Supplementary Information

Differentiation potential of Pluripotent Stem Cells correlates to the level of CHD7

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Figure S1. Gene expression of a subset of genes in ESC in the undifferentiated state and in EBs determined by qRT-PCR.

The expression of 96 genes in KhES-1 categorized as Self-renewal, Ectoderm-. Mesoderm-, Mesendoderm- or Endoderm-lineage before or after EB formation were determined by the qRT-PCR scorecard panel. Notably, genes related to self-renewal were not downregulated nor were those related to differentiation lineagesupregulated in EBs generated from KhES-1 cultured with RFF2. undiff Es8: undifferentiated KhES-1 culture with Es8. EBs Es8: EBs from KhES-1 cultured with Es8. undiff RFF2: undifferentiated KhES-1 cultured with RFF2. EBs RFF2: EBs from KhES-1 cultured with RFF2. undiff Es8 2nd: undifferentiated KhES-1 culture with Es8 again after transferred from RFF2 medium. EBs Es8 2nd: EBs from KhES-1 cultured with Es8 again after transferred from RFF2 medium.



Figure S2. The differentiation potential of iPSCs was altered by culture conditions The potential for EB formation by iPSCs can be altered reversibly by the culture conditions. iPSCs (PFX#9) in single-cell suspensions were seeded on VNT-N-coated dishes and cultured with Es8 medium (left, upper photograph) for 5 passages. The cells were then collected for EB formation assays (left, lower photograph) or transferred to Repro FF2 medium (RFF2, middle upper photograph). PFX#9 cells were cultured for 5 passages and collected for EB formation assays (middle, lower photo) or transferred to Es8 medium again (right upper photograph). PFX#9 cells were cultured for 5 passages, followed by EB formation assays (right, lower photograph). Photographs of PFX#9 cultures with Es8 or RFF2 (upper panels) at day 1 of culture and EBs on day 14 in EB formation assays (lower panels). Gene expression profiles in cells in the indicated culture conditions were determined using a qRT-PCR scorecard panel and appended below the relevant photograph. Scale bar: 1.0 mm.



Figure S3. Culture condition alters the differentiation potential of ESC. KhES-1 cells cultured on feeder were transferred to vitronectin-N (VNT-N)-coated dish in cell clumps and cultured for 5 passages for adaptation. The differentiation potential of cells was verified by EB formation assay. A: photos of KhES-1 cells in clumps before EB formation assay and its gene expression profile determined by qRT-PCR scorecard panel are appended in the right (Upper panels). Photos of Day 14-EBs and its genetic profile by scorecard panel (left panels). B. Expression of *CHD7* determined by qRT-PCR in designated culture conditions while maintained in the undifferentiated state (n=3 analytical replicates).



promoter RFF2 >0.2 and RFF2/S-P &Es8 \geq 1.5 \rightarrow 208 genes



Maintain potential for EB formation

С

35 genes

self-renewal	alf-renewal			
GENE_SYMBOL	RFF2	S-P&Es8	Ratio	
KLF4	0.02	0.02	1.02	
KLF2	0.21	0.19	1.12	
TFCP2L1	0.06	0.06	0.97	
SOX2	0.02	0.02	0.94	
EP300(p300)	0.04	0.04	0.85	
ZFP42(REX1)	0.03	0.07	0.43	
NANOG	0.36	0.23	1.58	
POU5F1	0.26	0.36	0.71	
HESX1	0.64	0.59	1.08	
LCK	0.73	0.69	1.07	
DNMT3B	0.69	0.71	0.97	
TRIM22	0.88	0.89	0.98	
IDO1	0.92	0.93	0.99	

