ChIP AS2	GAC TTC ACC ACC TAC CGT GCA CCA G	
94	hGLIS1 ChIP S3	TTG AGT AAT TTC TGG TGC GAG GCT G	
95	hGLIS1 ChIP AS3	GCT TTA TGG TGG TGT GCG TGT GTG C	

Microarray and gene ontology analyses

Fifty-nanograms of total RNA was labeled with Cyanine 3-CTP and used for hybridization with SurePrint G3 Human GE 8x60K (G4112F, Agilent technologies) or SurePrint G3 Mouse GE 8x60K (G4852A) with the one color protocol. The arrays were scanned with a Microarray Scanner System (G2565BA, Agilent technologies), and extracted signals were analyzed by using GeneSpring version11 software (Agilent technologies). Gene expression values were normalized by the 75% percentile shifts. The component 1 and 2 genes in Fig. 2c, d and e were narrowed down by cutting off as the rate of contribution was less than -0.6. Microarray datasets, GSE28024, was downloaded from Gene Expression Omnibus (GEO) in National Institute for biotechnology *Information (NCBI) website. Gene ontology* analyses were performed by using EASE program on DAVID bioinformatics database website (http://david.abcc.ncifcrf.gov/home.jsp).

Embryoid body formation

Small clamps of human ESC/iPSC transferred to low-binding

plate (Nunc) in DMEM/F12 containing 20% KSR, 1% Glutamax, 1% NEAA, 100 nM 2-ME, and 0.5% Pen/Strep. The medium was changed every other day. After 8-days floating culture, aggregates were transferred onto gelatinized plates and cultured for another 8 days. The medium was changed every other day.

Primitive streak differentiation

Differentiation of human ESC/iPSC into primitive streak was performed as described previously (*Nat Biotechnol* **28**, 1187-1194, doi:nbt.1683 [pii]). In brief, the single cell suspension of human ESC/iPSC were plated onto fibronectin-coated plate (BD biosciences) in DMEM/F12 supplemented with 1% Insulin-Transferrin-Selenite (ITS, Invitrogen), 1% Glutamax, 1% NEAA, 2% B27 (Invitrogen), 100 nM 2-ME, and 0.5% Pen/Strep. We added 3 μM CHIR99021 (Stemgent) and 50 ng/ml Activin A for day 1, 3 μM CHIR99021, 25 ng/ml Activin A and 20 ng/ml bFGF for day 2, 3 μM CHIR99021, 10 ng/ml Activin A, 20 ng/ml bFGF and 40 ng/ml BMP4 (R&D systems) for day 3.

Endoderm differentiation

Endoderm differentiation was performed as described previously with slight modification (*Proc Natl Acad Sci U S A* **109**, 12538-12543, doi:10.1073/pnas.1209979109 (2012)). The single cell suspension of human pluripotent stem cells were plated onto Matrigel-coated plate in RPMI1640 (Invitrogen) containing 2% B27, 100 ng/ml Activin A, 3 μM CHIR99021 and 0.5% Pen/Strep. We added 0.5 mM sodium butyrate (Sigma) for day 1 to 3, and then carried out sodium butyrate-free culture to day 7.

Mesoderm differentiation

The single cell suspension of human pluripotent stem cells were plated onto Collagen I-coated plate (BD biosciences) in DMEM/F12 containing 2% B27, 100 ng/ml Activin A, 3 μM CHIR99021 and 0.5% Pen/Strep. Forty eight hours later,

the medium was replaced with DMEM/F12 supplemented with 2% B27, 25 ng/ml BMP4, and 0.5% Pen/Strep. The medium was changed every other day to day 8.

Neural differentiation

Neural differentiation protocol with dual SMAD inhibition was according to previous report (*Nat Biotechnol* **27**, 275-280 (2009); *J Neurosci Res* **89**(2), 117-126. doi: 10.1002/jnr.22547. Epub 2010 Dec 8). The single cell suspension of pluripotent stem cells were transferred to Lipidure-coated low binding 96-well plate (NOF corporation) in DMEM/F12 containing 5% KSR, 1% NEAA, 1% Glutamax, 100 nM 2-ME, 2 μM Dorsomorphin (Stemgent) and 10 μM SB431542 (Stemgent). The medium was changed at day 5, 8 and 11. Differentiation period was 14 days.

