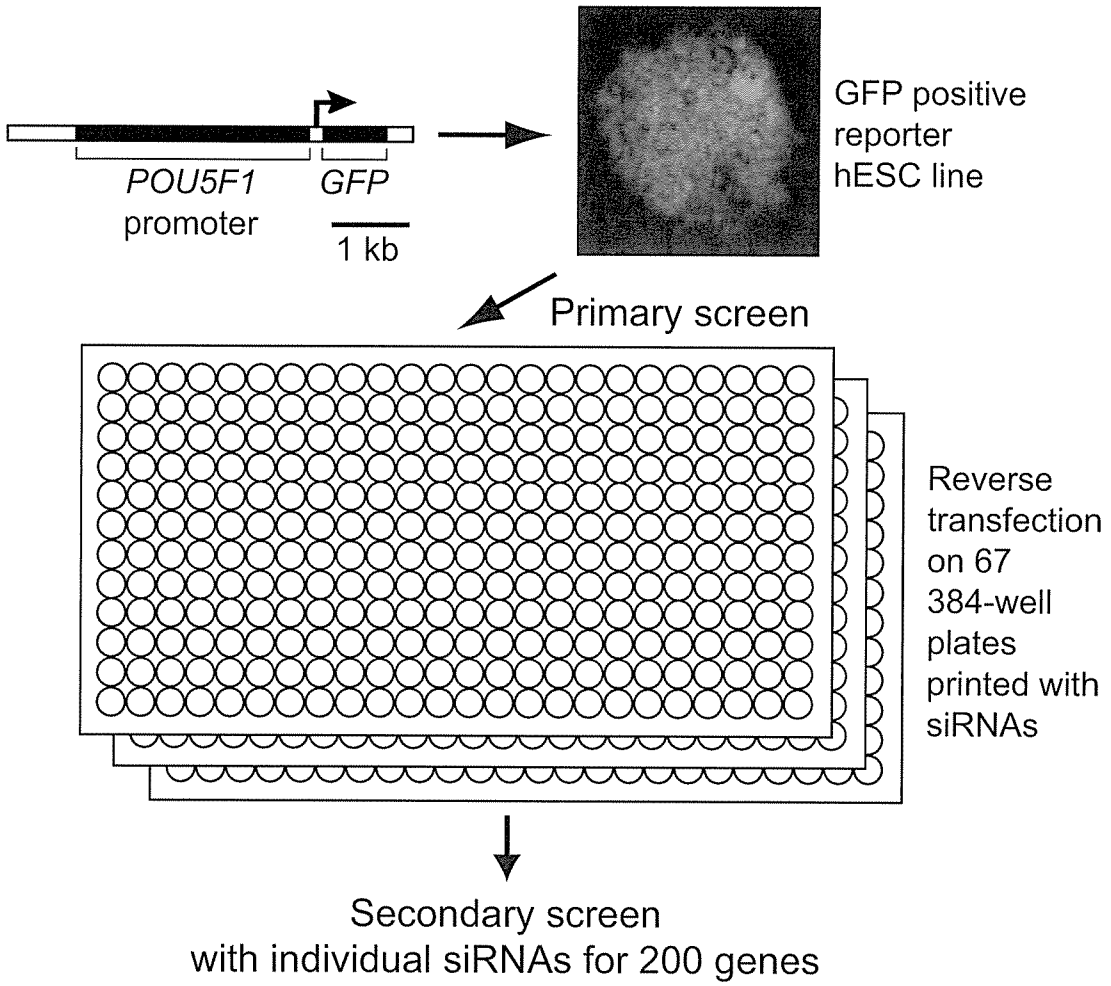

POU5F1
promoter
GFP
1 kb
GFP positive
reporter
hESC line
Primary screen
Reverse
transfection
on 67
384-well
plates
printed with
siRNAs
Secondary screen
with individual siRNAs for 200 genes

FIG. 1A

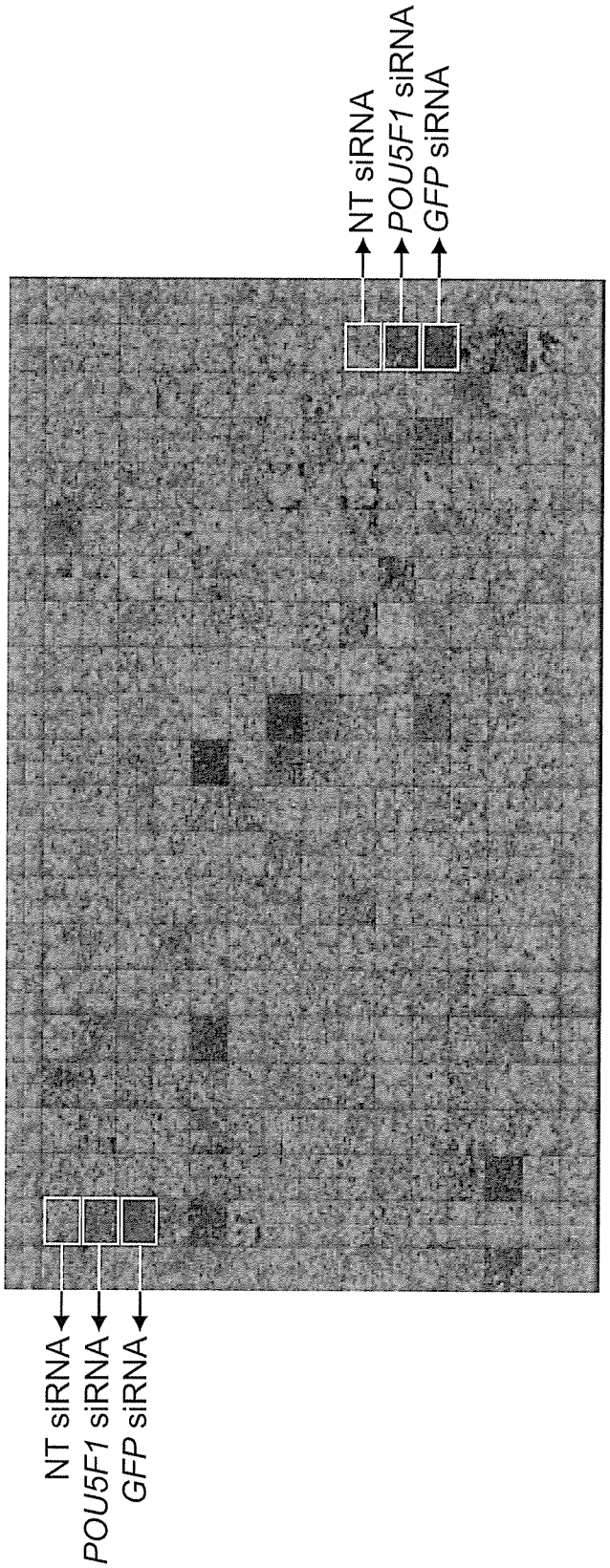

NT siRNA
POU5F1 siRNA
GFP siRNA
NT siRNA
POU5F1 siRNA
GFP siRNA

FIG. 1B

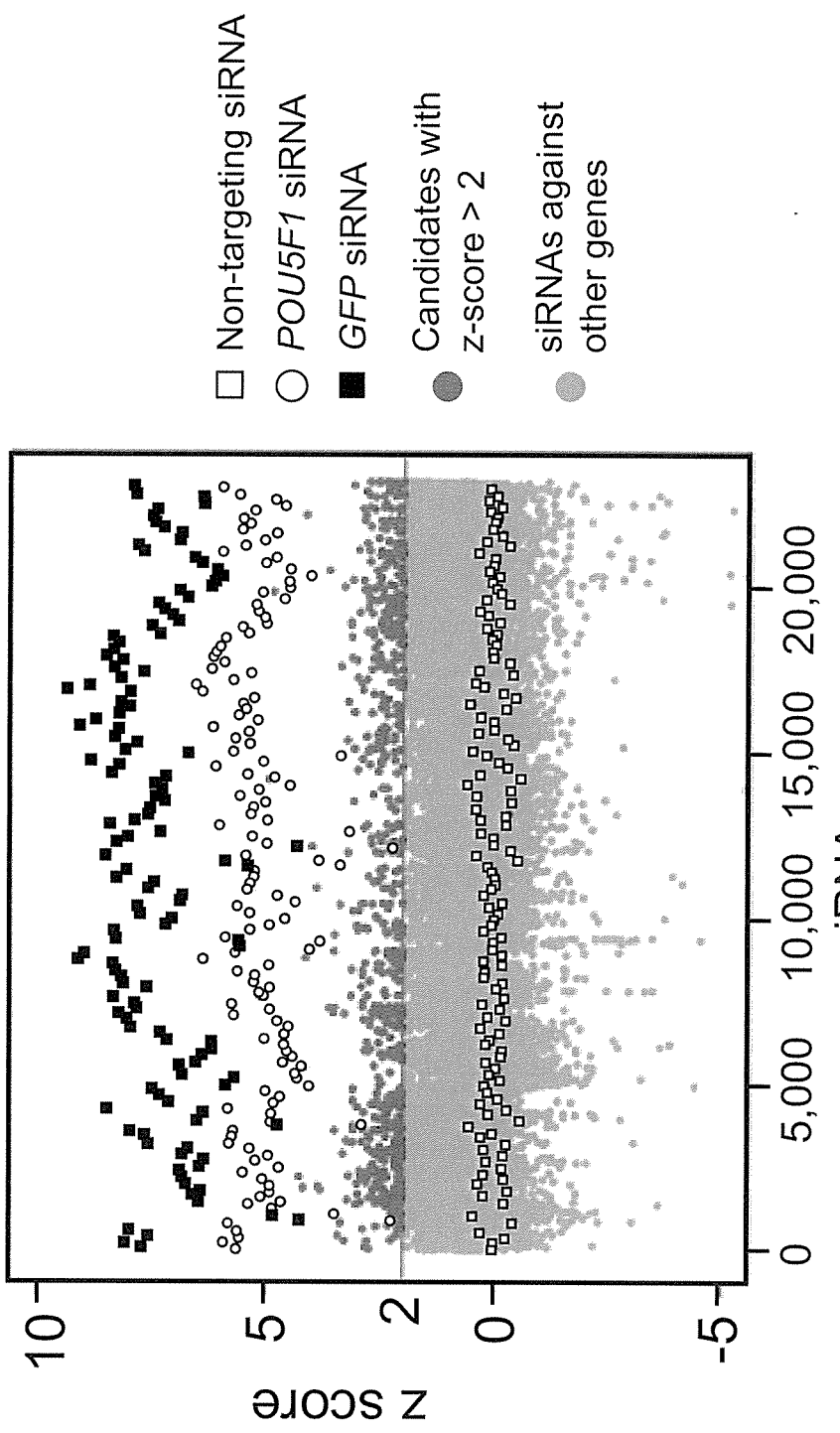

Non-targeting siRNA
POU5F1 siRNA
GFP siRNA
Candidates with z-score > 2
siRNAs against other genes
Z score
10
5
2
0
-5
0
5,000
10,000
15,000
20,000
siRNAs

FIG. 1C

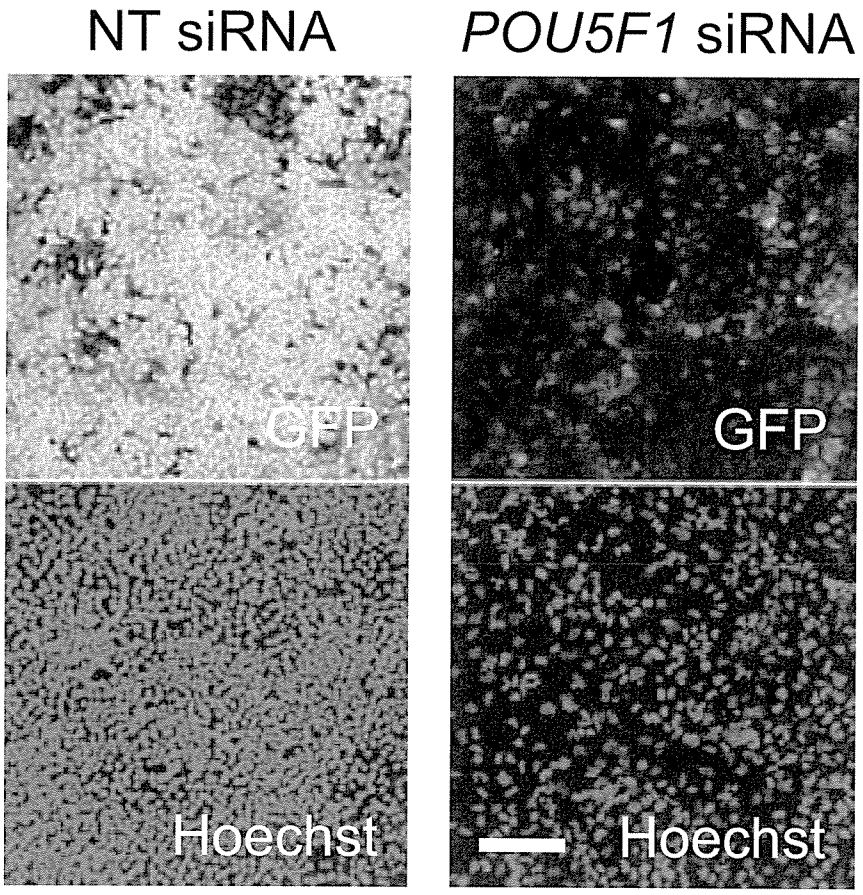


FIG. 2A

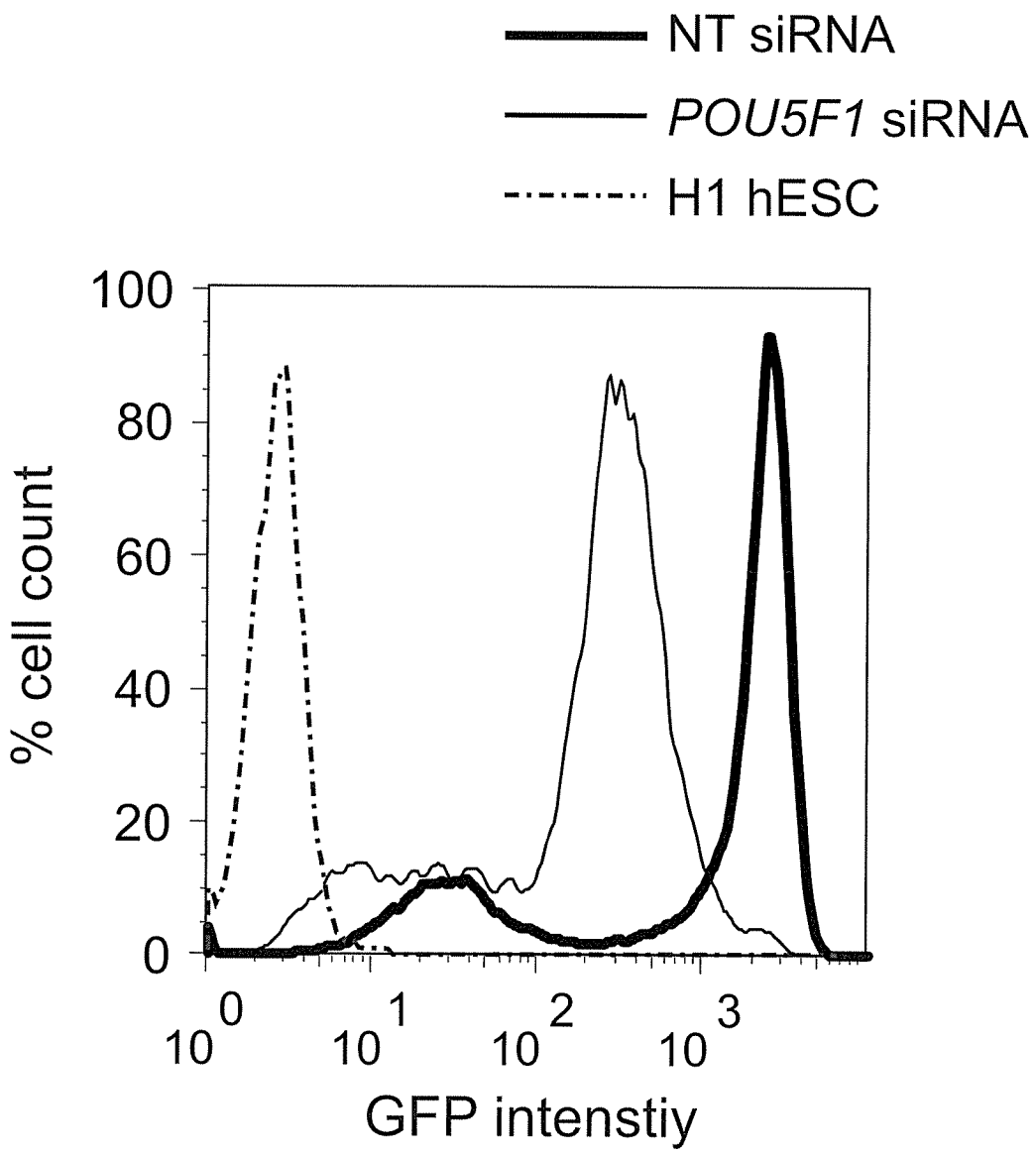

NT siRNA
POU5F1 siRNA
H1 hESC
100
80
60
40
20
0
% cell count
10^0
10^1
10^2
10^3
GFP intenstiy

FIG. 2B

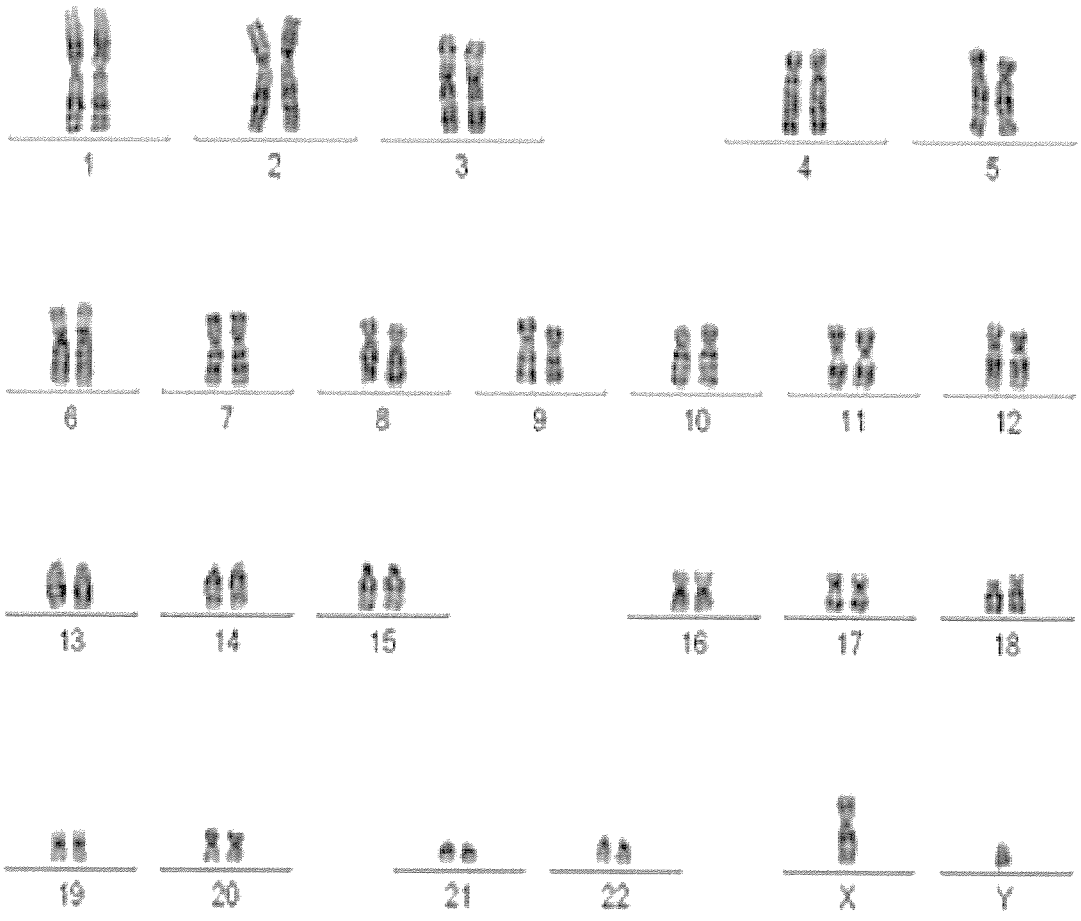


FIG. 2C

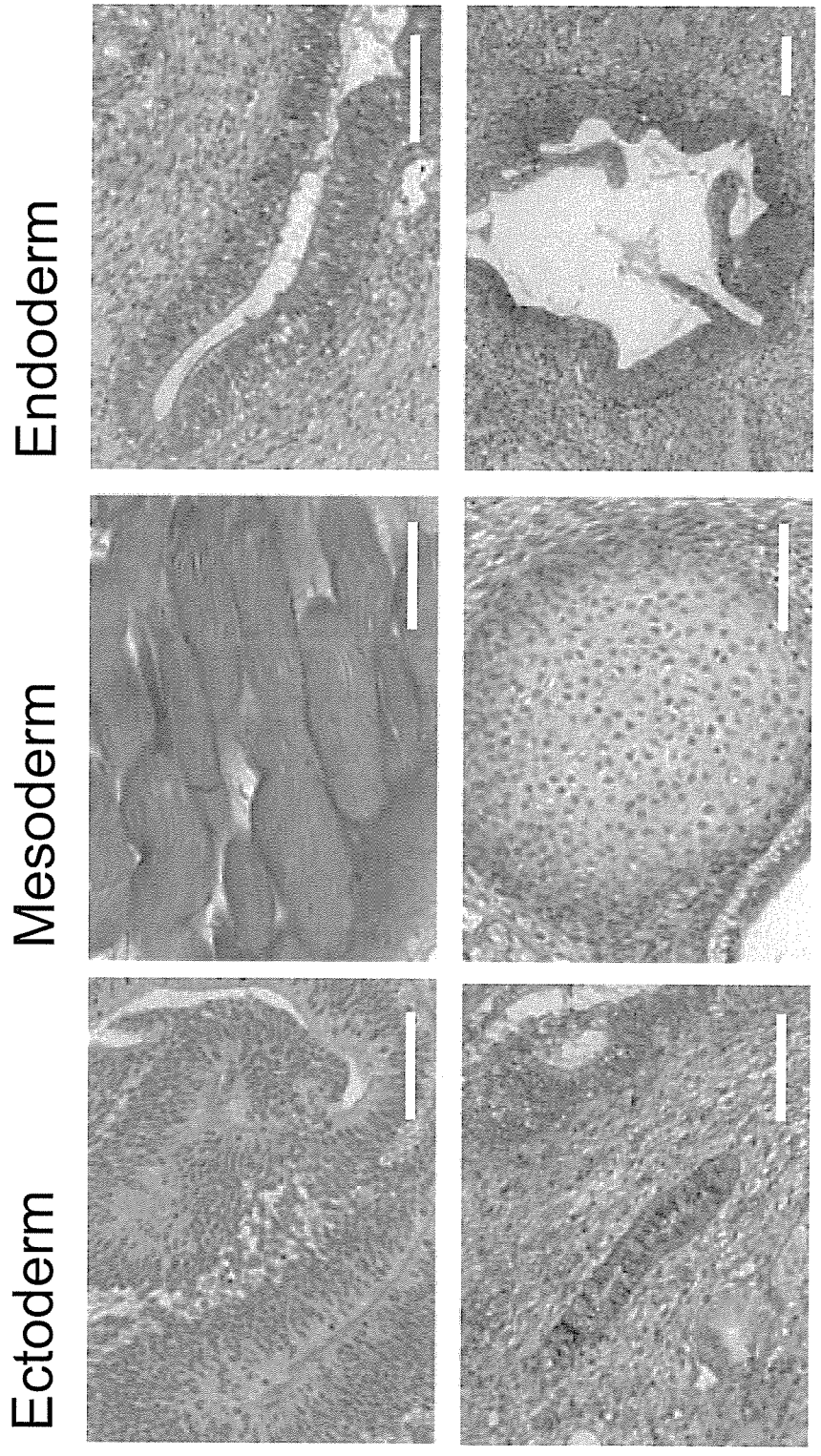
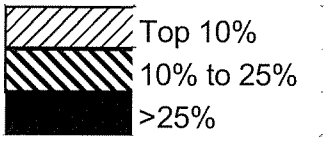


FIG. 2D

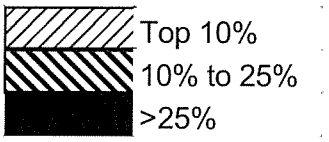
Gene	Ranking (% of 21,121 genes)	References
POU5F1	1 (0.005%)	
HCFC1	32 (0.15%)	(Dejosez et al, 2008. Cell)
TCL1A	145 (0.69%)	(Ivanova et al, 2006. Nature)
ZSCAN10	187 (0.89%)	(Wang et al, 2007. Stem Cells)
ZIC3	844 (3.99%)	(Lim et al, 2007. MBC)
NANOG	873 (4.13%)	(Chambers et al, 2003. Cell)
ZNF143	1024 (4.85%)	(Chen et al, 2008. Stem Cells)
RIF1	1350 (6.39%)	(Loh et al, 2006. Nat Genet)

FIG. 3A



Gene	Refseq ID	Ranking (% of 21,121 genes)
MED1	*NM_004774*	
MED4	*NM_014166*	
MED6	*NM_005466*	
MED7	*NM_004270*	
MED8	*NM_201542*	
MED9	*NM_01819*	
MED10	*NM_032286*	
MED11	*NM_001001683*	
MED12	*NM_005120*	
MED12L	*NM_053002*	
MED13	*NM_005121*	
MED13L	*NM_015335*	
MED14	*NM_004229*	
MED15	*NM_001003891*	
MED16	*NM_005481*	
MED17	*NM_004268*	
MED18	*NM_017638*	
MED19	*NM_153450*	
MED20	*NM_004275*	
MED21	*NM_004264*	
MED22	*NM_181491*	
MED23	*NM_015979*	
MED24	*NM_014815*	
MED25	*NM_030973*	
MED26	*NM_004831*	
MED27	*NM_004269*	
MED28	*NM_025205*	
MED29	*NM_017592*	
MED30	*NM_080651*	
MED31	*NM_016060*	

FIG. 3B



Gene	Alternative name	Ranking (% of 21,121 genes)
INO80		
ACTB		
ACTL6A	*Baf53a*	
ACTR5		
ACTR8		
RUVBL1		
RUVBL2b	*Tip49*	
INO80B		
INO80C		
YY1		
UCHL5		
INO80G	*NFRKB*	
INO80Q	*MCRS1*	
INO80F	*TFPT*	
INO80D	*FLJ20309*	
INO80E	*CCDC95*	