IDO1 ectoderm

GENE_SYMBOL	RFF2	S-P&Es8	Ratio	
COL2A1	0.04	0.04	0.98	
DRD4	0.04	0.06	0.78	
EN1	0.07	0.05	1.39	
LMX1A	0.03	0.03	1.09	
NR2F1	0.04	0.03	1.29	
NR2F2	0.08	1.32		
OLFM3	0.08	0.07	1.14	
PAPLN	0.10	0.11	0.91	
PAX3	0.05	0.04	1.45	
PAX6	0.03	0.03	1.00	
POU4F1	0.03	0.03	1.08	
PRKCA	0.03	0.03	0.97	
SDC2	0.04	0.03	1.17	
SOX1	0.06	0.04	1.47	
WNT1	0.11	0.09	1.27	
ZBTB16	0.06	0.05	1.22	
CDH9	0.35	0.25	1.42	
LMX1A	0.84	0.83	1.01	
DMBX1	0.82	0.83	0.99	
TRPM8	0.89	0.89	1.01	
NOS2	0.89	0.90	1.00	
MYO3B	0.92	0.93	0.99	

GENE_SYMBOL	RFF2	S-P&Es8	Ratio
ALOX15	0.12	0.11	1.10
CDX2	0.03	0.02	1.14
FOXF1	0.04	0.03	1.28
HAND1	0.03	0.03	1.06
HAND2	0.05	0.03	1.56
HEY1	0.01	0.02	0.86
IL6ST	0.04	0.04	1.02
NKX2-5	0.10	0.04	2.75
PDGFRA	0.04	0.03	1.09
SNAI2	0.05	0.03	1.35
TBX3	0.03	0.03	0.98
RGS4	0.33	0.19	1.71
HOPX	0.22	0.22	1.02
ESM1	0.79	0.82	0.97
CDH5	0.85	0.84	1.02
TM4SF1	0.85	0.86	0.99
PLVAP	0.87	0.90	0.98
ABCA4	0.89	0.90	0.98
FCN3	0.90	0.91	0.98
BMP10	0.92	0.92	1.00
COLEC10	0.94	0.94	1.00

mesendoderm

GENE_SYMBOL	RFF2	S-P&Es8	Ratio
FGF4	0.05	0.05	0.89
NPPB	0.14	0.09	1.44
PTHLH	0.03	0.03	1.18
Т	0.03	0.03	1.18
GDF3	0.80	0.83	0.97
NR5A2	0.91	0.92	0.99

GENE_SYMBOL	RFF2	S-P&Es8	Ratio	
CABP7	0.07	0.08	0.85	
CLDN1	0.03	0.03	1.01	
CPLX2	0.13	0.10	1.29	
EOMES	0.07	0.04	1.66	
FOXA1	0.03	0.03	1.06	
FOXA2	0.04	0.04	0.98	
GATA4	0.04	0.03	1.13	
GATA6	0.02	0.02	0.91	
HHEX	0.03	0.04	0.86	
HMP19	0.09	0.07	1.38	
HNF1B	0.03	0.03	1.22	
KLF5	0.03	0.03	1.04	
NODAL	0.06	0.07	0.83	
PHOX2B	0.09	0.05	1.75	
POU3F3	0.03	0.03	1.04	
PRDM1	0.03	0.03	0.94	
SOX17	0.04	0.03	1.35	
ELAVL3	0.25	0.21	1.16	
SST	0.42	0.40	1.05	
LEFTY1	0.70	0.74	0.96	
FOXP2	0.83	0.78	1.06	
LEFTY2	0.84	0.81	1.03	
HNF4A	0.91	0.90	1.01	
CDH20	0.91	0.93	0.98	
AFP	0.92	0.94	0.98	

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Figure S4. Methylation comparison study of PSCs cultured under various conditions