Immunocytochemistry

The cells were fixed with 4% paraformaldehyde and permeabilized with PBS containing 5% goat or donkey normal serum (Chemicon), 1% bovine serum albumin (BSA; Nacalai Tesque) and 0.2% TritonX-100 (Nacalai Tesque). Samples were incubated with primary antibodies for SOX17 (1:200, AF1924, R&D systems), α-smooth muscle actin (1:600, M085101, DAKO) and NESTIN (1:1000, ab5968, Abcam) which were diluted in staining solution (PBS containing 1% BSA) at 4°C overnight. After washing with PBS, samples were exposed to staining solution containing fluorescence-conjugated secondary antibodies such as Alexa488-conjugated anti-goat IgG (1:500, A-11055, Invitrogen), Alexa 546-conjugated anti-mouse IgG (1:500, A-11030, Invitrogen) or Alexa 488-conjugated anti-rabbit IgG (1:500, A-11034, Invitrogen), and Hoechst 33342 (1 μg/ml, H3570, Invitrogen). Images were obtained by using BZ9000 (KEYENCE).

Pyro-sequencing

Five-hundred micrograms of purified genomic DNA was used

for bisulfite CT conversion with EZ DNA methylation kit (Zymo research) according to manufacturer's recommendation. Resultant DNA samples were used for PCR with biotinated primers as templates, and amplified products were analyzed by Pyromark (Qiagen). Primer sequences were provided in Table 3.

Teratoma formation and histological analyses

Approximately 3 x 10^5 harvested cells suspended in DMEM/F12 containing 10 μM Y-27632 were injected into testes of severe combined immunodeficiency mice (6 weeks old) by using a Hamilton syringe. After 8 to 10 weeks, tumors were dissected and fixed with 4% paraformaldehyde and 70% ethanol in sequence. Paraffin-embedded sections were stained with hematoxylin and eosin. Images were obtained by using BZ9000.

RESULTS

Nascent reprogrammed cells are similar to PrS in gene expression

Large numbers of non-reprogrammed cells during induction of induced pluripotent stem cell (iPSC) inhibit accurate analyses of the reprogramming process. To overcome this issue, we used a pluripotent cell-specific surface antigen, TRA-1-60 to capture nascent reprogrammed cells (Fig. 1a). TRA-1-60 positive (+) cells initially appeared in human dermal fibroblast (HDF) culture at day 4 post-transduction of OSKM (Fig. 1b). We confirmed that most of induced pluripotent stem cell (iPSC) colonies were derived from TRA-1-60 (+) cells purified by magnetic activated cell sorting 7 days after transduction (Fig. 1d). The ability of TRA-1-60 (+) cells to form iPSC colonies also gradually increased and reached to an efficiency similar to ESCs/iPSCs on day 20 or 28 (Fig. 1c). In TRA-1-60 (+) cells, pluripotent stem cell markers such as NANOG progressively increased (Fig. 1e) and OSKM transgenes were silenced.

We examined the global and time-course gene expression

patterns of purified TRA-1-60 (+) cells with DNA microarrays. We predicted that most genes in TRA-1-60 (+) cells would show expression patterns somehow between HDFs and established iPSCs. Preliminary principle component analysis (PCA) identified component 1 characterized with gradual increases in ESC/iPSC-enriched genes and decreases in fibroblast-enriched genes, as expected (Fig. 2a). However, component 2 revealed substantial numbers of genes that showed transient fluctuation during iPSC generation, suggesting that the route from fibroblasts to iPSCs was not simple or straightforward (Fig. 2a). Gene ontology analyses showed that genes included in component 2 were mainly classified in processes related to "development" (Fig. 2b, lower panel). We compared gene expression of TRA-1-60 (+) cells with three germ lineages, including mesoderm (ME), endoderm (EN), and neuroectoderm (NE), as well as PrS, which were all differentiated from ESC/iPSC (Fig. 2c). PCA analyses showed that nascent reprogrammed cells are most similar to PrS in gene expression (Fig. 2d).