FIG. 3C

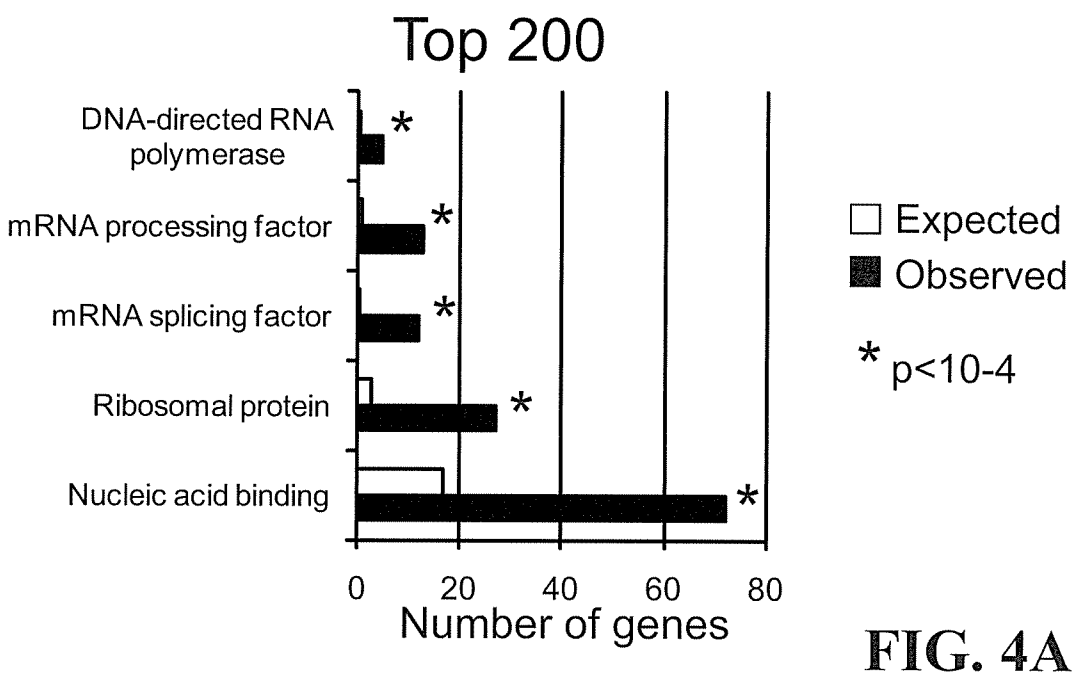


FIG. 4A

Gene	Alternative name	Ranking (% of 21,121 genes)
POLR2A	RPB1	
POLR2B	RPB2	
POLR2C	RPB3	
POLR2D	RBP4	
POLR2E	RPB5	
POLR2F	RPB6	
POLR2G	RPB7	
POLR2H	RPB8	
POLR2I	RPB9	
POLR2L	RBP10	
POLR2J4	RPB11	
POLR2J	RPB11	
POLR2J2	RPB11b1	
POLR2K	RPB12	

Top 10%
10% to 25%
>25%

FIG. 4B

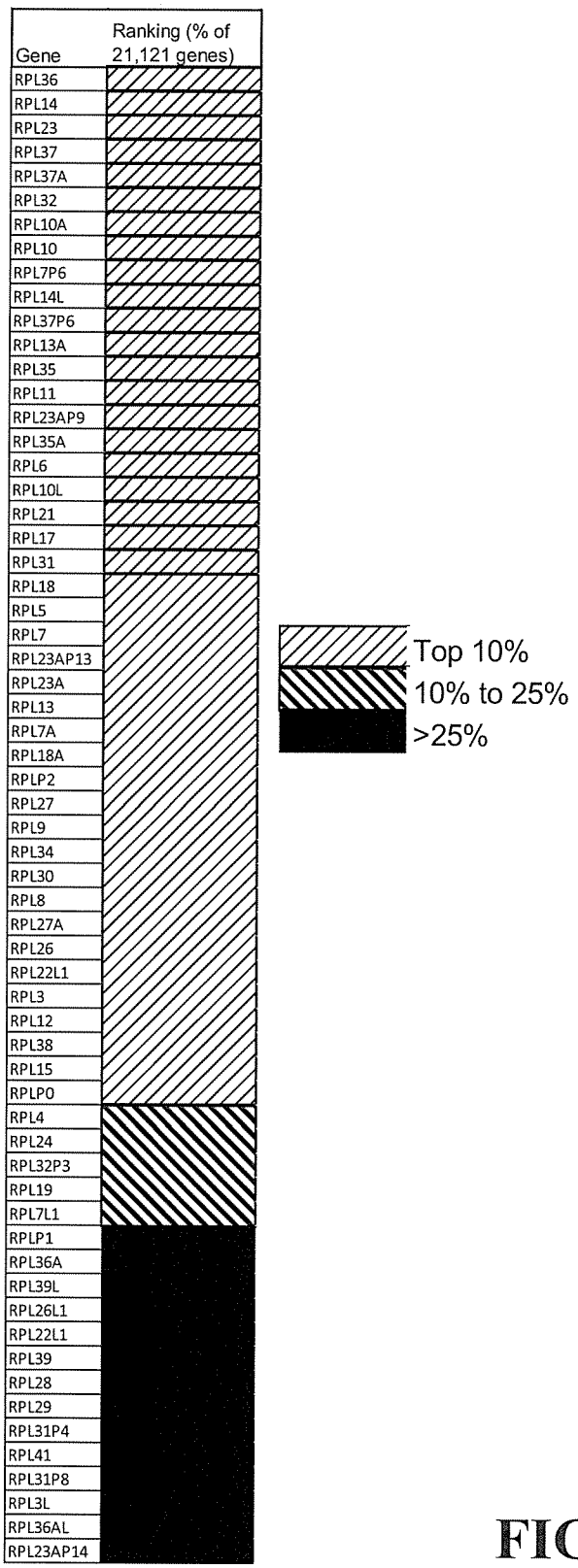

Gene
Ranking (% of 21,121 genes)
RPL36
RPL14
RPL23
RPL37
RPL37A
RPL32
RPL10A
RPL10
RPL7P6
RPL14L
RPL37P6
RPL13A
RPL35
RPL11
RPL23AP9
RPL35A
RPL6
RPL10L
RPL21
RPL17
RPL31
RPL18
RPL5
RPL7
RPL23AP13
RPL23A
RPL13
RPL7A
RPL18A
RPLP2
RPL27
RPL9
RPL34
RPL30
RPL8
RPL27A
RPL26
RPL22L1
RPL3
RPL12
RPL38
RPL15
RPLP0
RPL4
RPL24
RPL32P3
RPL19
RPL7L1
RPLP1
RPL36A
RPL39L
RPL26L1
RPL22L1
RPL39
RPL28
RPL29
RPL31P4
RPL41
RPL31P8
RPL3L
RPL36AL
RPL23AP14
Top 10%
10% to 25%
>25%

FIG. 4C

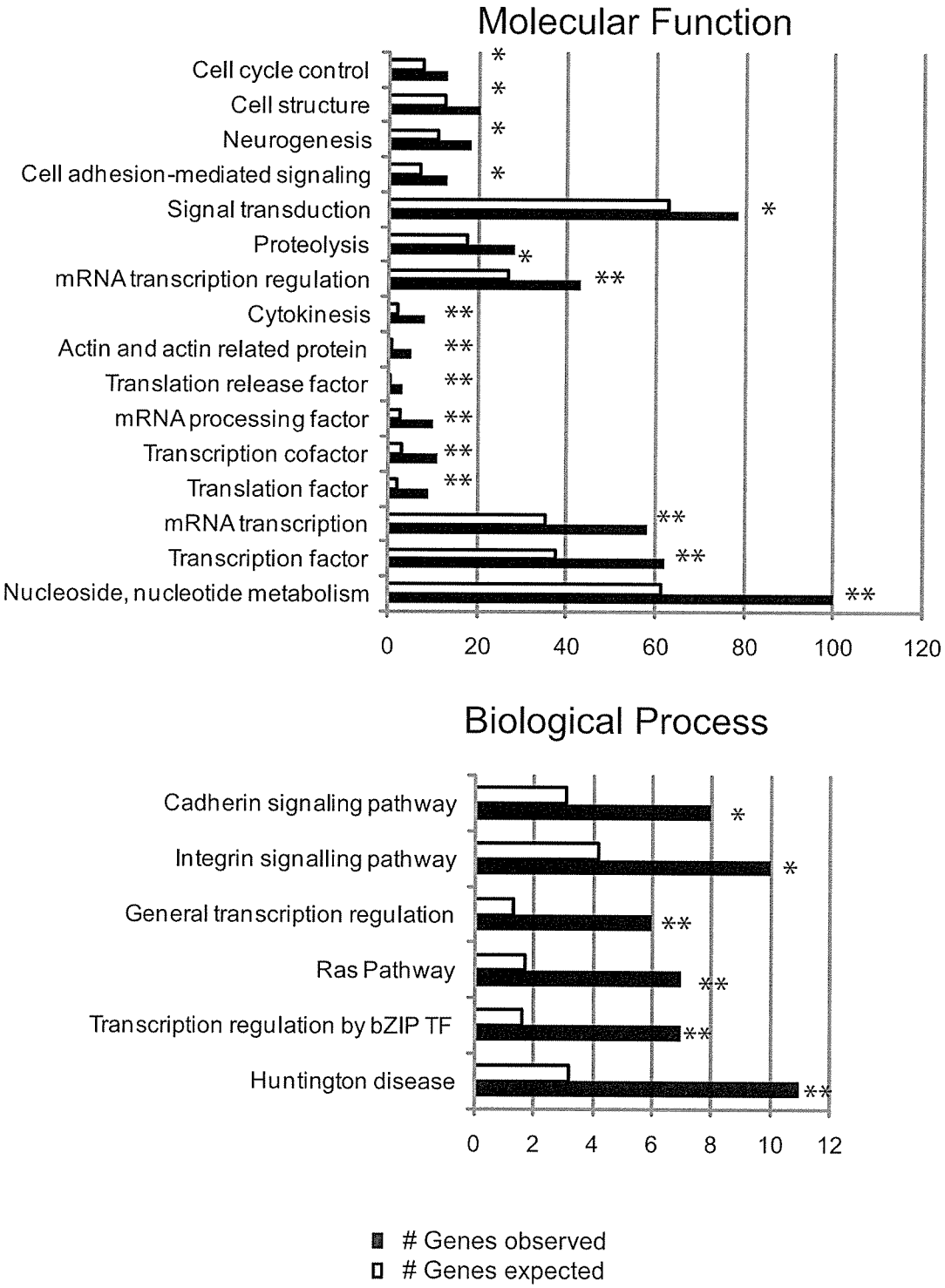

Molecular Function
Cell cycle control
Cell structure
Neurogenesis
Cell adhesion-mediated signaling
Signal transduction
Proteolysis
mRNA transcription regulation
Cytokinesis
Actin and actin related protein
Translation release factor
mRNA processing factor
Transcription cofactor
Translation factor
mRNA transcription
Transcription factor
Nucleoside, nucleotide metabolism
0
20
40
60
80
100
120
Biological Process
Cadherin signaling pathway
Integrin signalling pathway
General transcription regulation
Ras Pathway
Transcription regulation by bZIP TF
Huntington disease
0
2
4
6
8
10
12
Genes observed
Genes expected

FIG. 5A

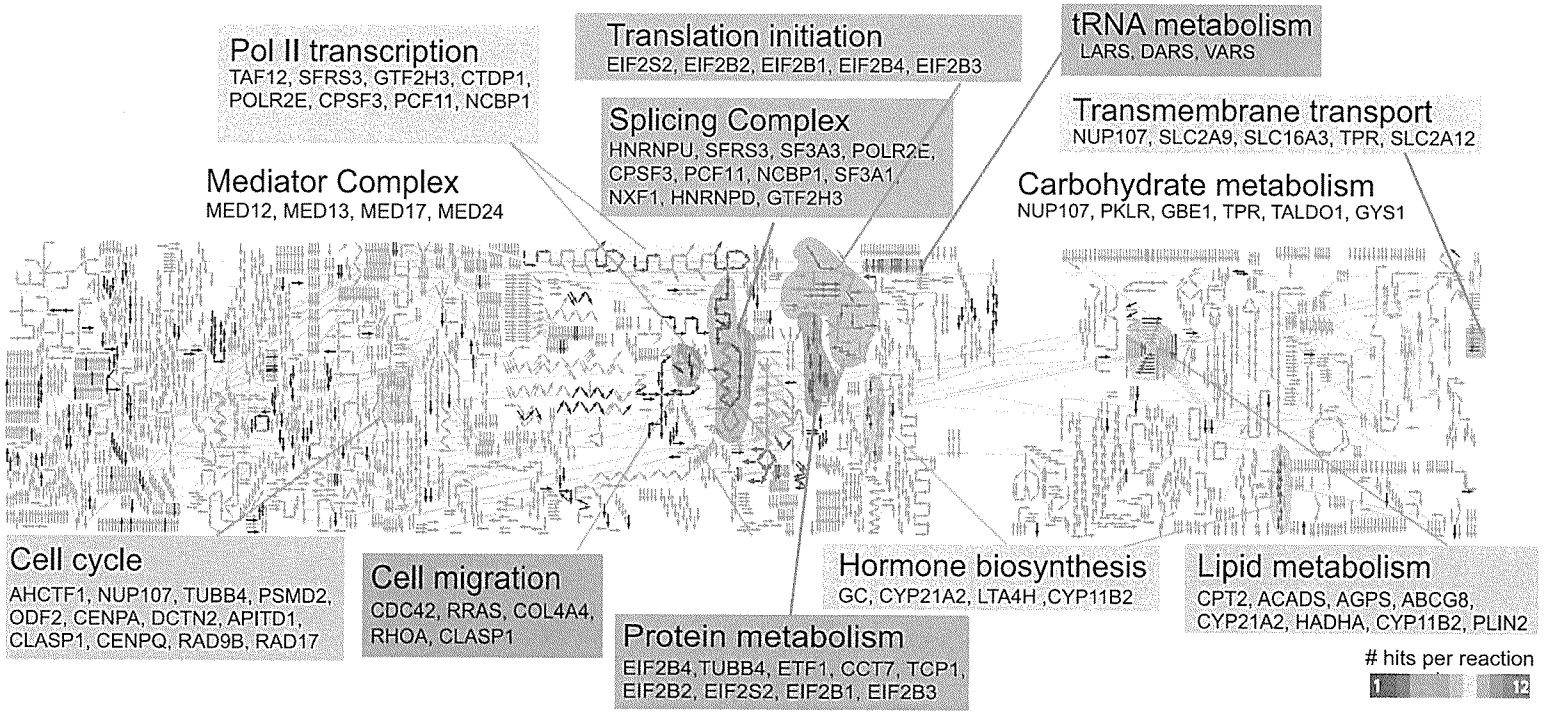

Pol II transcription
TAF12, SFRS3, GTF2H3, CTDP1, POLR2E, CPSF3, PCF11, NCBP1
Translation initiation
EIF2S2, EIF2B2, EIF2B1, EIF2B4, EIF2B3
tRNA metabolism
LARS, DARS, VARS
Splicing Complex
HNRNPU, SFRS3, SF3A3, POLR2E, CPSF3, PCF11, NCBP1, SF3A1, NXF1, HNRNPD, GTF2H3
Transmembrane transport
NUP107, SLC2A9, SLC16A3, TPR, SLC2A12
Mediator Complex
MED12, MED13, MED17, MED24
Carbohydrate metabolism
NUP107, PKLR, GBE1, TPR, TALDO1, GYS1
Cell cycle
AHCTF1, NUP107, TUBB4, PSMD2, ODF2, CENPA, DCTN2, APITD1, CLASP1, CENPQ, RAD9B, RAD17
Cell migration
CDC42, RRAS, COL4A4, RHOA, CLASP1
Hormone biosynthesis
GC, CYP21A2, LTA4H ,CYP11B2
Lipid metabolism
CPT2, ACADS, AGPS, ABCG8, CYP21A2, HADHA, CYP11B2, PLIN2
Protein metabolism
EIF2B4,TUBB4, ETF1, CCT7, TCP1, EIF2B2, EIF2S2, EIF2B1, EIF2B3
hits per reaction
1
12

FIG. 5B

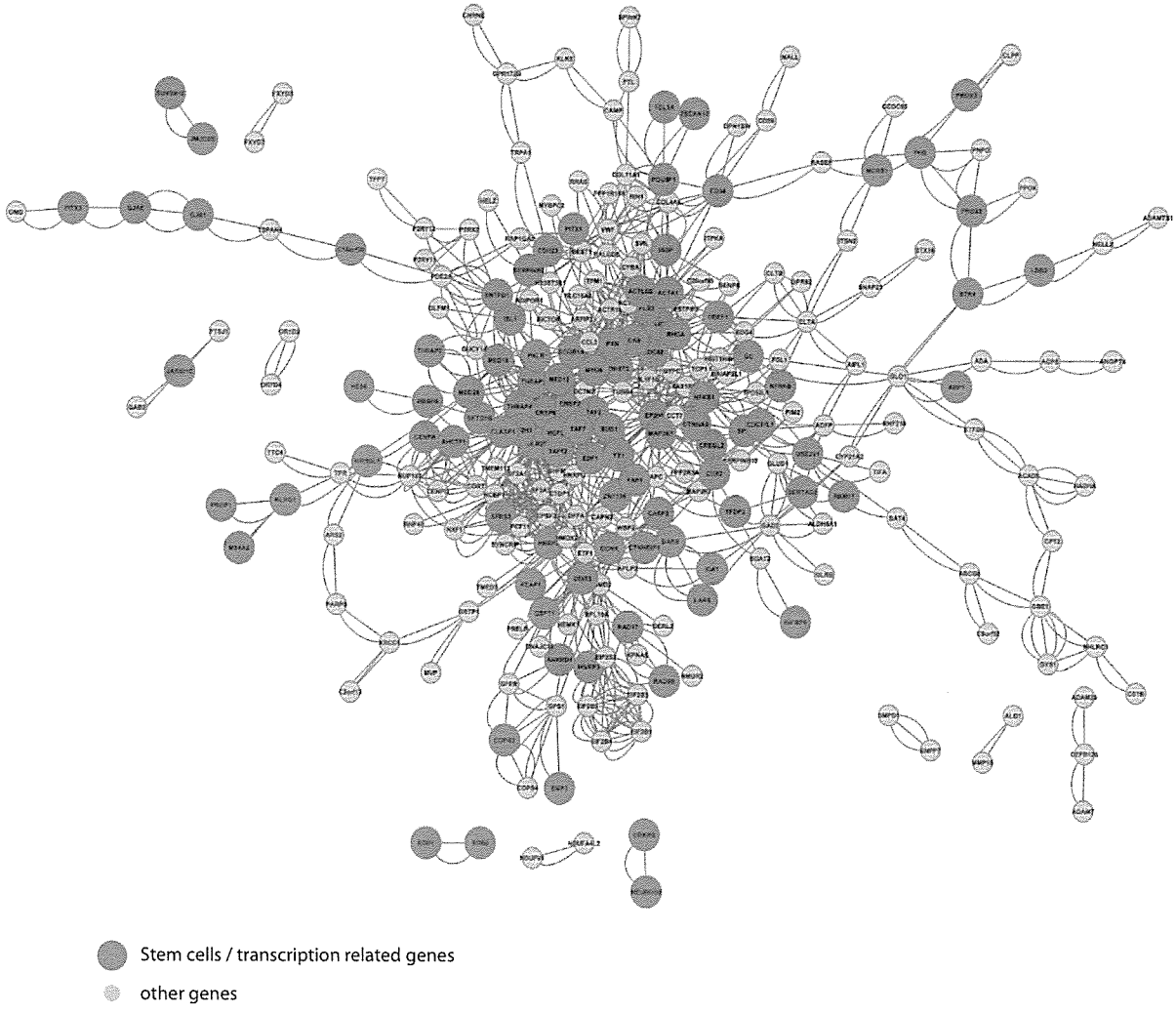


FIG. 5C

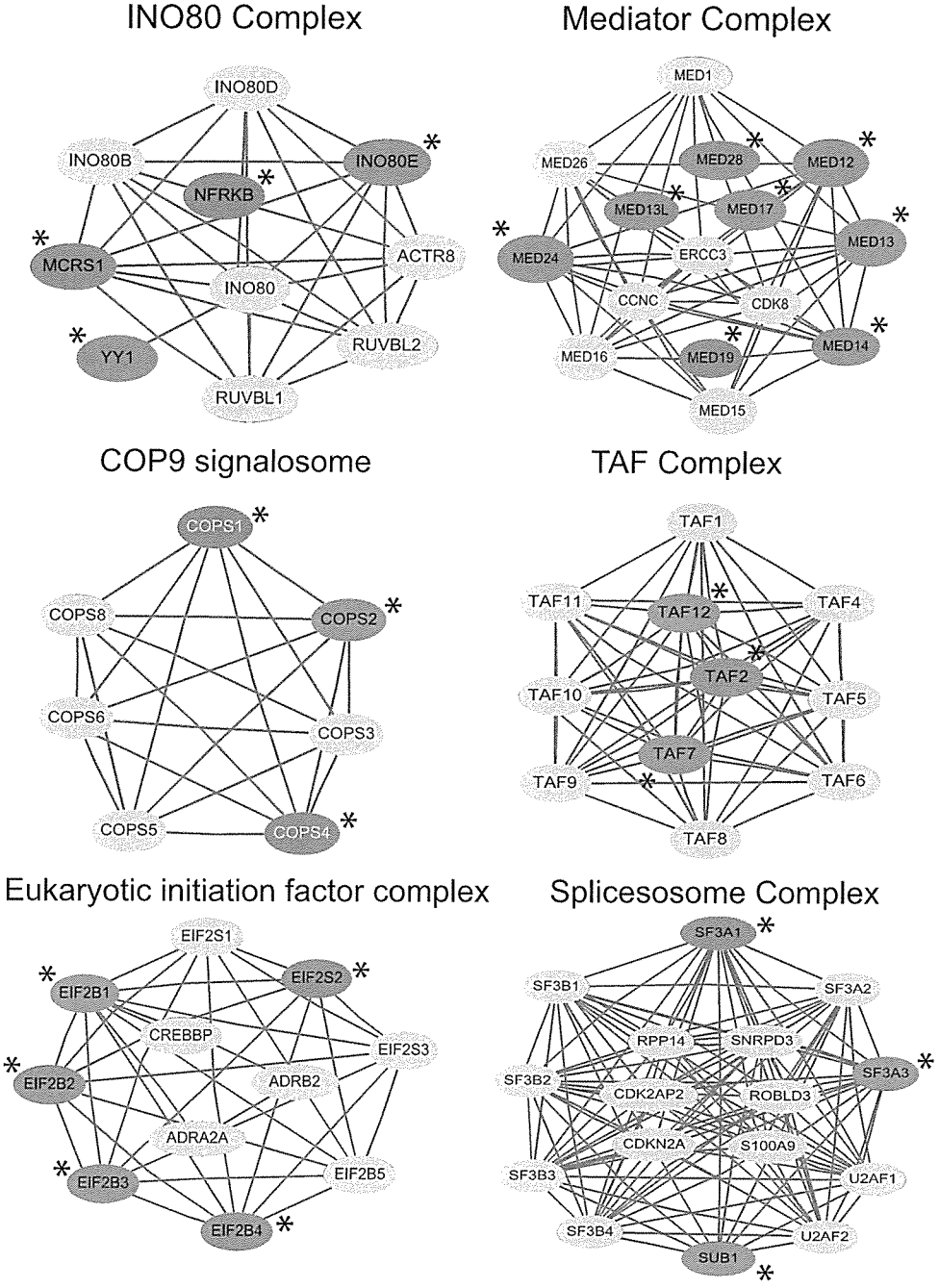

INO80 Complex
INO80D
INO80B
INO80E
NFRKB
MCRS1
ACTR8
INO80
YY1
RUVBL2
RUVBL1
Mediator Complex
MED1
MED26
MED28
MED12
MED13L
MED17
MED13
MED24
ERCC3
CCNC
CDK8
MED16
MED19
MED14
MED15
COP9 signalosome
COPS1
COPS8
COPS2
COPS6
COPS3
COPS5
COPS4
TAF Complex
TAF1
TAF11
TAF12
TAF4
TAF2
TAF10
TAF5
TAF7
TAF9
TAF6
TAF8
Eukaryotic initiation factor complex
EIF2S1
EIF2B1
EIF2S2
CREBBP
EIF2S3
EIF2B2
ADRB2
ADRA2A
EIF2B3
EIF2B5
EIF2B4
Splicesosome Complex
SF3A1
SF3B1
SF3A2
RPP14
SNRPD3
SF3B2
SF3A3
CDK2AP2
ROBLD3
CDKN2A
S100A9
SF3B3
U2AF1
SF3B4
U2AF2
SUB1

FIG. 5D

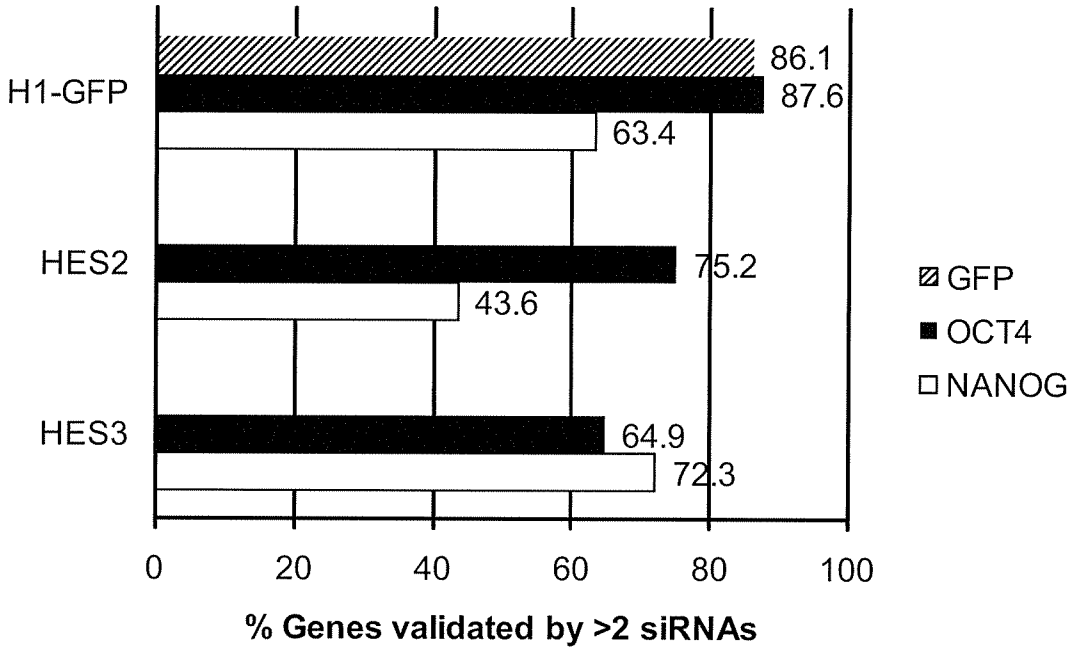

H1-GFP
HES2
HES3
86.1
87.6
63.4
75.2
43.6
64.9
72.3
0
20
40
60
80
100
% Genes validated by >2 siRNAs
GFP
OCT4
NANOG

FIG. 6A

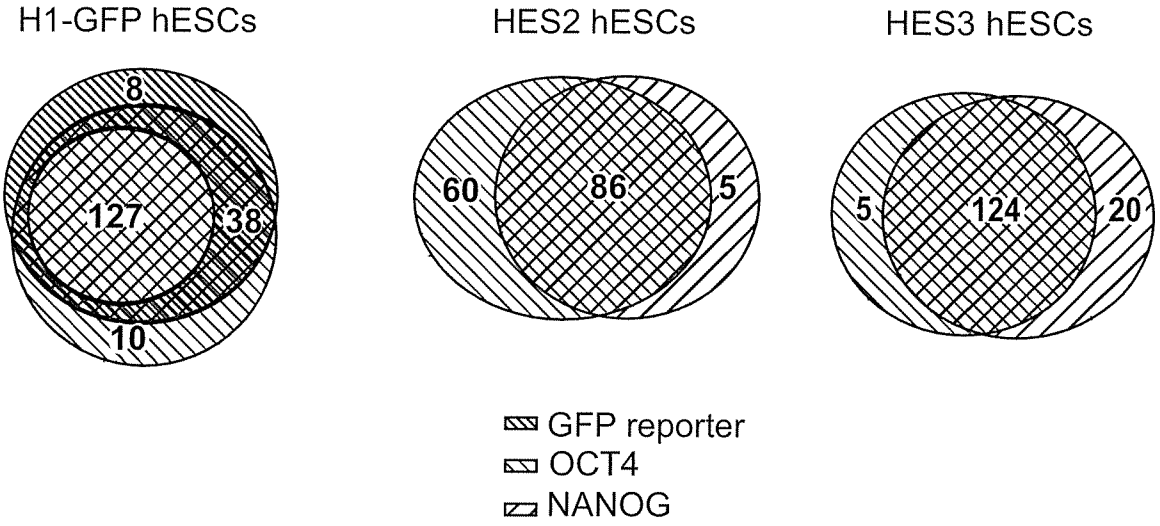

H1-GFP hESCs
HES2 hESCs
HES3 hESCs
8
127
38
10
60
86
5
5
124
20
GFP reporter
OCT4
NANOG

