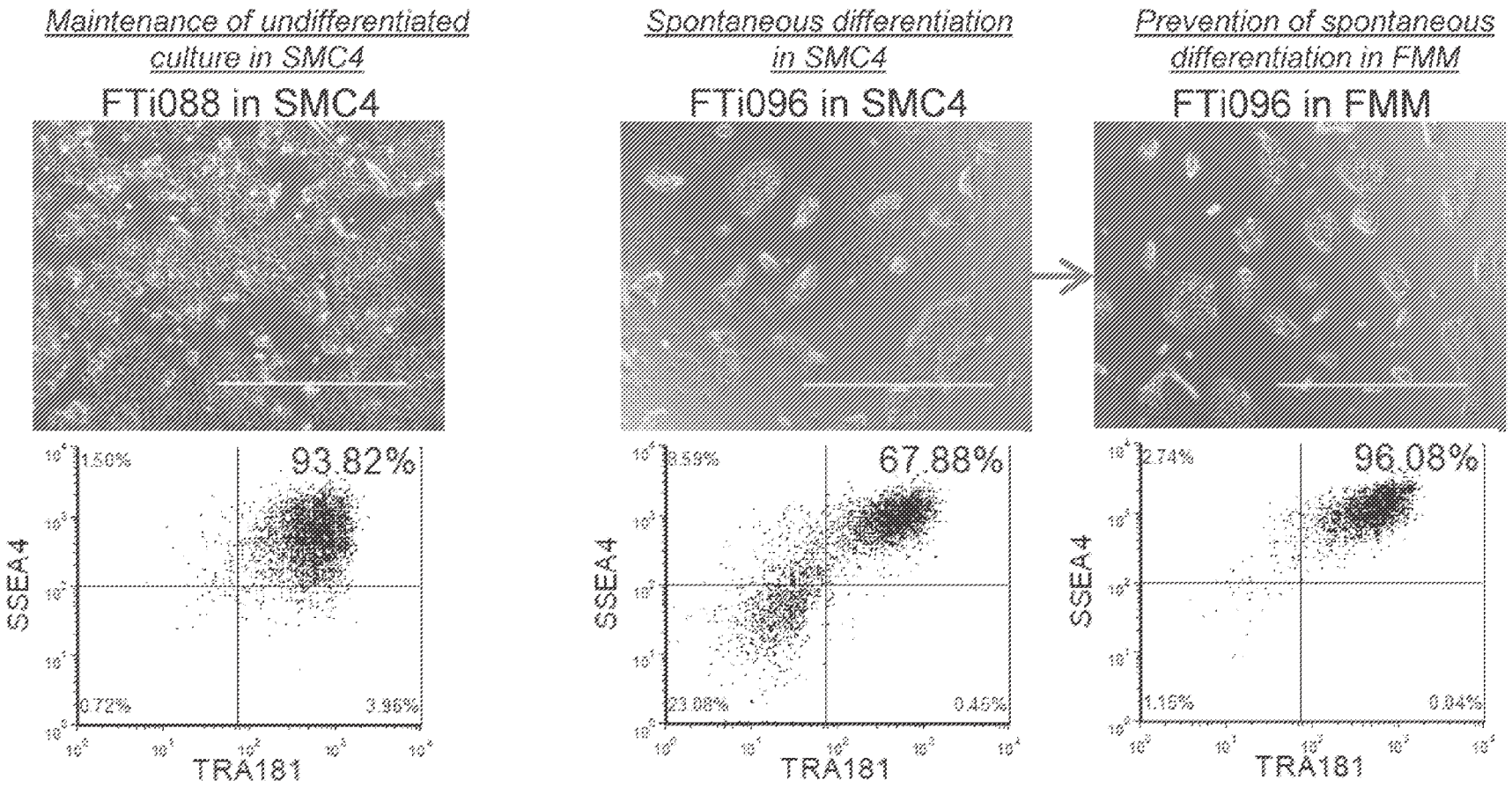

Maintenance of undifferentiated culture in SMC4
FTi088 in SMC4
Spontaneous differentiation in SMC4
FTi096 in SMC4
Prevention of spontaneous differentiation in FMM
FTi096 in FMM
93.82%
1.50%
0.72%
3.96%
67.88%
8.59%
23.08%
0.45%
96.08%
2.74%
1.15%
0.04%
SSEA4
TRA181

FIG. 1A

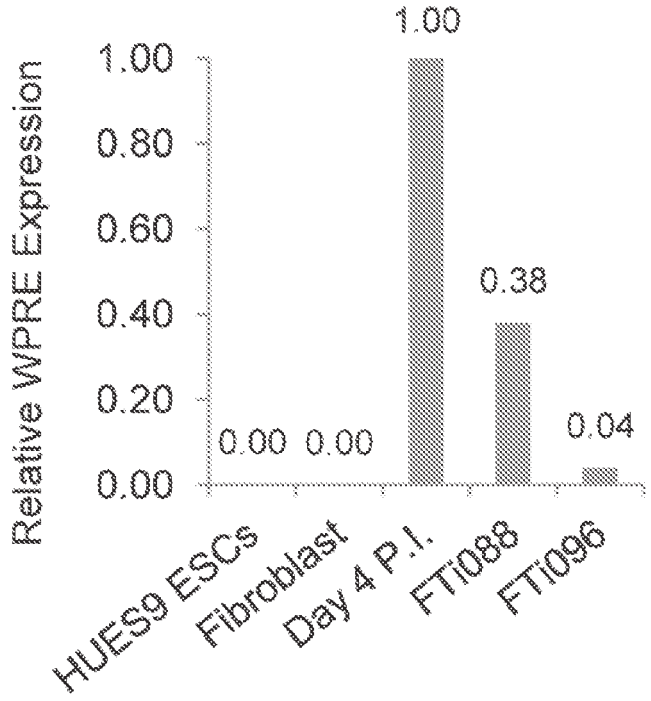

Relative WPRE Expression
1.00
0.80
0.60
0.40
0.20
0.00
0.00
0.00
1.00
0.38
0.04
HUES9 ESCs
Fibroblast
Day 4 P.I.
FTi088
FTi096

FIG. 1B

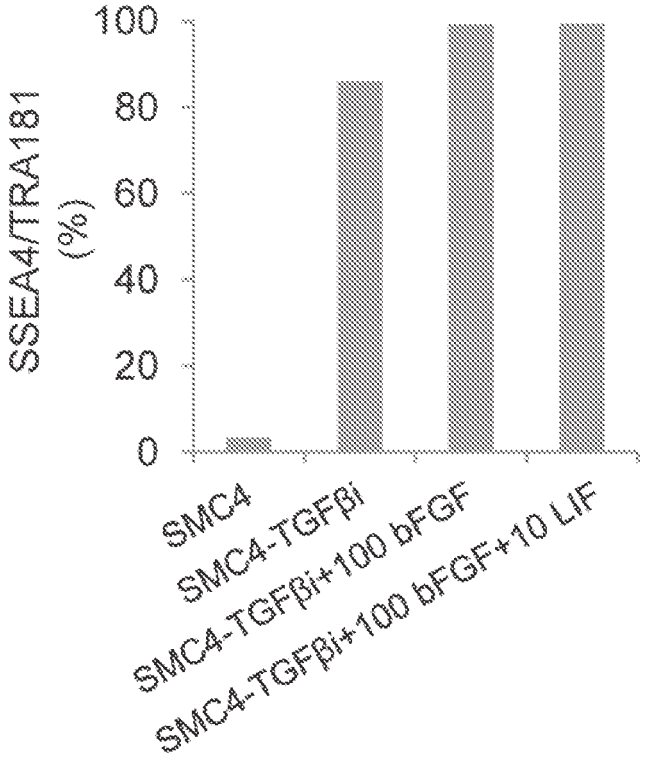

SSEA4/TRA181 (%)
100
80
60
40
20
0
SMC4
SMC4-TGFβi
SMC4-TGFβi+100 bFGF
SMC4-TGFβi+100 bFGF+10 LIF

FIG. 1C

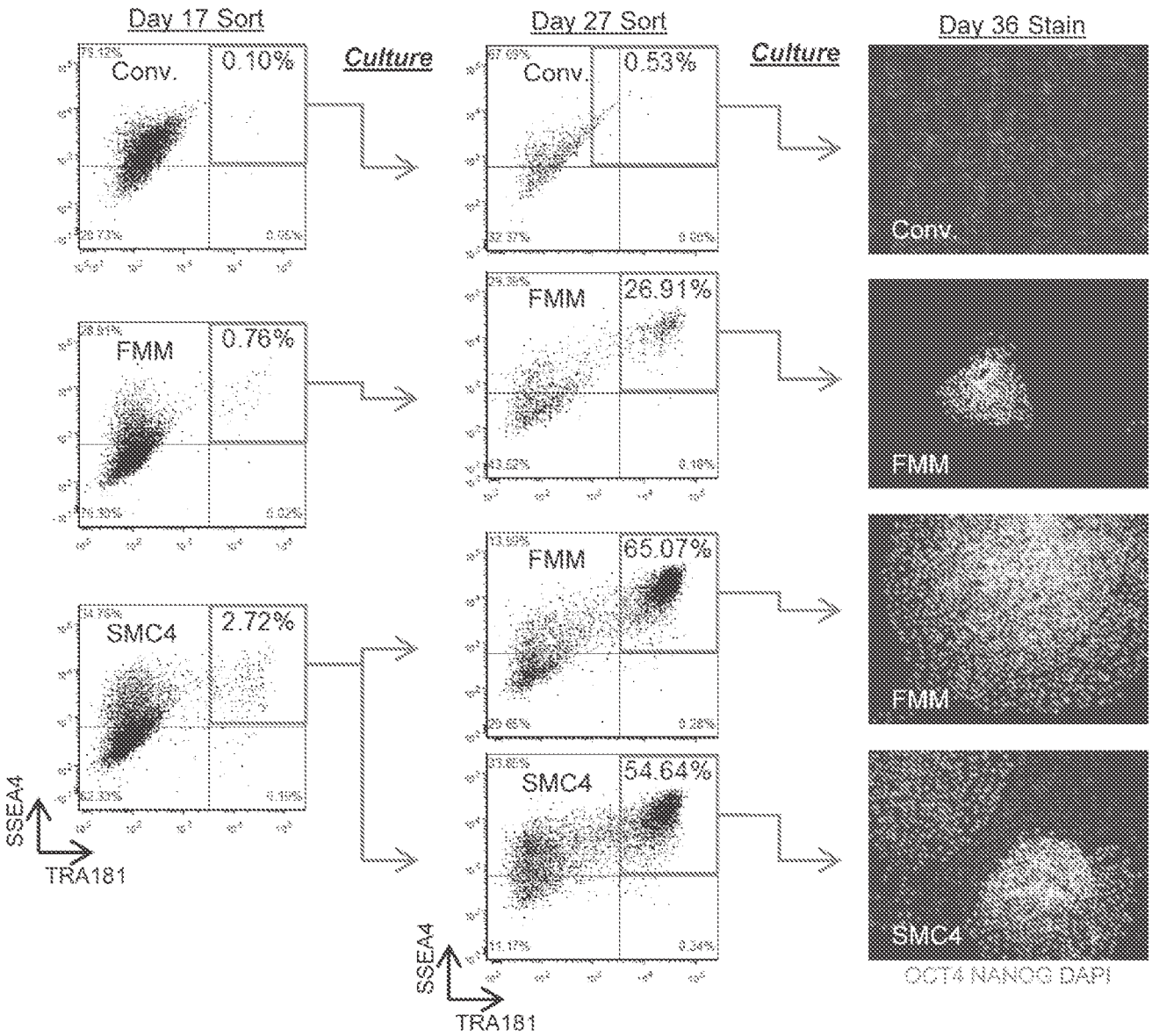

Day 17 Sort
Day 27 Sort
Day 36 Stain
Culture
Culture
Conv.
0.10%
Conv
0.53%
Conv.
FMM
0.76%
FMM
26.91%
FMM
FMM
65.07%
FMM
SMC4
2.72%
SMC4
54.64%
SMC4
SSEA4
TRA181
SSEA4
TRA181
OCT4 NANOG DAPI

FIG. 1D

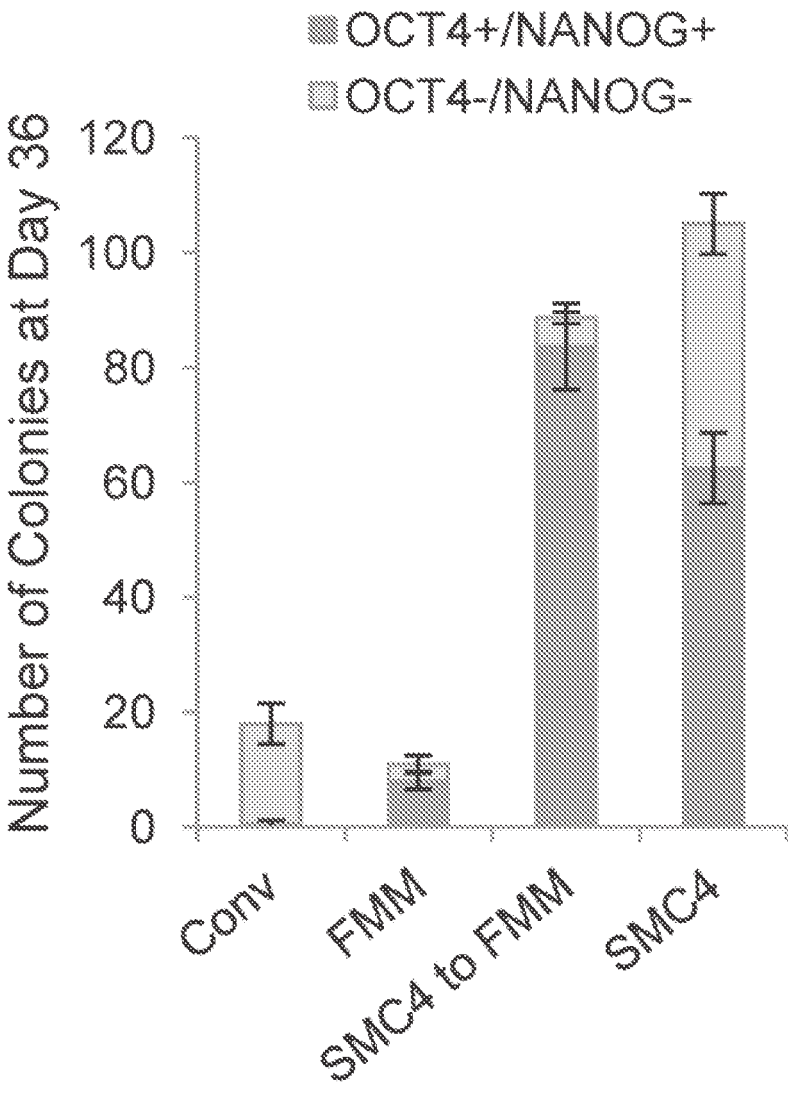

OCT4+/NANOG+
OCT4-/NANOG-
Number of Colonies at Day 36
120
100
80
60
40
20
0
Conv
FMM
SMC4 to FMM
SMC4

FIG. 1E

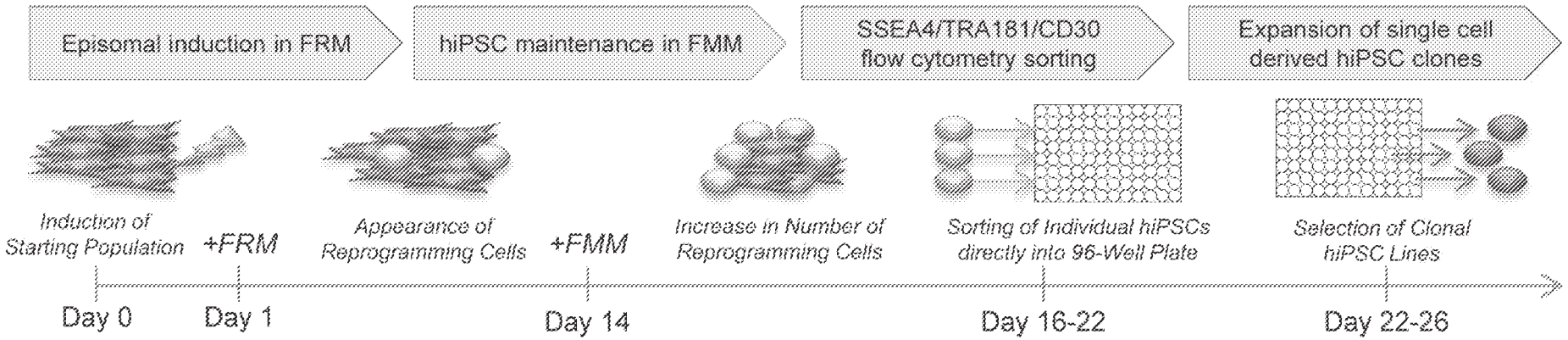

Episomal induction in FRM
hiPSC maintenance in FMM
SSEA4/TRA181/CD30 flow cytometry sorting
Expansion of single cell derived hiPSC clones
Induction of Starting Population
+FRM
Appearance of Reprogramming Cells
+FMM
Increase in Number of Reprogramming Cells
Sorting of Individual hiPSCs directly into 96-Well Plate
Selection of Clonal hiPSC Lines
Day 0
Day 1
Day 14
Day 16-22
Day 22-26