Further PCA analyses revealed that the expression levels of significant number of genes in TRA-1-60 (+) cells were not intermediate between HDFs and iPSCs, but were transiently activated or suppressed during iPSC generation (Fig. 2e). Gene ontology analyses demonstrated that transiently-downregulated genes were mainly categolized as metabolic terms (Fig. 2f, upper panel). On the other hand, transiently-activated genes were associated with terms related to development (Fig. 2f, lower panel). The hierarchical clustering suggested that the fate of TRA-1-60 (+) cells in the first-half of reprogramming (d3-15) verged to those of epithelial cells including epidermis (EDM) (green box in Fig. 2g). Actually, in this stage, some EDM-associated genes were transiently increased, although the correlation coefficient between EDM and nascent reprogrammed cells on day 3-15 were 0.9082-0.9105. Furthermore, the drastic suppression of mesenchymal genes and activation of epithelial genes were observed (Fig. 2h). These data suggest

that epitheliarization is one of dominant events in TRA-1-60 (+) intermediate cells in fisrt-half of reprogramming.

Nascent human reprogrammed cells transiently acquire a PrS-like state

We found that TRA-1-60 (+) cells in the last-half of reprogramming (d20-49) were involved in the cluster with not only ESCs/iPSCs but also differentiated lineages such as mesoderm (ME), endoderm (EN) and primitive streak (PrS) which have early mesendodermal features (red box in Fig. 2g). The PCA and the hierarchical clustering for the comparison of TRA-1-60 (+) cells with differentiated lineages including EDM and PrS showed that the route of reprogramming made a close passage to PrS in the last-half of reprogramming (Fig. 3a).

We then checked the expression levels of marker genes for various developmental lineages. Marker genes for PrS such as BRACHYURY (T), GDF3, LEFTY2, MIXL1, LHX1, and NODAL showed a transient activation during iPSC generation in TRA-1-60 (+) cells (Fig. 3c). Approximately 40% of PrS-enriched genes were included in transiently-upregulated genes in TRA-1-60 (+) cells (Fig. 3b). Genes such as *GDF3, LEFTY2, NODAL, HAND1, WNT3* and *NOG* were induced at as early as day 3 (Fig. 4a). On the other hand, genes such as *T, FOXA2, EOMES, LHX1, SOX17* and *MIXL1* rose up at relative late stages at day 15 or later (Fig. 4b). In contrast, marker genes for other lineages, including pluripotent stem cell, ME, EN and neuroectoderm (NE), did not show such transient changes.

The PCA and hierarchical clustering revealed that TRA-1-60 (+) cells on day 20 post-transduction were more similar but not identical to PrS than to NE, EN, ME or ESC/iPSC (Fig. 3a). The correlation coefficient of global gene expression between TRA-1-60 (+) cells on day 20 and PrS was 0.9718 which was quite similar level to the clonal variation of ESCs/iPSCs (0.9634-0.9862). The occupancy of tri-methylated lysine 4 of histone H3 (H3K4me3), which is a mark of activated promoter,

also transiently increased in PrS-related gene loci during reprogramming (Fig. 3d). Single cell qRT-PCR and immunocytochemistry revealed that vertically all of TRA-1-60 (+) cells on day 20 but not HDFs and ESCs expressed T (Fig. 3e and 3f). These data suggest that TRA-1-60 (+) cells in late stage of reprogramming possess gene expression profiles partially resembling PrS. TRA-1-60 (+) cells derived from adipose-derived stem cells (ASC), as well as non-mesodermal lineages such as astrocytes (HA, ectoderm), bronchial epithelium (NHBE, endoderm), and prostate epithelial cells (PrEC, endoderm), also showed similarities in global gene expression with PrS (Fig. 3g and 4c).

GLIS1 has a PrS induction activity

Another set of evidence connecting reprogramming and PrS arose from GLIS1, which we recently reported as a maternal transcription factor enhancing iPSC generation. We found, in this study, GLIS1 is also expressed in a proximal region of epiblast at embryonic day (E) 5.5 and in mesoderm, extraembryonic ectoderm, and PrS including node at E6.5 (Fig. 5a). We also found high expressions of GLIS1 in PrS and mesoendoderm derived from human ESC/iPSC (Fig. 5b). In contrast, Glis1 is barely expressed in undifferentiated human pluripotent stem cells.