FIG. 6B

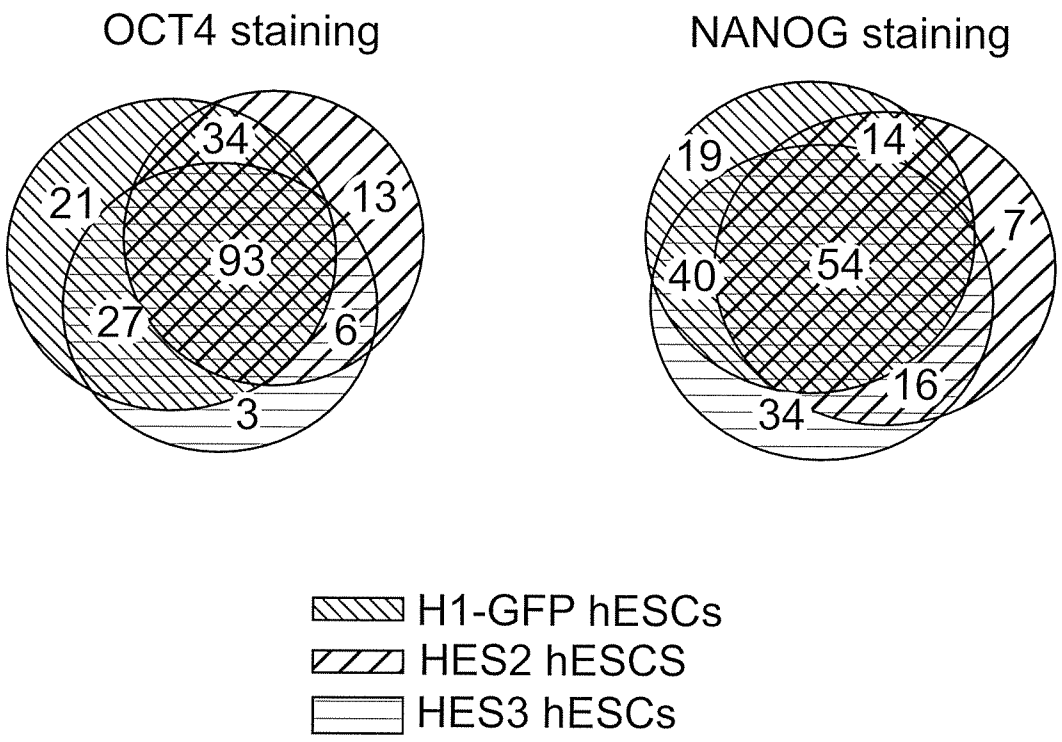

OCT4 staining
NANOG staining
34
21
13
93
27
6
3
19
14
7
40
54
16
34
H1-GFP hESCs
HES2 hESCS
HES3 hESCs

FIG. 6C

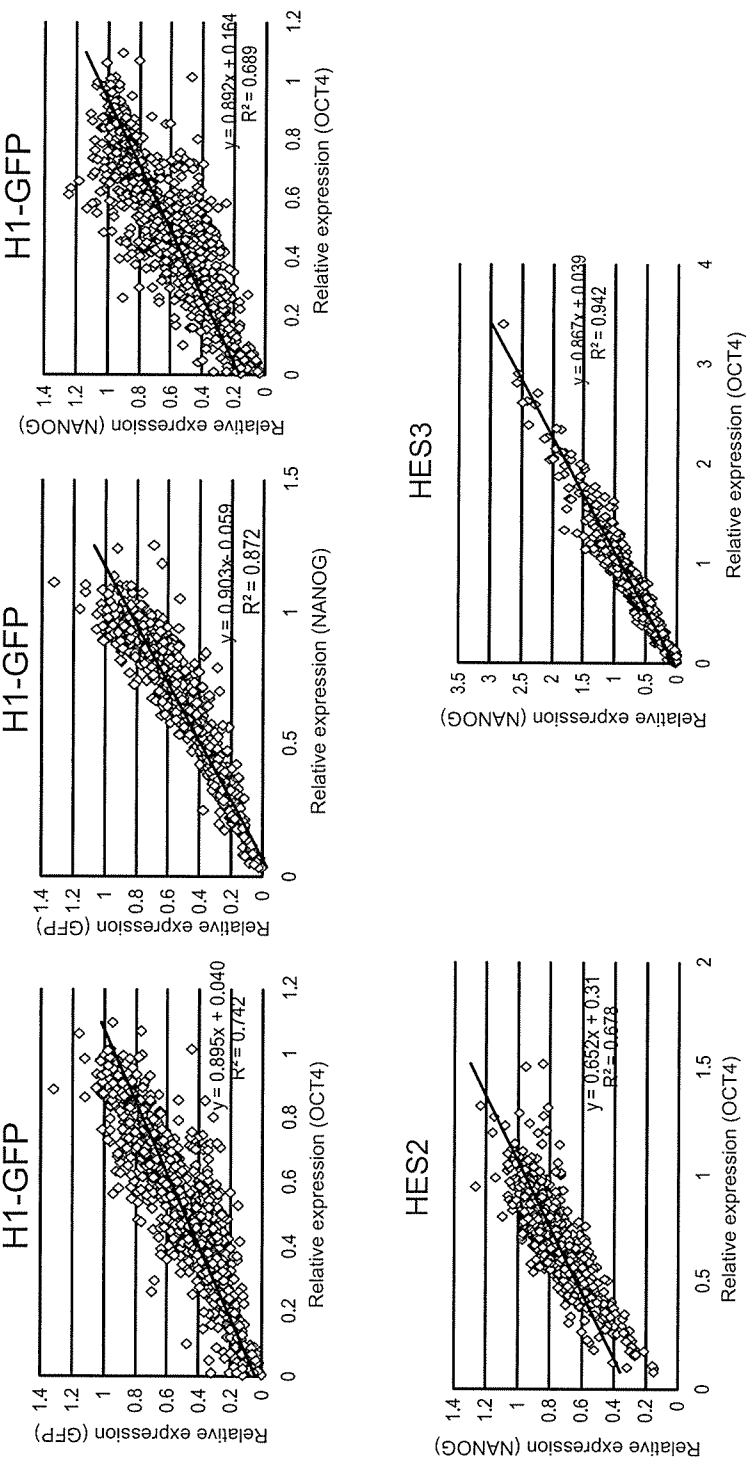

H1-GFP
Relative expression (GFP)
Relative expression (OCT4)
y = 0.895x + 0.040
R² = 0.742
H1-GFP
Relative expression (GFP)
Relative expression (NANOG)
y = 0.903x - 0.059
R² = 0.872
H1-GFP
Relative expression (NANOG)
Relative expression (OCT4)
y = 0.892x + 0.164
R² = 0.689
HES2
Relative expression (NANOG)
Relative expression (OCT4)
y = 0.652x + 0.31
R² = 0.678
HES3
Relative expression (NANOG)
Relative expression (OCT4)
y = 0.867x + 0.039
R² = 0.942

FIG. 6D

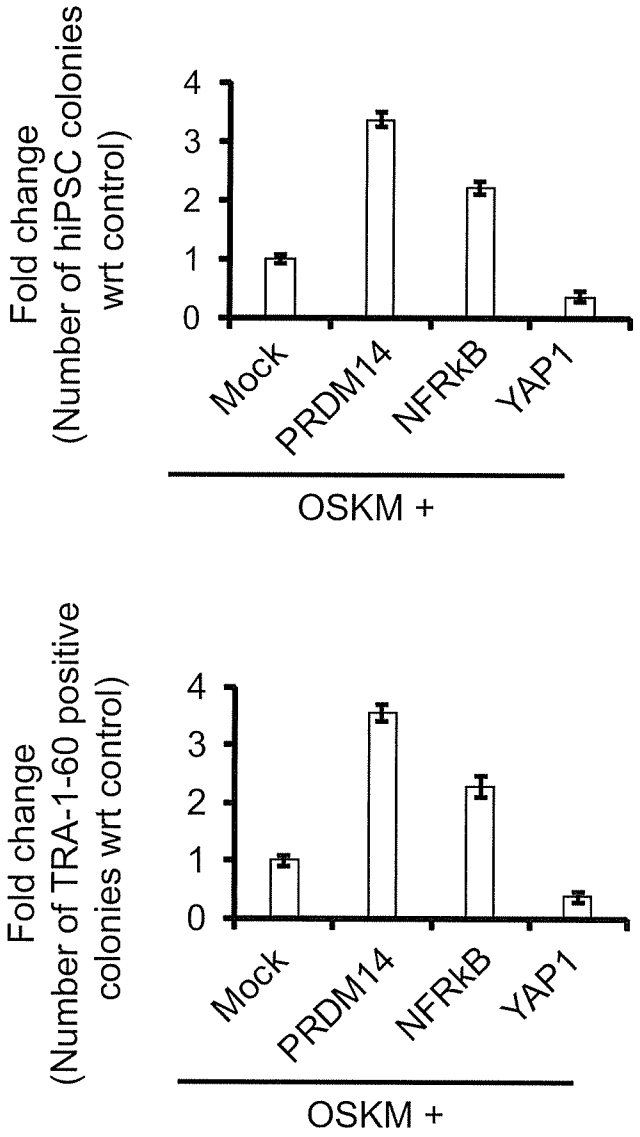

Fold change
(Number of hiPSC colonies
wrt control)
4
3
2
1
0
Mock
PRDM14
NFRkB
YAP1
OSKM +
Fold change
(Number of TRA-1-60 positive
colonies wrt control)
4
3
2
1
0
Mock
PRDM14
NFRkB
YAP1
OSKM +

FIG. 7A

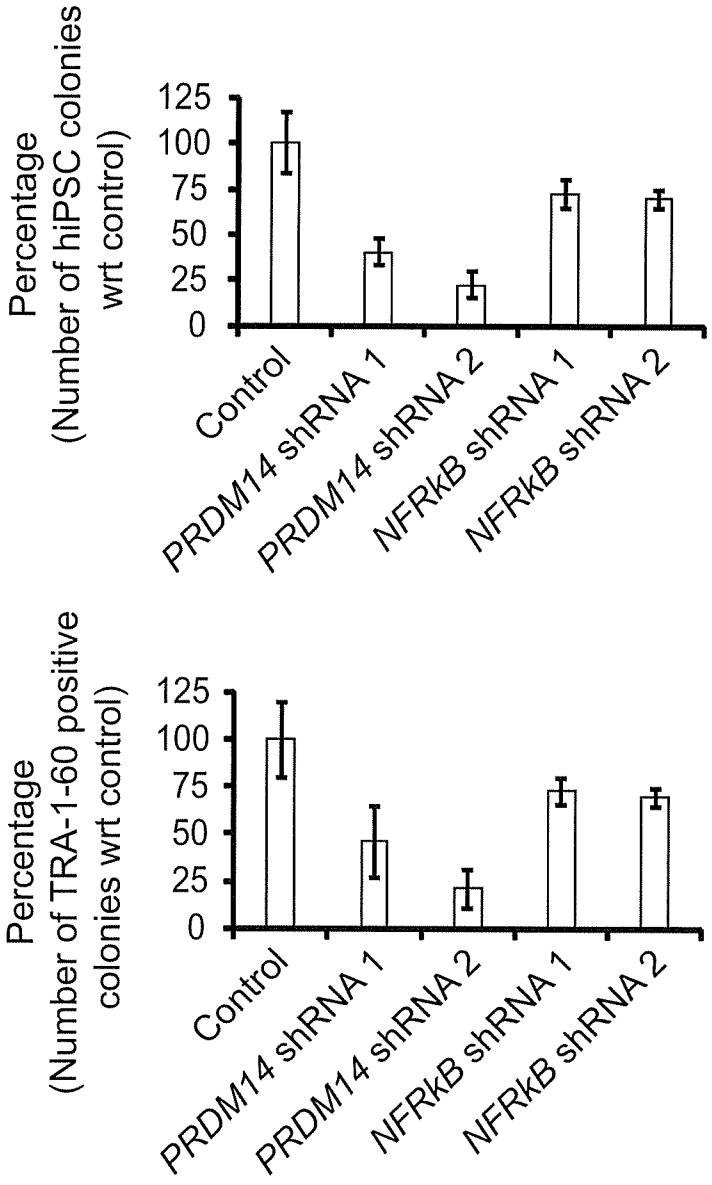

Percentage
(Number of hiPSC colonies wrt control)
125
100
75
50
25
0
Control
PRDM14 shRNA 1
PRDM14 shRNA 2
NFRkB shRNA 1
NFRkB shRNA 2
Percentage
(Number of TRA-1-60 positive colonies wrt control)
125
100
75
50
25
0
Control
PRDM14 shRNA 1
PRDM14 shRNA 2
NFRkB shRNA 1
NFRkB shRNA 2

FIG. 7B

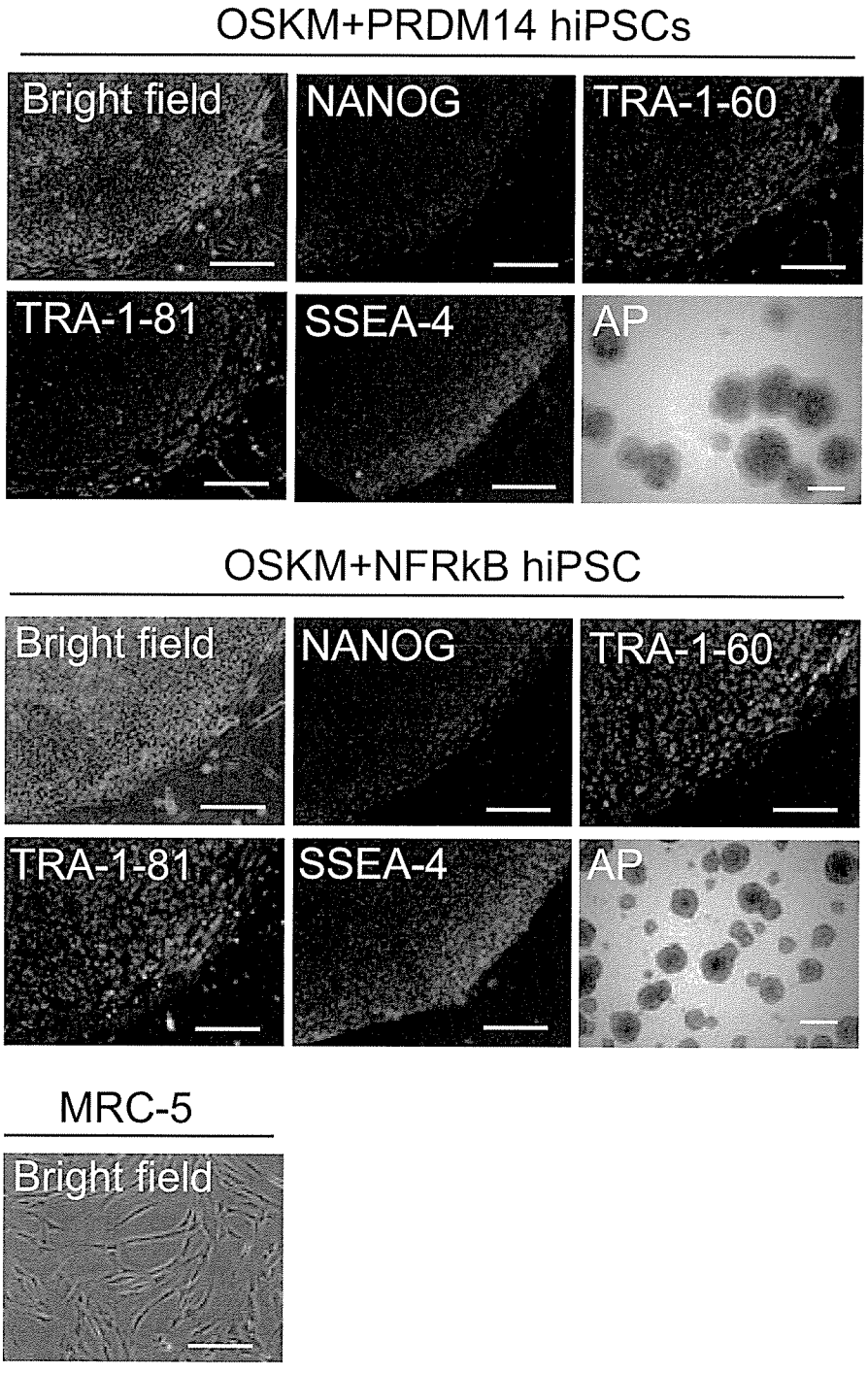

OSKM+PRDM14 hiPSCs
Bright field
NANOG
TRA-1-60
TRA-1-81
SSEA-4
AP
OSKM+NFRkB hiPSC
Bright field
NANOG
TRA-1-60
TRA-1-81
SSEA-4
AP
MRC-5
Bright field

FIG. 7C

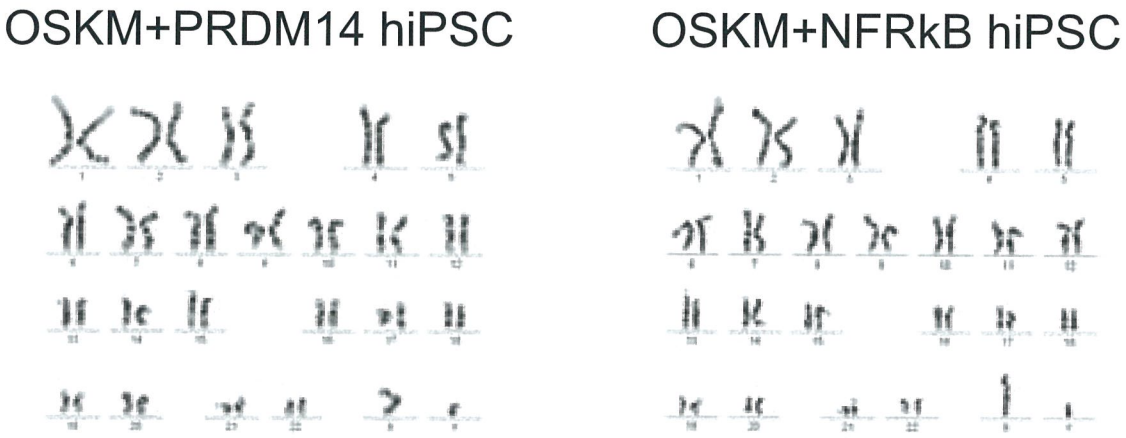

OSKM+PRDM14 hiPSC
OSKM+NFRkB hiPSC

FIG. 7D

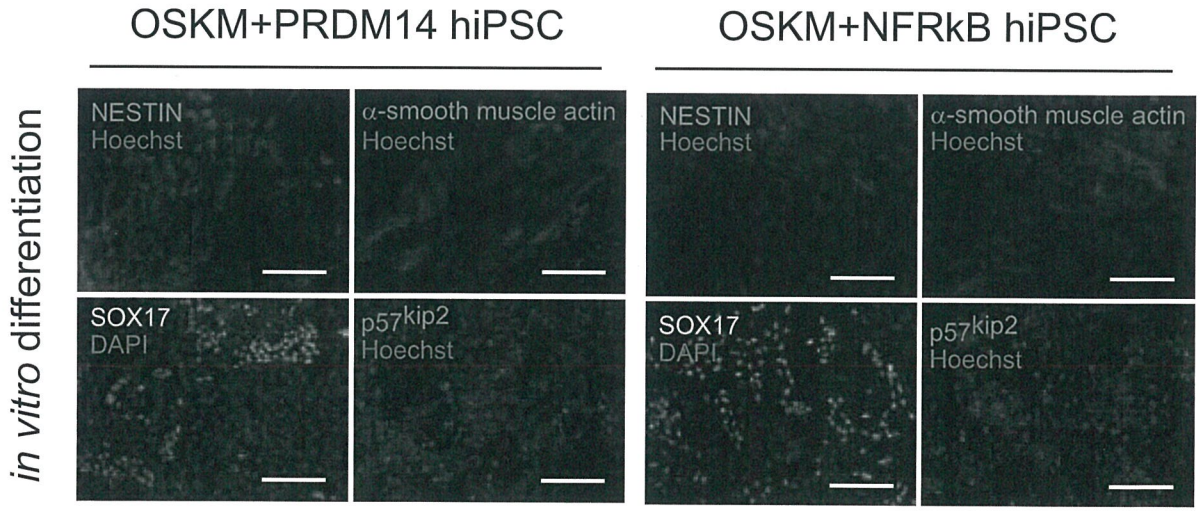

OSKM+PRDM14 hiPSC
OSKM+NFRkB hiPSC
in vitro differentiation
NESTIN
Hoechst
α-smooth muscle actin
Hoechst
SOX17
DAPI
p57kip2
Hoechst
NESTIN
Hoechst
α-smooth muscle actin
Hoechst
SOX17
DAPI
p57kip2
Hoechst

FIG. 7E

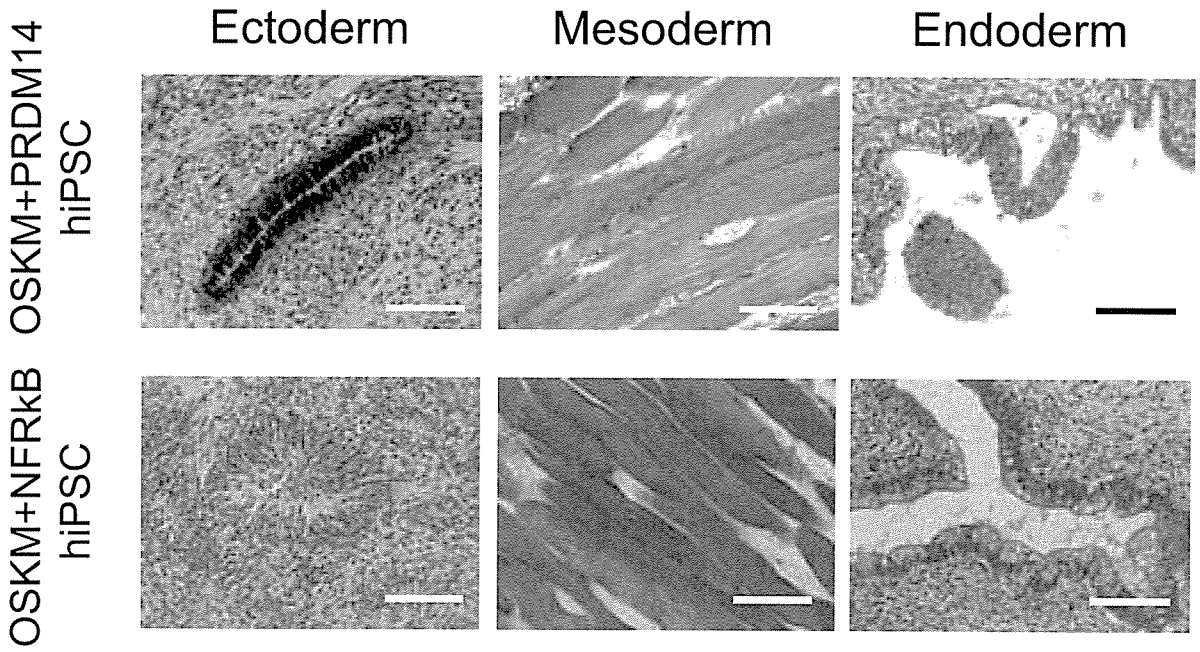

Ectoderm
Mesoderm
Endoderm
OSKM+PRDM14 hiPSC
OSKM+NFRkB hiPSC

FIG. 7F

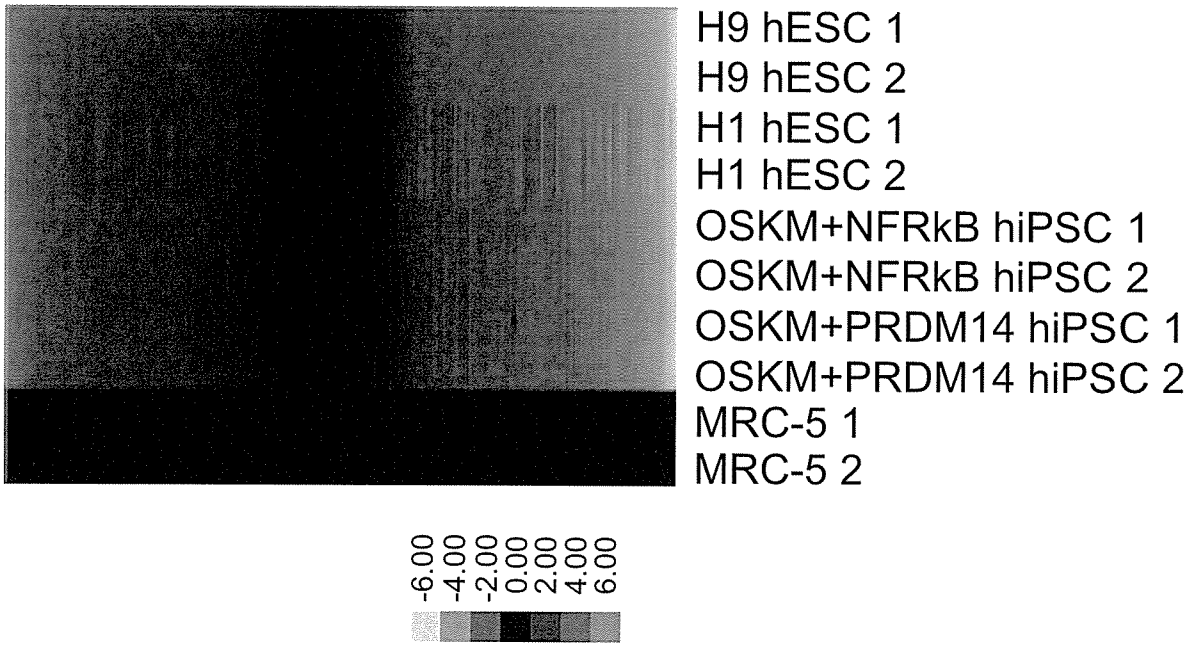

H9 hESC 1
H9 hESC 2
H1 hESC 1
H1 hESC 2
OSKM+NFRkB hiPSC 1
OSKM+NFRkB hiPSC 2
OSKM+PRDM14 hiPSC 1
OSKM+PRDM14 hiPSC 2
MRC-5 1
MRC-5 2
-6.00
-4.00
-2.00
0.00
2.00
4.00
6.00

FIG. 7G

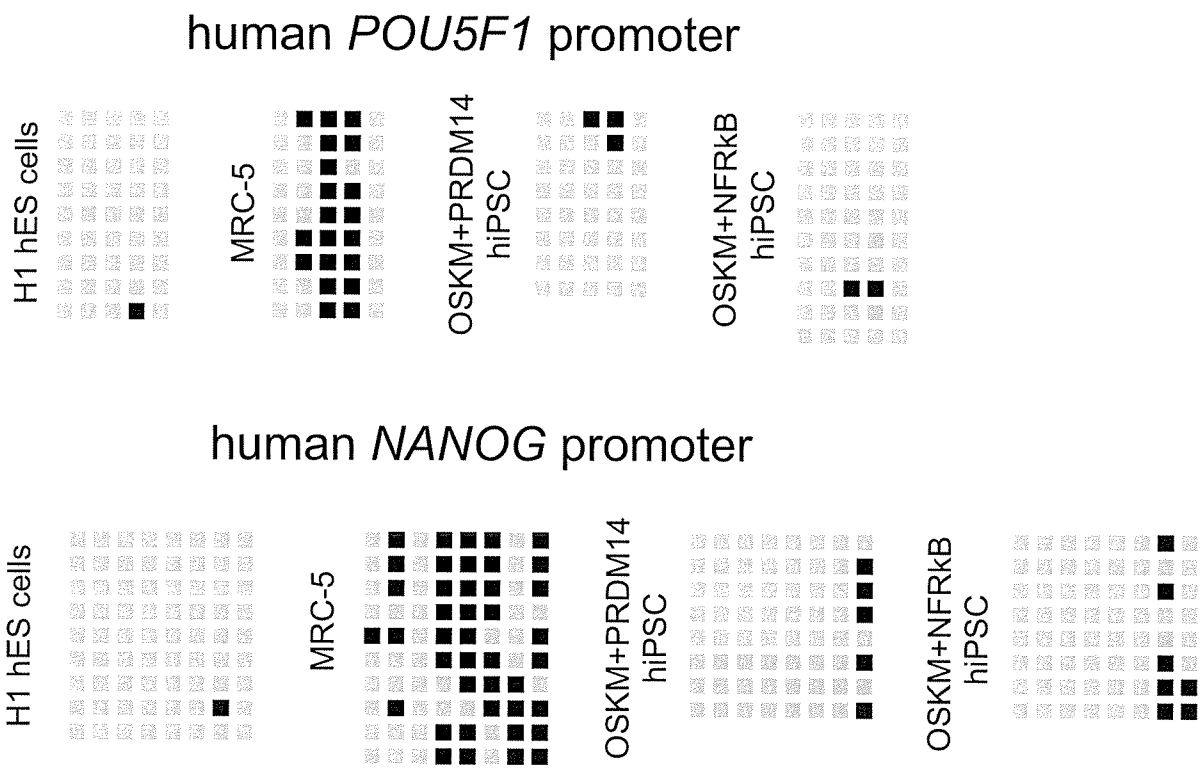

human *POU5F1* promoter
H1 hES cells
MRC-5
OSKM+PRDM14 hiPSC
OSKM+NFRkB hiPSC
human *NANOG* promoter
H1 hES cells
MRC-5
OSKM+PRDM14 hiPSC
OSKM+NFRkB hiPSC