FIG. 2A

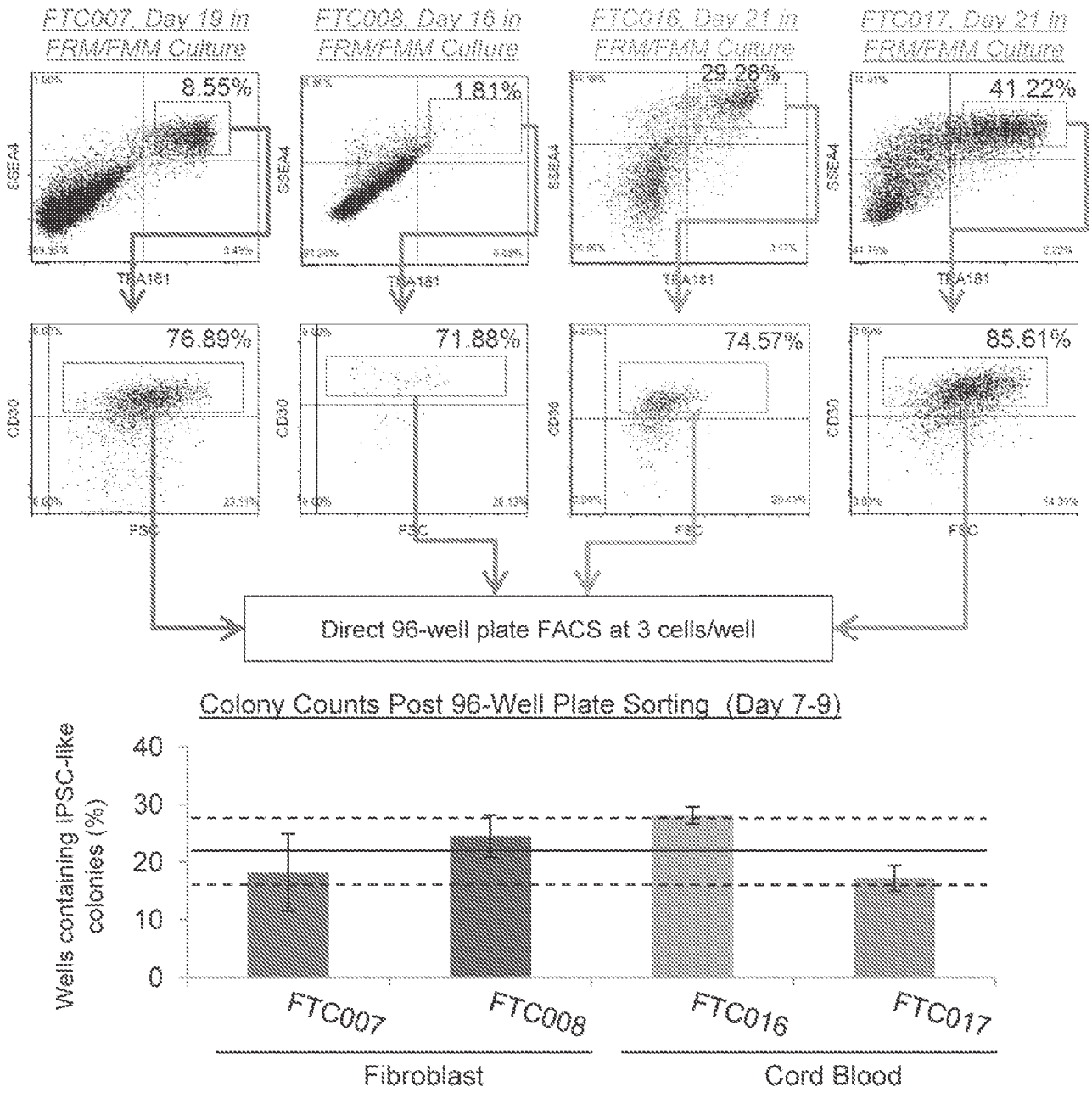

FTC007, Day 19 in FRM/FMM Culture
FTC008, Day 19 in FRM/FMM Culture
FTC016, Day 21 in FRM/FMM Culture
FTC017, Day 21 in FRM/FMM Culture
8.55%
1.81%
29.28%
41.22%
SSEA4
TRA181
76.89%
71.88%
74.57%
85.61%
CD30
FSC
Direct 96-well plate FACS at 3 cells/well
Colony Counts Post 96-Well Plate Sorting (Day 7-9)
Wells containing iPSC-like colonies (%)
40
30
20
10
0
FTC007
FTC008
FTC016
FTC017
Fibroblast
Cord Blood

FIG. 2B

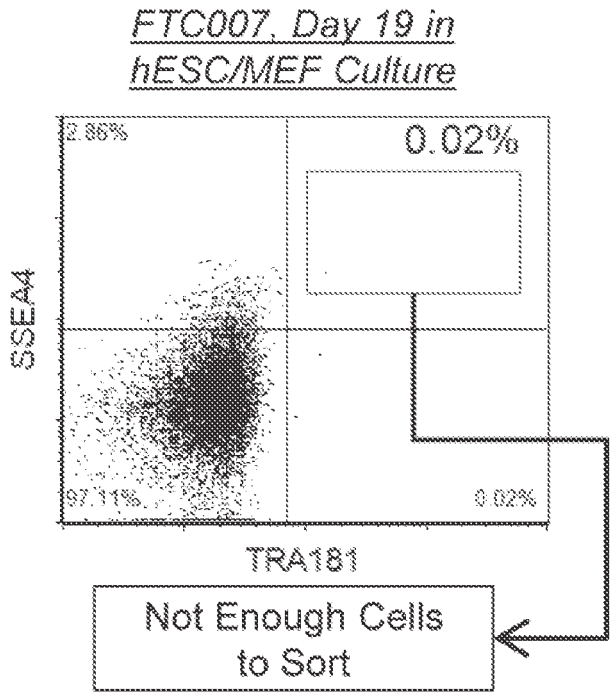

FTC007, Day 19 in
hESC/MEF Culture
2.86%
0.02%
97.11%
0.02%
SSEA4
TRA181
Not Enough Cells
to Sort

FIG. 2C

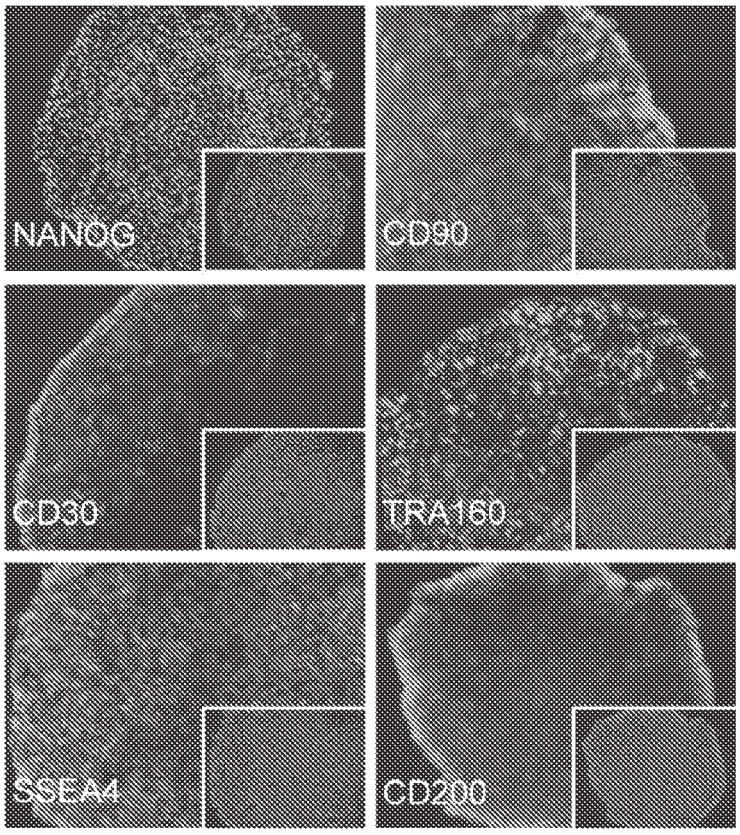

NANOG
CD90
CD30
TRA160
SSEA4
CD200

FIG. 2D

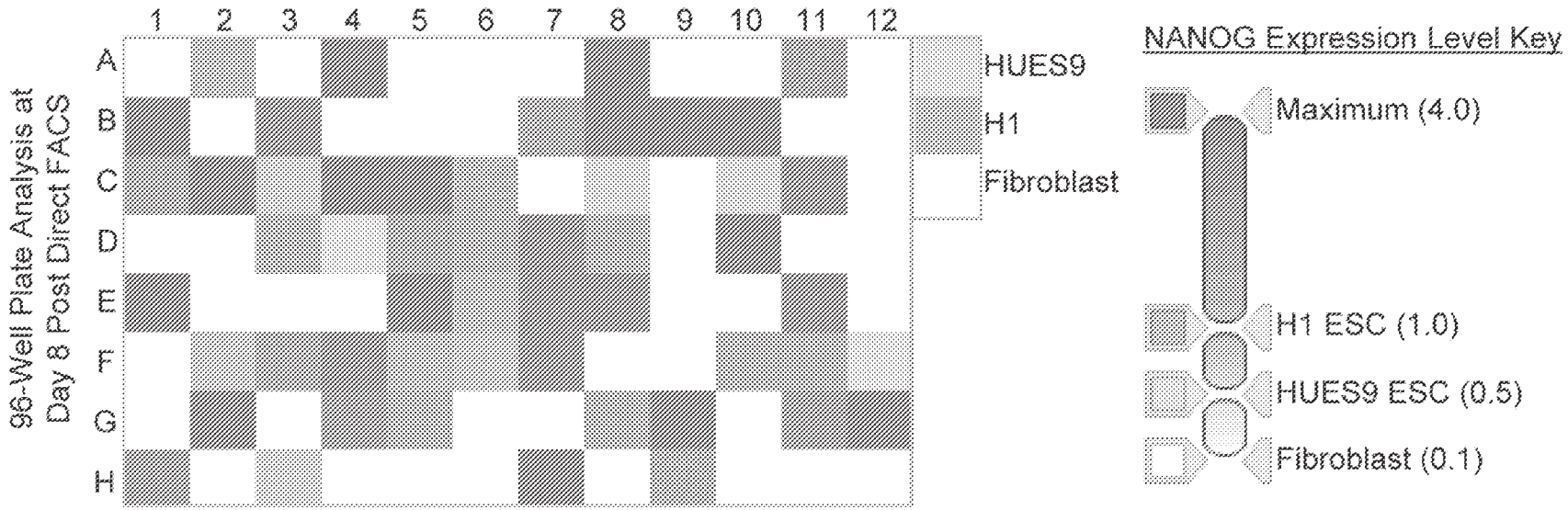

96-Well Plate Analysis at
Day 8 Post Direct FACS
1 2 3 4 5 6 7 8 9 10 11 12
A
B
C
D
E
F
G
H
HUES9
H1
Fibroblast
NANOG Expression Level Key
Maximum (4.0)
H1 ESC (1.0)
HUES9 ESC (0.5)
Fibroblast (0.1)