To further examine functions of GLIS1, we introduced an expression vector of GLIS1 into human ESC. We found that forced-expression of GLIS1 in human ESC resulted in morphological changes characterized with looser cell-cell interactions and a slower proliferation rate (Fig. 5c). In consistent with our previous report, GLIS1 enhanced expression of pluripotency-related genes, including OCT3/4, NANOG, LIN28A and c-MYC (Fig. 5d). On the other hand, GLIS1 markedly increased expression of PrS-related genes, such as T, GSC, FOXH1, and NODAL (Fig. 5e). Global gene expression analyses with microarray revealed that GLIS1 significantly activated

the expression of mesoderm- and PrS-related genes (106 out of 196 genes, $P < 0.05$) (Fig. 5f). Furthermore, GLIS1 markedly enhanced PrS differentiation potentials of human ESC, whereas reduced neural differentiation (Fig. 5g). These data suggest that the reprogramming enhancer GLIS1 also has a PrS induction activity.

FOXH1 markedly enhances human iPSC generation

Our findings led us to hypothesize that genes that play important roles in PrS formation during development may facilitate iPSC generation. We initially focused on FOXH1, since knockout mouse experiments have shown that the transcription factor is essential for PrS formation. We confirmed that suppression of FOXH1 prevented the differentiation of human ESC/iPSC into PrS (Fig. 6a).

Next, we selected 23 transcription factors that were highly expressed in mesendoderm and transduced each of them together with OSKM into HDFs (Fig. 6b). We found that five factors, including FOXA2, FOXF1, FOXH1, LHX1, and T, significantly increased the numbers of iPSC colonies. Among them, FOXH1 showed the strongest effect (Fig. 6b). FOXH1 functions as a downstream target of the Nodal signal and is required for the specification of anterior PrS.

On studying in more detail the effect of markedly increasing the number of iPSC colonies by transduction of *FOXH1* along with OSKM (OSKMF), its effect was stronger than short-hairpin RNA mediated depletion of p53 (p53 shRNA) and Glis1, two of the strongest known enhancers of reprogramming (Fig. 6c). FOXH1 and p53 shRNA showed synergistic effects, suggesting that FOXH1 enhances reprogramming independently of p53 activities. We confirmed that human iPSC generated with FOXH1 were indistinguishable from those with OSKM alone (Fig. 7). Taken together, these data suggest that FOXH1 has a strong activity to enhance human iPSC generation.

During human iPSC generation, endogenous FOXH1 increased

in late stages (Fig. 6d). Stage-specific activation of FOXH1 demonstrated that FOXH1 clearly facilitated reprogramming efficiency in late stages (Fig.6e and 6g). These results are in contrast to those using GLIS1, which facilitated reprogramming in the earlier stages and increased the proportion of TRA-1-60 (+) cells (Fig. 6f and 6g). This may suggest that GLIS1 promotes induction of a PrS-like state whereas FOXH1 promotes its maturation. Actually, the proportion of TRA-1-60 (+) cells were reproducibly reduced by FOXH1 on day 7 but turned back on day 11 and 15 compared to OSKM with GLIS1 (Fig. 6g). In addition, FOXH1 did not increase the proportion of TRA-1-60 (+) cells at day 7 (Fig. 6h). We found that FOXH1 promoted the downregulation of a fibroblast marker, CD13, and the upregulation of an epithelial marker, EpCAM in TRA-1-60 (+) cells on day 11 and 15 (Fig. 6i). In addition, the expression of late reprogramming markers such as DPPA4, DNMT3B, LIN28A, ZFP42 and endogenous SOX2 were significantly enhanced by FOXH1 action (Fig. 6j). These results further support our hypothesis that GLIS1 promotes induction of a PrS-like state whereas FOXH1 promotes its maturation.