FIG. 7H

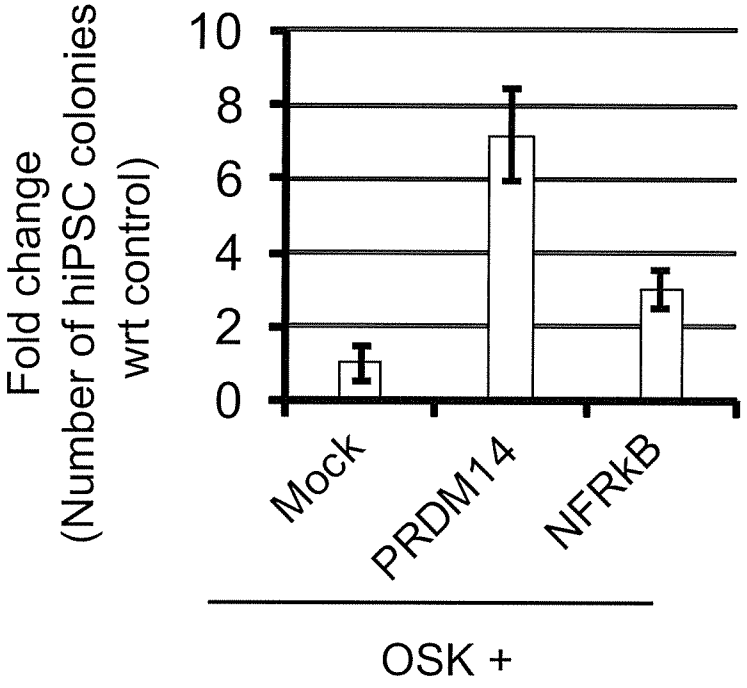

Fold change
(Number of hiPSC colonies
wrt control)
10
8
6
4
2
0
Mock
PRDM14
NFRkB
OSK +

FIG. 8A

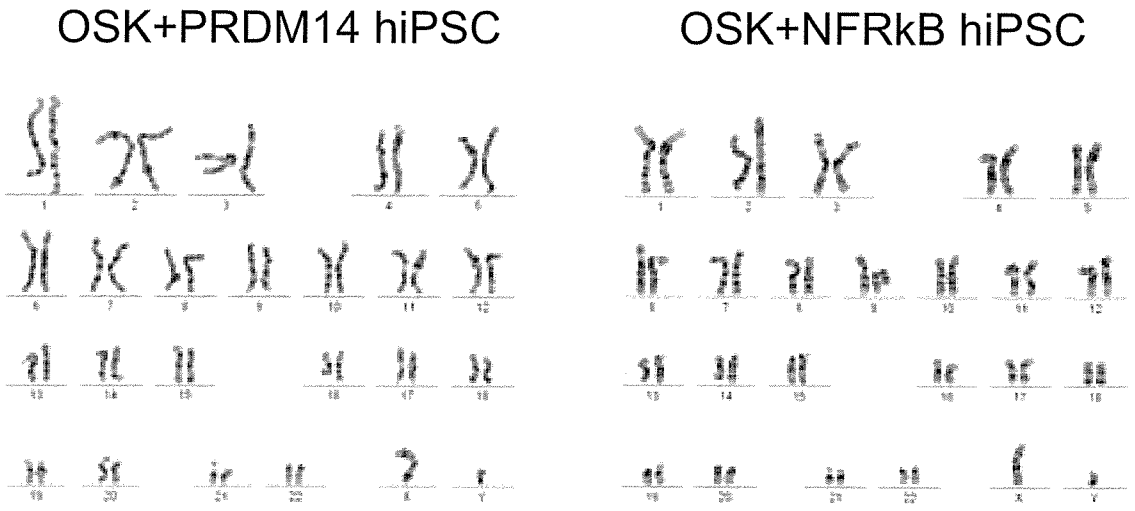

OSK+PRDM14 hiPSC
OSK+NFRkB hiPSC

FIG. 8B

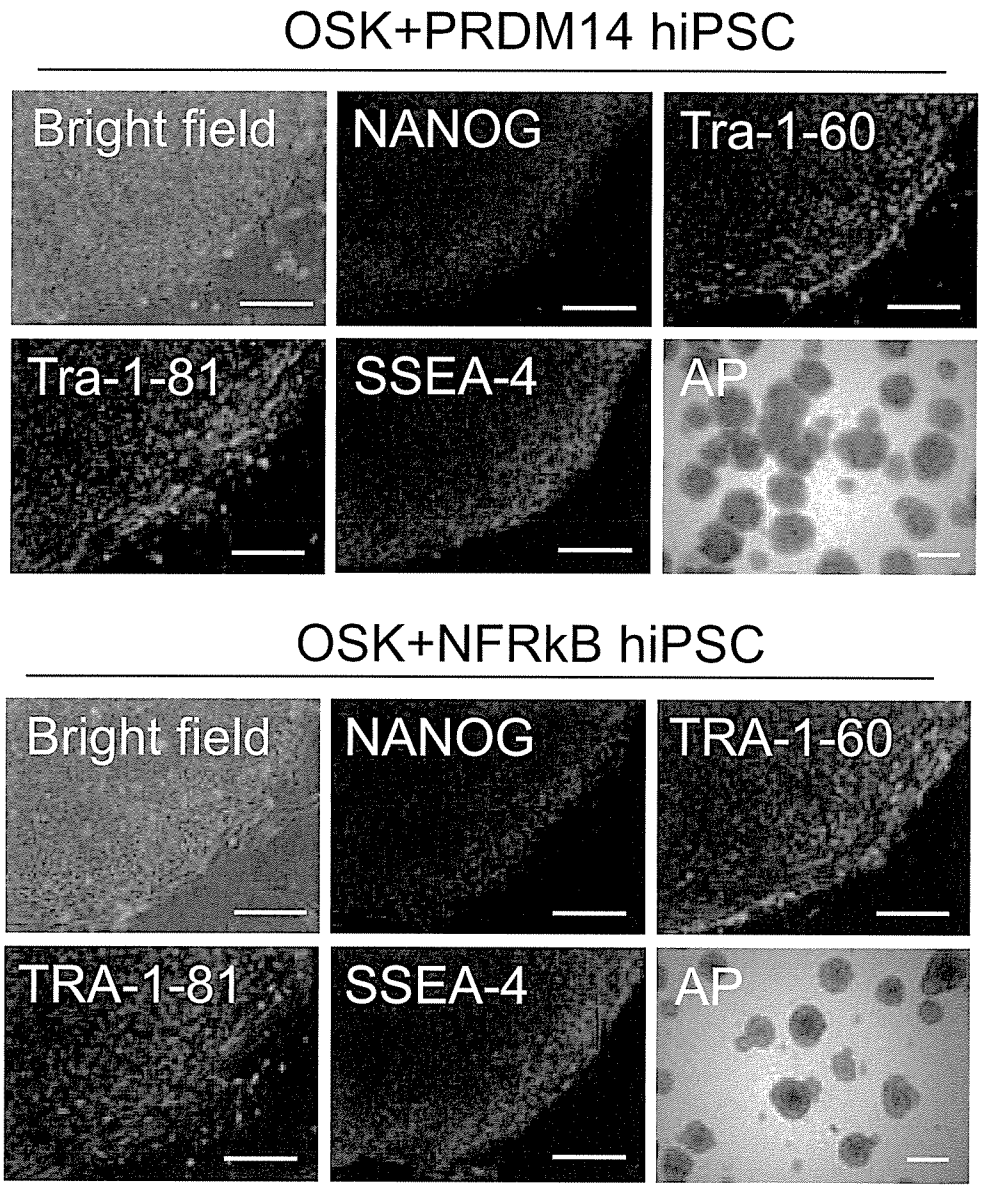

OSK+PRDM14 hiPSC
Bright field
NANOG
Tra-1-60
Tra-1-81
SSEA-4
AP
OSK+NFRkB hiPSC
Bright field
NANOG
TRA-1-60
TRA-1-81
SSEA-4
AP

FIG. 8C

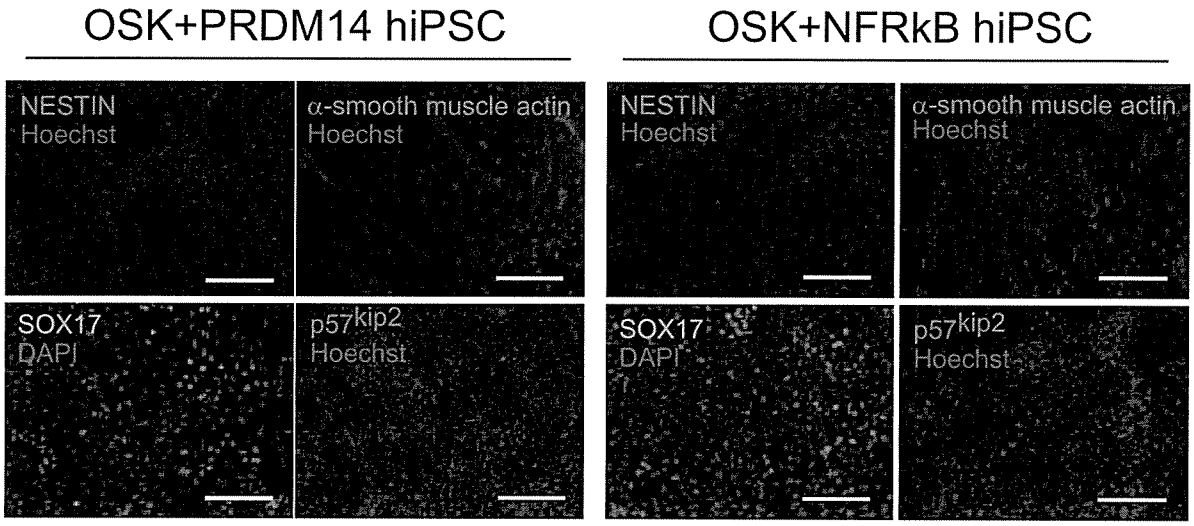

OSK+PRDM14 hiPSC
OSK+NFRkB hiPSC
NESTIN
Hoechst
α-smooth muscle actin
Hoechst
NESTIN
Hoechst
α-smooth muscle actin
Hoechst
SOX17
DAPI
p57kip2
Hoechst
SOX17
DAPI
p57kip2
Hoechst

FIG. 8D

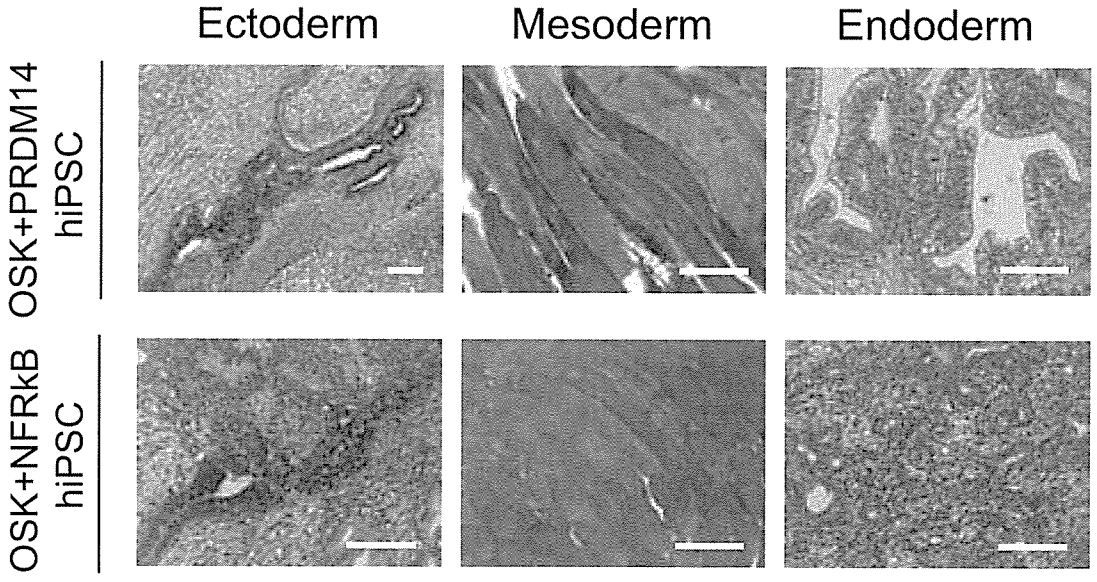

Ectoderm
Mesoderm
Endoderm
OSK+PRDM14 hiPSC
OSK+NFRkB hiPSC

FIG. 8E

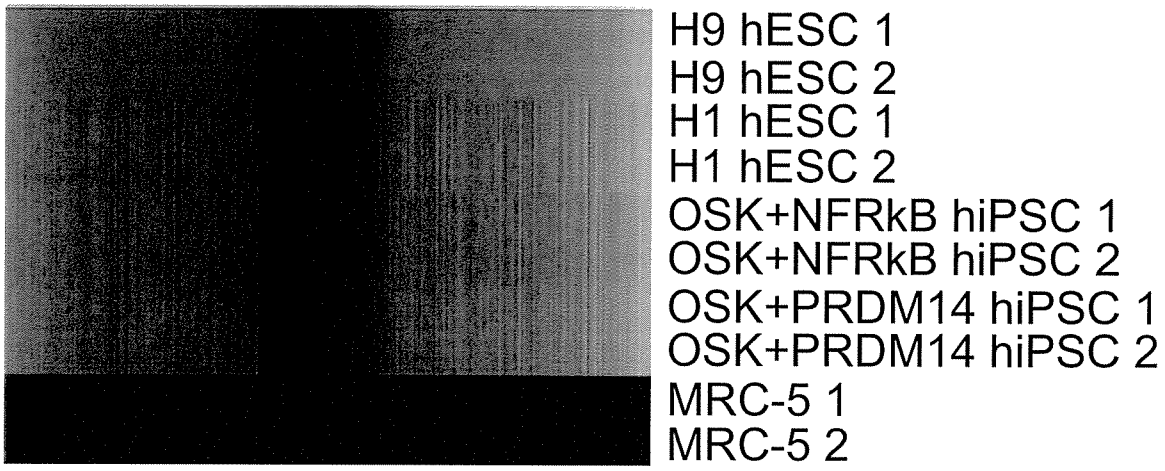

H9 hESC 1
H9 hESC 2
H1 hESC 1
H1 hESC 2
OSK+NFRkB hiPSC 1
OSK+NFRkB hiPSC 2
OSK+PRDM14 hiPSC 1
OSK+PRDM14 hiPSC 2
MRC-5 1
MRC-5 2

FIG. 8F

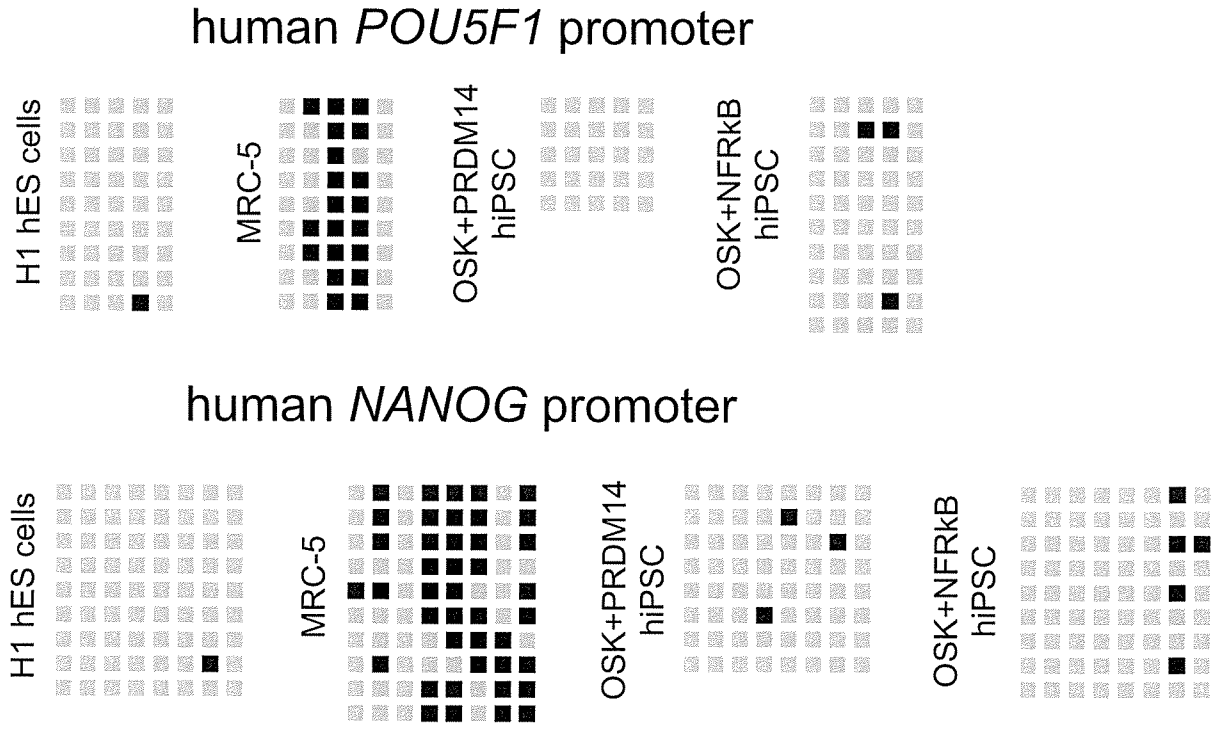

human *POU5F1* promoter
H1 hES cells
MRC-5
OSK+PRDM14 hiPSC
OSK+NFRkB hiPSC
human *NANOG* promoter
H1 hES cells
MRC-5
OSK+PRDM14 hiPSC
OSK+NFRkB hiPSC

FIG. 8G

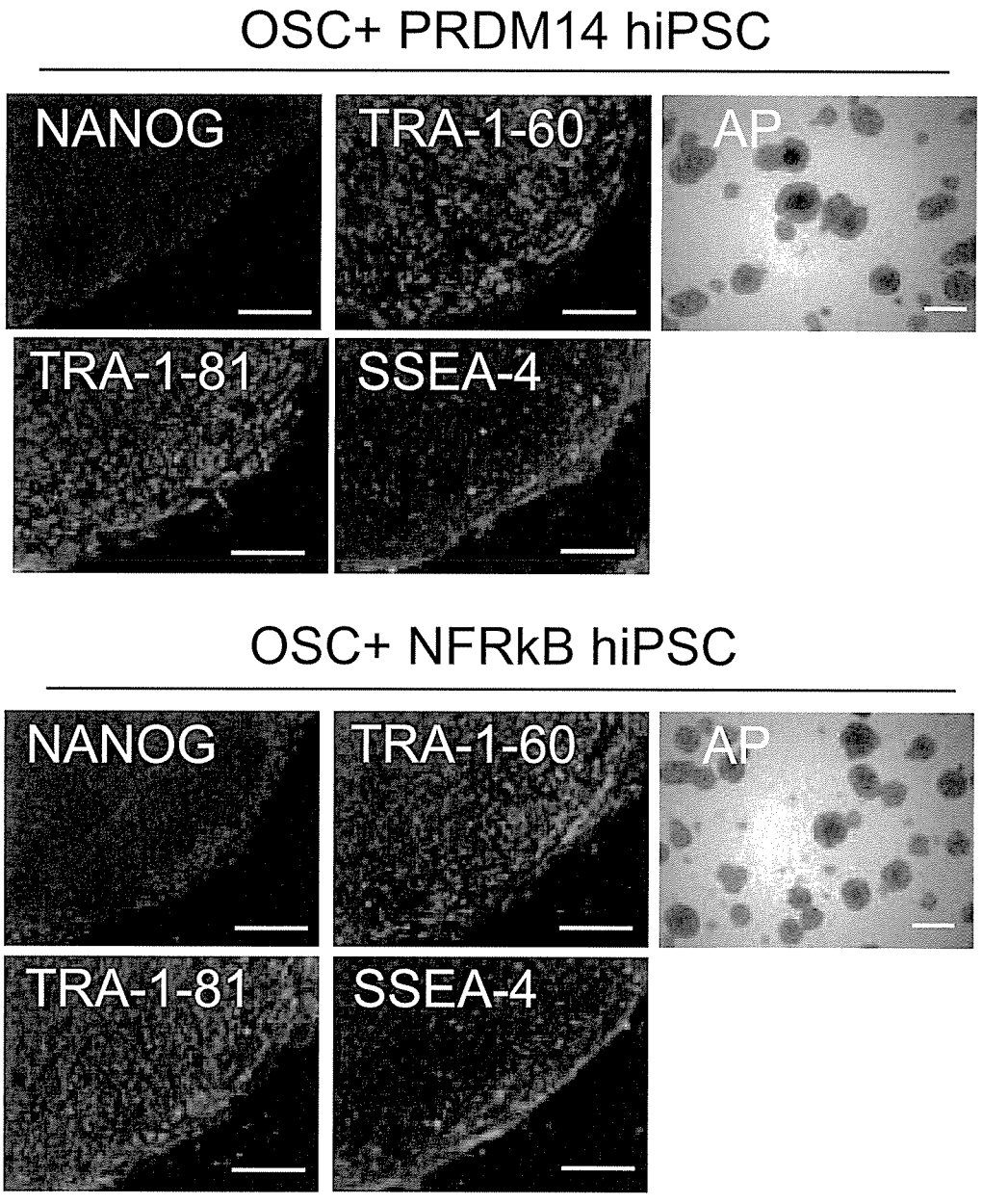

OSC+ PRDM14 hiPSC
NANOG
TRA-1-60
AP
TRA-1-81
SSEA-4
OSC+ NFRkB hiPSC
NANOG
TRA-1-60
AP
TRA-1-81
SSEA-4

FIG. 8H

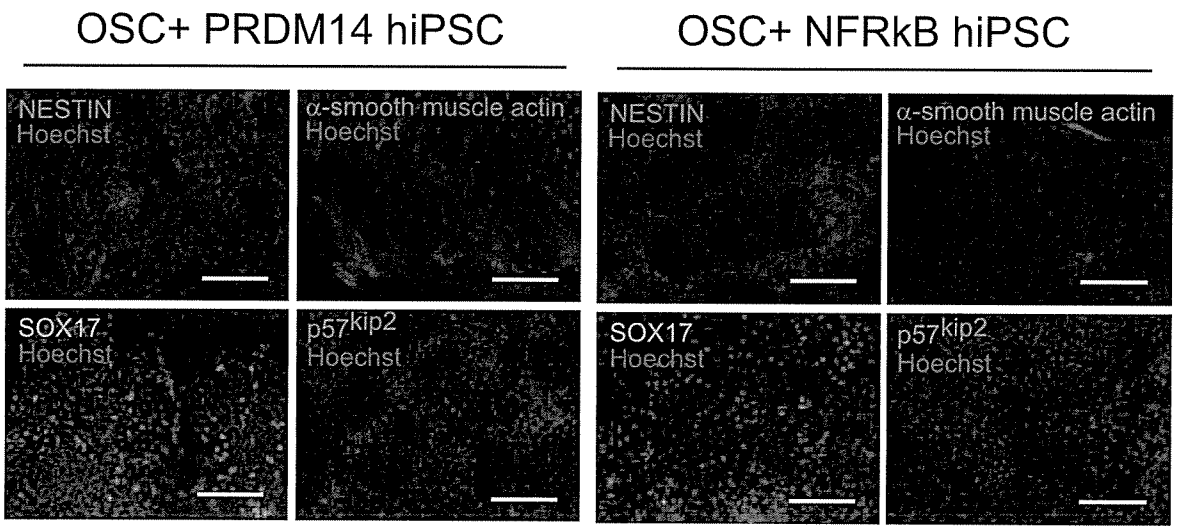

OSC+ PRDM14 hiPSC
OSC+ NFRkB hiPSC
NESTIN
Hoechst
α-smooth muscle actin
Hoechst
NESTIN
Hoechst
α-smooth muscle actin
Hoechst
SOX17
Hoechst
p57kip2
Hoechst
SOX17
Hoechst
p57kip2
Hoechst

FIG. 8I

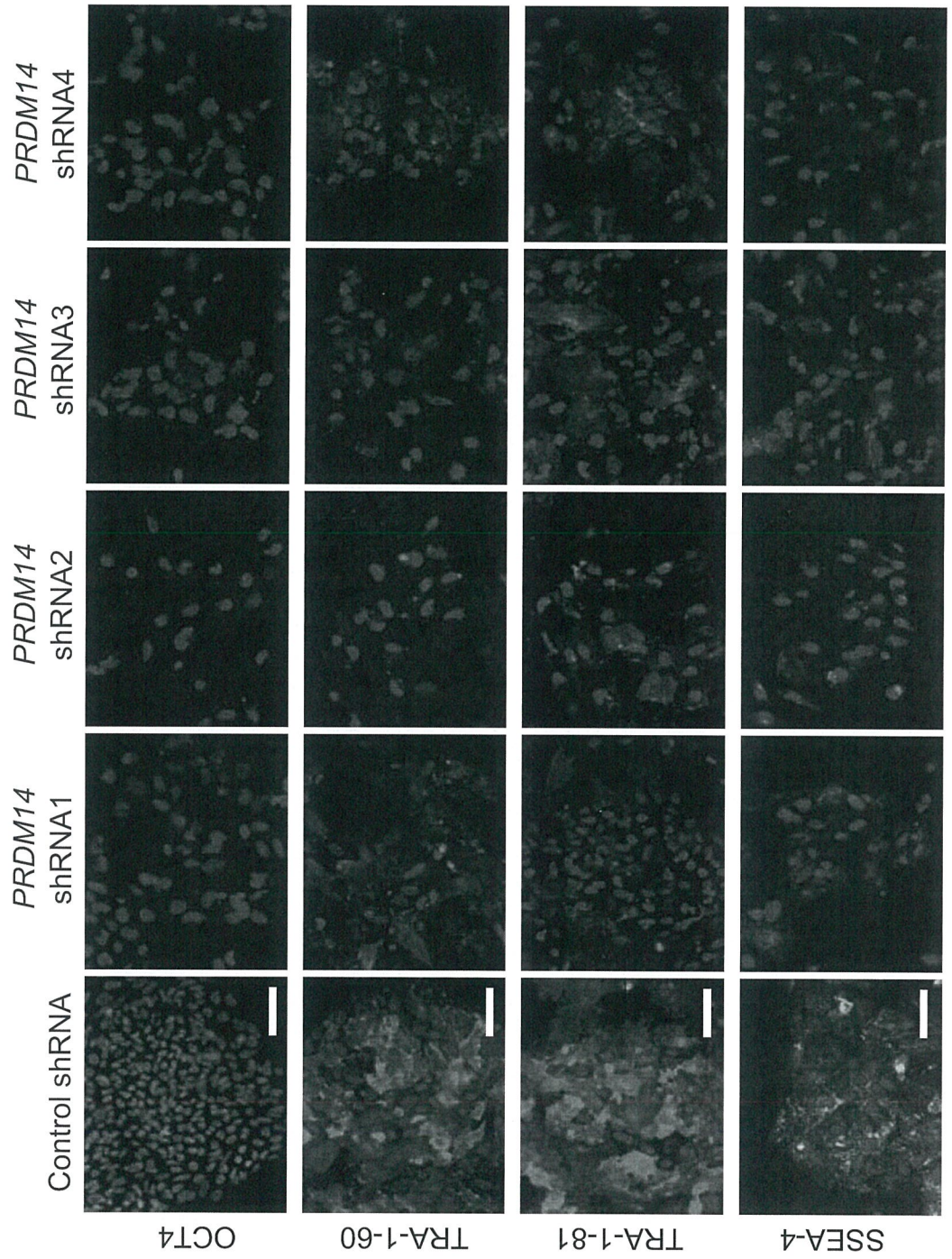

Control shRNA
PRDM14 shRNA1
PRDM14 shRNA2
PRDM14 shRNA3
PRDM14 shRNA4
OCT4
TRA-1-60
TRA-1-81
SSEA-4