FIG. 2E

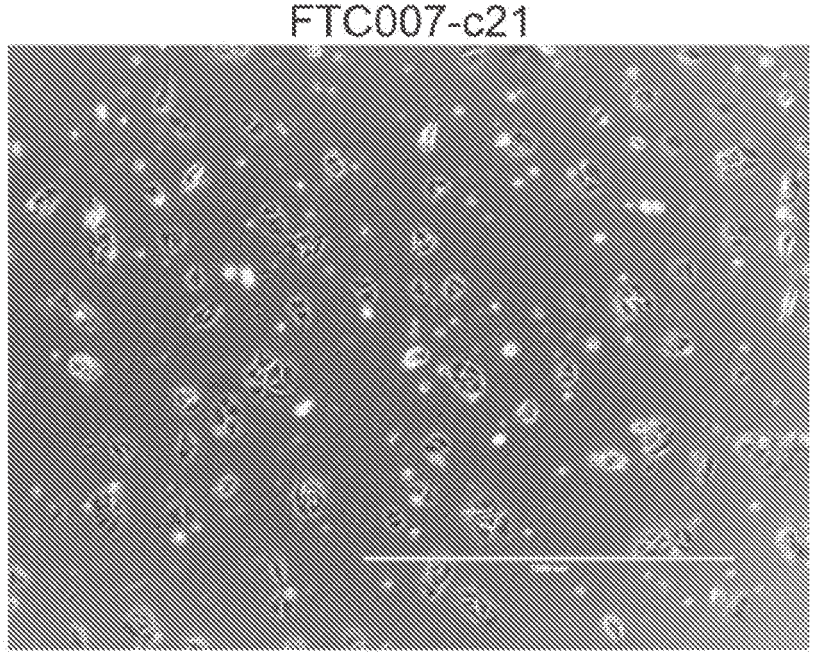


FIG. 3A

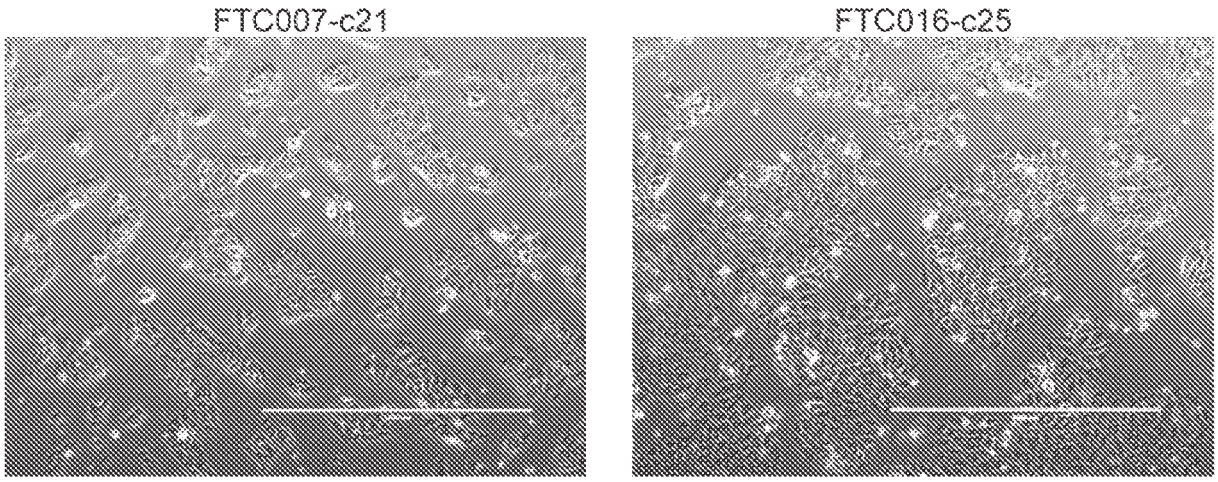


FIG. 3B

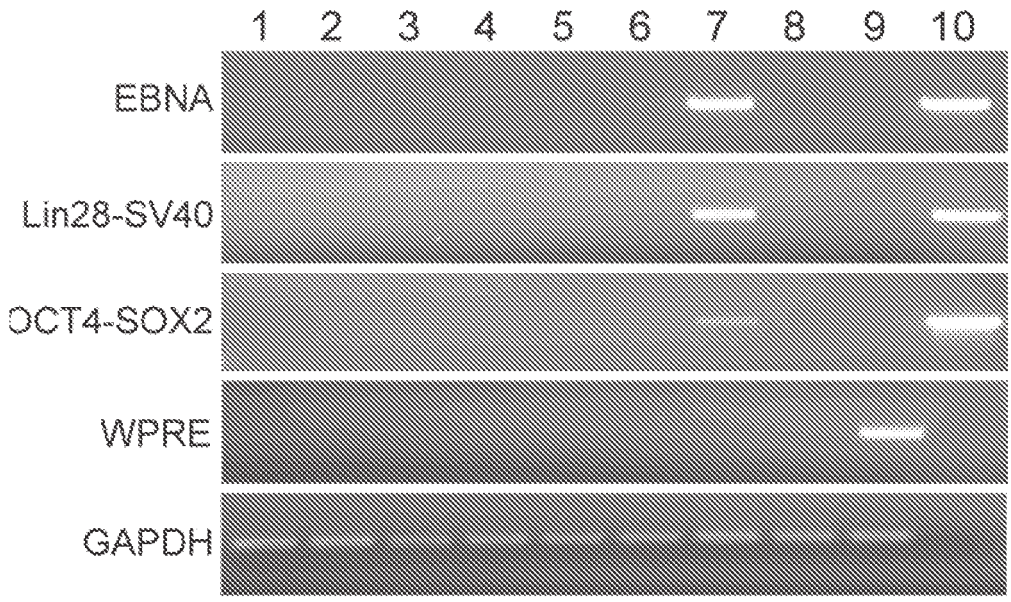


FIG. 3C

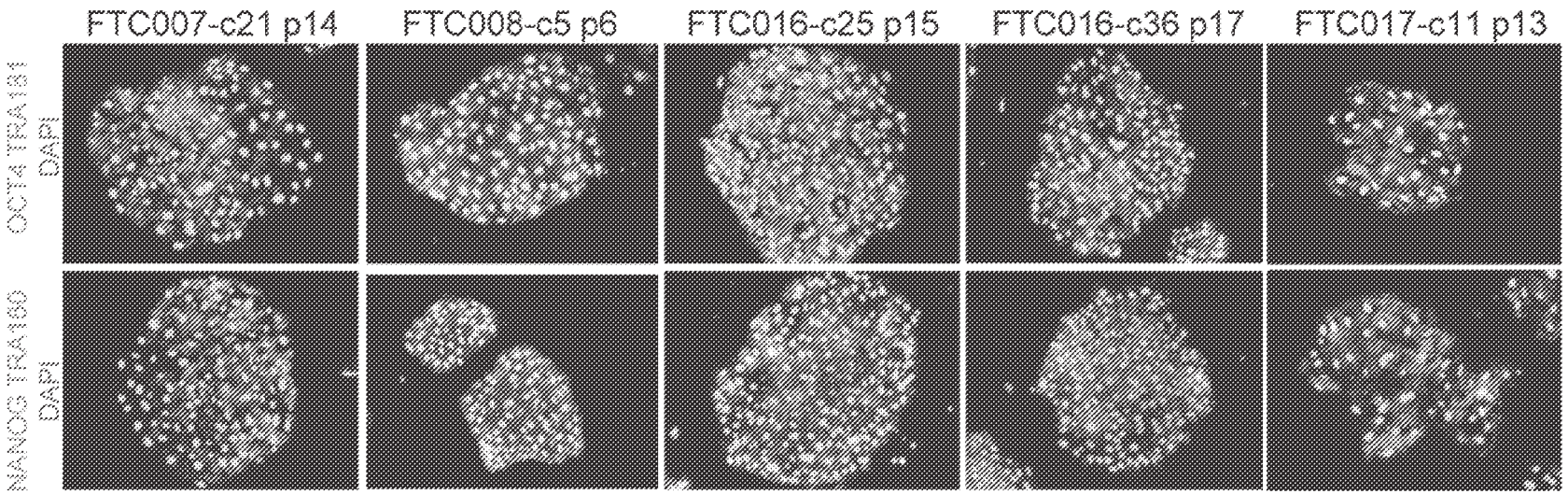

FTC007-c21 p14
FTC008-c5 p6
FTC016-c25 p15
FTC016-c36 p17
FTC017-c11 p13
OCT4 TRA181
DAPI
NANOG TRA160
DAPI

FIG. 3D

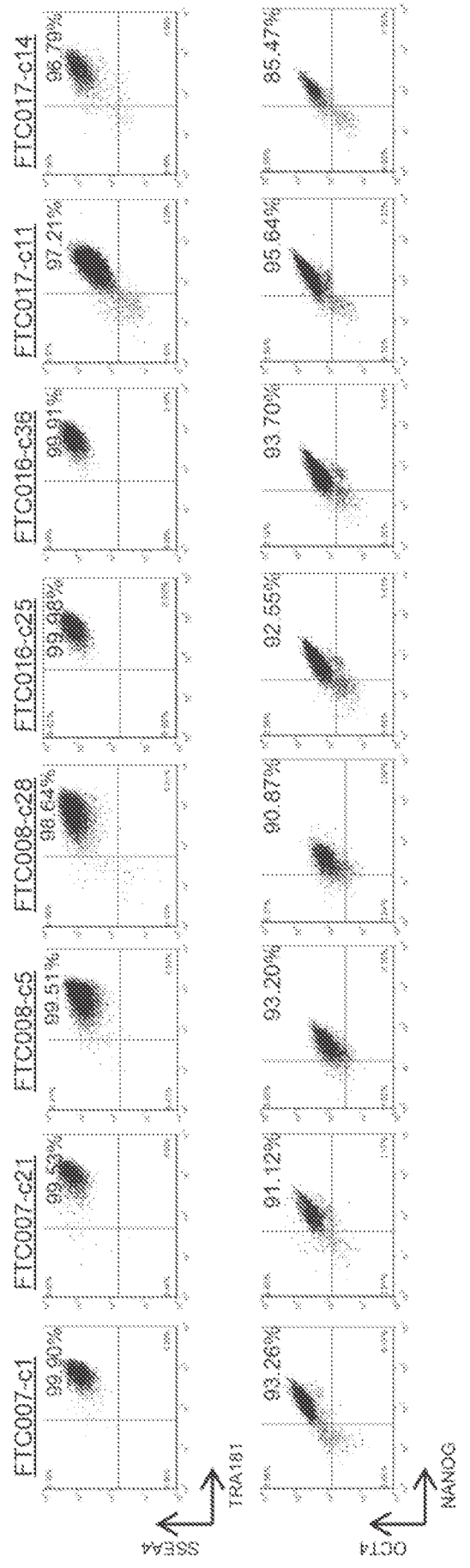

FTC007-c1
99.80%
FTC007-c21
99.62%
FTC008-c5
99.51%
FTC008-c28
98.64%
FTC016-c25
99.48%
FTC016-c36
99.01%
FTC017-c11
97.21%
FTC017-c14
96.79%
SSEA4
TRA181
93.26%
91.12%
93.20%
90.87%
92.55%
93.70%
95.64%
85.47%
OCT4
NANOG

FIG. 3E

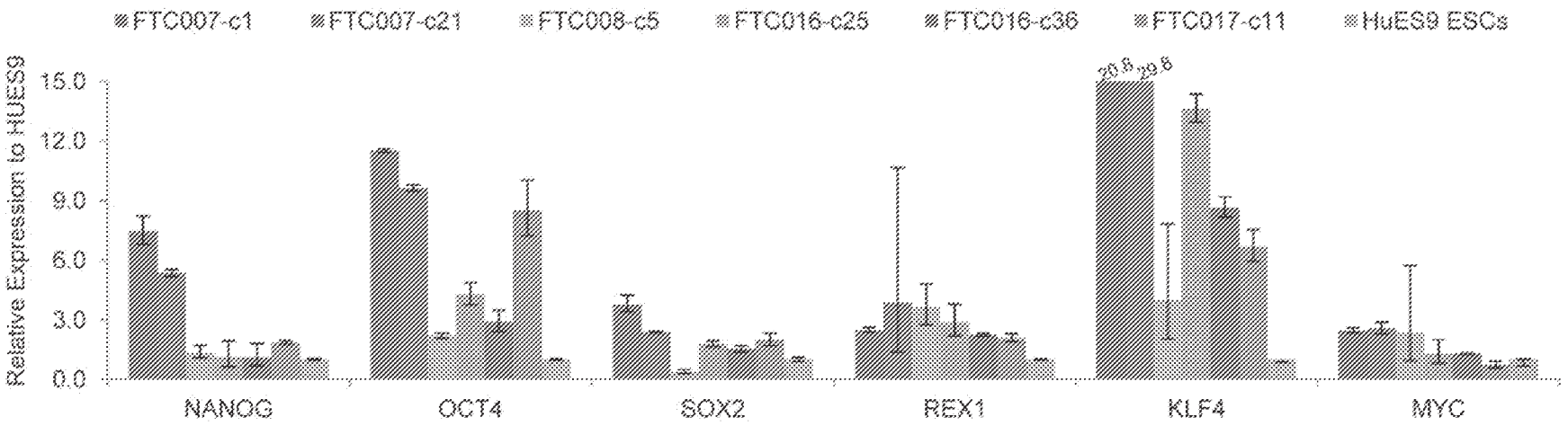

FTC007-c1
FTC007-c21
FTC008-c5
FTC016-c25
FTC016-c36
FTC017-c11
HuES9 ESCs
Relative Expression to HUES9
15.0
12.0
9.0
6.0
3.0
0.0
20.8
29.6
NANOG
OCT4
SOX2
REX1
KLF4
MYC

FIG. 3F

FTC007-c1 p10
46,XY
FTC007-c21 p10
46,XY
FTC016-c25 p11
46,XX
FTC016-c36 p14
46,XX
FTC016-c28 p13
46,XX
FTC017-c11 p13
46,XY

FIG. 4A

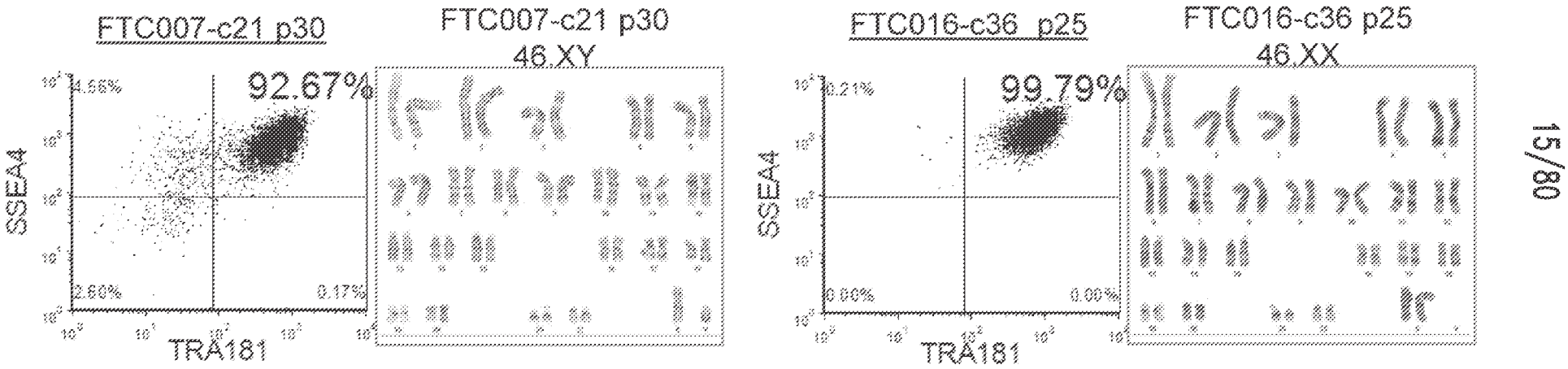

FTC007-c21 p30
FTC007-c21 p30
46,XY
FTC016-c36 p25
FTC016-c36 p25
46,XX
92.67%
99.79%
SSEA4
TRA181
4.56%
2.60%
0.17%
0.21%
0.00%
0.00%

FIG. 4B

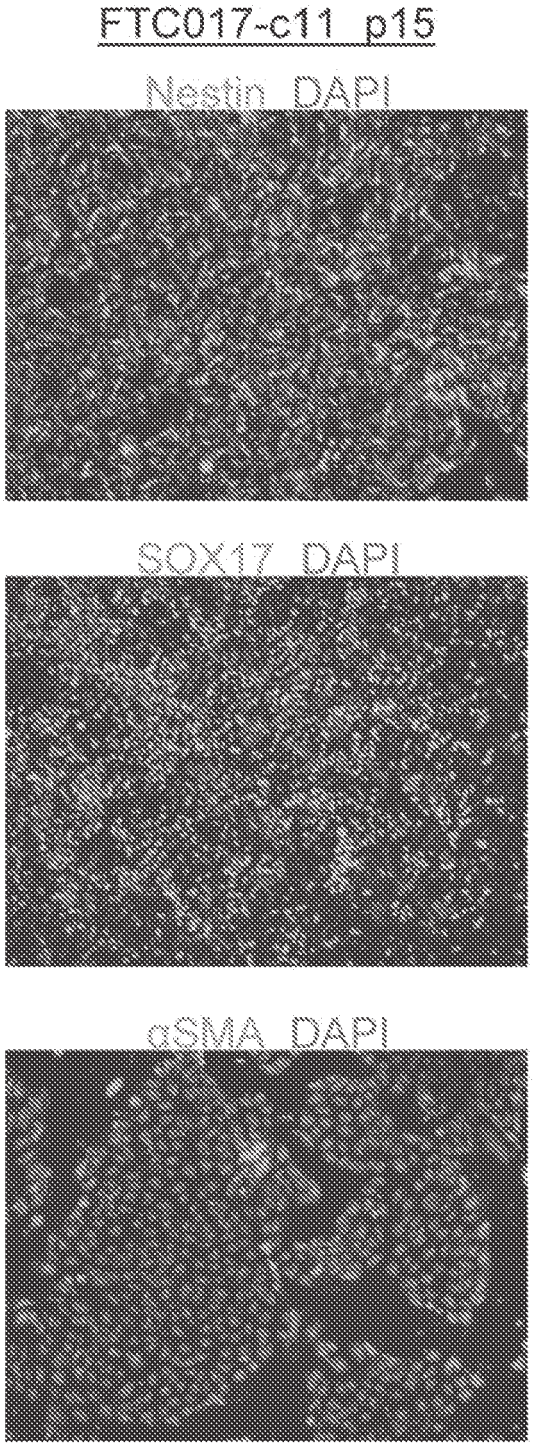


FIG. 4C

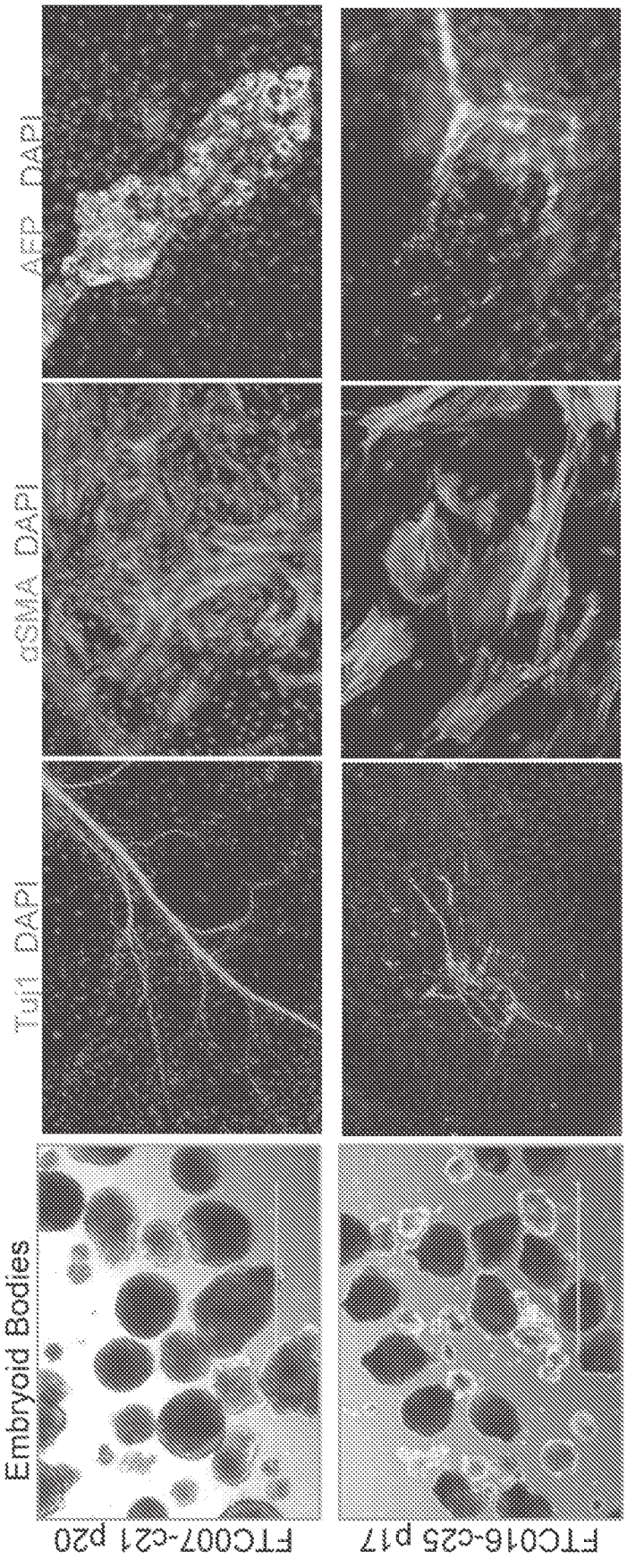

Embryoid Bodies
Tuj1 DAPI
αSMA DAPI
AFP DAPI
FTC007-c21 p20
FTC016-c25 p17

FIG. 4D

FIG. 4E

Vector System	Abbreviation
EF1a-OCT4-2A-NANOG-2A-SOX2	ONS
EF1a-OCT4-2A-SOX2	OS
EF1a-OCT4-2A-OCT4	2xO
EF1a-SV40LT	T