Next, we again examined whether the endogenous FOXH1 is required for human iPSC generation and PrS differentiation in more detail. Knockdown of FOXH1 in ESC significantly interfered the differentiation into PrS (Fig. 6k). The expression of endogenous FOXH1 was ever-increased in TRA-1-60 (+) cells during reprogramming toward iPSC (Fig. 6d). Three out of six shRNAs (#1, 3 and 6) suppressed the expression of endogenous FOXH1 in ESC or OSKM-transduced HDF with ~90%, 70% and 50% efficiencies, respectively (Fig. 6l). When co-introduced with OSKM, shRNA #1 nearly abolished the generation of iPSC colonies (Fig. 6l). In addition, shRNA #3 decreased iPSC colony formation by 50%. In contrast, the suppression of FOXH1 did not ameliorate proliferation of transduced HDFs (Fig. 6m). These data suggest that FOXH1 plays an important role in

the reprogramming process toward iPSCs.

A Fox family member enhances human iPSC generation

Finally, we examined the effects of other FOX family transcription factors on human iPSC generation. We found that 5 factors such as FOXA2, FOXB1, FOXF1 (same as FOXF2), FOXG1, and FOXH1 out of selected 36 FOX genes significantly increased numbers of iPSC colonies (Fig. 8). As similar to SOX, KLF and MYC families, some of FOX family transcription factors have overlapping effects on human iPSC generation (Fig. 9).

In summary, our analyses of purified nascent reprogrammed cells revealed that the route to induced pluripotency in human goes through a PrS-like state. This led us to demonstrate that FOXH1, one of the key factors for PrS identify, markedly enhances human iPSC generation.

While the present invention has been described with emphasis on preferred embodiments, it is obvious to those skilled in the art that the preferred embodiments can be modified. The present invention intends that the present invention can be embodied by methods other than those described in detail in the present specification. Accordingly, the present invention encompasses all modifications encompassed in the gist and scope of the appended "CLAIMS."

The contents disclosed in any publication cited herein, including patents and patent applications, are hereby incorporated in their entireties by reference, to the extent that they have been disclosed herein.

This application is based on US provisional patent application No. 61/717,250 filed on October 23, 2012, the contents of which are incorporated in full herein.

CLAIMS

[1] A method of improving iPS cell establishment efficiency, comprising contacting a protein involved in primitive streak (PrS) formation or a nucleic acid that encodes the same with a somatic cell in a nuclear reprogramming step.

[2] The method according to claim 1, wherein the protein is selected from the group consisting of Foxh1, brachyury, goosecoid, Foxa2, eomesodermin, LHX1, Sox17, MIXL1, Lefty2, Nodal1, Hand1, Wnt3, noggin, CER1, Foxf1, GATA4, GATA6, GSC, HESX1, HNF1A, HNF4A, OTX2, RNF111, Sox7, SP5, TBX6, Foxb1, Foxf2 and Foxg1.

[3] The method according to claim 1, wherein the protein is selected from the group consisting of Foxh1, brachyury, Foxa2, LHX1, Foxf1, Foxb1, Foxf2 and Foxg1.

[4] The method according to claim 1, wherein the protein is Foxh1.

[5] The method according to any one of claims 1 to 4, wherein the somatic cell is further contacted with Glis1 or a nucleic acid that encodes the same and/or a p53 inhibitor in a nuclear reprogramming step.

[6] An agent for improving iPS cell establishment efficiency comprising a protein involved in primitive streak (PrS) formation or a nucleic acid that encodes the same.

[7] The agent according to claim 6, wherein the protein is selected from the group consisting of Foxh1, brachyury, goosecoid, Foxa2, eomesodermin, LHX1, Sox17, MIXL1, GDF3, Lefty2, Nodal, Hand1, Wnt3, noggin, CER1, Foxf1, GATA4, GATA6, HESX1, HNF1A, HNF4A, OTX2, RNF111, Sox7, SP5, TBX6, Foxb1, Foxf2 and Foxg1.

[8] The agent according to claim 6, wherein the protein is selected from the group consisting of Foxh1, brachyury, Foxa2, LHX1, Foxf1, Foxb1, Foxf2 and Foxg1.

[9] The agent according to claim 6, wherein the protein is Foxh1.

[10] The agent according to any one of claims 6 to 9, further

comprising Glis1 or a nucleic acid that encodes the same and/or a p53 inhibitor.

[11] A method of producing an iPS cell, comprising contacting a protein involved in primitive streak (PrS) formation or a nucleic acid that encodes the same, and nuclear reprogramming substance(s) with a somatic cell.