FIG. 9A

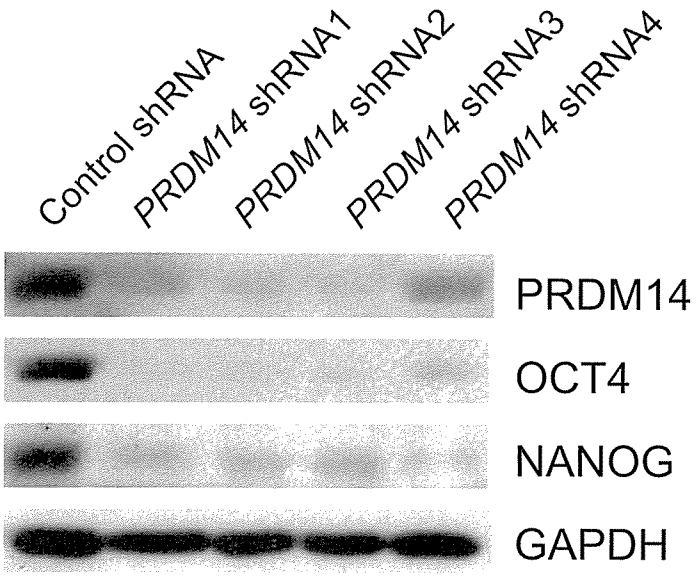

Control shRNA
PRDM14 shRNA1
PRDM14 shRNA2
PRDM14 shRNA3
PRDM14 shRNA4
PRDM14
OCT4
NANOG
GAPDH

FIG. 9B

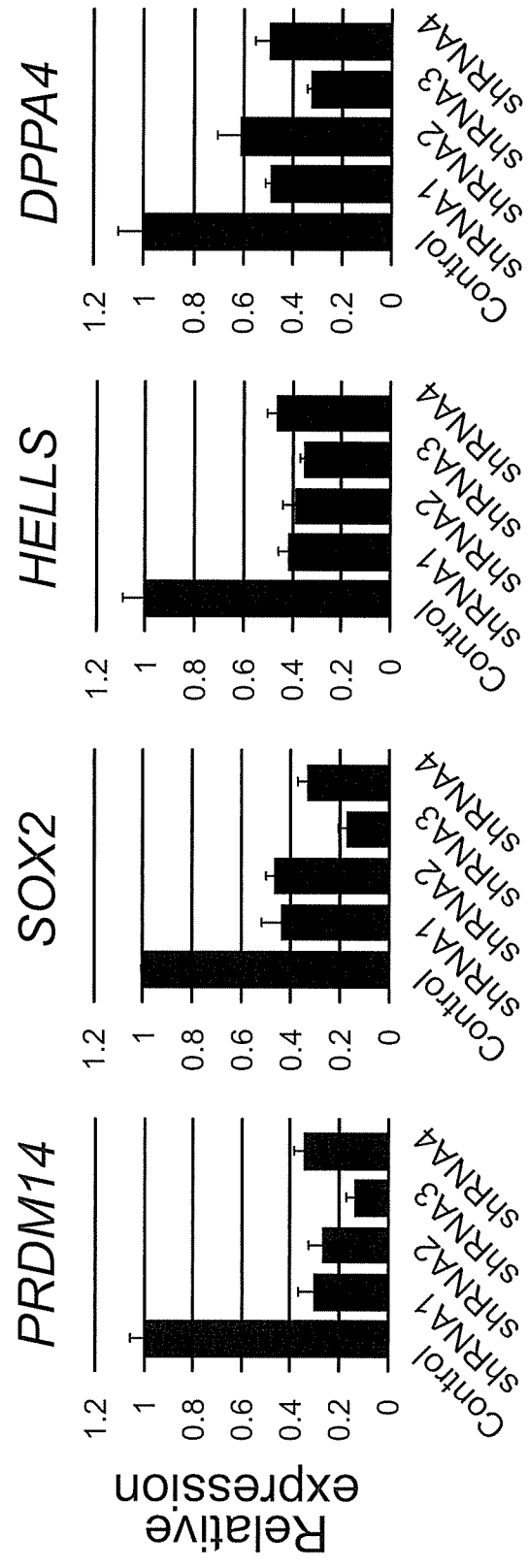

Relative expression
PRDM14
SOX2
HELLS
DPPA4
1.2
1
0.8
0.6
0.4
0.2
0
Control
shRNA1
shRNA2
shRNA3
shRNA4

FIG. 9C

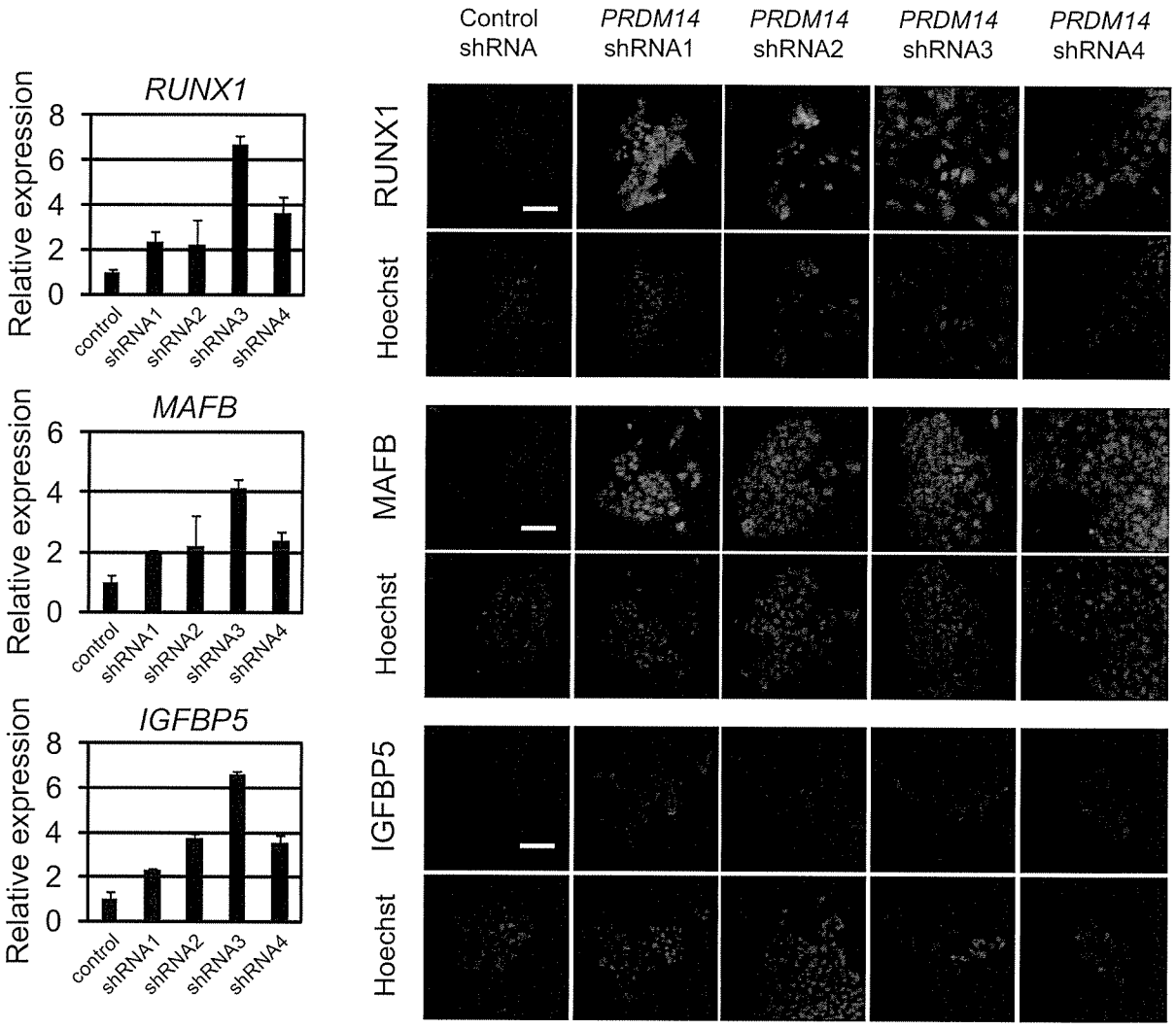

Control shRNA
PRDM14 shRNA1
PRDM14 shRNA2
PRDM14 shRNA3
PRDM14 shRNA4
RUNX1
Hoechst
MAFB
Hoechst
IGFBP5
Hoechst
RUNX1
Relative expression
0
2
4
6
8
control
shRNA1
shRNA2
shRNA3
shRNA4
MAFB
Relative expression
0
2
4
6
control
shRNA1
shRNA2
shRNA3
shRNA4
IGFBP5
Relative expression
0
2
4
6
8
control
shRNA1
shRNA2
shRNA3
shRNA4

FIG. 9D

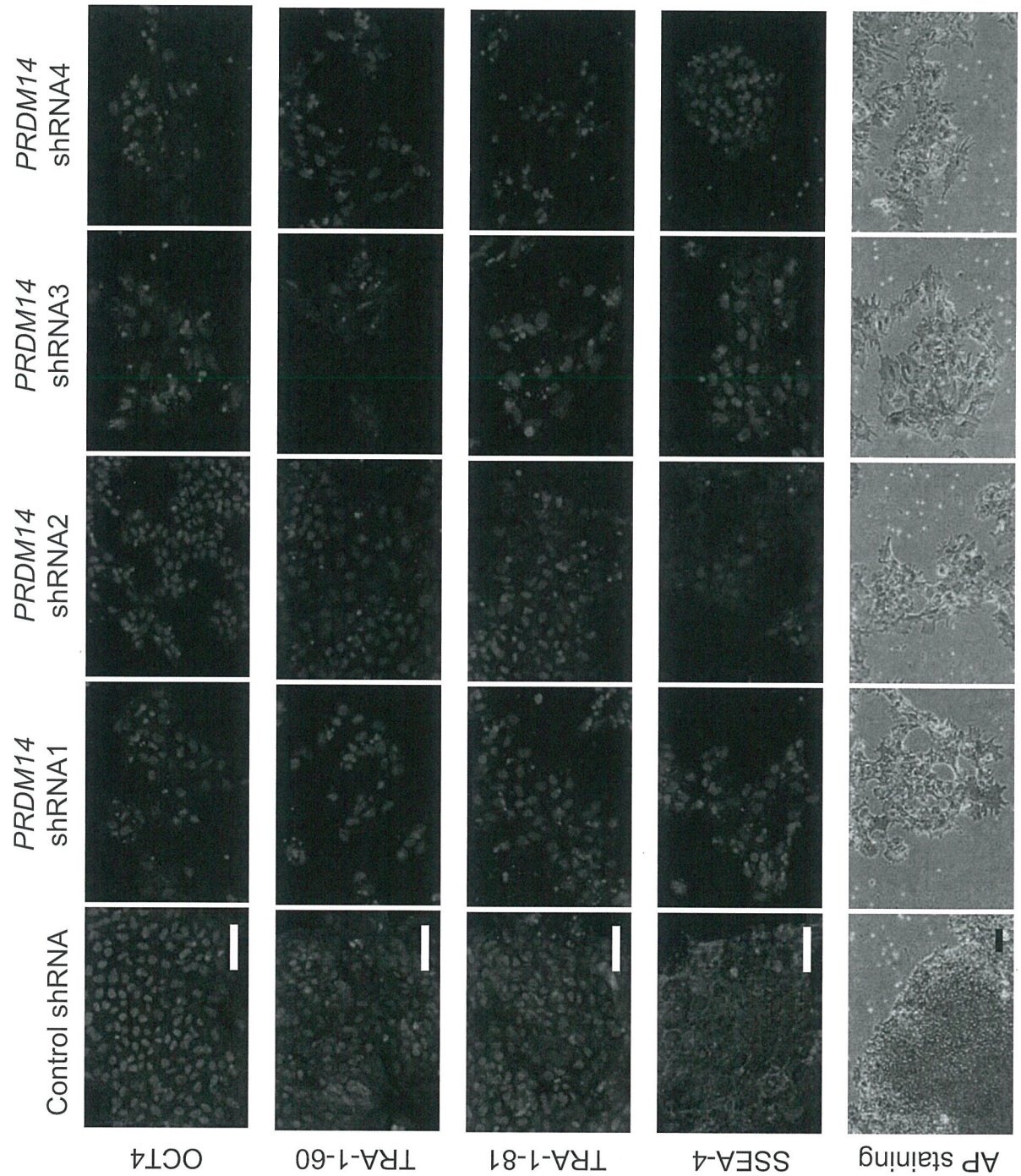

Control shRNA
PRDM14 shRNA1
PRDM14 shRNA2
PRDM14 shRNA3
PRDM14 shRNA4
OCT4
TRA-1-60
TRA-1-81
SSEA-4
AP staining

FIG. 10A

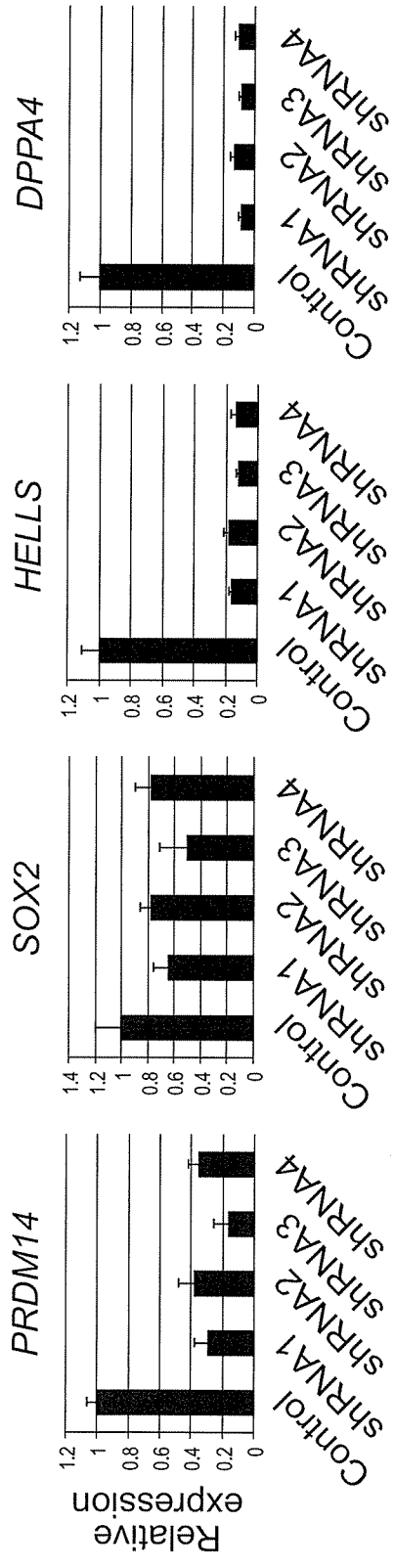

Relative expression
PRDM14
SOX2
HELLS
DPPA4
Control
shRNA1
shRNA2
shRNA3
shRNA4
0
0.2
0.4
0.6
0.8
1
1.2
1.4

FIG. 10B

Control shRNA
PRDM14 shRNA1
PRDM14 shRNA2
PRDM14 shRNA3
PRDM14 shRNA4
OCT4
TRA-1-60
TRA-1-81
SSEA-4
AP staining

FIG. 11A

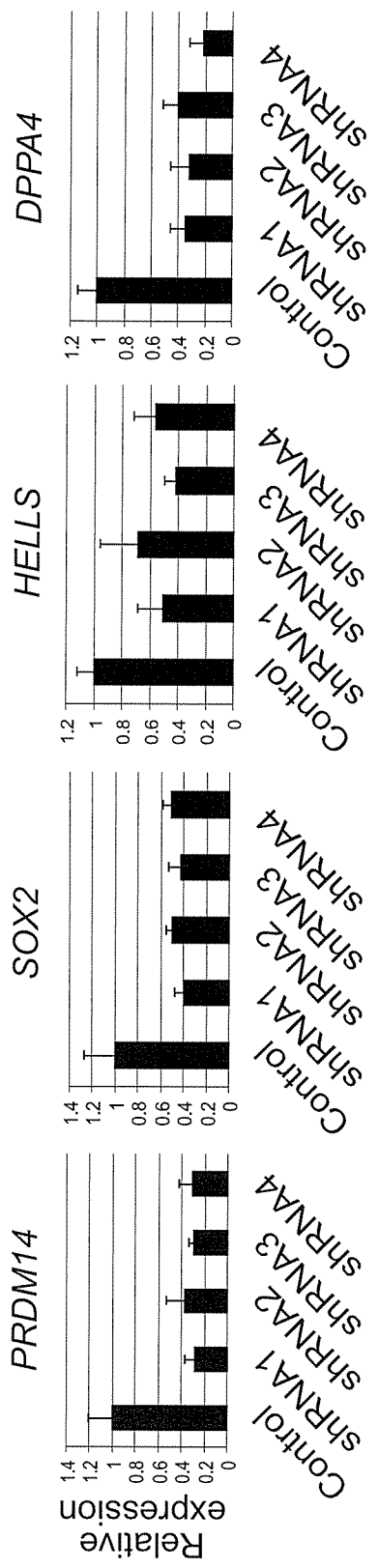

PRDM14
SOX2
HELLS
DPPA4
Relative expression
1.4
1.2
1
0.8
0.6
0.4
0.2
0
Control
shRNA1
shRNA2
shRNA3
shRNA4