FIG. 5A

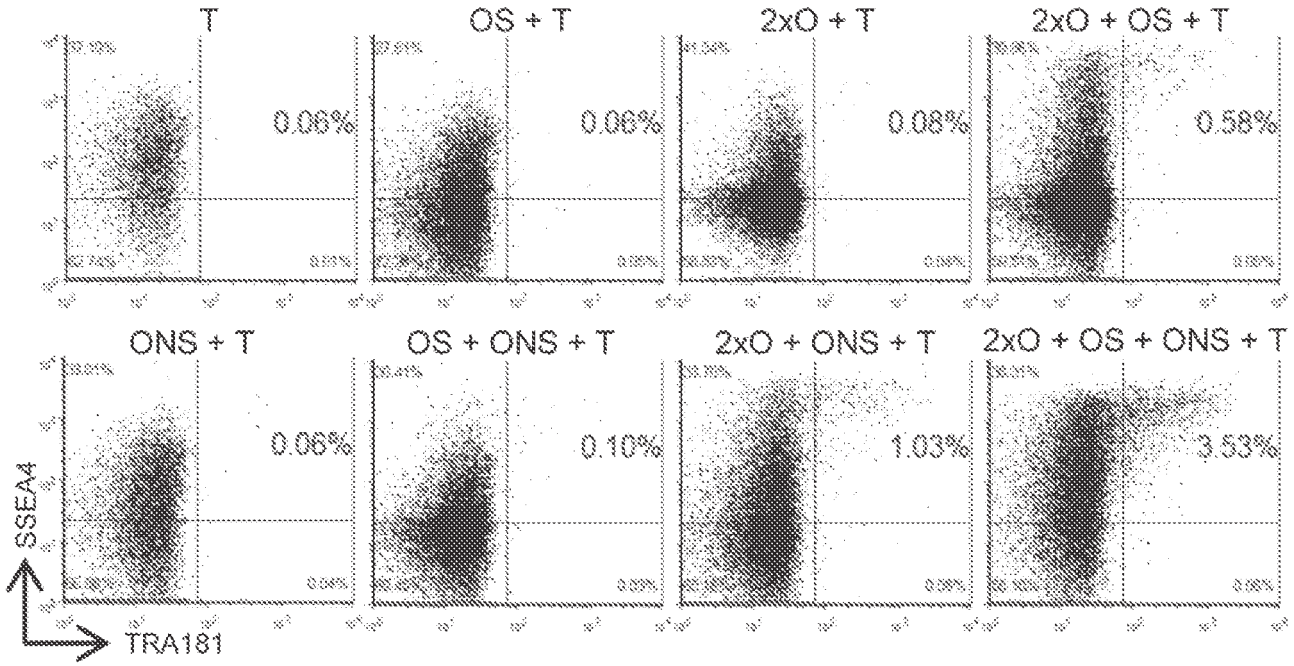


FIG. 5B

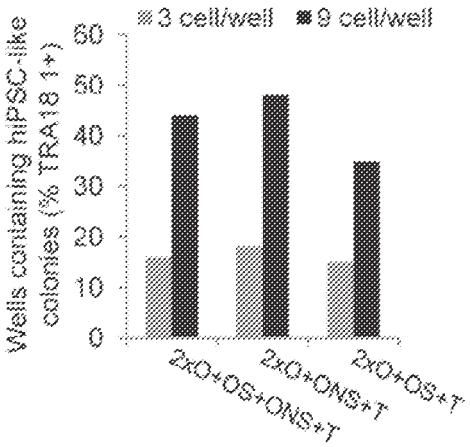


FIG. 5C

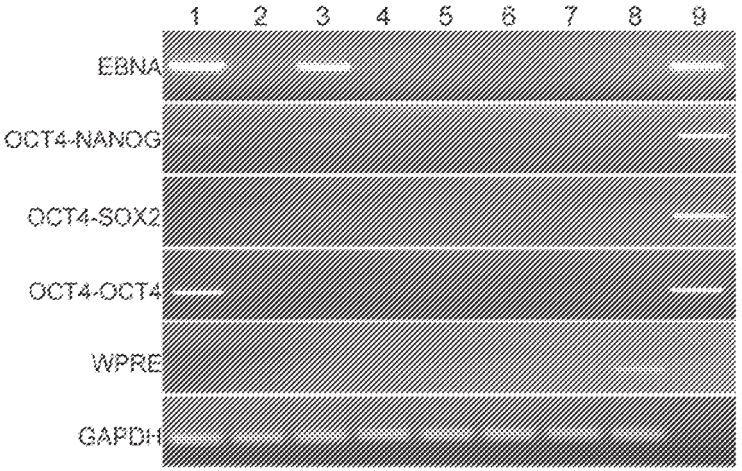


FIG. 5D

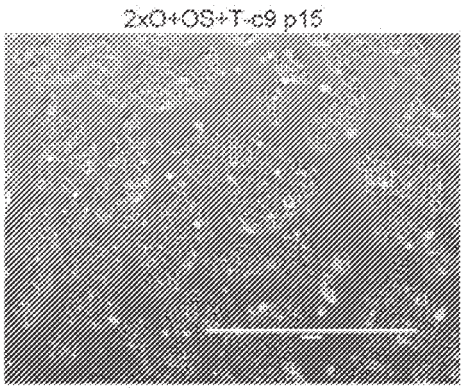


FIG. 5E

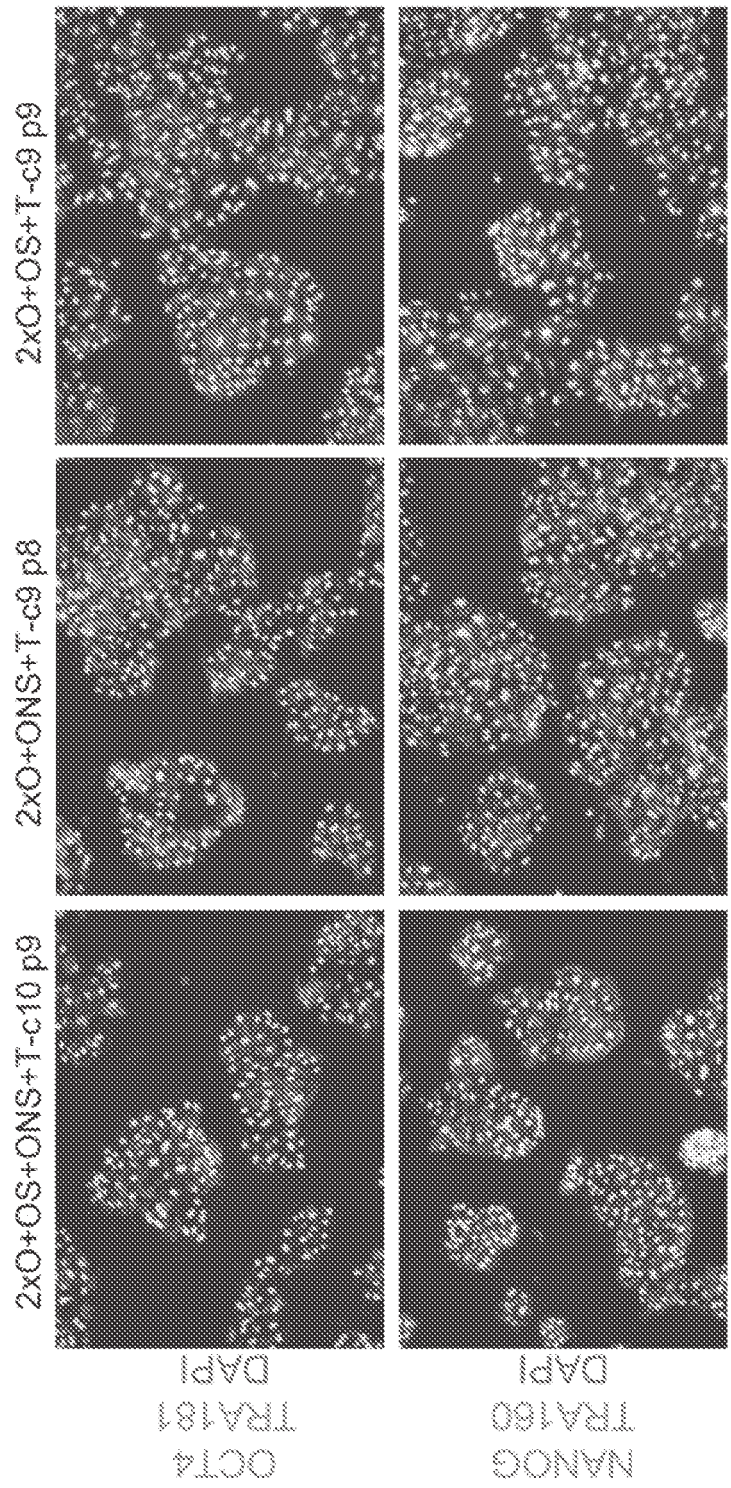

2xO+OS+T-c9 p9
2xO+ONS+T-c9 p8
2xO+OS+ONS+T-c10 p9
NANOG
TRA160
DAPI
OCT4
TRA181
DAPI

FIG. 5F

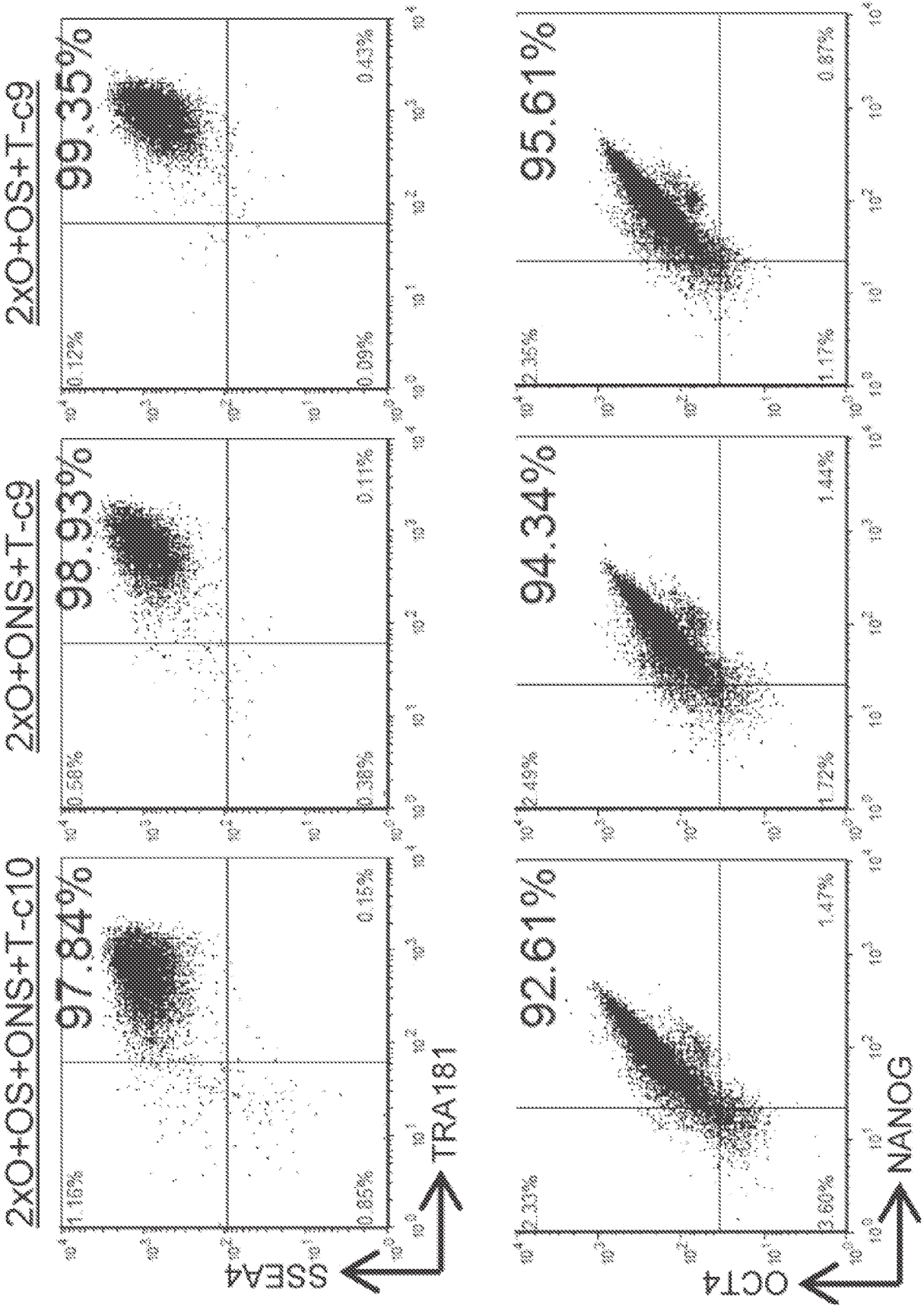

2xO+OS+ONS+T-c10
2xO+ONS+T-c9
2xO+OS+T-c9
97.84%
98.93%
99.35%
92.61%
94.34%
95.61%
1.16%
0.85%
0.15%
0.58%
0.38%
0.11%
0.12%
0.09%
0.43%
2.33%
3.60%
1.47%
2.49%
1.72%
1.44%
2.35%
1.17%
0.87%
SSEA4
TRA181
OCT4
NANOG