- A. The methylation status of the cells was determined with an Illumina Human Methylation Bead Chip. Average methylation scores from 6 PSC samples cultured with RFF2 (3 iPSC [PFX#9] samples and 3 ESC [KhES-1] samples). Scores were compared with the average of 6 PSC samples in S-P or Es8 medium (1 sample of PFX#9 with S-P; 1 sample of KhES-1 with S-P; 1 sample of H9 with S-P; 1 sample of PFX#9 with Es8; 2 samples of H9 with Es8). The number of gene promoter regions or all regions whose methylation scores exceeded 0.2 by culturing with RFF2 or S-P and Es8 is displayed in a Venn diagram.
- B. Clustering of methylation patterns in the promoter region of PSCs cultured with RFF2, S-P, or Es8 medium. Lanes #1-3: iPSCs (PFX#9) cultured with RFF2 medium. Lanes #4-6: ESCs (KhES-1) cultured with RFF2 from 6 independent experiments. Lane #7: PFX#9 cells with S-P. Lane #8: KhES-1 cells with S-P. Lane #9: H9 ESCs with S-P. Lane #10: PFX#9 cells with Es8. Lanes #11, 12: H9 cells with Es8 from 6 independent experiments.
- C. Table of methylation status of promoters of representative genes for self-renewal, ectoderm, mesoderm, mesendoderm, and endoderm lineage in PSCs cultured with RFF2, S-P, or Es8 medium. The average methylation status in 6 PSCs (3 iPSCs plus 3 ESCs) cultured with RFF2 or 6 PSCs (1 iPSC sample and 2 ESC samples with S-P and 1 iPSC sample and 2 ESCs with Es8) cultured with S-P or Es8 (S-P & Es8) are shown in the table. All cells were maintained in the undifferentiated state. Methylation status defined as follow: hypomethylated, < 0.2; moderate, 0.2 to < 0.5; hypermethylated, > 0.5. Shown in blue, yellow, and orange columns, respectively.



Figure S5. Table for 96 genes expression of *mock*- or si*CHD7*-transfected KhES-1 in EB formation assay day 4, 5 or 14 determined by qRT-PCR scorecard panel. This is a raw data before normalization for bar graphs in Figure 2D.



Figure S6. Differentiation potential of KhES-1 correlates to the expression level of *CHD7. CHD7* in KhES-1 was downregulated by introducing either 10, 30 or 50 pmol of si*CHD7* into cells (A) subsequently, differentiation potential was determined by qRT-PCR of 96 genes with a scorecard panel (B). Ectoderm differentiation potential after normalized was as bar graph (C).



Figure S7. Downregulation of *CHD7* supported the survival of ESCs cultured with nutrient-depleted media.

- A. Protocol for induction of differentiation by nutrient-depleted Es8 medium and transfection with *siCHD7*. *siCHD7* or control siRNA (mock) was transfected into cells after changing the medium (Es8) on day 0. The medium was then changed every 2 days (days 2 and 4). Cells were harvested 42 h (day 2), 72 h, and 96 h after transfection with siRNA for cell counting and determination of gene expression by qRT-PCR. ESCs were normally cultured in Es8 medium with daily medium changes and passaged every 3 days to maintain an undifferentiated state.
- B. CHD7 gene expression was determined by qRT-PCR in KhES-1 cells transfected with siCHD7 or control siRNA (mock) or in non-transfected cells on days 0, 1, 2, 3 and 4. CHD7 gene expression was standardized according to the average CHD7 expression in KhES-1 cells cultured with Es8 medium measured independently 3 times.
- C. Photomicrographs of non-transfected regular cultures of KhES-1 cells (upper panels, daily medium changes), *siCHD7*-transfected KhES-1 cells (middle panels, medium changes every 2 days), and control siRNA-transfected (mock) KhES-1 cells (lower panels, medium changes every 2 days) on days 2, 3, and 4 are shown. Gene expression profiles of KhES-1 cells, as determined by qRT-PCR scorecard panel, are shown below the corresponding photograph. Scale bar: 1 mm.
- D. Numbers of non-transfected KhES-1 cells (blue line), *siCHD7*-transfected cells (red line), or mock-transfected cells (green line) on the designated cultured day are plotted as a linear graph. Representative data sets from 3 independent experiments are shown.



Figure S8. Gene expression data from ESC after introduction of *mCHD7* determined by the qRT-PCR.

mRNA encoding *CHD7* isoform 2 (mCHD7) or *mock* RNA (mock) was transfected into KhES-1 cells cultured with RFF2 medium, and the expression levels of 96 genes in KhES-1 at 1, 2, and 3 days after transfection were determined by the qRT-PCR scorecard panel. Notably, three germ layer differentiation was observed simultaneously with upregulation of *CHD7* isoform 2 mRNA.



Figure S9. Table depicting the expression of a 96-gene panel from *mock-*, *DN1-*, *DN2-* or *DN1+DN2*-transfected KhES-1 in an EB formation assay at day 0 or 3 determined by a qRT-PCR scorecard panel. This is a raw data before normalization for bar graphs in Figure 4C.