[12] The method according to claim 11, wherein the nuclear reprogramming substance(s) is(are) selected from the group consisting of members of the Oct family, members of the Sox family, members of the Klf family, members of the Myc family, members of the Lin family and the Nanog, as well as nucleic acids that encode the same.

[13] The method according to claim 11, wherein the nuclear reprogramming substances are Oct3/4, Sox2 and Klf4, or nucleic acids that encode the same.

[14] The method according to claim 11, wherein the nuclear reprogramming substances are Oct3/4, Sox2, Klf4 and L-Myc or c-Myc, or nucleic acids that encode the same.

[15] The method according to any one of claims 11 to 14, wherein the protein involved in primitive streak (PrS) formation is selected from the group consisting of a Fox family member, brachyury, goosecoid, eomesodermin, LHX1, Sox17, MIXL1, Lefty2, Nodal1, Hand1, Wnt3, noggin, CER1, GATA4, GATA6, GSC, HESX1, HNF1A, HNF4A, OTX2, RNF111, Sox7, SP5 and TBX6.

[16] The method according to claim 15, wherein the Fox family member is selected from the group consisting of Foxa1, Foxa2, Foxa3, Foxb1, Foxc1, Foxc2, Foxd1, Foxd3, Foxd5, Foxe3, Foxf1, Foxf2, Foxg1, Foxh1, Foxi1, Foxi2, Foxj1, Foxj2, Foxj3, Foxk1, Foxk2, Foxl2, Foxm1, Foxn1, Foxan2, Foxn3, Foxn4, Foxo3, Foxo4, Foxp1, Foxp3, Foxp4, Foxr1, Foxr2 and Foxs1.

[17] The method according to any one of claims 11 to 14, wherein the protein is selected from the group consisting of Foxh1, brachyury, Foxa2, LHX1, Foxf1, Foxb1, Foxf2 and Foxg1.

[18] The method according to any one of claims 11 to 14, wherein the protein involved in primitive streak (PrS) formation is

Foxh1.

[19] The method according to any one of claims 11 to 18, wherein the somatic cell is further contacted with Glis1 or a nucleic acid that encodes the same and/or a p53 inhibitor.

[20] An agent for inducing an iPS cell from a somatic cell, comprising a protein involved in primitive streak (PrS) formation or a nucleic acid that encodes the same, and nuclear reprogramming substance(s).

[21] The agent according to claim 20, wherein the nuclear reprogramming substance(s) is(are) selected from the group consisting of members of the Oct family, members of the Sox family, members of the Klf family, members of the Myc family, members of the Lin family and the Nanog, as well as nucleic acids that encode the same.

[22] The agent according to claim 20, wherein the nuclear reprogramming substances are Oct3/4, Sox2 and Klf4, or nucleic acids that encode the same.

[23] The agent according to claim 20, wherein the nuclear reprogramming substances are Oct3/4, Sox2, Klf4 and L-Myc or c-Myc, or nucleic acids that encode the same.

[24] The agent of any one of claims 20 to 23, wherein the protein involved in primitive streak (PrS) formation is selected from the group consisting of a Fox family member, brachyury, goosecoid, eomesodermin, LHX1, Sox17, MIXL1, GDF3, Lefty2, Nodal1, Hand1, Wnt3, noggin, CER1, GATA4, GATA6, GSC, HESX1, HNF1A, HNF4A, OTX2, RNF111, Sox7, SP5 and TBX6.

[25] The method according to claim 24, wherein the Fox family member is selected from the group consisting of Foxa1, Foxa2, Foxa3, Foxb1, Foxc1, Foxc2, Foxd1, Foxd3, Foxd5, Foxe3, Foxf1, Foxf2, Foxg1, Foxh1, Foxi1, Foxi2, Foxj1, Foxj2, Foxj3, Foxk1, Foxk2, Foxl2, Foxm1, Foxn1, Foxan2, Foxn3, Foxn4, Foxo3, Foxo4, Foxp1, Foxp3, Foxp4, Foxr1, Foxr2 and Foxs1.