FIG. 5G

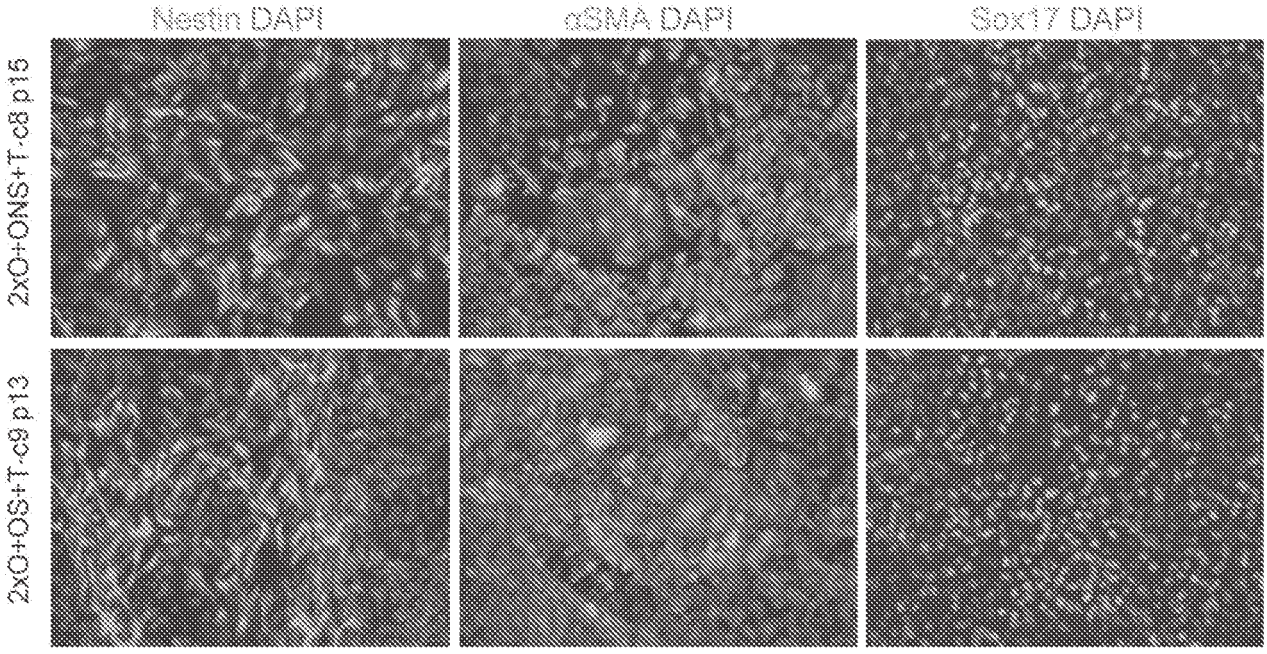

Nestin DAPI
αSMA DAPI
Sox17 DAPI
2xO+ONS+T-c8 p15
2xO+OS+T-c9 p13

FIG. 5H

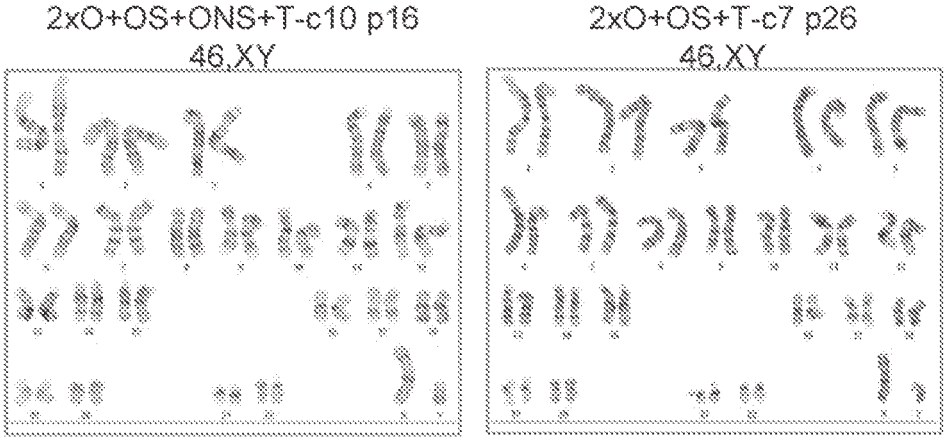

2xO+OS+ONS+T-c10 p16
46,XY
2xO+OS+T-c7 p26
46,XY

FIG. 5I

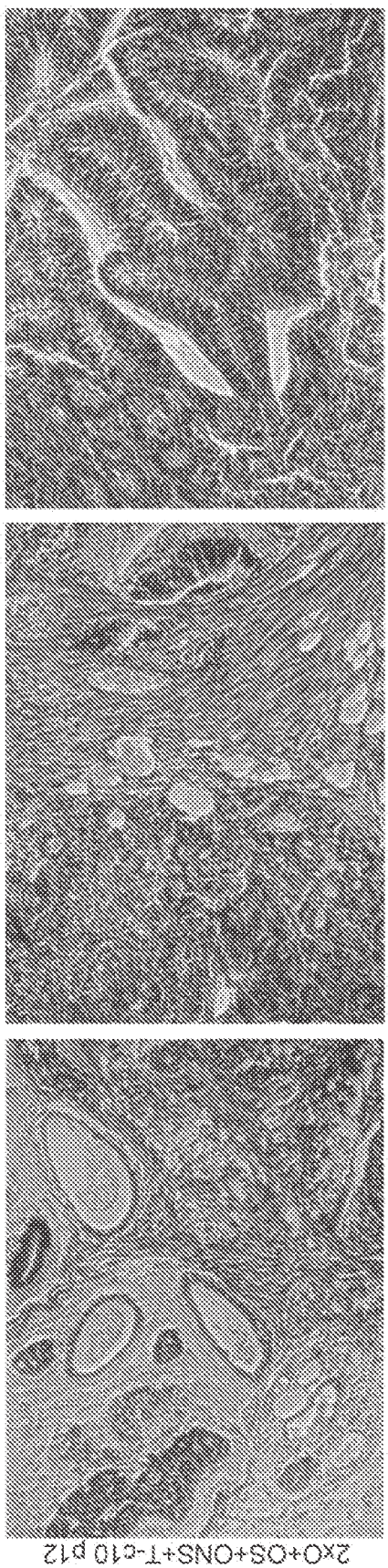


FIG. 5J

Cell Type	Cell Line	NANOG	OCT4	SOX2	KLF4	REX1	DNMT3B	LIN28	MYC
Conventionally maintained hiPSCs on MEF	OKS hiPSC	0.437	0.617	0.781	0.761	0.783	0.764	0.968	0.928
	OKS hiPSC	1.423	0.841	0.837	1.547	0.990	0.837	1.033	0.439
	OKS hiPSC	0.904	1.189	1.028	1.109	1.068	1.497	0.833	1.496
	OKS hiPSC	0.641	1.395	0.972	0.902	1.010	1.014	1.112	1.078
	OKS hiPSC	1.107	1.308	1.618	1.839	1.088	1.217	0.561	1.184
hESC on MEF	H1 ESCs	1.239	0.271	1.078	0.839	0.965	0.986	1.156	0.385
OSNKLMT Episomal hiPSCs in FMM	FTC016-c5	1.211	0.447	1.335	2.513	1.227	1.897	1.233	0.719
	FTC007-c1	1.389	1.478	1.929	5.413	1.668	2.015	1.506	2.076
	FTC016-c25	1.084	0.453	1.120	4.130	1.444	1.362	1.231	1.037
	FTC016-c36	0.955	0.462	1.448	4.597	1.416	1.115	1.249	0.873
	FTC016-c28	0.885	0.419	1.483	1.501	1.293	1.499	1.506	0.626
	FTC017-c11	0.905	1.520	1.639	5.825	1.478	1.498	1.405	0.821
	FTC016-c31	1.040	0.393	1.353	3.249	1.207	0.991	1.040	0.607
	FTC017-c14	0.522	6.003	1.717	14.024	1.292	2.306	0.243	7.228
	FTC007-c21	1.862	1.733	2.025	2.800	1.692	1.940	1.495	1.674
Minimal Factor Episomal hiPSCs in FMM	ONS+OS+2xO-c7	1.270	1.248	1.642	7.658	1.563	1.659	1.304	0.949
	ONS+OS+2xO-c10	1.243	0.856	1.167	8.475	1.395	1.541	1.270	0.843
	ONS+2xO-c5	1.172	0.794	1.399	4.352	1.105	1.865	1.432	0.547
	ONS+2xO-c8	1.114	1.007	1.162	8.367	1.091	1.544	1.448	0.542
	ONS+2xO-c9	1.183	0.856	1.015	9.251	1.303	1.218	1.507	0.536
	OS+2xO-c7	1.203	0.866	1.740	9.434	1.529	1.152	1.402	0.766
	OS+2xO-c9	1.406	0.863	1.650	8.231	1.379	2.053	1.534	0.662

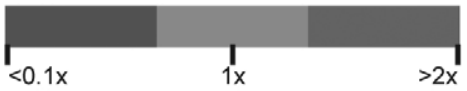


FIG. 6A

Cell Type	Cell Line	T	CXCR4	NODAL	GATA4	SOX17	FOXA2	OTX2	TUJ1
Conventionally maintained hiPSCs on MEF	OKS hiPSC	0.361	0.002	0.000	1.567	2.668	0.001	0.000	0.000
	OKS hiPSC	1.431	1.489	2.023	0.563	0.993	1.205	0.648	1.853
	OKS hiPSC	1.200	2.269	3.673	2.329	1.600	4.834	1.770	1.641
	OKS hiPSC	0.102	1.185	0.494	0.579	0.581	0.830	1.543	1.200
	OKS hiPSC	2.247	0.844	2.996	2.056	0.702	4.476	2.126	0.834
hESC on MEF	H1 ESCs	0.833	0.001	0.000	0.638	1.007	0.000	0.000	0.000
OSNKLMT Episomal hiPSCs in FMM	FTC016-c5	0.011	0.046	0.171	0.001	0.002	0.001	0.892	2.023
	FTC007-c1	0.006	0.128	1.105	0.020	0.006	0.046	2.085	2.031
	FTC016-c25	0.035	0.001	0.000	0.015	0.001	0.000	0.000	0.001
	FTC016-c36	0.026	0.001	0.000	0.010	0.003	0.000	0.000	0.001
	FTC016-c28	0.004	0.075	0.093	0.000	0.001	0.011	1.117	2.257
	FTC017-c11	0.046	0.001	0.000	0.092	0.001	0.000	0.000	0.001
	FTC016-c31	0.015	0.095	0.401	0.002	0.002	0.009	0.531	2.895
	FTC017-c14	0.460	0.377	0.003	0.145	0.435	0.141	0.007	0.016
	FTC007-c21	0.094	0.003	0.000	0.089	0.002	0.001	0.000	0.001
Minimal Factor Episomal hiPSCs in FMM	ONS+OS+2xO-c7	0.081	0.003	0.000	0.020	0.003	0.001	0.001	0.004
	ONS+OS+2xO-c10	0.322	0.002	0.000	0.069	0.008	0.001	0.000	0.003
	ONS+2xO-c5	0.044	0.001	0.000	0.023	0.004	0.000	0.000	0.001
	ONS+2xO-c8	0.011	0.001	0.000	0.027	0.002	0.000	0.000	0.001
	ONS+2xO-c9	0.074	0.001	0.000	0.036	0.003	0.000	0.000	0.000
	OS+2xO-c7	0.005	0.001	0.000	0.019	0.000	0.000	0.000	0.002
	OS+2xO-c9	0.145	0.001	0.000	0.028	0.009	0.000	0.000	0.001

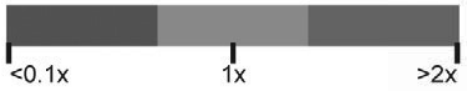


FIG. 6B

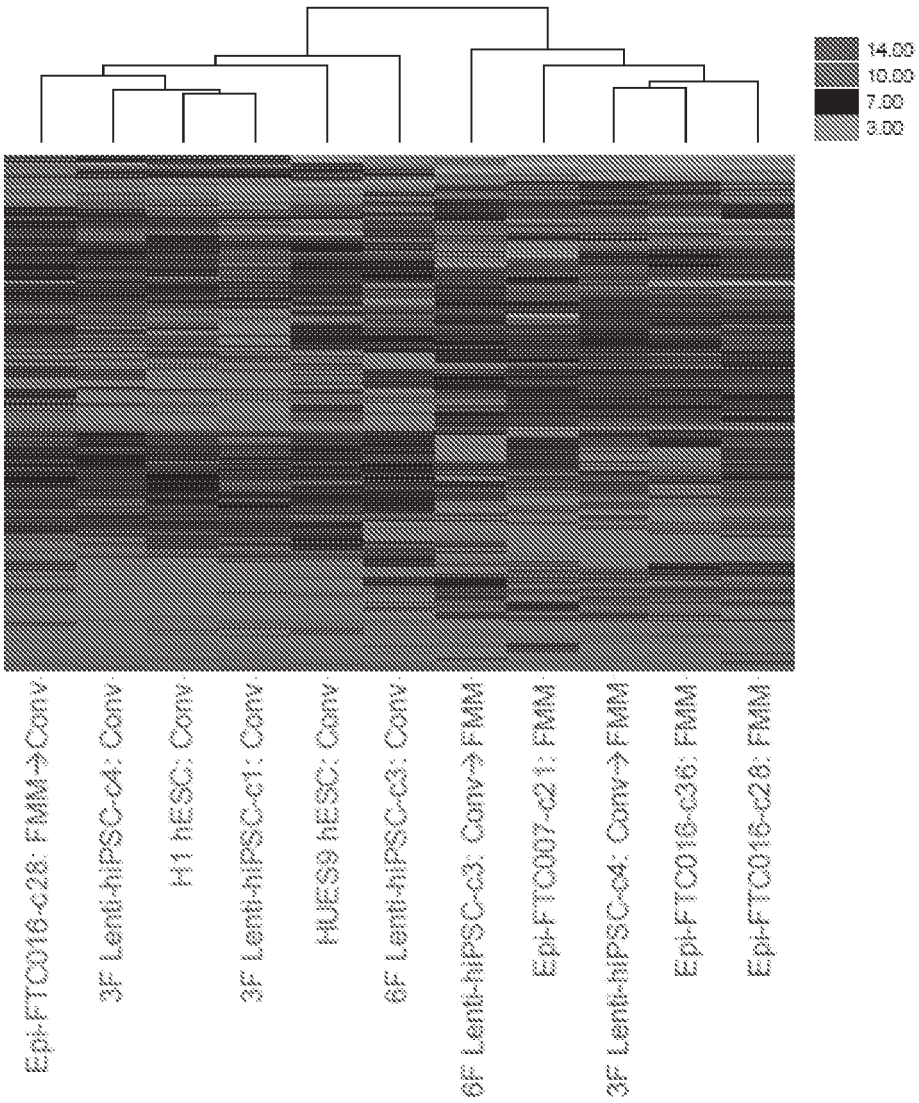

14.00
10.00
7.00
3.00
Epi-FTC016-c28: FMM→Conv
3F Lenti-hiPSC-c4: Conv
H1 hESC: Conv
3F Lenti-hiPSC-c1: Conv
HUES9 hESC: Conv
6F Lenti-hiPSC-c3: Conv
6F Lenti-hiPSC-c3: Conv→FMM
Epi-FTC007-c21: FMM
3F Lenti-hiPSC-c4: Conv→FMM
Epi-FTC016-c36: FMM
Epi-FTC016-c28: FMM

FIG. 7A

213 Probe sets upregulated in conventional hESC culture group vs. FMM culture group			
GO ID	GO Term	%	p-value
GO:0007389	pattern specification process	11.2	2.20E-10
GO:0003002	regionalization	8.1	1.90E-07
GO:0048598	embryonic morphogenesis	8.1	1.90E-05
GO:0009952	anterior/posterior pattern formation	5.6	3.60E-05
GO:0043009	chordate embryonic development	6.2	2.90E-03
GO:0009792	embryonic development ending in birth or egg hatching	6.2	3.10E-03
GO:0001756	somitogenesis	2.5	3.40E-03
GO:0001775	cell activation	5.6	4.20E-03
GO:0001667	ameboidal cell migration	2.5	4.30E-03
GO:0048568	embryonic organ development	4.4	4.50E-03
GO:0040029	regulation of gene expression, epigenetic	3.1	5.00E-03
GO:0010557	positive regulation of macromolecule biosynthetic process	8.8	5.70E-03
GO:0010628	positive regulation of gene expression	8.1	5.80E-03
GO:0045321	leukocyte activation	5	6.00E-03
GO:0048562	embryonic organ morphogenesis	3.8	6.80E-03
GO:0030111	regulation of Wnt receptor signaling pathway	2.5	8.00E-03
GO:0031328	positive regulation of cellular biosynthetic process	8.8	8.20E-03
GO:0046649	lymphocyte activation	4.4	8.90E-03
GO:0035282	segmentation	2.5	9.00E-03
GO:0009891	positive regulation of biosynthetic process	8.8	9.20E-03
GO:0010604	positive regulation of macromolecule metabolic process	10	9.40E-03

FIG. 7B

Ground State Associated Gene Set
KLF4
KLF2
POU5F1
STAT3
UTF1
FGF4
ID4
TBX3
GDF3
DNMT3L
ESRRB
DPPA2
DPPA3
DPPA5
ZFP42
ZSCAN4
TRIM43
TFCP2L1

Metastable State Associated Gene Set		
MYC	FOXA2	T
DKK1	FGF5	SOX17
BMP2	XIST	NODAL
LEFTY2	COL13A1	OTX2
HES1	DUSP6	EOMES
CDX2	NR2F2	NR0B1
GNAS	CXCR4	CYP2B6
EGR1	GATA3	ERBB4
COL3A1	GATA6	HOXC6
TCF4	INHA	SMAD6
HEPH	RORA	NIPBL
KDR	TNFSF11	CDH11
TOX	ZIC4	GAL
FOXA1	SOX3	PITX2
LCK	APOA2	CXCL5
PCDH7	CER1	FOXQ1
CD1D	MLL5	DPP10
FOXG1	GSC	PCDH10
LEFTY1	CTCFL	PCDH20
ZIC1	TSHZ1	MEGF10