Figure S10. Introduction of mCHD7 failed to generate CHD7 overexpressing ESCs in culture with Es8 medium.

- A. Protocol for transfection with mRNA for *CHD7* isoform 2 (*mCHD7*) and cell culture.
- B. Evaluation of *mCHD7* expression by qRT-PCR on days 1 and 2. The 3' PCR primer sets to detect all of CHD7 isoforms (isoform 1, 2 and X4) was used. *CHD7* gene expression was standardized according to the average *CHD7* expression in KhES-1 cells cultured with Es8 medium and measured independently 3 times. A representative result from 3 biological replicates is shown. (n=3 analytical replicates).
- C. Cell counting and cell morphology of *CHD7* or mock-transfected KhES-1 cells on days 1 and 2. The cell numbers in one well of a 6-well plate is appended in the upper right corner of the relevant photograph.



Figure S11. ChIP-seq 18 factors (H1) and BRG1 (H9). Heat map were obtained from a public ESC ChIP-seq database. The odds ratio representing the correlation between binding sites for each pair of factors was calculated. Green indicates high homology between factors and red indicates no high homology between factors.

Human ESC H1 or H9

Gene	Accession No.
CHD7	GSM1003473
P300	GSM1003513
SUZ12	GSM1003573
EZH2	GSM1003524
POU5F1	GSM803438
NANOG	GSM803437
CTCF	GSM803419
KLF4	GSM447584
C-MYC	GSM447585
SOX2	GSM456570
BRG1	GSM602297
H3K4me1	GSM733782
H3K4me2	GSM733670
H3K4me3	GSM733657
H3K9me3	GSM1003585
H3K27me3	GSM733748
H3K27ac	GSM733718
H3K9ac	GSM733773

Figure S12. List of accession numbers from the GEO public database

GSM accession numbers in the GEO database used for odds ratios mapping and gene expression profiles.