FIG. 11B

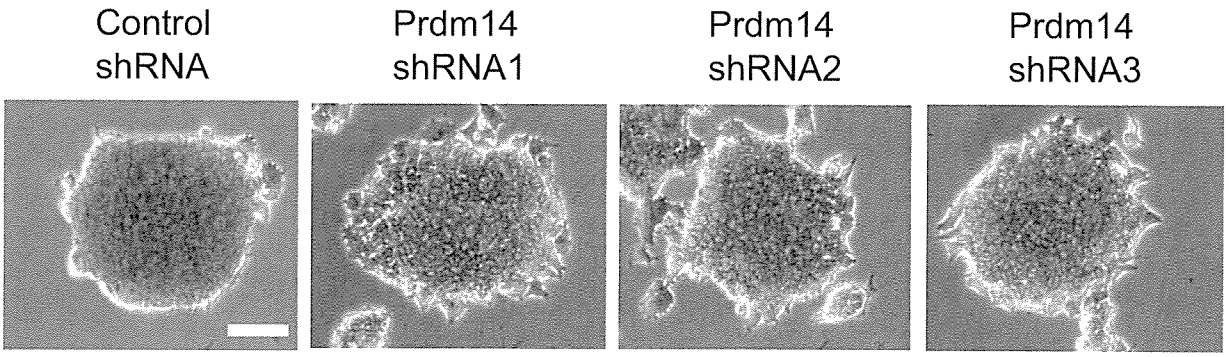


FIG. 12A

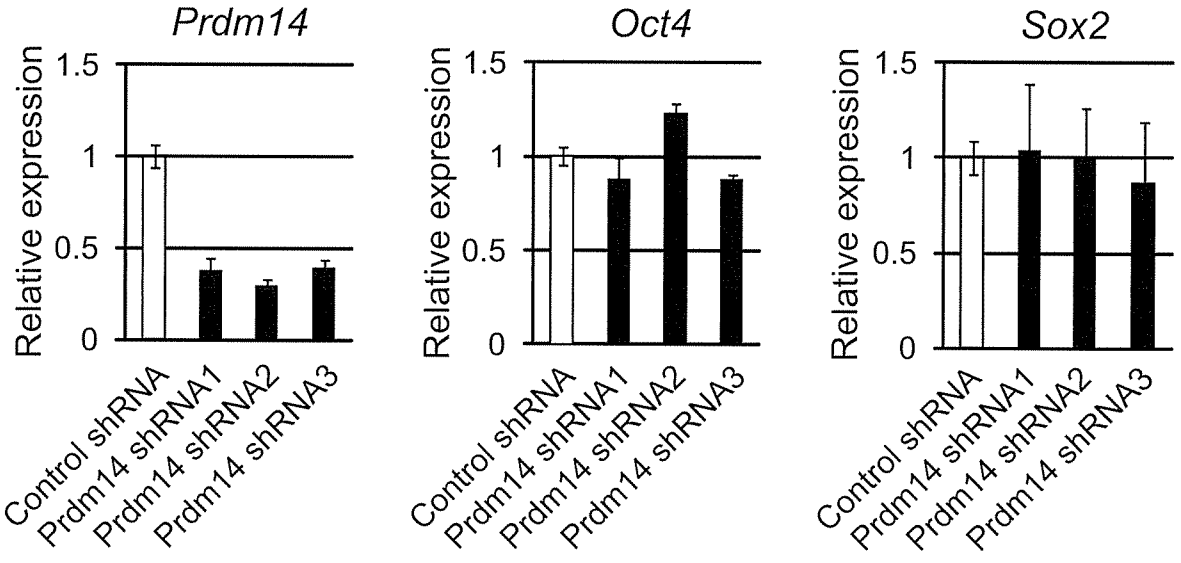


FIG. 12B

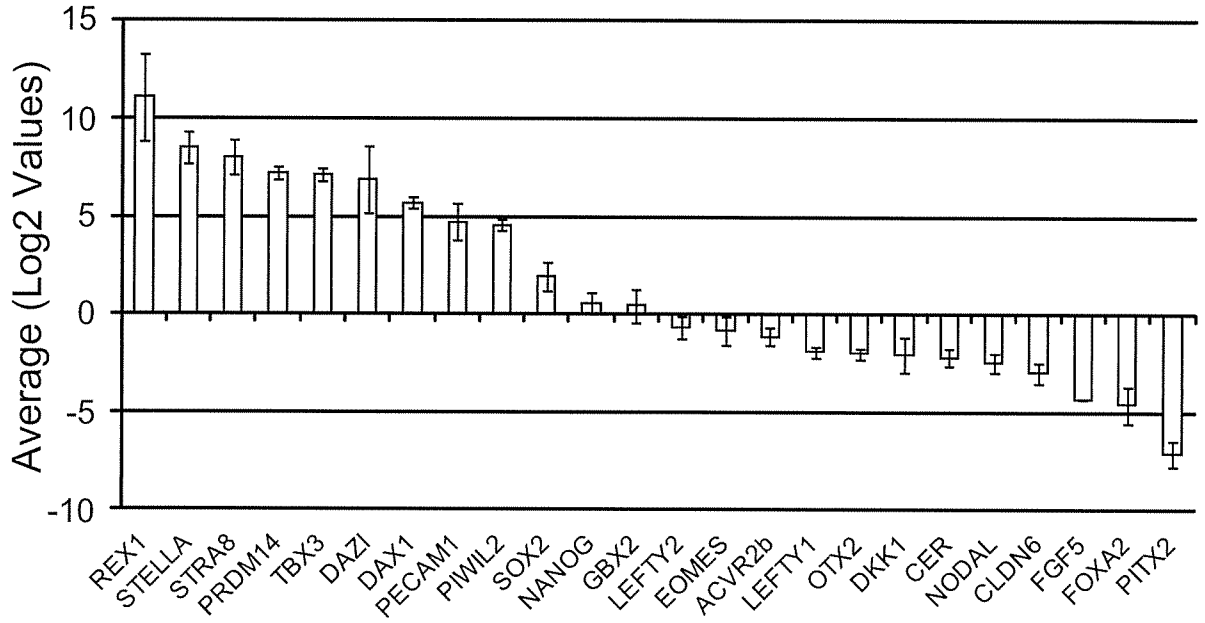


FIG. 12C

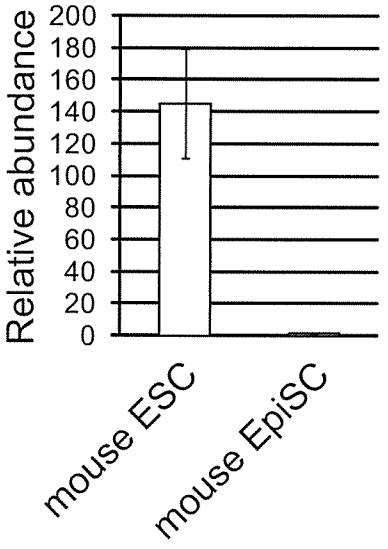


FIG. 12D

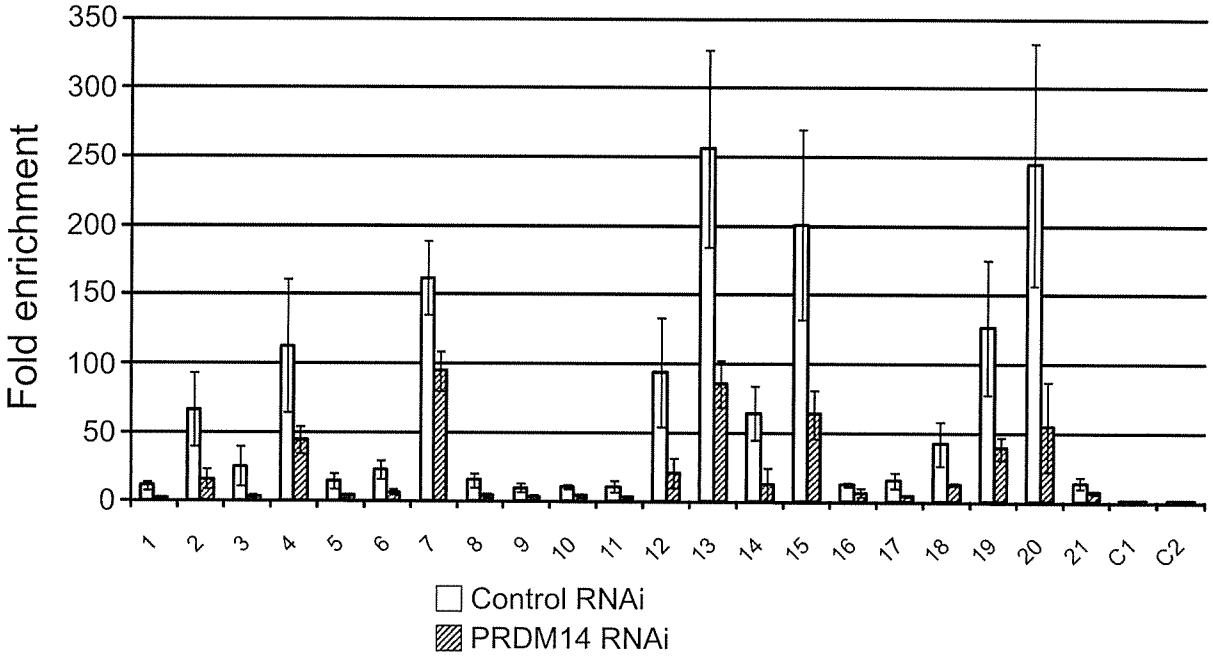


FIG. 13A

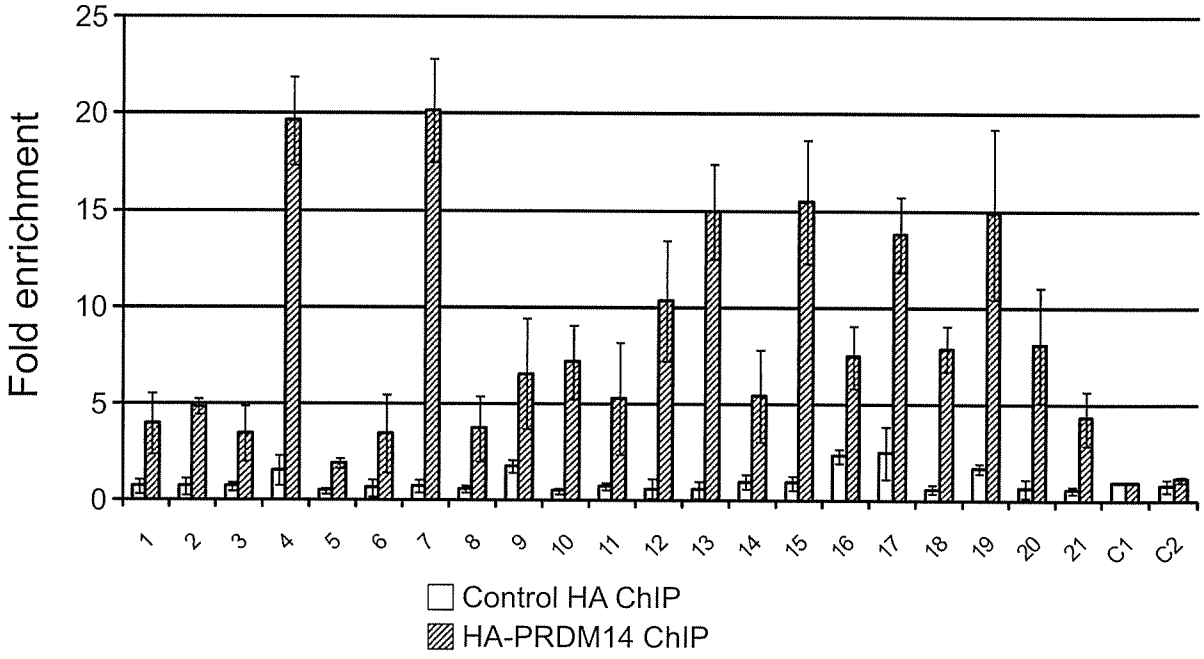


FIG. 13B

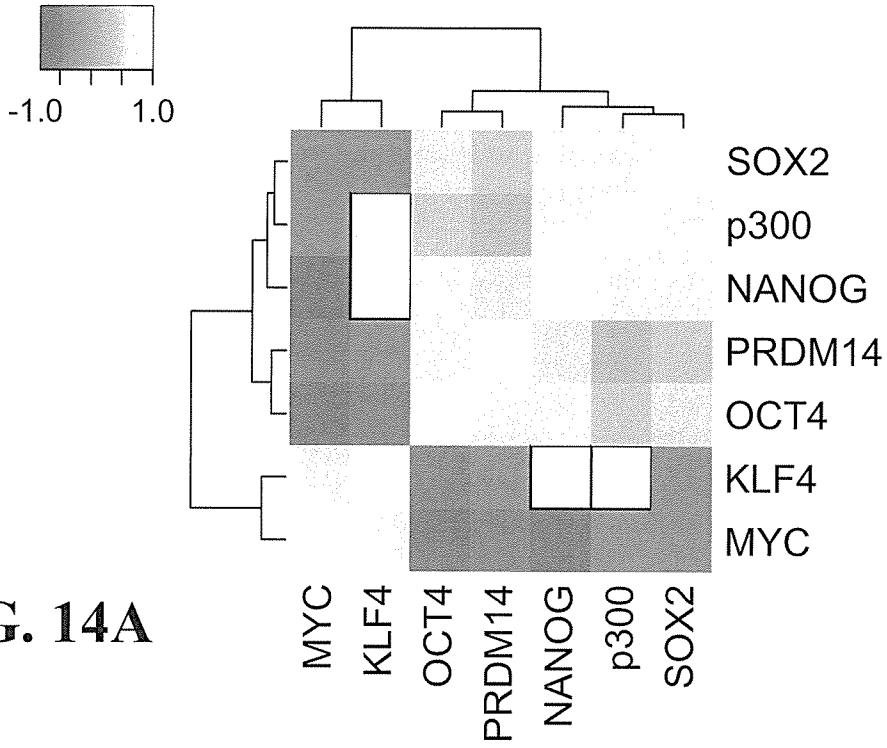


FIG. 14A

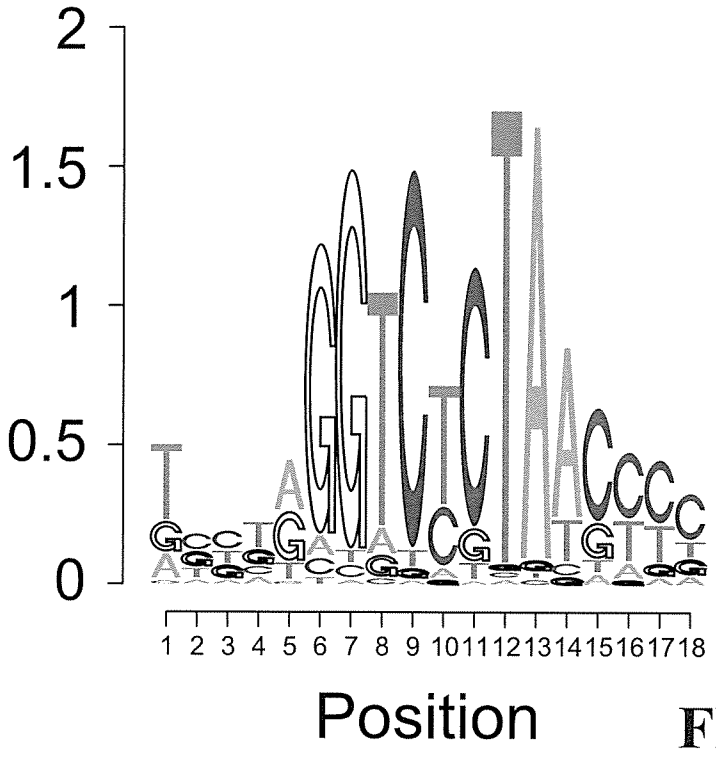


FIG. 14B

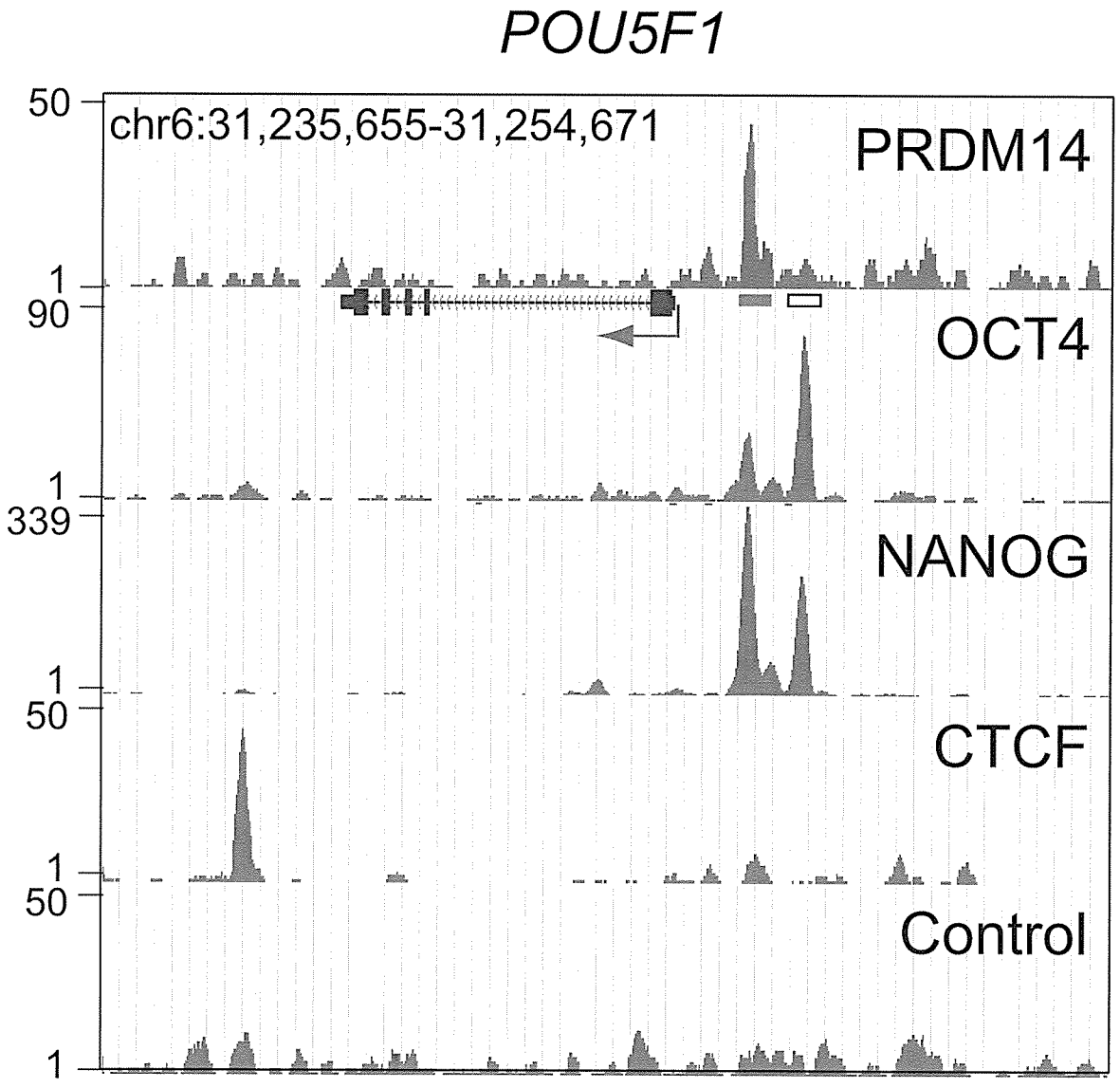

POU5F1
chr6:31,235,655-31,254,671
PRDM14
OCT4
NANOG
CTCF
Control
50
1
90
1
339
1
50
1
50
1

FIG. 14C

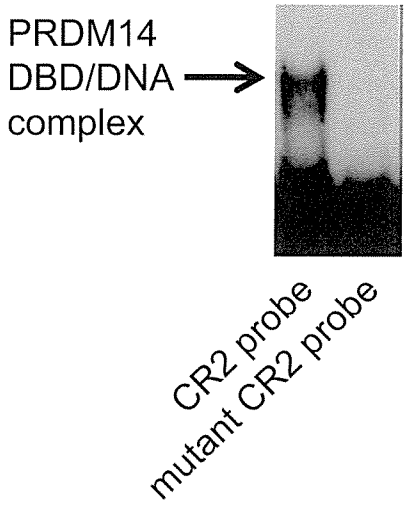


FIG. 14D

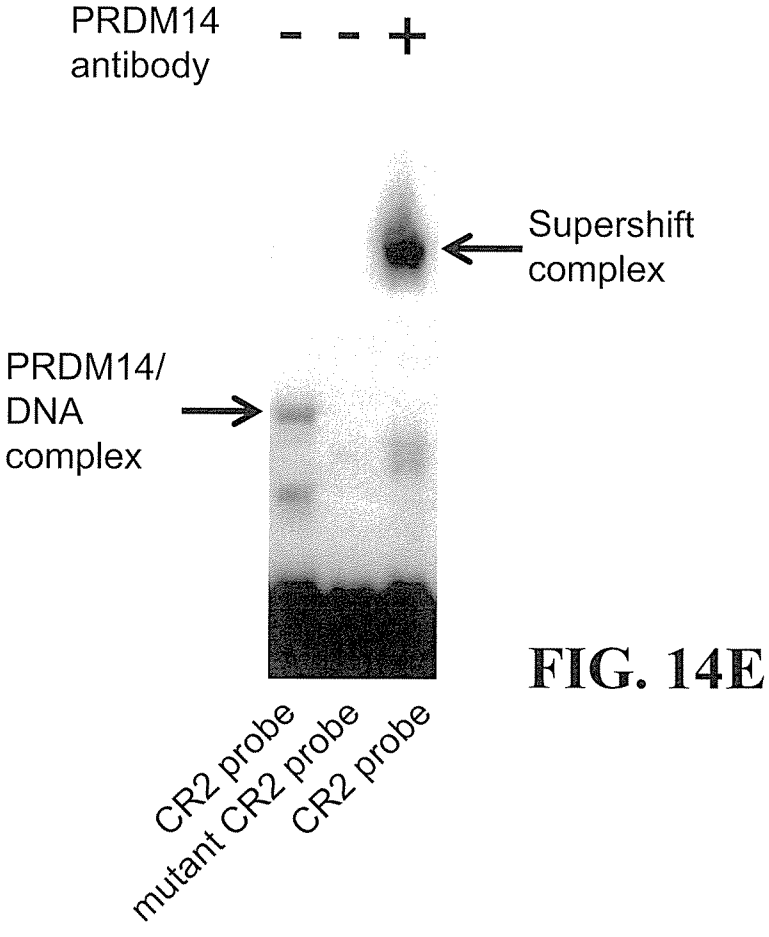


FIG. 14E

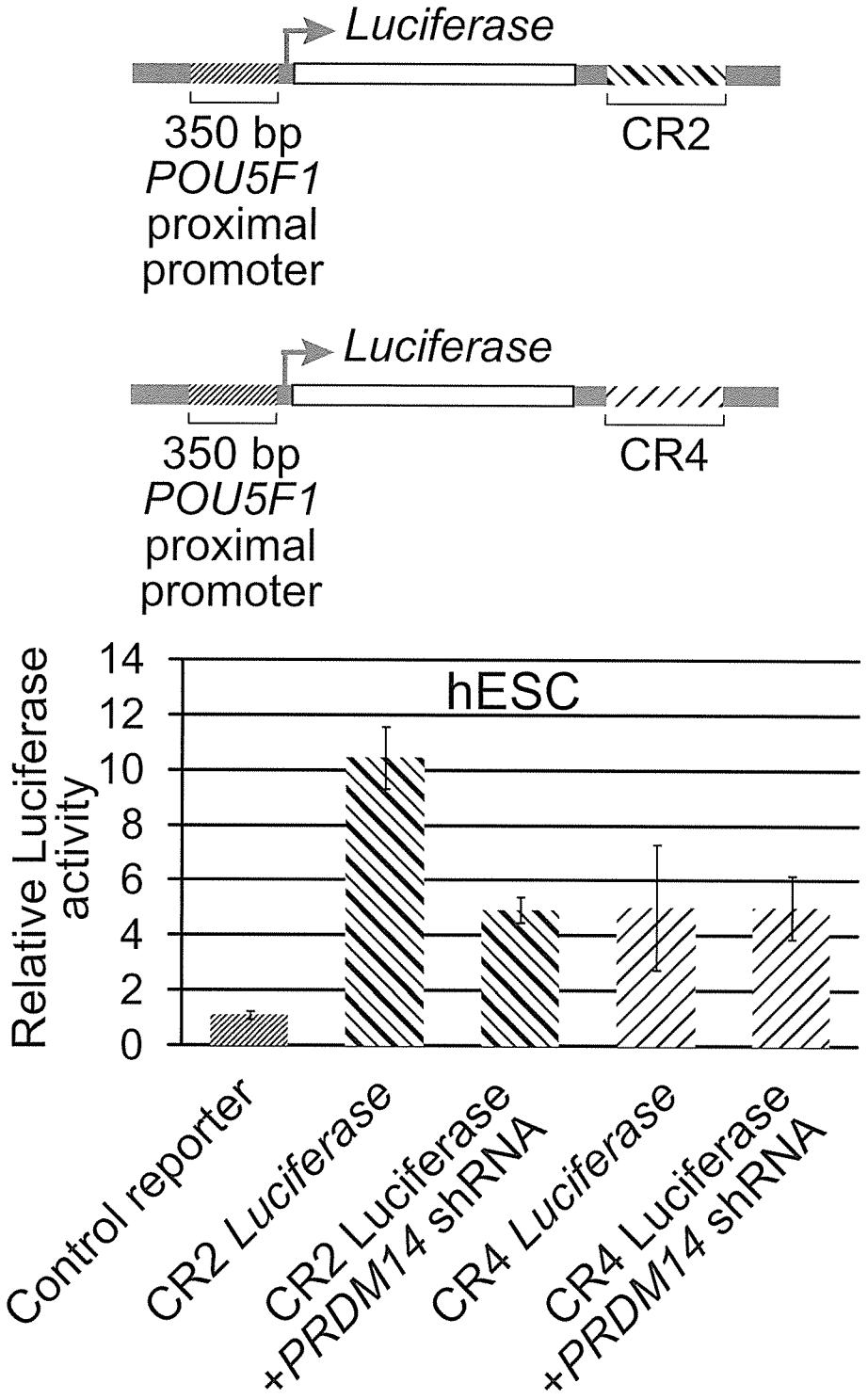

Luciferase
350 bp
POU5F1
proximal
promoter
CR2
Luciferase
350 bp
POU5F1
proximal
promoter
CR4
hESC
Relative Luciferase activity
0
2
4
6
8
10
12
14
Control reporter
CR2 Luciferase
CR2 Luciferase +PRDM14 shRNA
CR4 Luciferase
CR4 Luciferase +PRDM14 shRNA

FIG. 14F

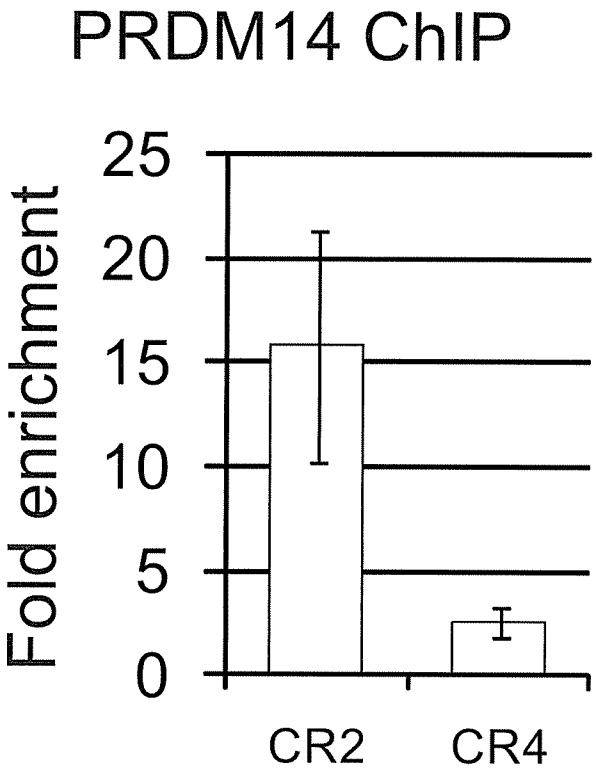


FIG. 14G

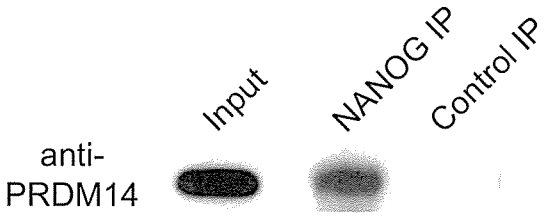


FIG. 14H

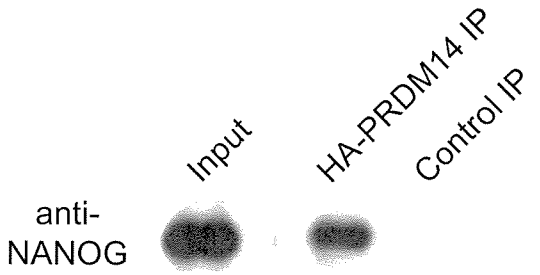


FIG. 14I

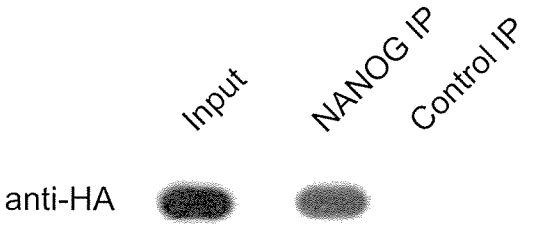
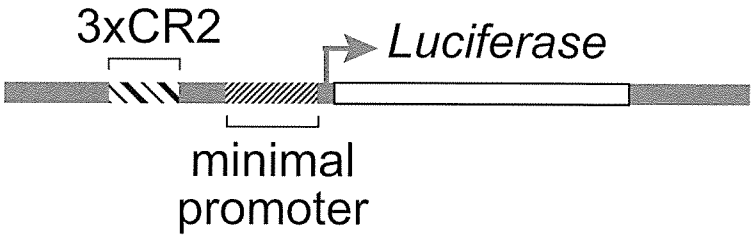


FIG. 14J



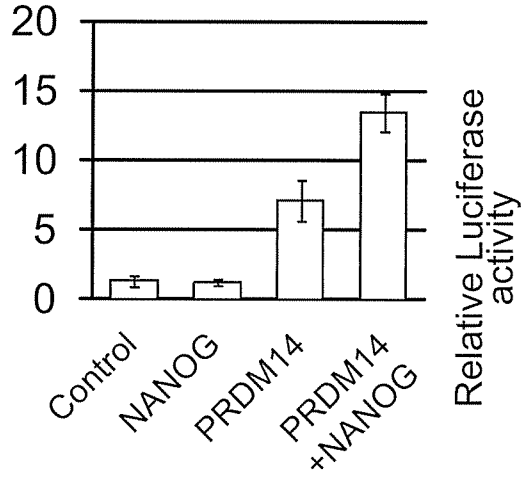


FIG. 14K

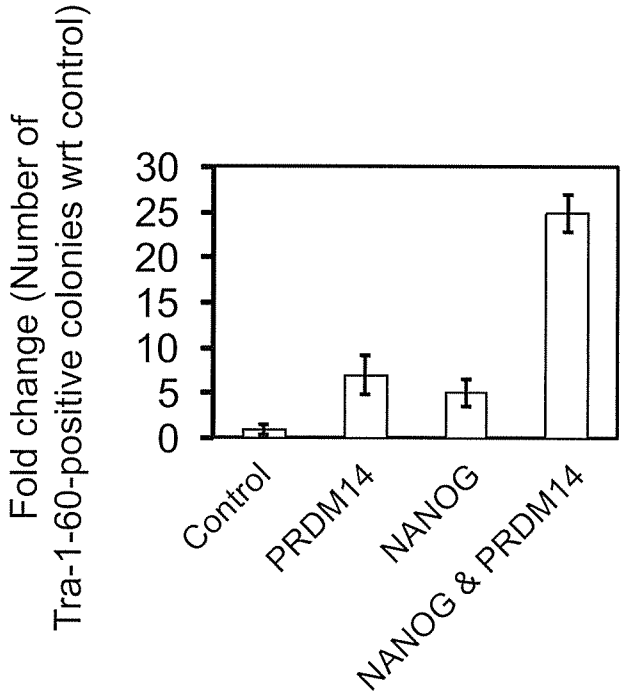


FIG. 14L

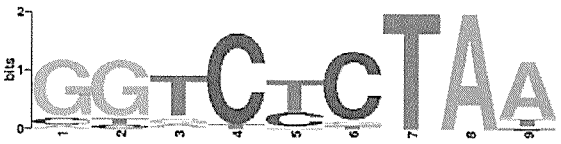
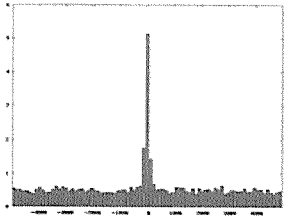
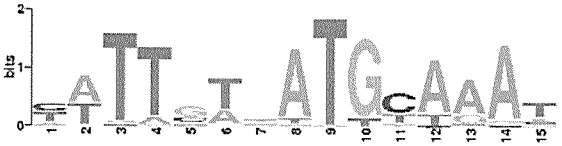
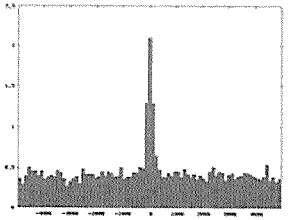
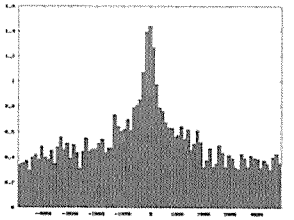
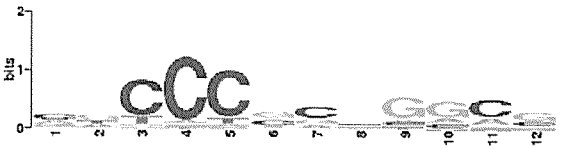
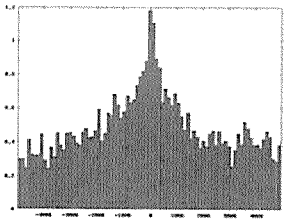
Motif	Logo	Enrichment score	Distribution around PRDM14 ChIP-seq peaks
PRDM14		16	
V_OCT4_01		7.5	
V_SP1_Q6_01		5.7	
V_AP2_Q6		4.2	

FIG. 15

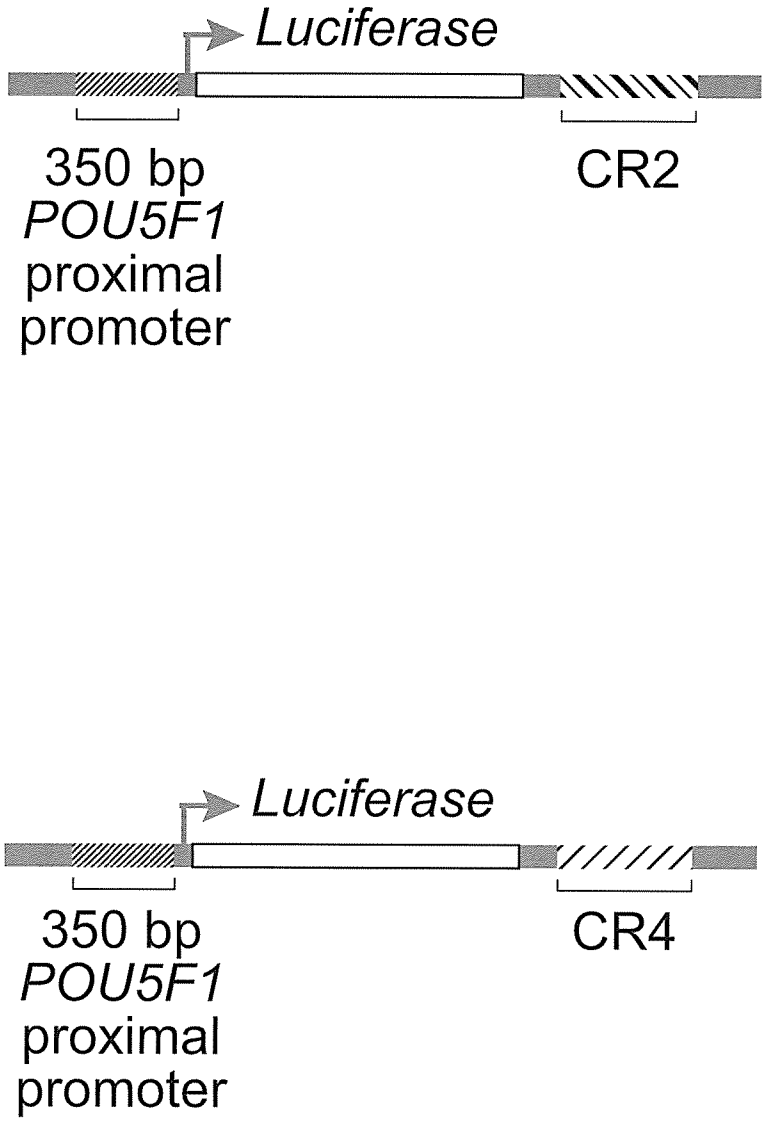

Luciferase
350 bp
POU5F1
proximal
promoter
CR2
Luciferase
350 bp
POU5F1
proximal
promoter
CR4