FIG. 7C

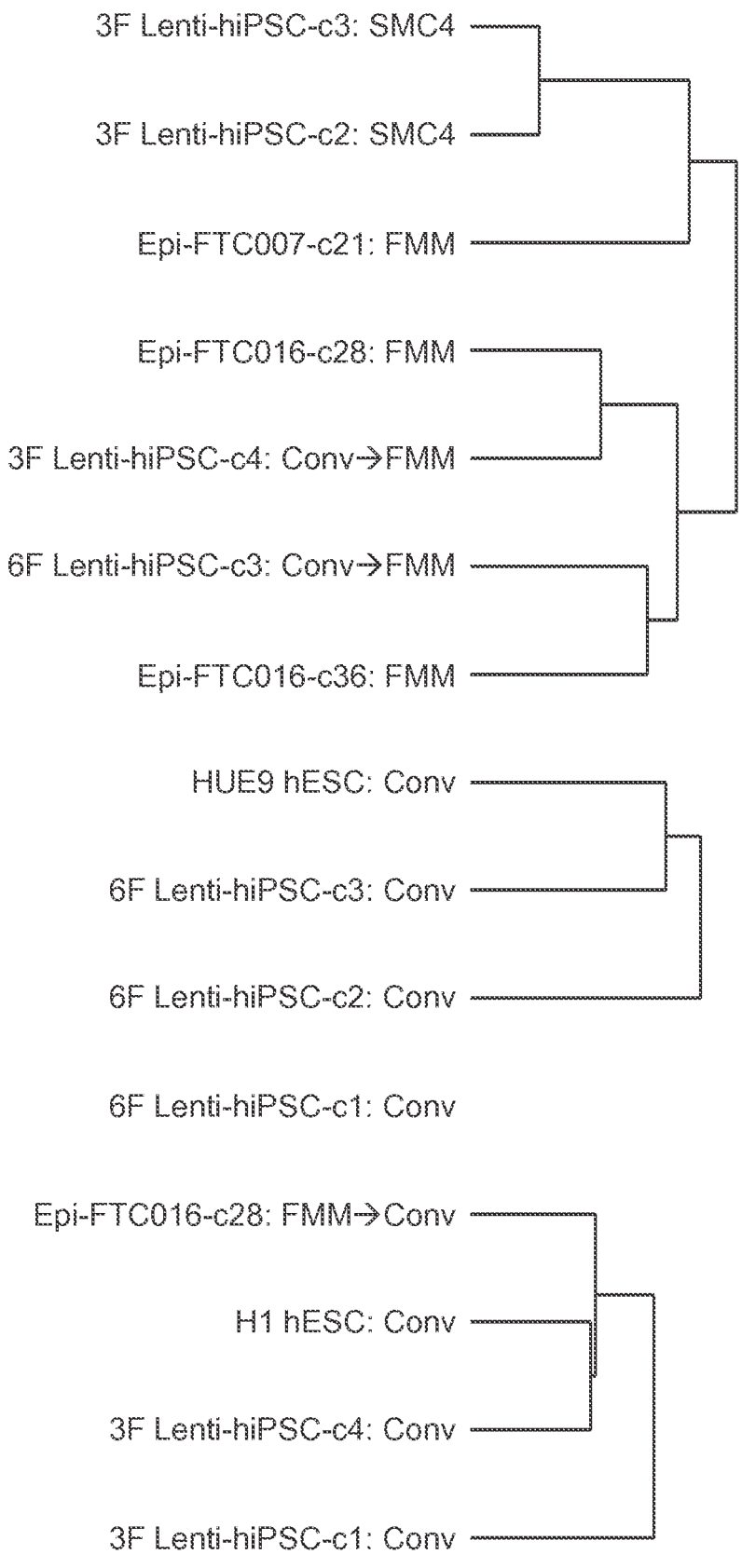

3F Lenti-hiPSC-c3: SMC4
3F Lenti-hiPSC-c2: SMC4
Epi-FTC007-c21: FMM
Epi-FTC016-c28: FMM
3F Lenti-hiPSC-c4: Conv→FMM
6F Lenti-hiPSC-c3: Conv→FMM
Epi-FTC016-c36: FMM
HUE9 hESC: Conv
6F Lenti-hiPSC-c3: Conv
6F Lenti-hiPSC-c2: Conv
6F Lenti-hiPSC-c1: Conv
Epi-FTC016-c28: FMM→Conv
H1 hESC: Conv
3F Lenti-hiPSC-c4: Conv
3F Lenti-hiPSC-c1: Conv

FIG. 7D

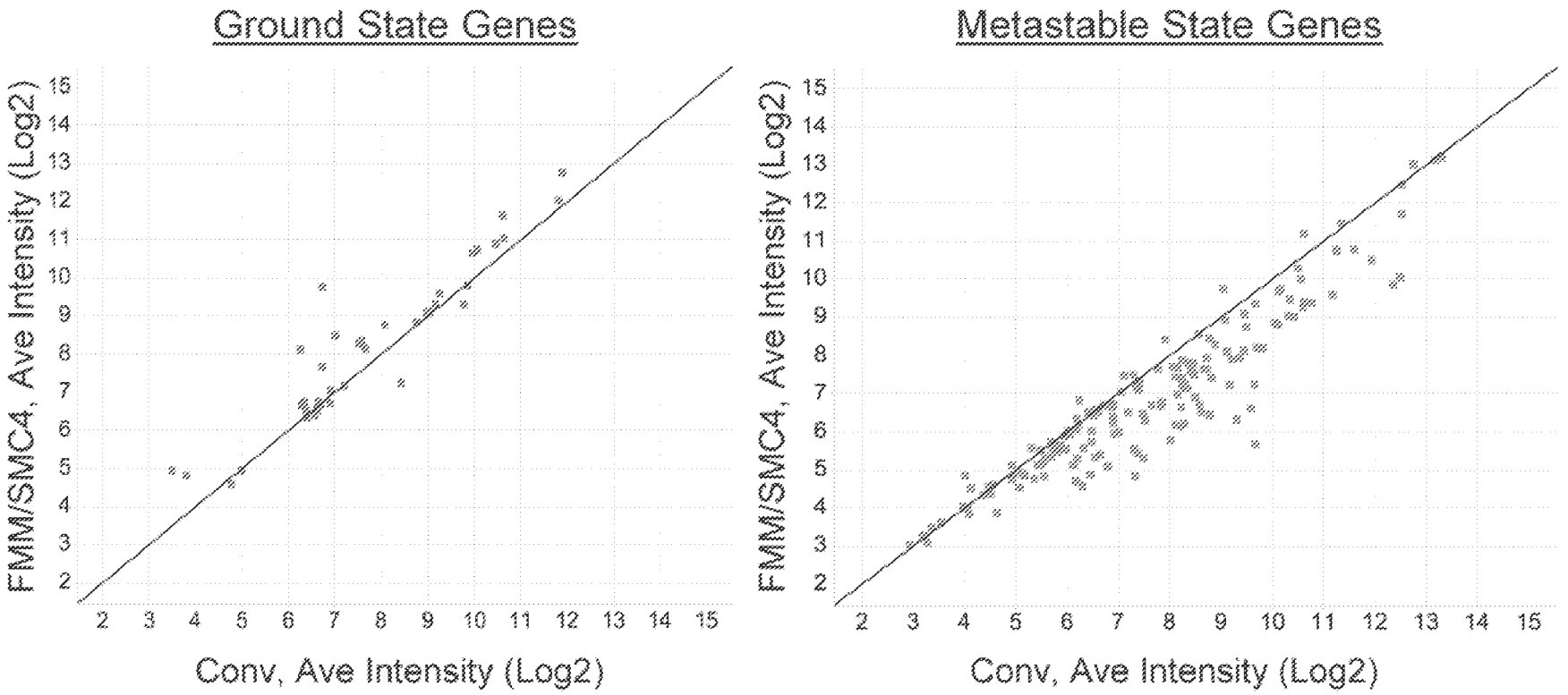

Ground State Genes
FMM/SMC4, Ave Intensity (Log2)
Conv, Ave Intensity (Log2)
Metastable State Genes
FMM/SMC4, Ave Intensity (Log2)
Conv, Ave Intensity (Log2)

FIG. 7E

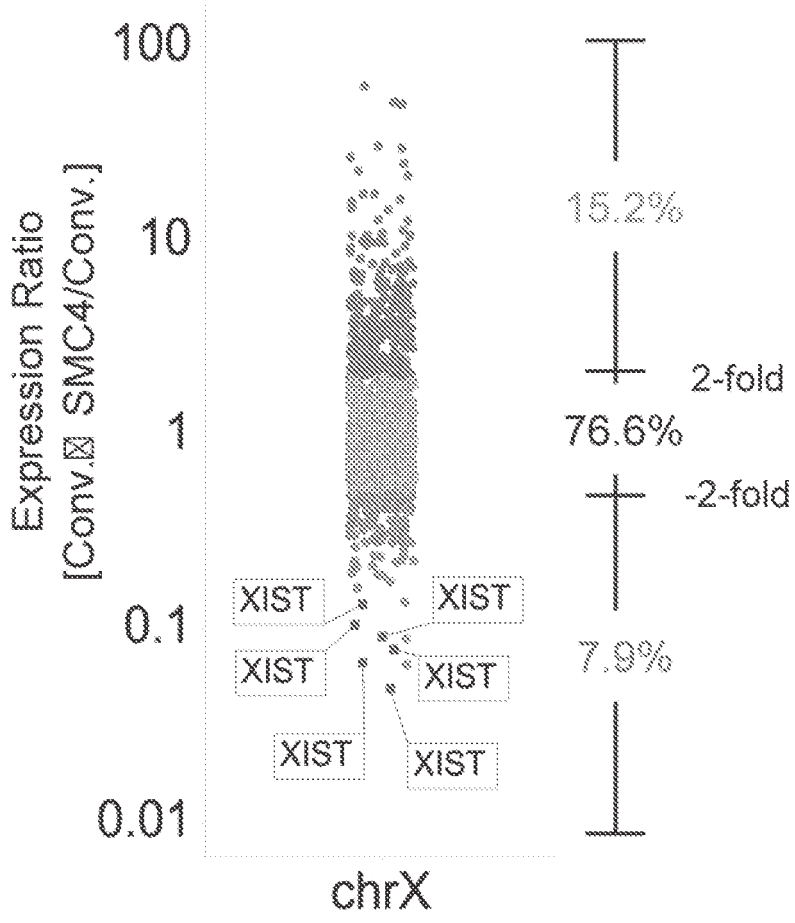

100
10
1
0.1
0.01
Expression Ratio
[Conv.⊠ SMC4/Conv.]
XIST
XIST
XIST
XIST
XIST
XIST
15.2%
2-fold
76.6%
-2-fold
7.9%
chrX