POU5F1 POU5F1 SOX2 SOX2 NANOG P300 P300 CHD7 CHD7	F R F R F R F R		CG CTT GCC C GG AAA TGC C TG CGT GAG T CTC AGC TAC A CC CTG GTG G TG AAT GTA CA	CT GCA GCA GA TT CTG GCG IAG GGG TGC AAA AGA GG GT GGA TGG GAT TGG TG AA CAG GTG AAG AC TA GCA AGA GTA AA	Refseq No. NM_20328 NM_02486
POU5F1 SOX2 NANOG NANOG p300 CHD7 CHD7	R F F F R		CG CTT GCC C GG AAA TGG G TG CGT GAG T CTC AGC TAC A CC CTG GTG G TG AAT GTA CA	TT CTG GCG AG GGG TGC AAA AGA GG GT GGA TGG GAT TGG TG AA CAG GTG AAG AC TA GGA AGA GTA AA	Refseq No. NM_20328 NM_02486
SOX2 SOX2 NANOG P300 P300 CHD7 CHD7	F R F R	C T T T	GGG AAA TGG G TG CGT GAG T CTC AGC TAC A CC CTG GTG G TG AAT GTA CA	AG GGG TGC AAA AGA GG GT GGA TGG GAT TGG TG AA CAG GTG AAG AC TA GGA AGA GTA AA	NM_20328 NM_02486
SOX2 NANOG P300 P300 CHD7 CHD7	R F R		TG CGT GAG TO CTC AGC TAC AA CCC CTG GTG G TG AAT GTA CA	GT GGA TGG GAT TGG TG AA CAG GTG AAG AC TA GGA AGA GTA AA	NM_20328 NM_02486
NANOG NANOG p300 p300 CHD7 CHD7	F	с с т	TC AGC TAC A	AA CAG GTG AAG AC	NM 02486
NANOG p300 p300 CHD7 CHD7	R F	T	CC CTG GTG G	TA GGA AGA GTA AA	
p300 p300 CHD7 CHD7	F	T	TG AAT GTA CA		NM 00142
p300 p300 CHD7 CHD7	R		IGAAI GIA CA	C ACT CCC CAA CA	
CHD7 CHD7			10 100 0170	G AGT GCG GAA GA	NM_00112
CHD7			AC AGE CAT CA	AC AGA CGA ATC C	NM_00307
CHD7		G	GT TCC CAC A	CI CGI GCA IA	NM 01535
	R	<u>с</u> т	GC GCC TCG G	GA CAG A	
CHD7 isoform 2	F	0	CCC ATG AAA G	CA ATG AGT AAT CC	NM_15299
CHD7 isoform 2	R	: т	CC ATT GGT AT	TC CCA GCA CTT C	NM_00445
CHD7 Chromodomain	n F	Т	GATGGACTTGG	GAACACAAAGTG	
CHD7 Chromodomain	n R	: Т	GAAGGGAAGC	GACTTGGTT	
CHD7 sant slide	F	C	CAAACATGGCTA	ATGAGAAGTACAACTC	
CHD7 sant slide	R		CGACTCGTTC	CAGAAAGCA	
GAPDH	F	C	CA CTC CTC C	AC CTT TGA CG	
GAPDH	R	A	TG AGG TCC A	CC ACC CTG TT	
rimer set 1					
Refseg No.	Gene			Tagman probe	
NM_017780 XM_011517553.2 XM_011517554.2 XM_011517555.2 XM_017013612.1 XM_017013613.1 XM_011517560	CHD7			Hs00215010_m1	
rimer set 2					
Refseq No.	G	Gene	P/F/ R	seq (5'-3')	
	C	HD7	P	TATGACTCAGAAACCGAAACA	GAAACGACA
IM_001316690	C	HD7	F	GCCCTTTCTAGAGAAACCAGT	G
	C	HD7	R	AGGCACCCTTTCTTCTCCTG	
rimer set 3					
Refseq No.	(Gene	P/F/ R	seq (5'-3')	
NM_017780	C	CHD7	Р	CACGGACGCTATAAACGCCA	ACTCACTG
XM_011517553.2					
XM_011517554.2	C	CHD7	F	GAATCTGCTTGTCTATGGTTG	GG
XM_011517555.2 XM_017013612.1 XM_017013613.1	C	CHD7	R	AGGATGGTTCTGCAGATGGT	
	CHD7 isoform 2 CHD7 Chromodomain CHD7 Chromodomain CHD7 sant slide CHD7 sant slide CHD7 sant slide GAPDH irriner set 1 Refseq No. KM_011517553.2 XM_011517554.2 XM_011517554.2 XM_011517554.2 XM_011517554.2 XM_011517554.2 XM_011517550.2 XM_011517552.2 XM_011517553.2 XM_0153753.2 XM_0153753.2 XM_0153753.2 XM_015375	CHD7 isoform 2 R CHD7 Chromodomain F CHD7 Chromodomain F CHD7 sant slide F CHD7 sant slide F CHD7 sant slide F GAPDH F GAPDH F Refseq No. Gene NM_0115755.2 XM_0115755.2 XM_0115755.2 CHD7 XM_0115756.2 CHD7 XM_0115756.2 CHD7 XM_0115756.2 CHD7 XM_0115756.2 CHD7 XM_0115756.2 CC rimer set 2 CC VM_001316690 CC Crimer set 3 CC Refseq No. CC XM_0115755.2 XM_01151755.2 XM_01151755.2 CC XM_01151755.2 