FIG. 16A

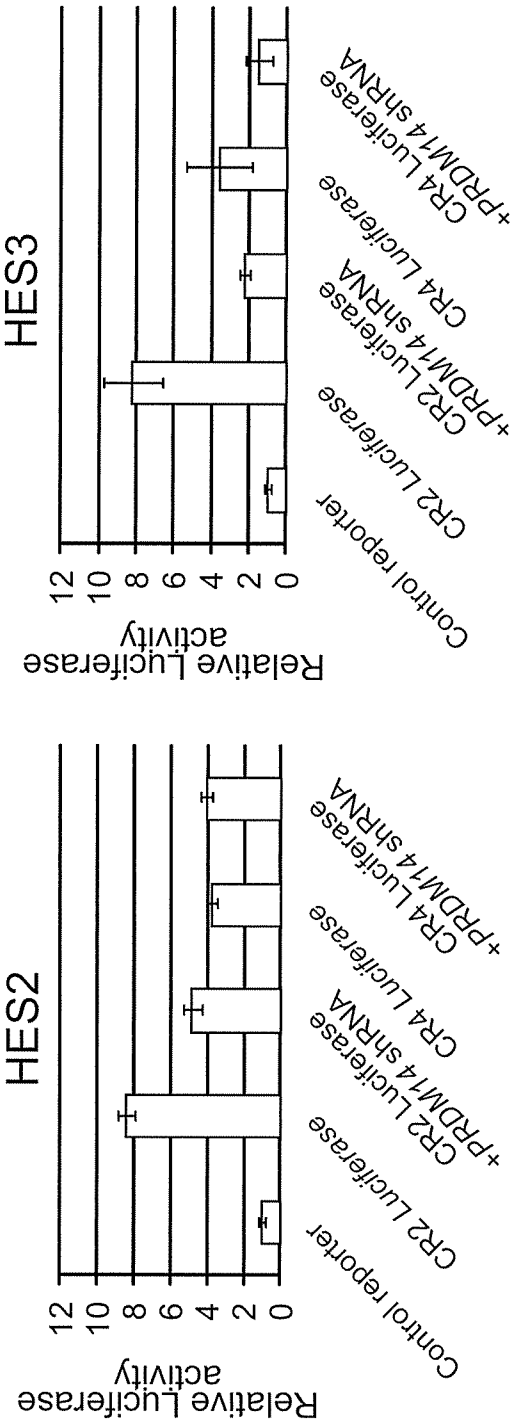

HES2
Relative Luciferase activity
0
2
4
6
8
10
12
Control reporter
CR2 Luciferase
+PRDM14 shRNA
CR4 Luciferase
HES3
Relative Luciferase activity
0
2
4
6
8
10
12
Control reporter
CR2 Luciferase
+PRDM14 shRNA
CR4 Luciferase

FIG. 16B

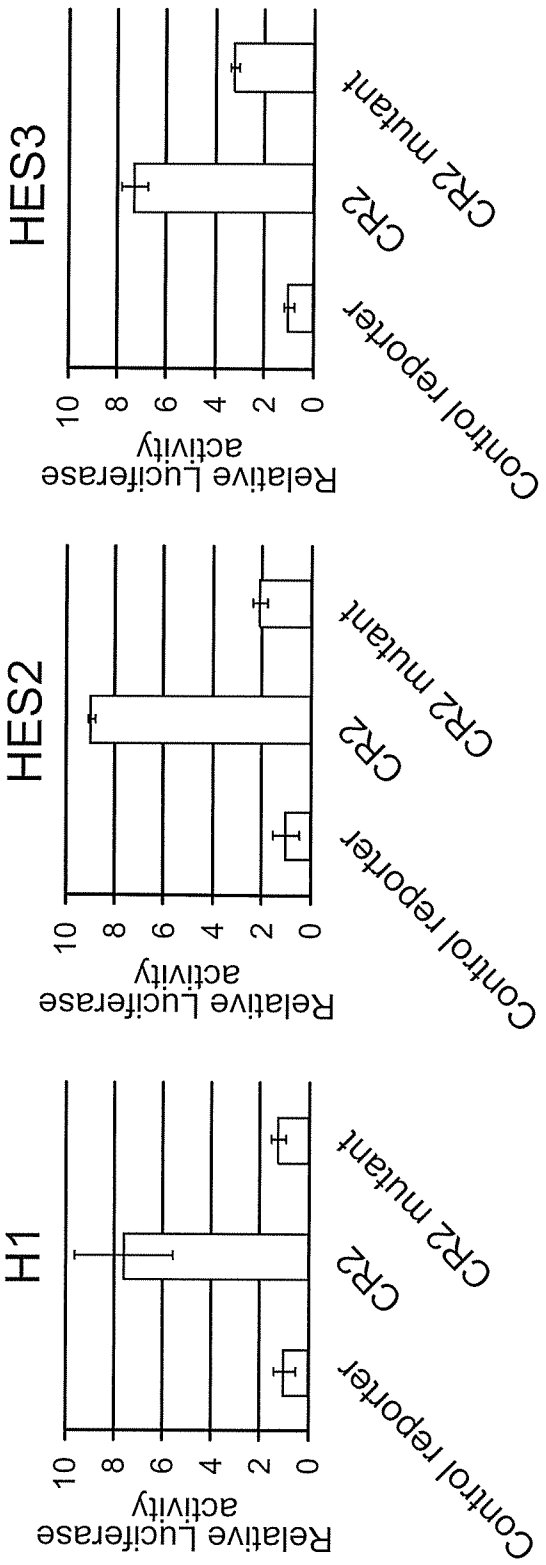

H1
HES2
HES3
Relative Luciferase activity
0
2
4
6
8
10
Control reporter
CR2
CR2 mutant

FIG. 16C

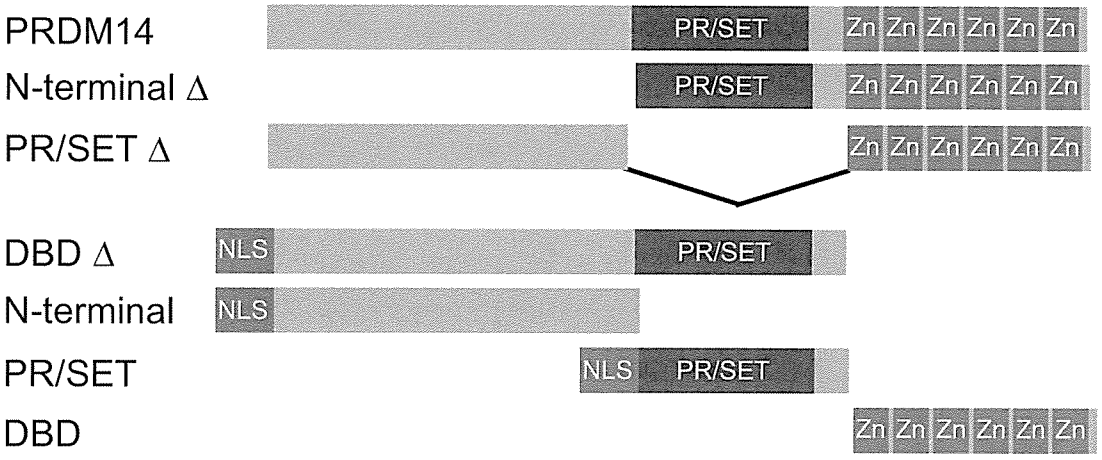


FIG. 17A

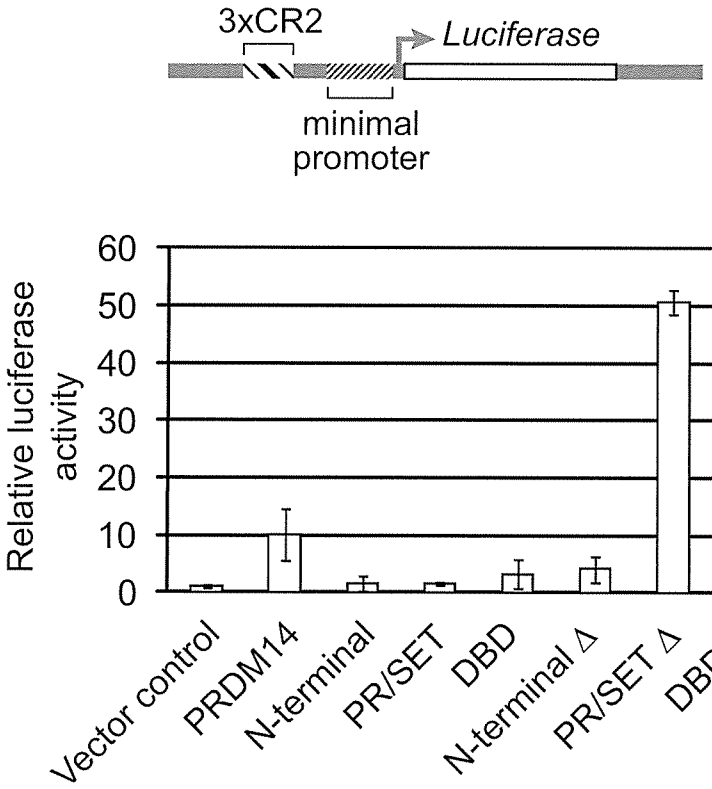


FIG. 17B

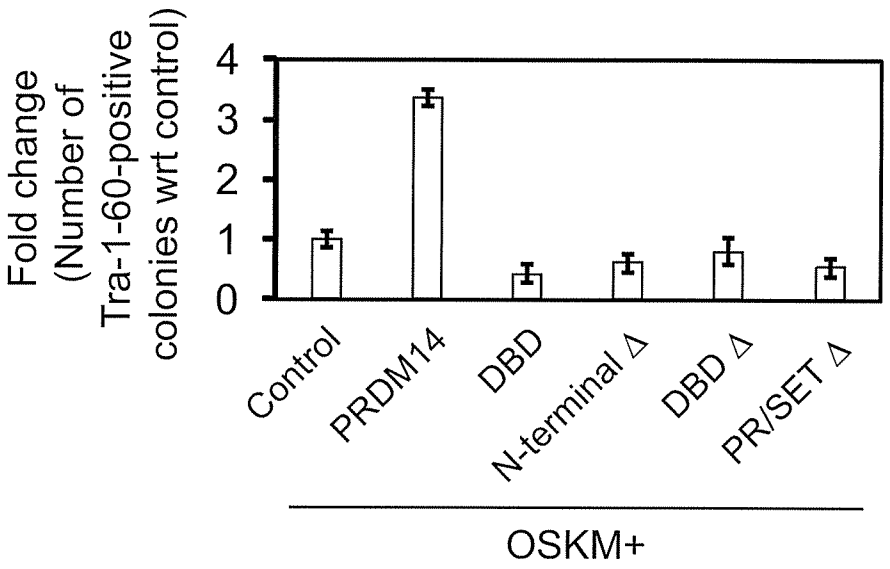


FIG. 17C

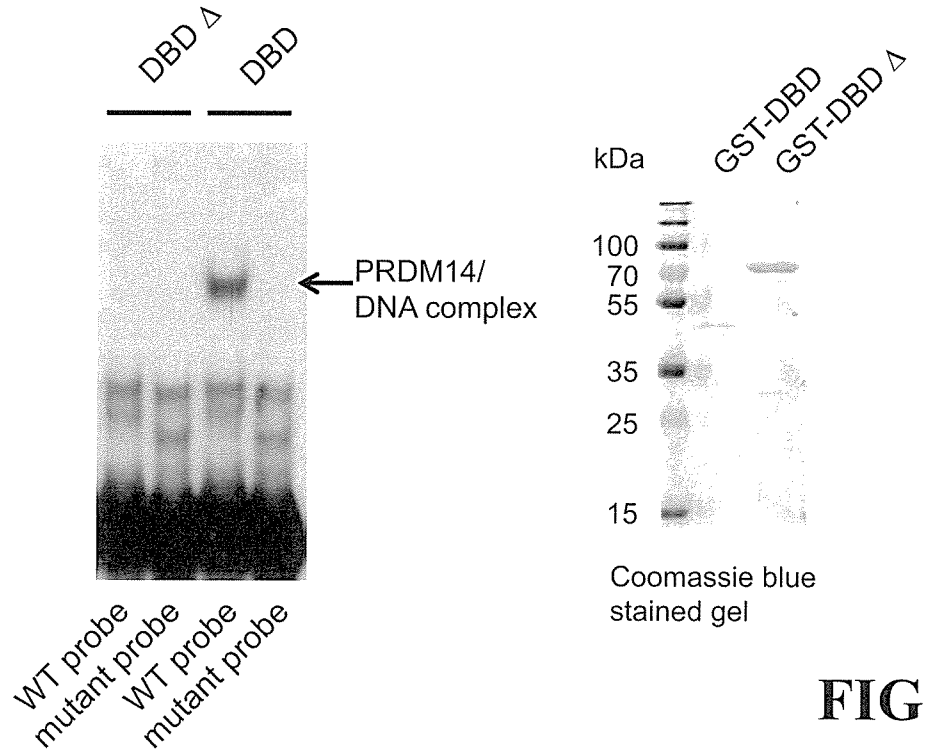
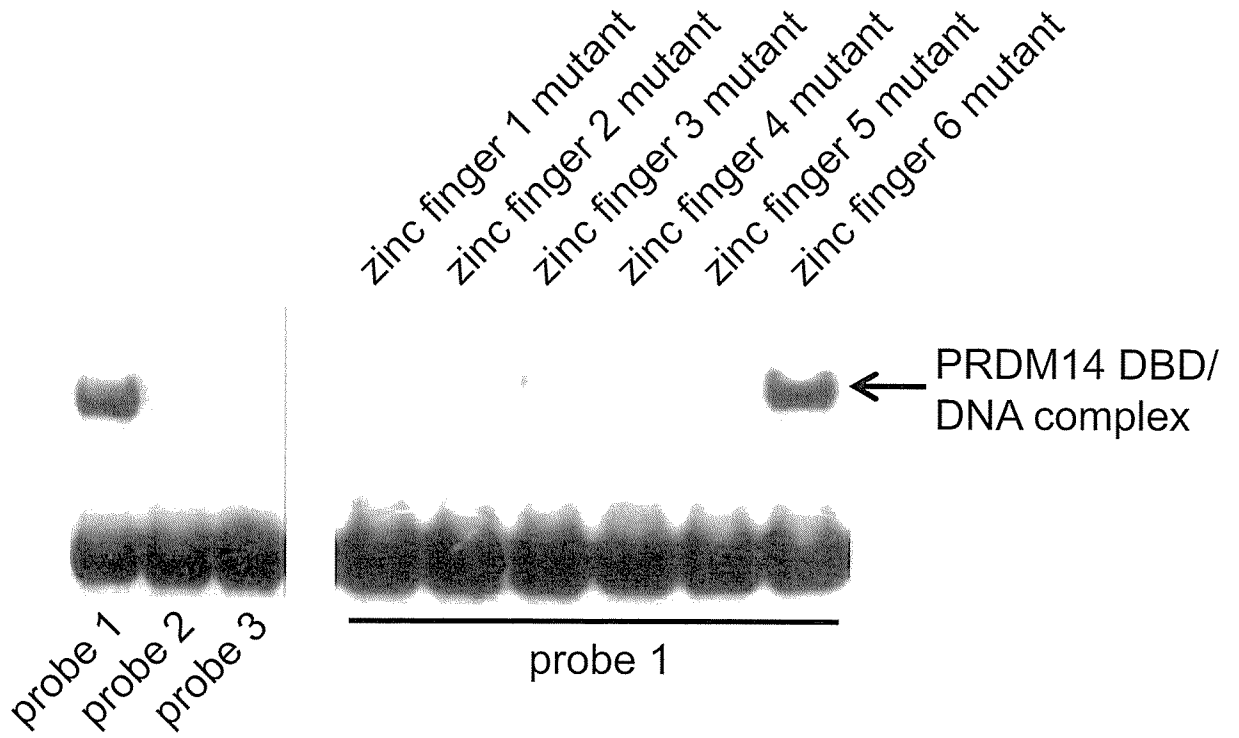


FIG. 17D




```
Probe 1 - CGGGGACAAGATGCCCATCAGGGTCTCTAACTGCCCCCCACCCCCTCGCC WT
Probe 2 - CGGGGACAAGATGCCCATCAGGGTCCCCAACTGCCCCCCACCCCCTCGCC mutant probe 1
Probe 3 - CGGGGACAAGATGCCCATCAGGGCCCCCAACTGCCCCCCACCCCCTCGCC mutant probe 2
```

FIG. 17E

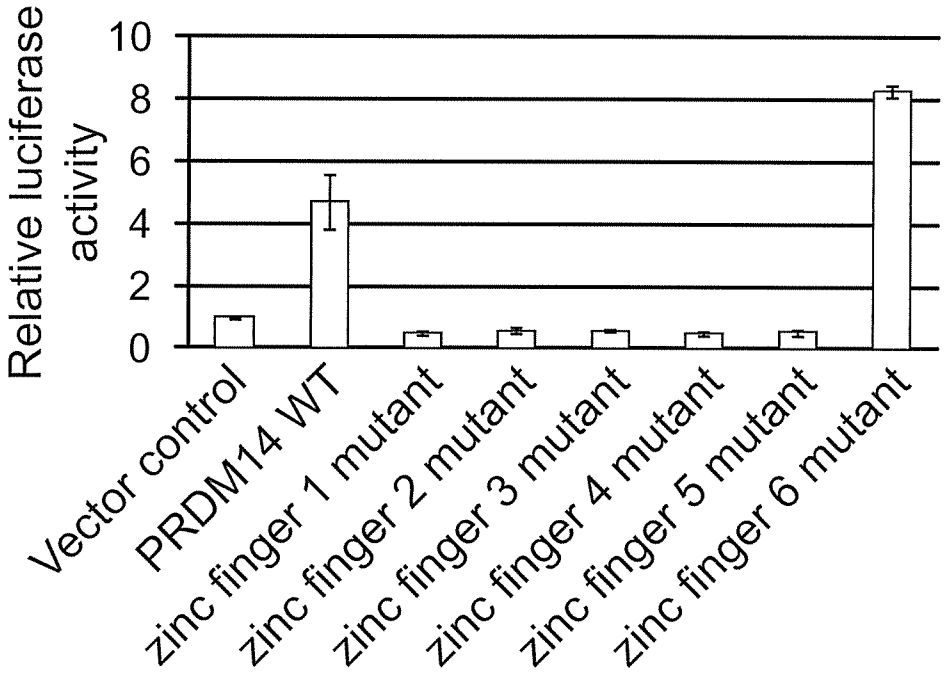

Relative luciferase activity
10
8
6
4
2
0
Vector control
PRDM14 WT
zinc finger 1 mutant
zinc finger 2 mutant
zinc finger 3 mutant
zinc finger 4 mutant
zinc finger 5 mutant
zinc finger 6 mutant

FIG. 17F

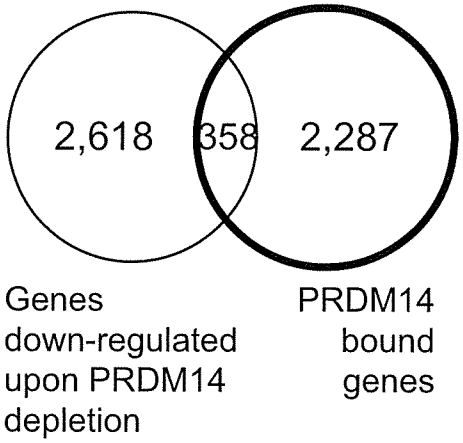


FIG. 18A

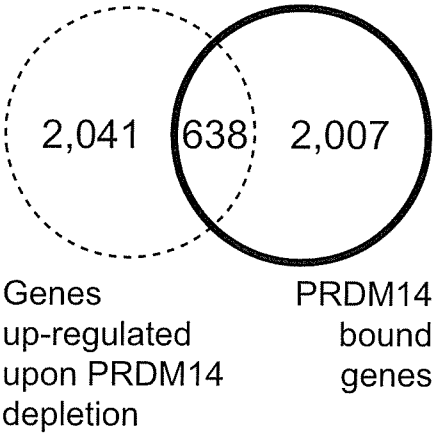


FIG. 18B

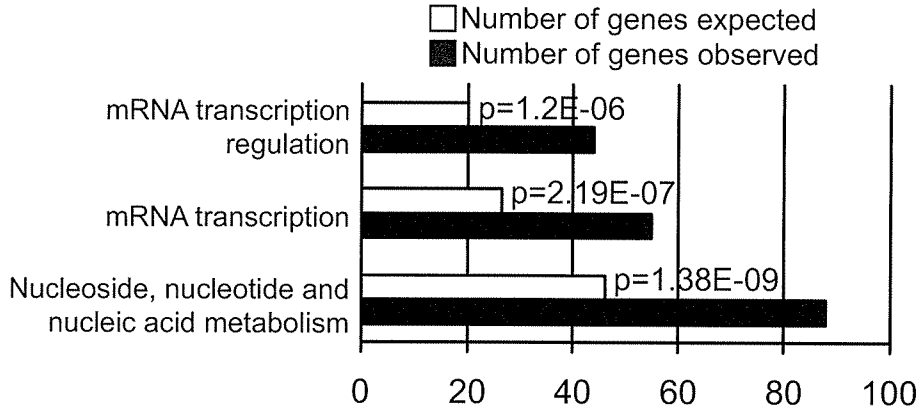


FIG. 18C

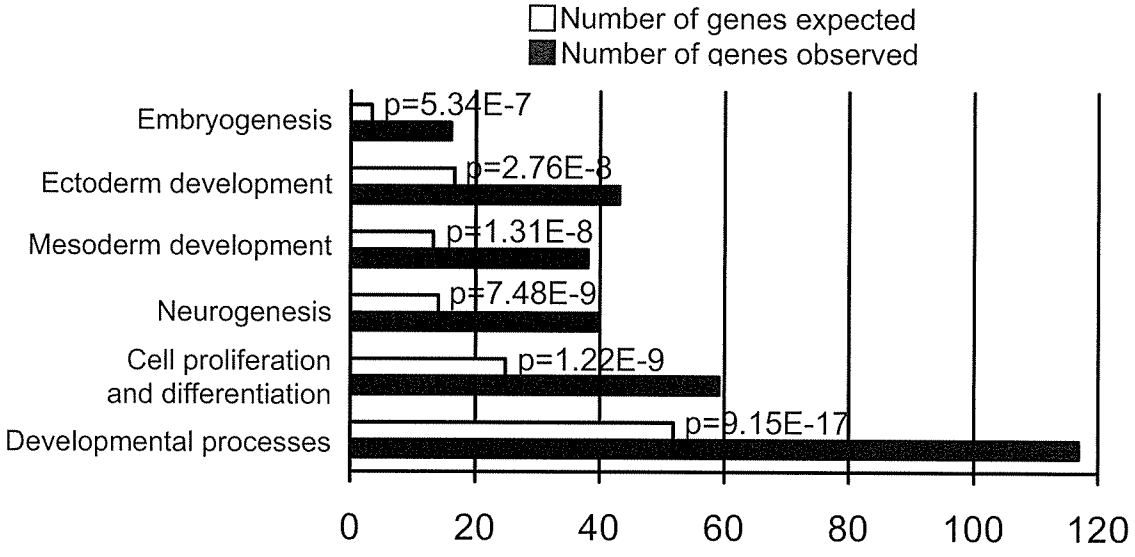


FIG. 18D

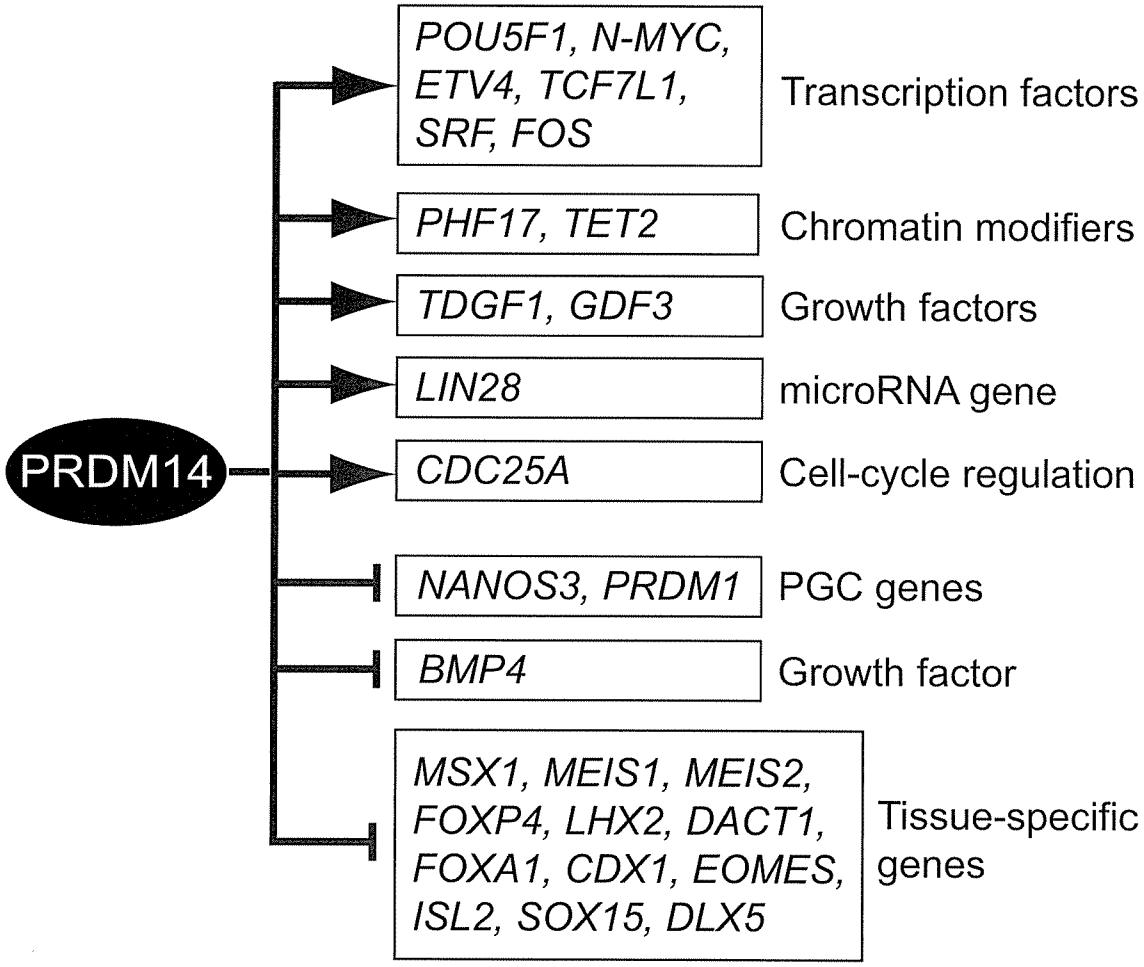

PRDM14
POU5F1, N-MYC, ETV4, TCF7L1, SRF, FOS
Transcription factors
PHF17, TET2
Chromatin modifiers
TDGF1, GDF3
Growth factors
LIN28
microRNA gene
CDC25A
Cell-cycle regulation
NANOS3, PRDM1
PGC genes
BMP4
Growth factor
MSX1, MEIS1, MEIS2, FOXP4, LHX2, DACT1, FOXA1, CDX1, EOMES, ISL2, SOX15, DLX5
Tissue-specific genes