FIG. 7F

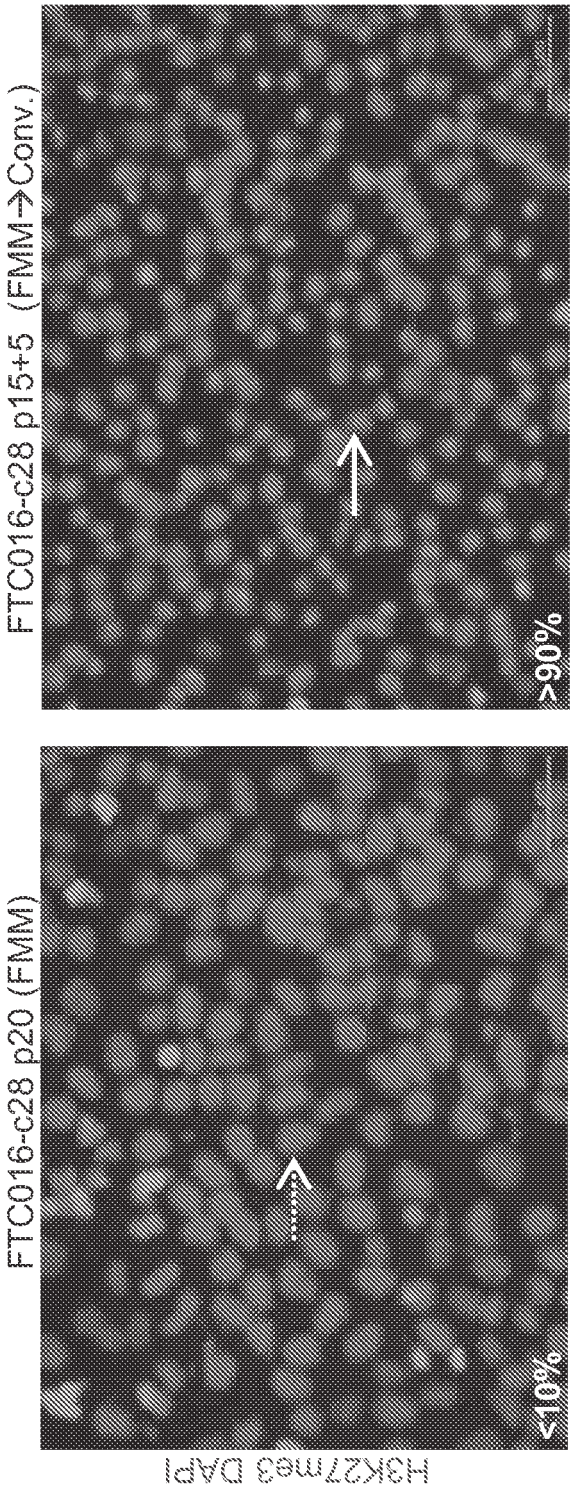

FTC016-c28 p20 (FMM)
<10%
FTC016-c28 p15+5 (FMM→Conv.)
>90%
H3K27me3 DAPI

FIG. 7G

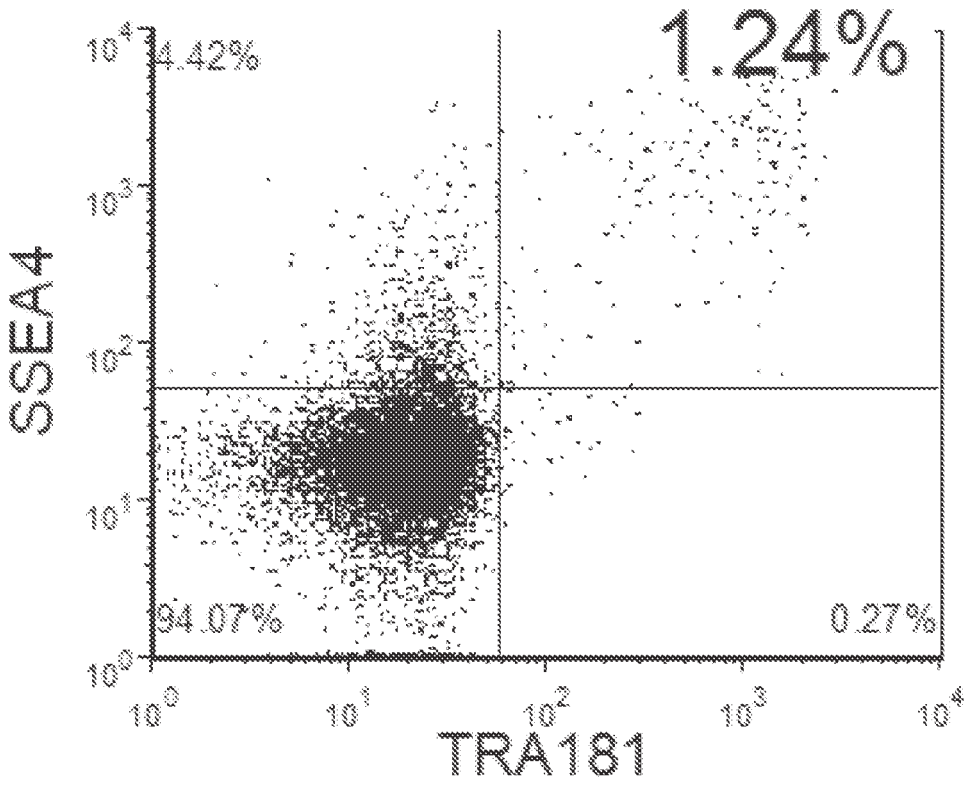


FIG. 8A

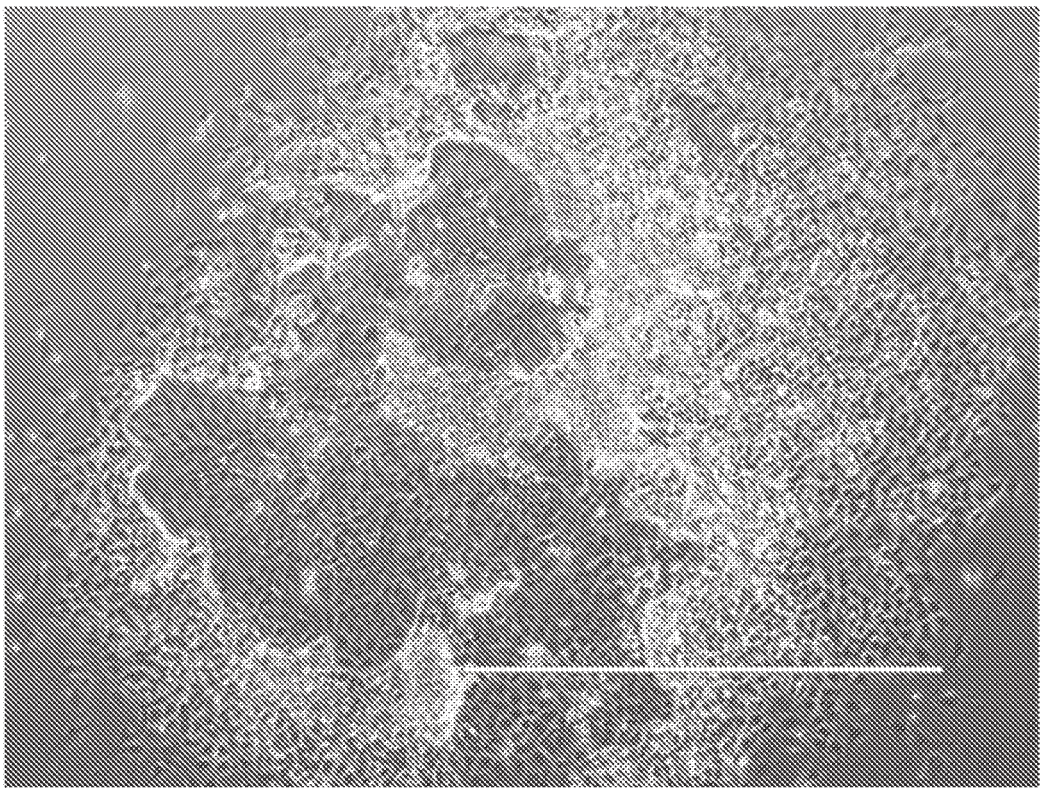


FIG. 8B

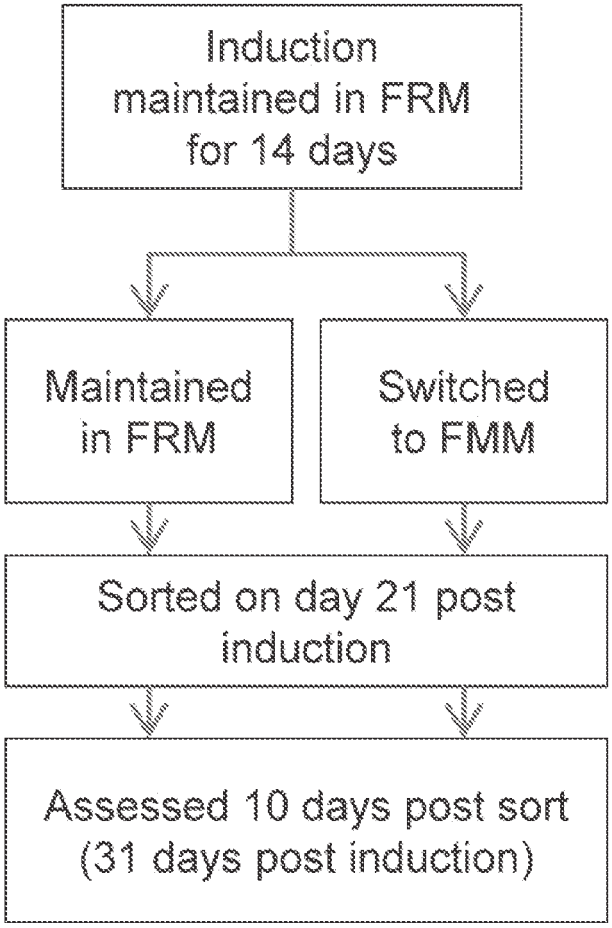

Induction maintained in FRM for 14 days
Maintained in FRM
Switched to FMM
Sorted on day 21 post induction
Assessed 10 days post sort (31 days post induction)

FIG. 8C

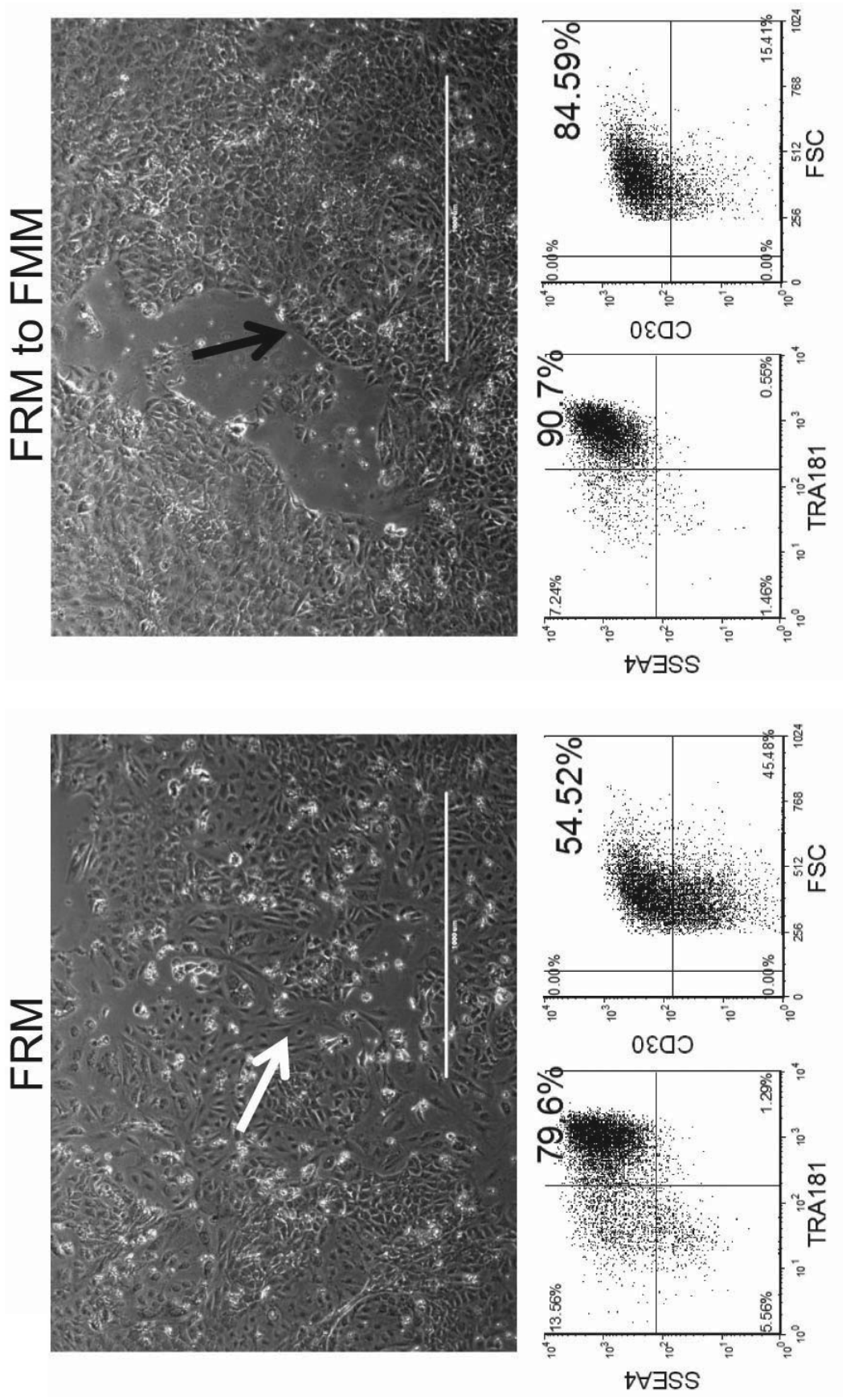

FRM
FRM to FMM
79.6%
13.56%
5.56%
1.29%
54.52%
0.00%
0.00%
45.48%
90.7%
7.24%
1.46%
0.55%
84.59%
0.00%
0.00%
15.41%
SSEA4
TRA181
CD30
FSC

FIG. 8D

Nomenclature	Cell Type	Source	Ethnicity	Gender	Age	Culture Medium	Percent SSEA4/TRA181 Positive Population At Time of 96-Well Plate FACS
FTC007	Fibroblast	Neonatal Foreskin	Caucasian	Male	Neonatal	DMEM + 10%FBS	8.55% (Day 19 post induction)
FTC008	Fibroblast	Dermal Skin	Asian	Female	Adult	DMEM + 10%FBS	1.81% (Day 16 post induction)
FTC016	CD34+ Hematopoietic Cells	Cord Blood, AllCells	Pool	Pool	Neonatal	Stempro + CC110	29.3% (Day 19 post induction)
FTC017	CD34+ Hematopoietic Cells	Cord Blood, Fate derived	African American	Male	Neonatal	Stempro + CC110	41.2% (Day 21 post induction)

FIG. 9A

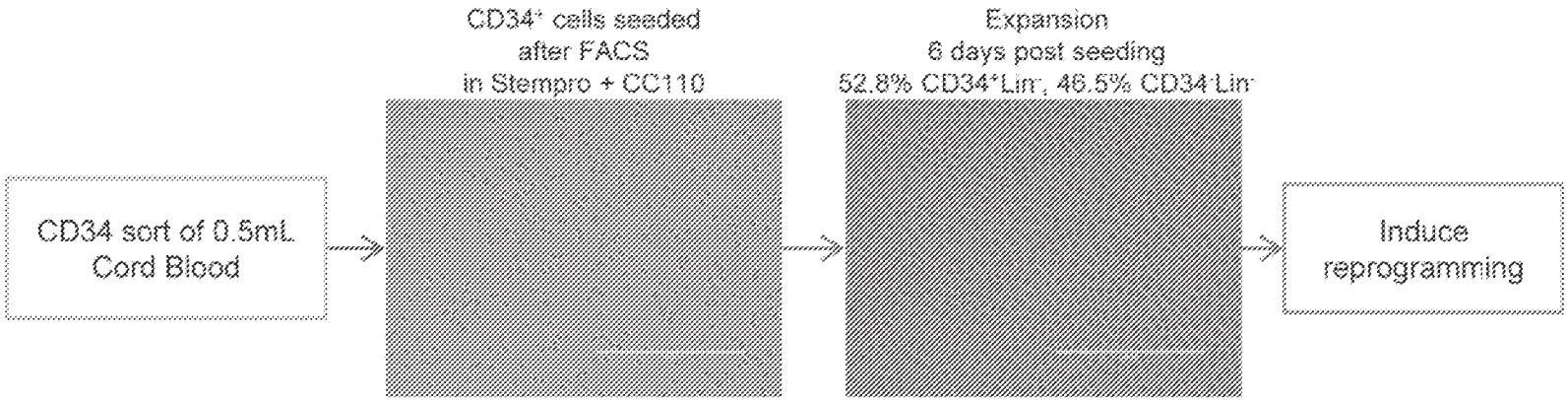

CD34 sort of 0.5mL Cord Blood
CD34+ cells seeded after FACS in Stempro + CC110
Expansion 6 days post seeding 52.8% CD34+Lin-, 46.5% CD34-Lin-
Induce reprogramming