CC XM_01151755.2 CC XM_01151755.2 CC XM_01151755.2 CC XM_01151755.2 CC XM_017013612.1 CC	CHD7 isoform 2 R T CHD7 Chromodomain F T CHD7 Chromodomain R T CHD7 Sant slide R T CHD7 sant slide R C GAPDH F C GAPDH R A rimer set 1 Refseq No. Gene Refseq No. Gene NM_01151755.2 XM_011517554.2 XM_011517554.2 CHD7 XM_011517554.2 CHD7 XM_011517554.2 XM_011517554.2 CHD7 XM_011517554.2 XM_011517554.2 CHD7 XM_011517554.2 XM_011517554.2 CHD7 CHD7 rimer set 2 CHD7 CHD7 XM_001316690 CHD7 CHD7 rimer set 3 Refseq No. Gene XM_011517554.2 CHD7 XM_011517554.2 XM_011517554.2 CHD7 XM_011517554.2 XM_011517554.2 CHD7 XM_011517554.2 XM_011517554.2 CHD7 XM_011517554.2	CHD7 isoform 2 R TCC ATT GGT AT CHD7 Chromodomain F TGATGGACTTGG CHD7 Chromodomain F TGATGGACTTGG CHD7 sant slide F CAAAGATGGCT/ CHD7 sant slide R CCGACTCGTCG GAPDH F CCA CTC CTC C, GAPDH R ATG AGG TCC A rimer set 1 Refseq No. Gene Refseq No. Gene NM_011517554.2 XM_011517554.2 CHD7 XM_011517554.2 XM_011517554.2 CHD7 XM_011517554.2 XM_011517554.2 CHD7 P MM_01703613.1 XM_011517554.2 CHD7 XM_011517554.2 CHD7 P IM_001316690 CHD7 P IM_001316690 CHD7 P rimer set 3 CHD7 P Rift17553.2 CHD7 P XM_011517553.2 CHD7 F XM_011517554.2 CHD7 F XM_011517554.2 CHD7 F <t< td=""><td>CHD7 isoform 2 R TCC ATT GGT ATC CCA GCA CTT C CHD7 Chromodomain F TGATGGAACTGGAACCAAAAGTG CHD7 sant slide F CAAACATGGCTATGAAACAAAGTG CHD7 sant slide F CAAACATGGCTATGAAAGTACAAACTC CHD7 sant slide R CCGACTCGTTCCAGAAAGTACAACTC CHD7 sant slide R CCGACTCGTTCCAGAAAGCA GAPDH F CCA CT C CT C CAC C TT TGA CG GAPDH R ATG AGG TCC ACC ACC ACC TG TT rimer set 1 Refseq No. Gene Taqman probe NM_011517553.2 XM_011517554.2 XM_011517554.2 XM_011517564.2 XM_0115175612.1 XM_011517560 Hs00215010_m1 XM_011517560 virmer set 2 CHD7 P TATGACTCAGAAACCGAAACAGT Refseq No. Gene P/F/ R seq (5'-3') rimer set 3 CHD7 F GCCCTTTCTAGAGAAACCGAAACAGT Refseq No. Gene P/F/ R seq (5'-3') rimer set 3 CHD7 F GCACGGACCCTTTCTAGAGAAACCGAAACCAGT XM_011517552.2 CHD7 F<!--</td--></td></t<>	CHD7 isoform 2 R TCC ATT GGT ATC CCA GCA CTT C CHD7 Chromodomain F TGATGGAACTGGAACCAAAAGTG CHD7 sant slide F CAAACATGGCTATGAAACAAAGTG CHD7 sant slide F CAAACATGGCTATGAAAGTACAAACTC CHD7 sant slide R CCGACTCGTTCCAGAAAGTACAACTC CHD7 sant slide R CCGACTCGTTCCAGAAAGCA GAPDH F CCA CT C CT C CAC C TT TGA CG GAPDH R ATG AGG TCC ACC ACC ACC TG TT rimer set 1 Refseq No. Gene Taqman probe NM_011517553.2 XM_011517554.2 XM_011517554.2 XM_011517564.2 XM_0115175612.1 XM_011517560 Hs00215010_m1 XM_011517560 virmer set 2 CHD7 P TATGACTCAGAAACCGAAACAGT Refseq No. Gene P/F/ R seq (5'-3') rimer set 3 CHD7 F GCCCTTTCTAGAGAAACCGAAACAGT Refseq No. Gene P/F/ R seq (5'-3') rimer set 3 CHD7 F GCACGGACCCTTTCTAGAGAAACCGAAACCAGT XM_011517552.2 CHD7 F </td

Primers

Refseq No.	Gene	Primer
NM_203289.3	POU5F1	GPH1024786(-)01A
NM_024865.2	NANOG	GPH1002937(-)01A
NM_001429.3	p300	GPH1008986(-)01A
NM_001128844.1 NM_003072.3	BRG1	GPH1006548(-)01A
NM_015355.2	SUZ12	GPH1005657(-)01A
NM_152998.1 NM_004456.3	EZH2	GPH1025912(-)01A

Figure S13. List of primer sets used for qRT-PCR.