FIG. 18E

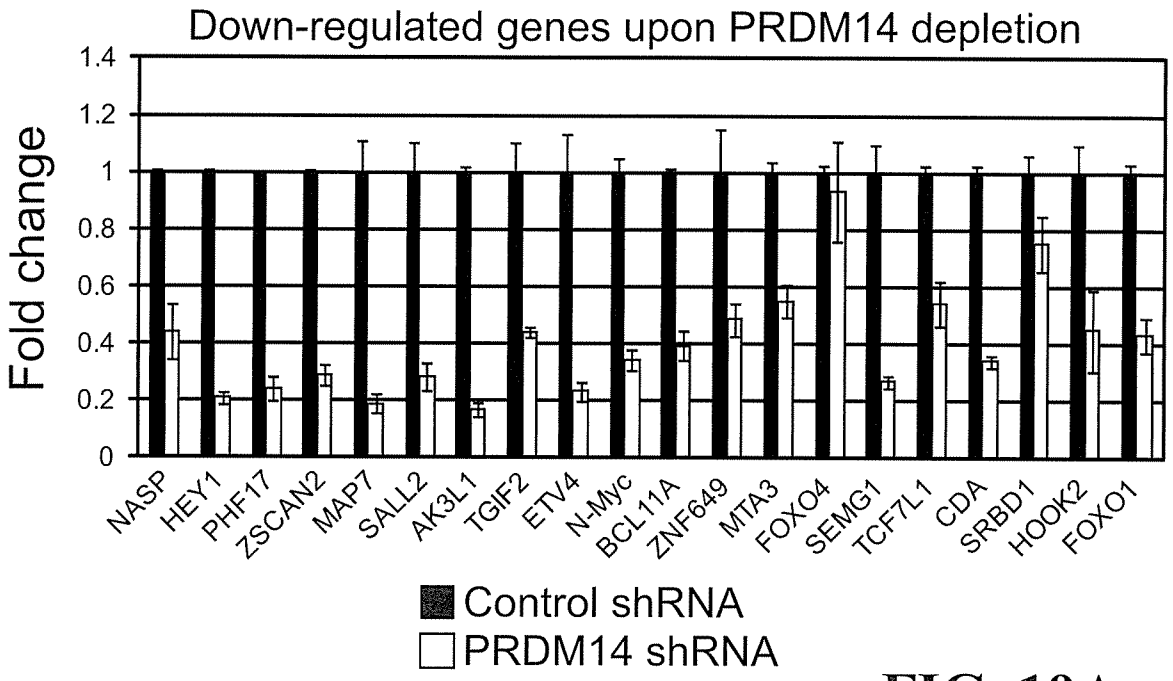


FIG. 19A

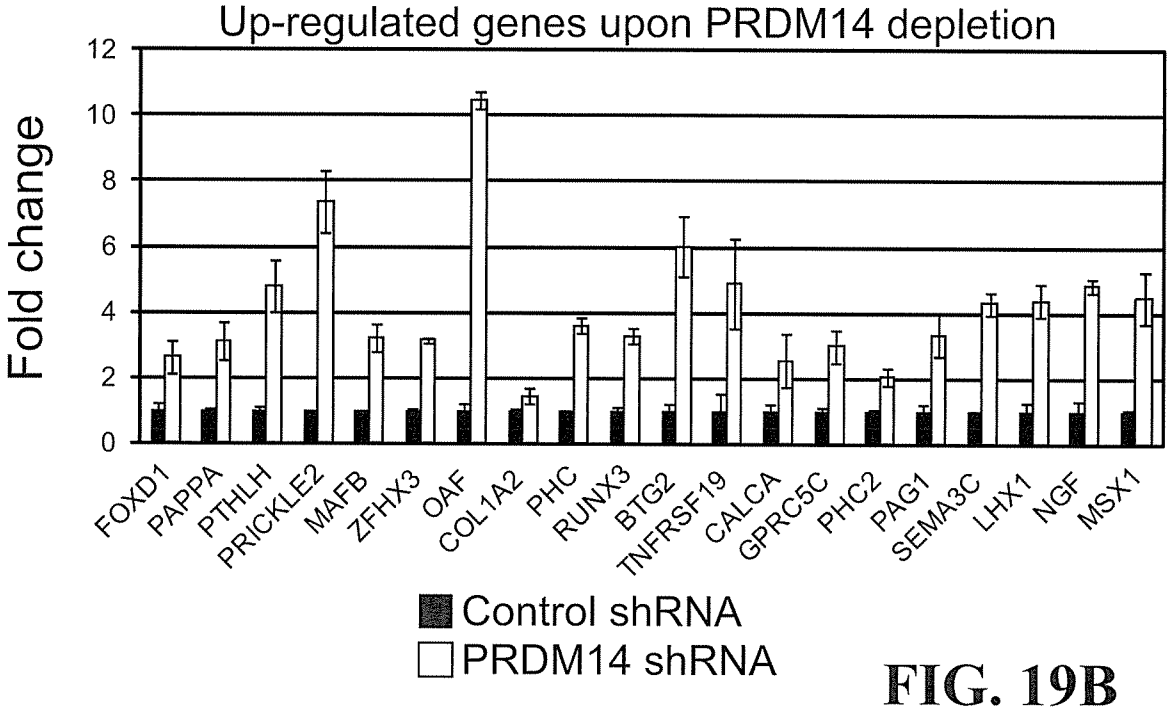


FIG. 19B

TF family	TRANSFAC PWM	p-value
FXR	V_PXR_Q2	3.27E-12
OCT	V_OCT4_01	3.61E-12
ETS	V_ETS1_B	3.88E-12
WHN	V_WHN_B	5.44E-12
EGR	V_EGR3_01	5.73E-12
AP2	V_AP2ALPHA_01	6.37E-12
E2F	V_E2F_Q6_01	6.49E-12
NRF	V_NRF1_Q6	7.21E-12
ZF5	V_ZF5_B	7.64E-12
SP1	V_SP1_Q6	7.66E-12
WT1	V_WT1_Q6	7.67E-12
HIC1	V_HIC1_02	8.29E-12
ZNF219	V_ZNF219_01	8.48E-12
MOVO	V_MOVOB_01	9.68E-12
GGG	V_CHCH_01	9.92E-12
CREB	V_NRSE_B	2.72E-10
P300	V_P300_01	1.26E-09
VMYB	V_VMYB_02	1.31E-07
HEN	V_HEN1_02	3.36E-07
LEF	V_LEF1_Q2_01	3.68E-05

FIG. 20A

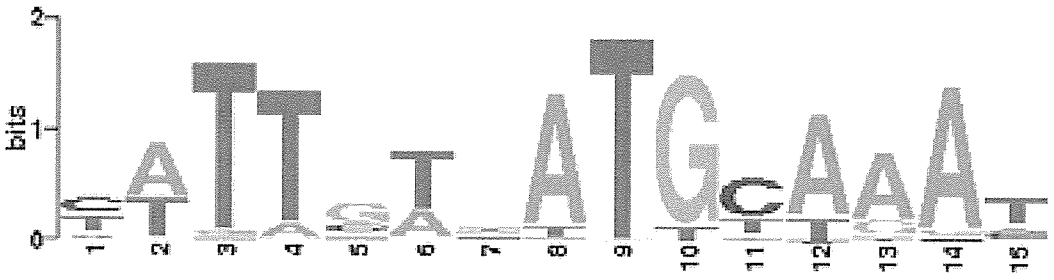
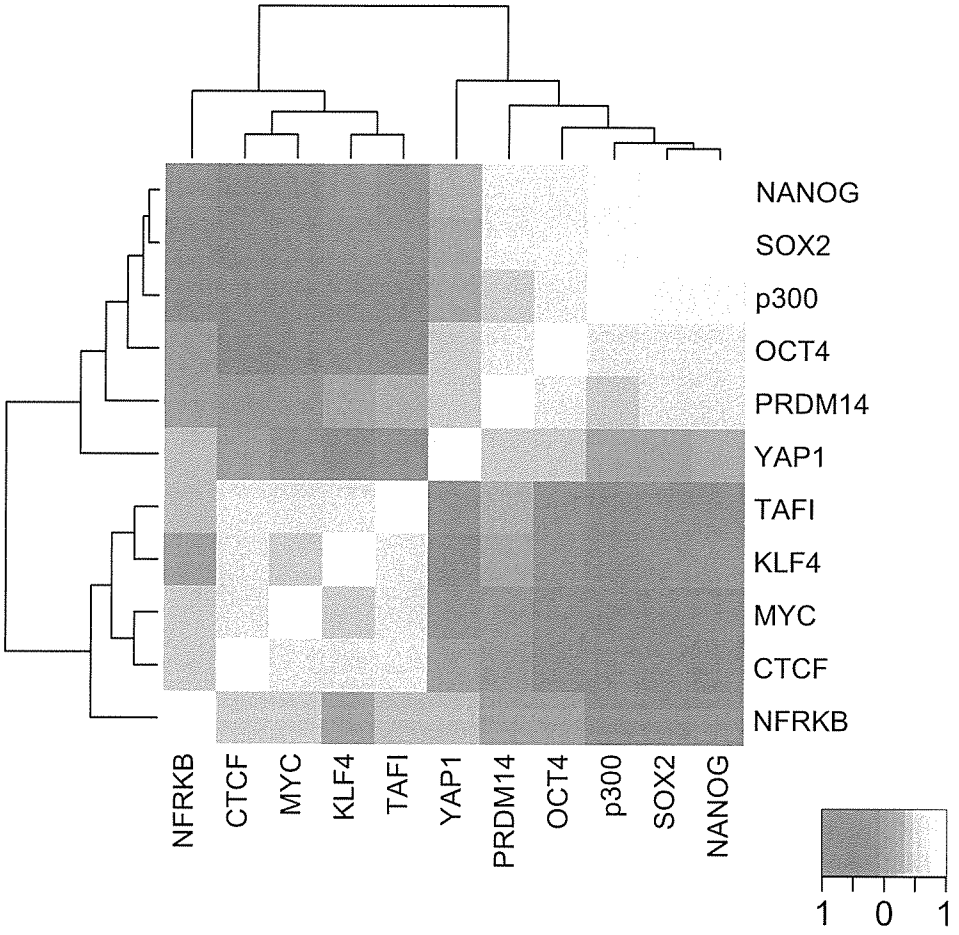


FIG. 20B

TF family	TRANSFAC PWM	p-value
BARBIE	V_BARBIE_01	Not significant, p>0.05
BLIMP1	V_BLIMP1_Q6	Not significant, p>0.05
BRCA	V_BRCA_01	Not significant, p>0.05
CHOP	V_CHOP_01	Not significant, p>0.05
GFI	V_GFI1_Q6	Not significant, p>0.05
HSF	V_HSF_Q6	Not significant, p>0.05
POLYA	V_LPOLYA_B	Not significant, p>0.05
LYF1	V_LYF1_01	Not significant, p>0.05
P53	V_P53_DECAMER_Q2	Not significant, p>0.05
RP58	V_RP58_01	Not significant, p>0.05

FIG. 20C



PRDM14 vs TF:	Kendall tau correlation coefficient	p-level	Significance
CTCF	-0.14680	5.30E-01	No
KLF4	0.14680	5.30E-01	No
MYC	-0.12963	5.79E-01	No
NANOG	0.61111	8.88E-03	*(p<0.05)
NFRKB	-0.05661	8.08E-01	No
OCT4	0.59816	1.04E-02	*(p<0.05)
P300	0.46296	4.74E-02	*(p<0.05)
SOX2	0.56077	1.63E-02	*(p<0.05)
TAFI	0.18692	4.24E-01	No
YAP1	0.37385	1.09E-01	No

FIG. 20D

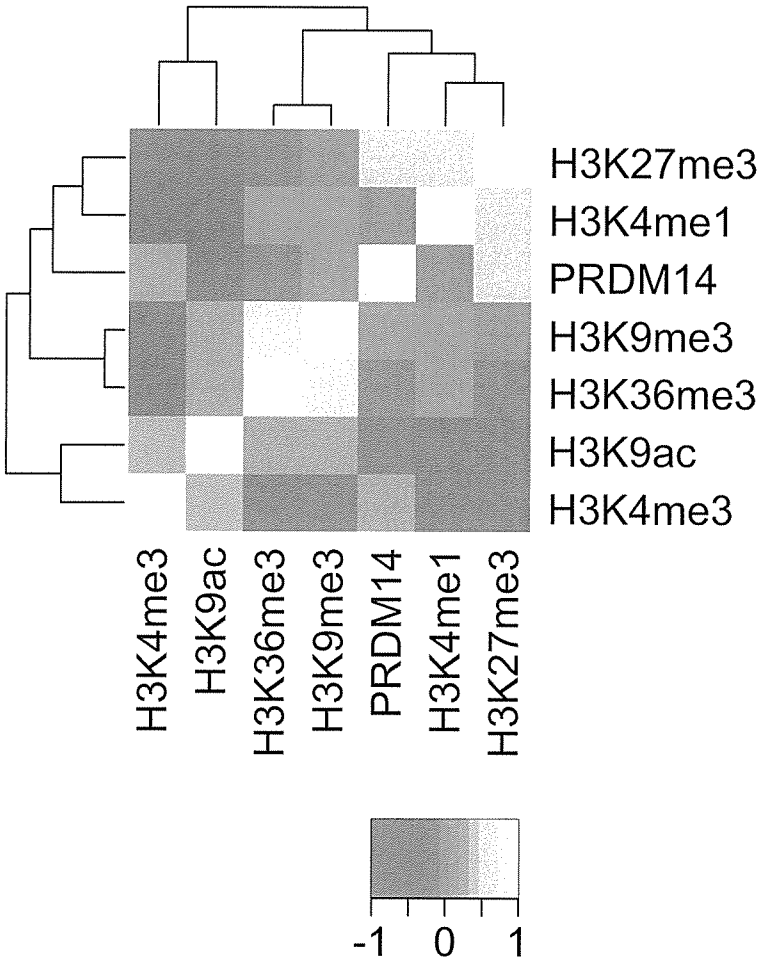

H3K27me3
H3K4me1
PRDM14
H3K9me3
H3K36me3
H3K9ac
H3K4me3
H3K4me3
H3K9ac
H3K36me3
H3K9me3
PRDM14
H3K4me1
H3K27me3
-1
0
1

FIG. 21A

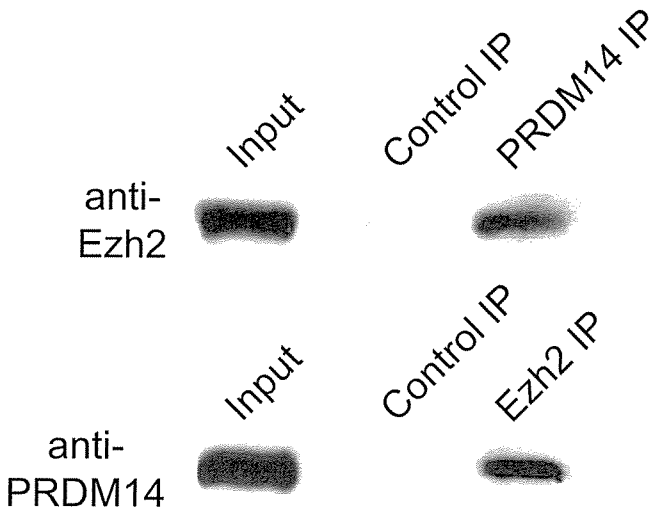


FIG. 21B

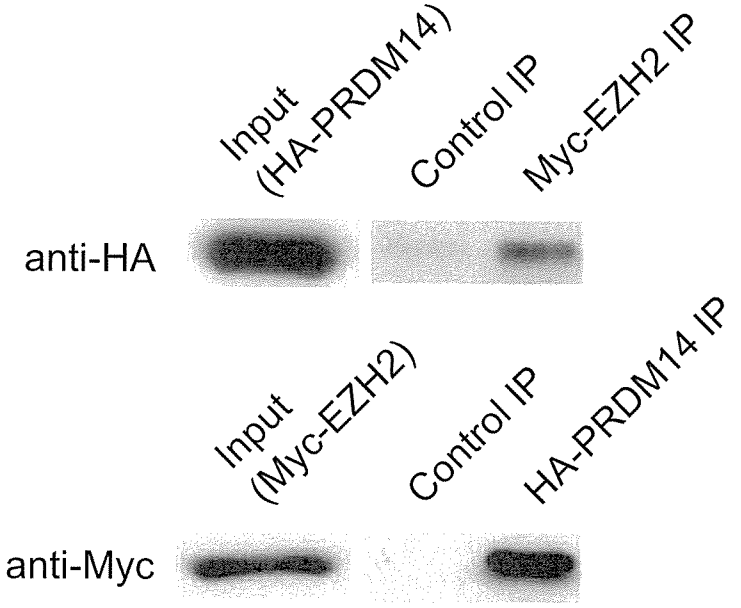


FIG. 21C

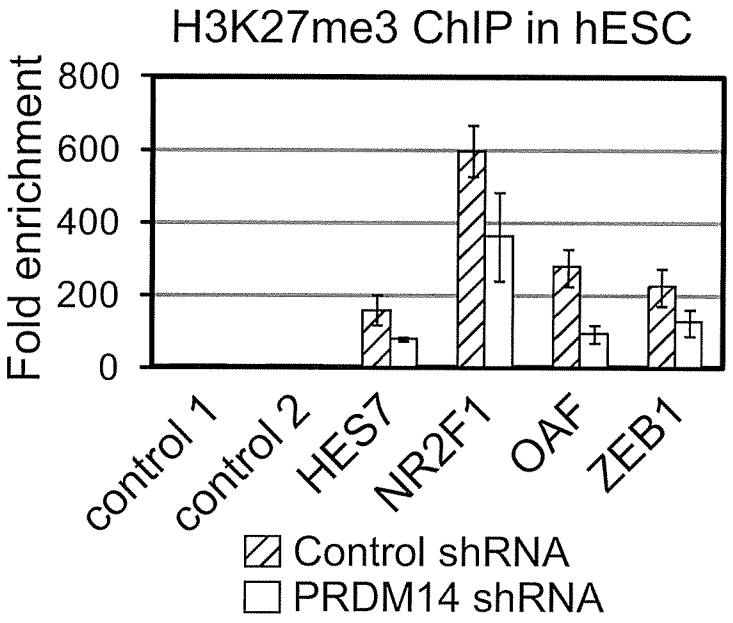


FIG. 21D

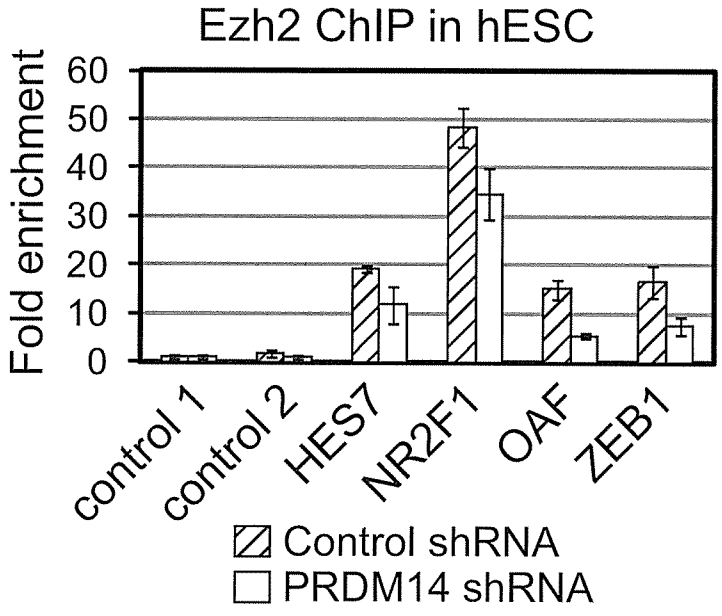


FIG. 21E

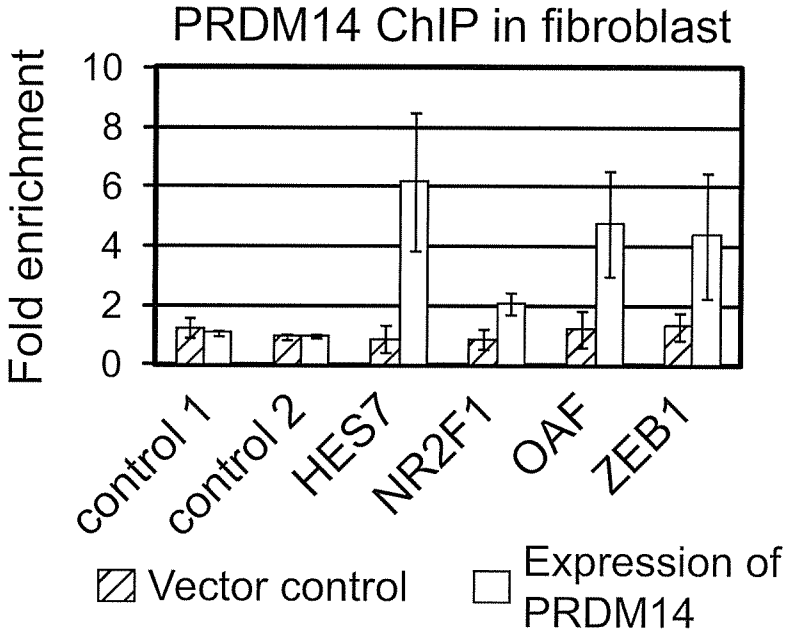


FIG. 21F

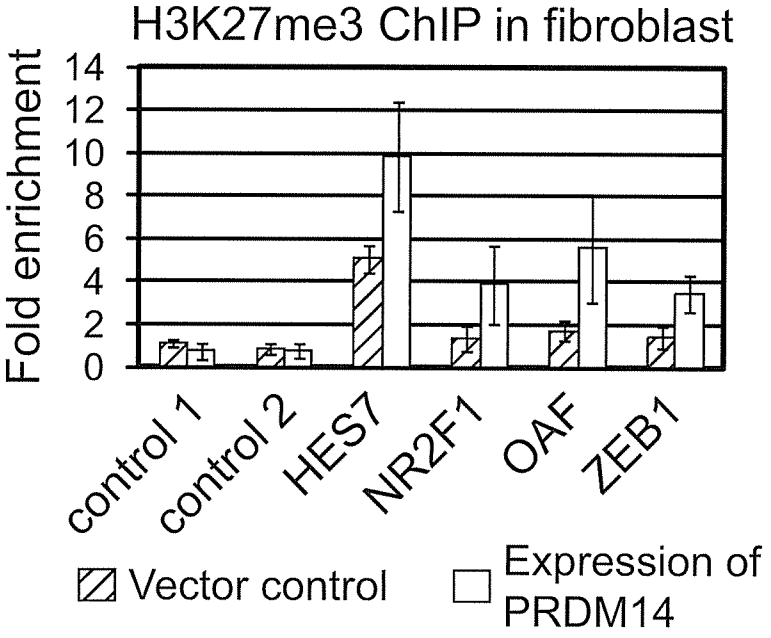


FIG. 21G

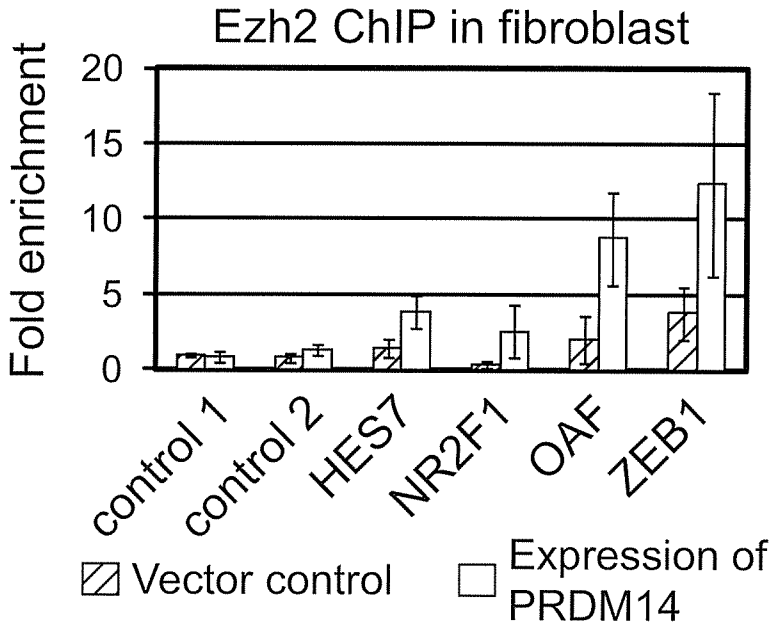


FIG. 21H

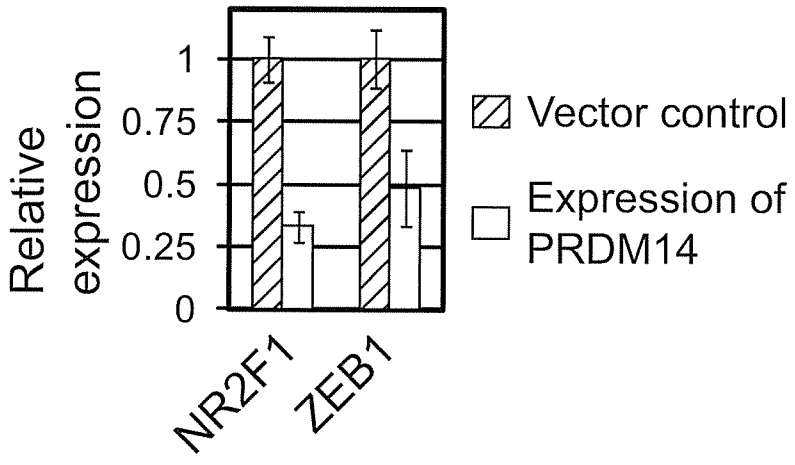


FIG. 21I

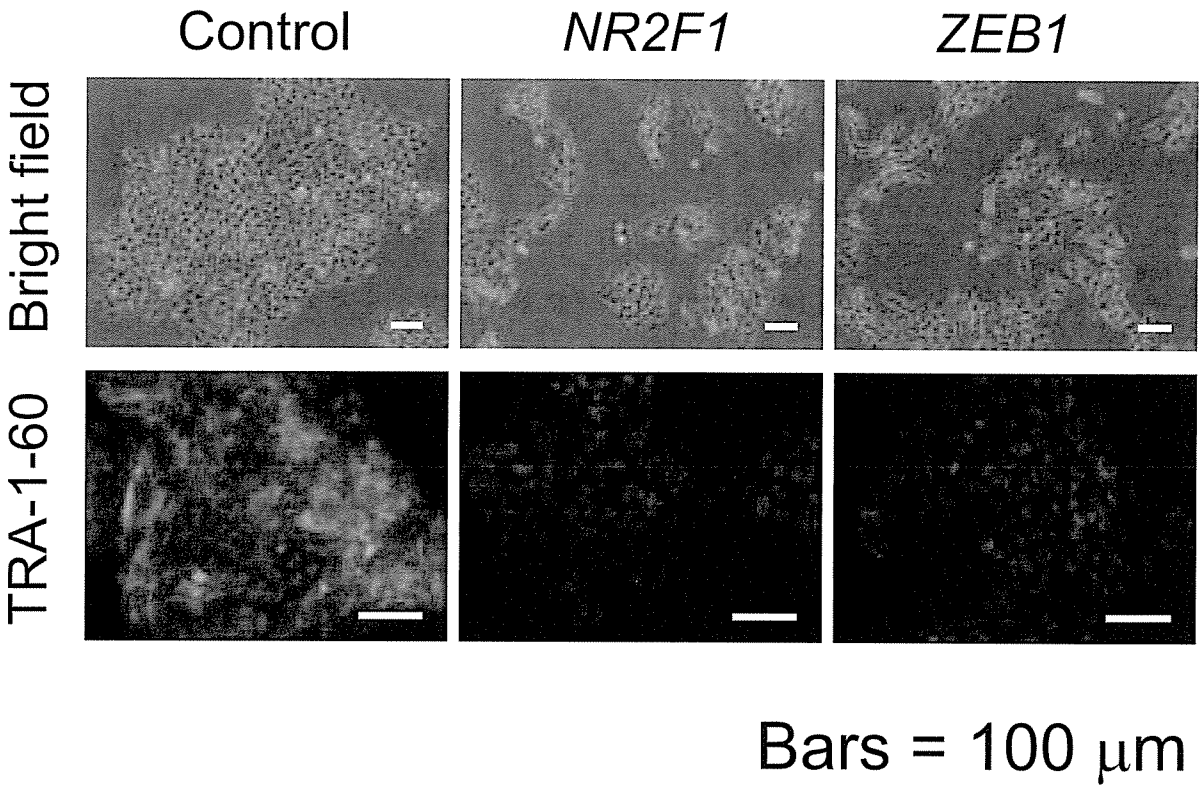


FIG. 21J