[26] The agent according to any one of claims 20 to 23, wherein the protein is selected from the group consisting of Foxh1, brachyury, Foxa2, LHX1, Foxf1, Foxb1, Foxf2 and Foxg1.

[27] The agent of any one of claims 20 to 23, wherein the protein involved in primitive streak (PrS) formation is Foxh1.

[28] The agent of any one of claims 20 to 27, further comprising Glis1 or a nucleic acid that encodes the same and/or a p53 inhibitor.

[29] An iPS cell containing an exogenous nucleic acid that encodes Foxh1.

[30] The iPS cell according to claim 29, wherein the exogenous nucleic acid is integrated in the genome.

[31] A method of producing a somatic cell, comprising performing a differentiation induction treatment on the iPS cell according to claim 29 or 30 to cause the iPS cell to differentiate into a somatic cell.

[32] A method of producing a somatic cell, comprising the steps of:

(1) producing an iPS cell by the method according to any one of claims 11 to 19, and

(2) performing a differentiation induction treatment on the iPS cell obtained through the step (1) to cause the iPS cell to differentiate into a somatic cell.

[33] A use of a protein involved in primitive streak (PrS) formation or a nucleic acid that encodes the same for improving the efficiency of establishment of iPS cells.

[34] The use according to claim 33, wherein the protein is selected from the group consisting of Foxh1, brachyury, goosecoid, Foxa2, eomesodermin, LHX1, Sox17, MIXL1, Lefty2, Nodal, Hand1, Wnt3, noggin, CER1, GATA4, GATA6, GSC, HESX1, HNF1A, HNF4A, OTX2, RNF111, Sox7, SP5 and TBX6, Foxb1, Foxf2 and Foxg1.

[35] The use according to claim 33, wherein the protein is selected from the group consisting of Foxh1, brachyury, Foxa2, LHX1, Foxf1, Foxb1, Foxf2 and Foxg1.

[36] The use according to claim 33, wherein the protein is Foxh1.

[37] A use of a protein involved in primitive streak (PrS)

formation or a nucleic acid that encodes the same in combination with nuclear reprogramming substance(s) for producing an iPS cell.

[38] The use according to claim 37, wherein the nuclear reprogramming substance(s) is(are) selected from the group consisting of members of the Oct family, members of the Sox family, members of the Klf family, members of the Myc family, members of the Lin28 family, and the Nanog, as well as nucleic acids that encode the same.

[39] The use according to claim 37, wherein the nuclear reprogramming substances are Oct3/4, Sox2 and Klf4, or nucleic acids that encode the same.

[40] The use according to claim 37, wherein the nuclear reprogramming substances are Oct3/4, Sox2, Klf4 and L-Myc or c-Myc, or nucleic acids that encode the same.

[41] The use according to any one of claims 37 to 40, wherein the protein involved in primitive streak (PrS) formation is selected from the group consisting of a Fox family member, brachyury, goosecoid, eomesodermin, LHX1, Sox17, MIXL1, Lefty2, Nodal, Hand1, Wnt3, noggin, CER1, GATA4, GATA6, GSC, HESX1, HNF1A, HNF4A, OTX2, RNF111, Sox7, SP5 and TBX6.

[42] The method according to claim 41, wherein the Fox family member is selected from the group consisting of Foxa1, Foxa2, Foxa3, Foxb1, Foxc1, Foxc2, Foxd1, Foxd3, Foxd5, Foxe3, Foxf1, Foxf2, Foxg1, Foxh1, Foxi1, Foxi2, Foxj1, Foxj2, Foxj3, Foxk1, Foxk2, Foxl2, Foxm1, Foxn1, Foxan2, Foxn3, Foxn4, Foxo3, Foxo4, Foxp1, Foxp3, Foxp4, Foxr1, Foxr2 and Foxs1.

[43] The use according to any one of claims 37 to 40, wherein the protein is selected from the group consisting of Foxh1, brachyury, Foxa2, LHX1, Foxf1, Foxb1, Foxf2 and Foxg1.

[44] The use according to any one of claims 37 to 40, wherein the protein is Foxh1.

[45] A use of the iPS cell according to claim 29 or 30 in producing a somatic cell.

[46] The iPS cell according to claim 29 or 30 as a source of

cells for producing a somatic cell.