FIG. 9B

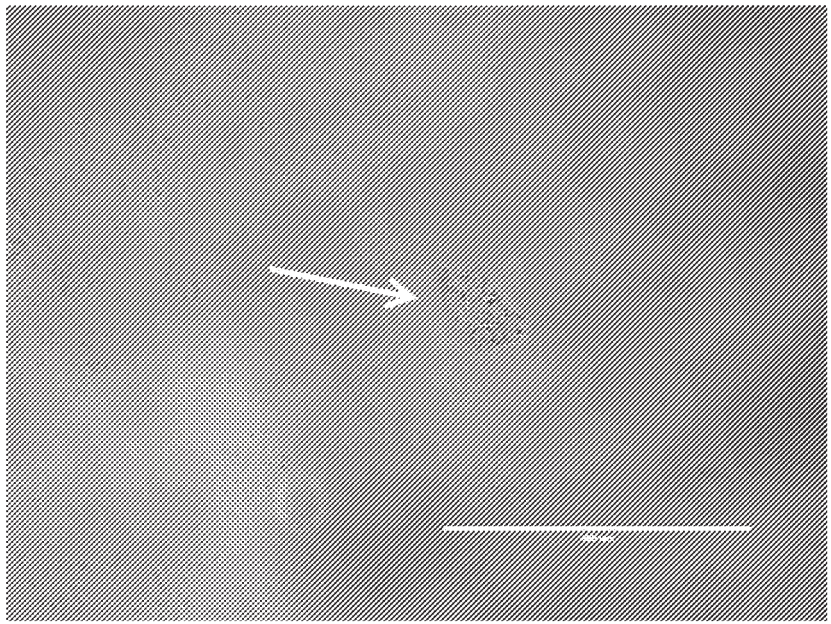


FIG. 10A

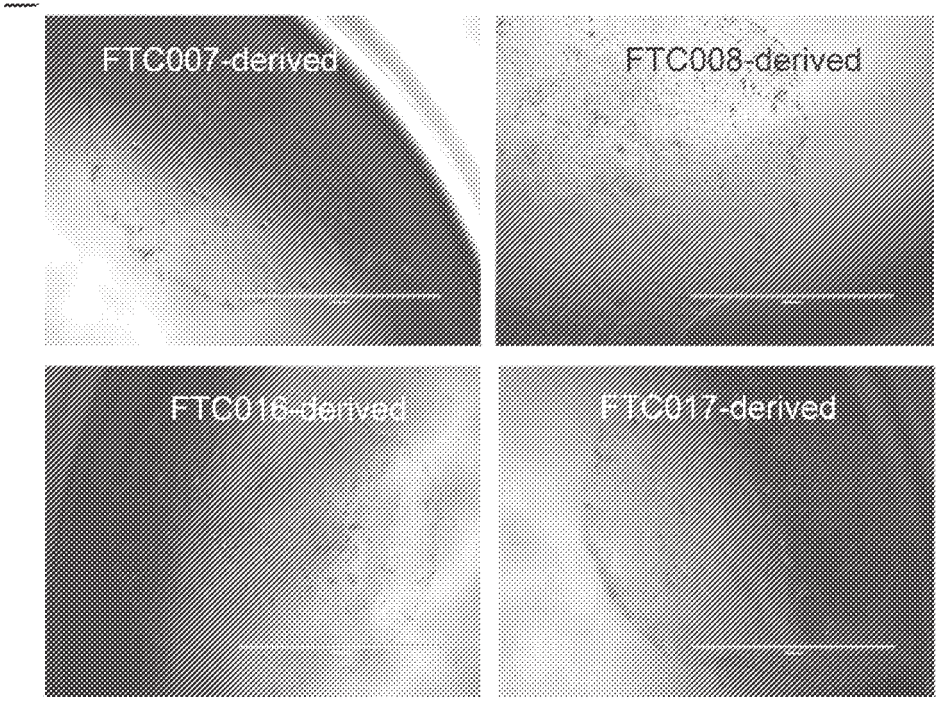


FIG. 10B

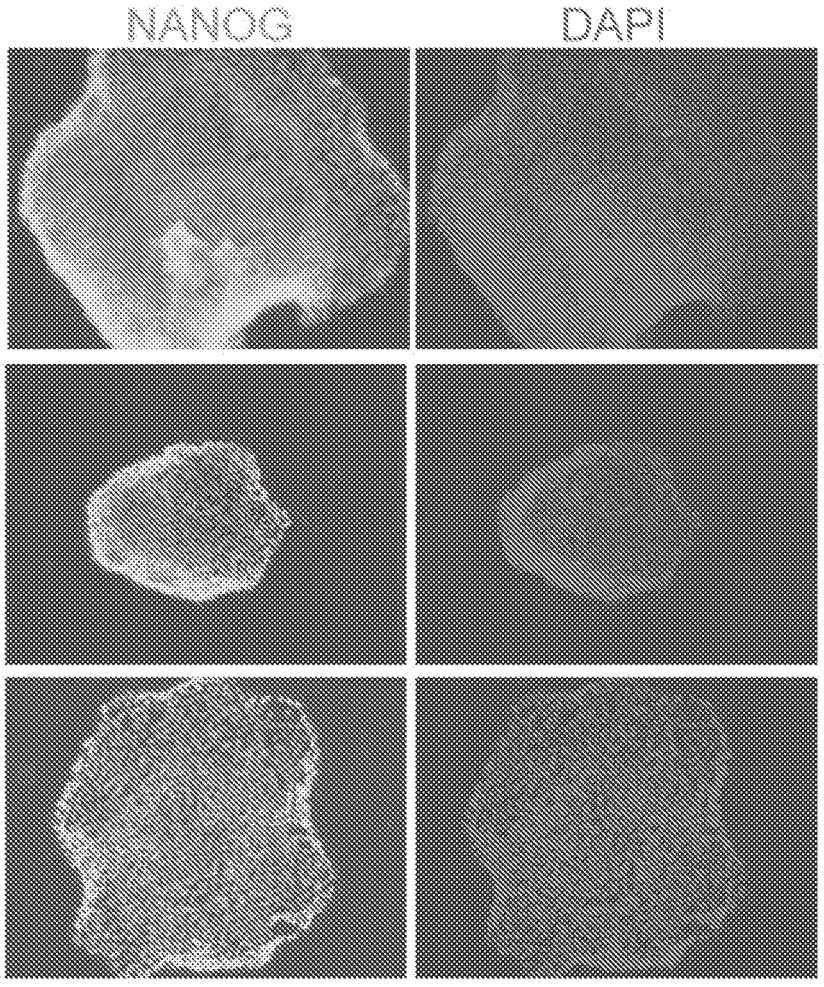


FIG. 10C

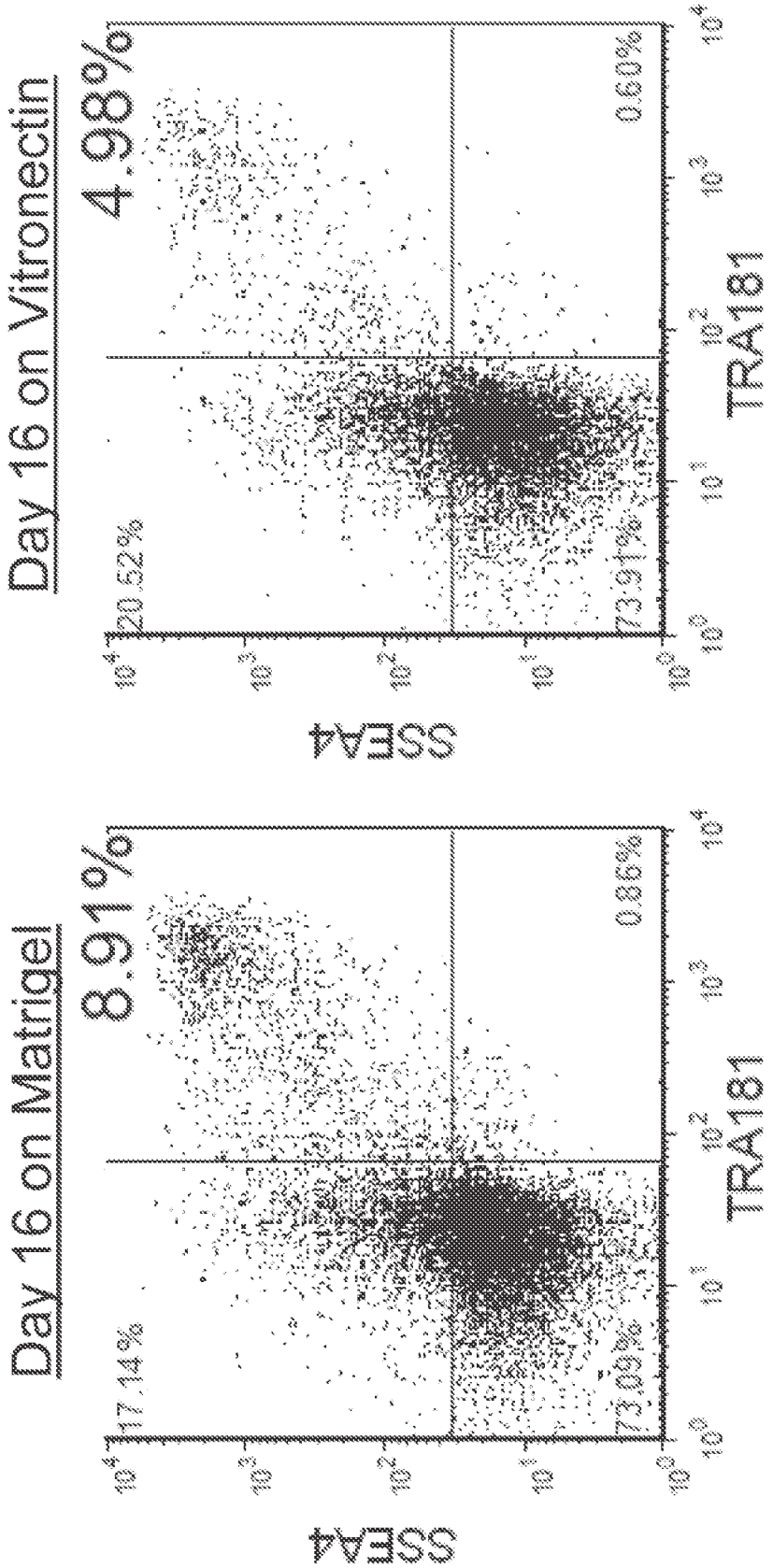

Day 16 on Matrigel
8.91%
0.86%
17.14%
73.09%
SSEA4
TRA181
Day 16 on Vitronectin
4.98%
0.60%
20.52%
73.91%
SSEA4
TRA181

FIG. 10D

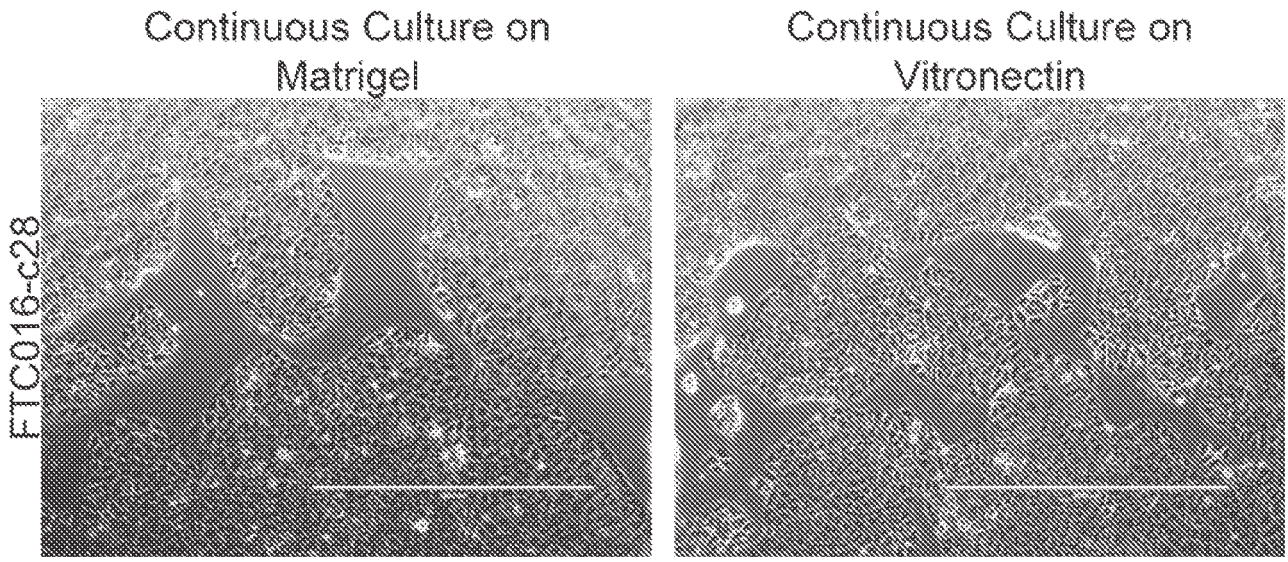


FIG. 10E

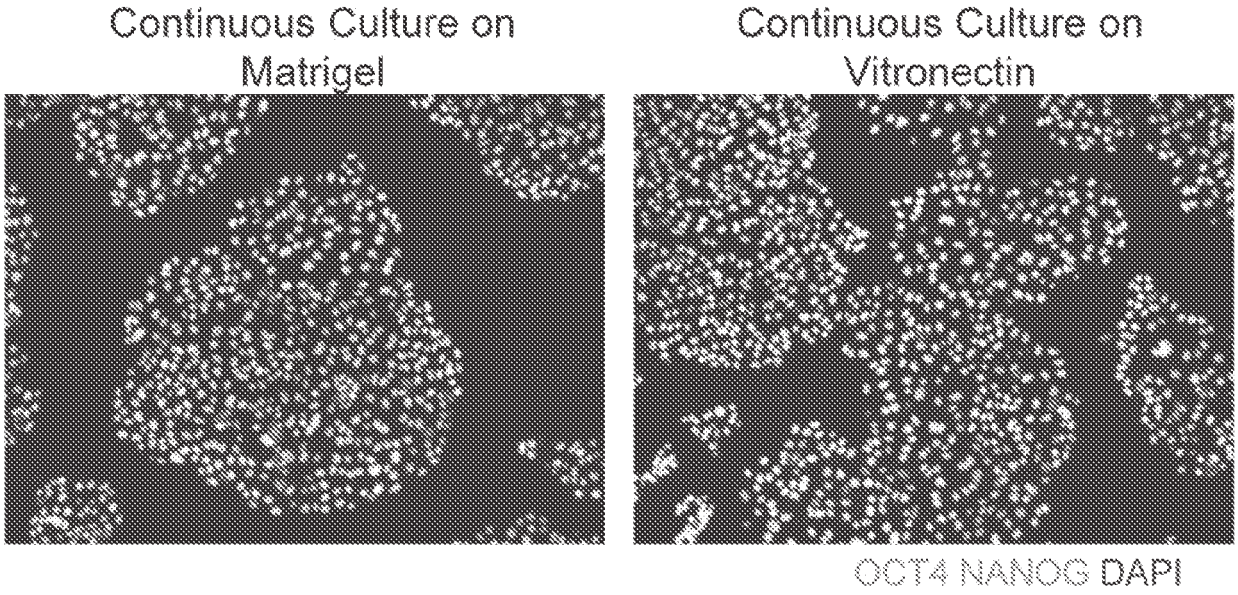


FIG. 10F

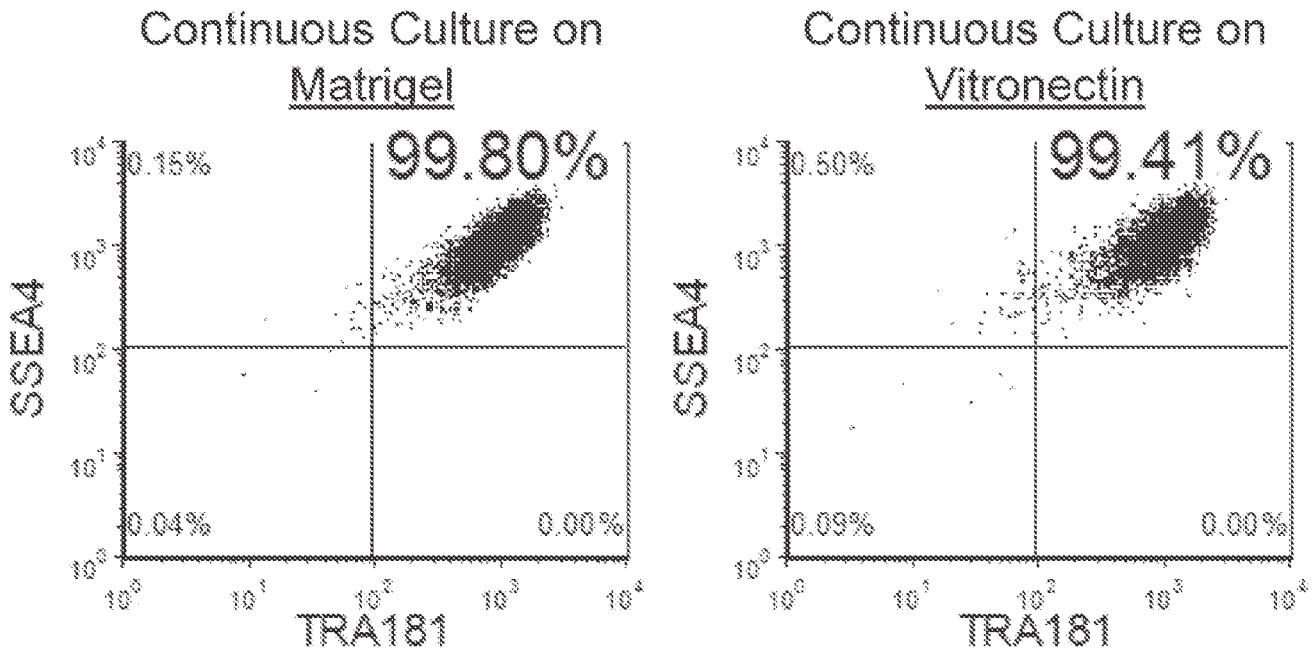

Continuous Culture on
Matrigel
99.80%
0.15%
0.04%
0.00%
SSEA4
TRA181
Continuous Culture on
Vitronectin
99.41%
0.50%
0.09%
0.00%
SSEA4
TRA181

FIG. 10G

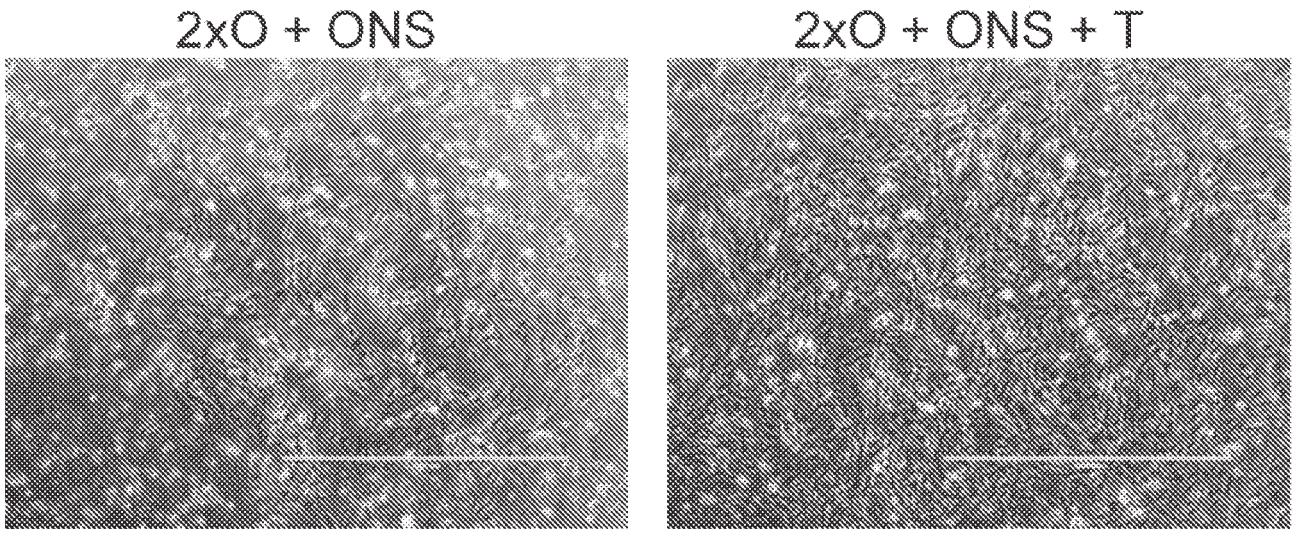


FIG. 11A

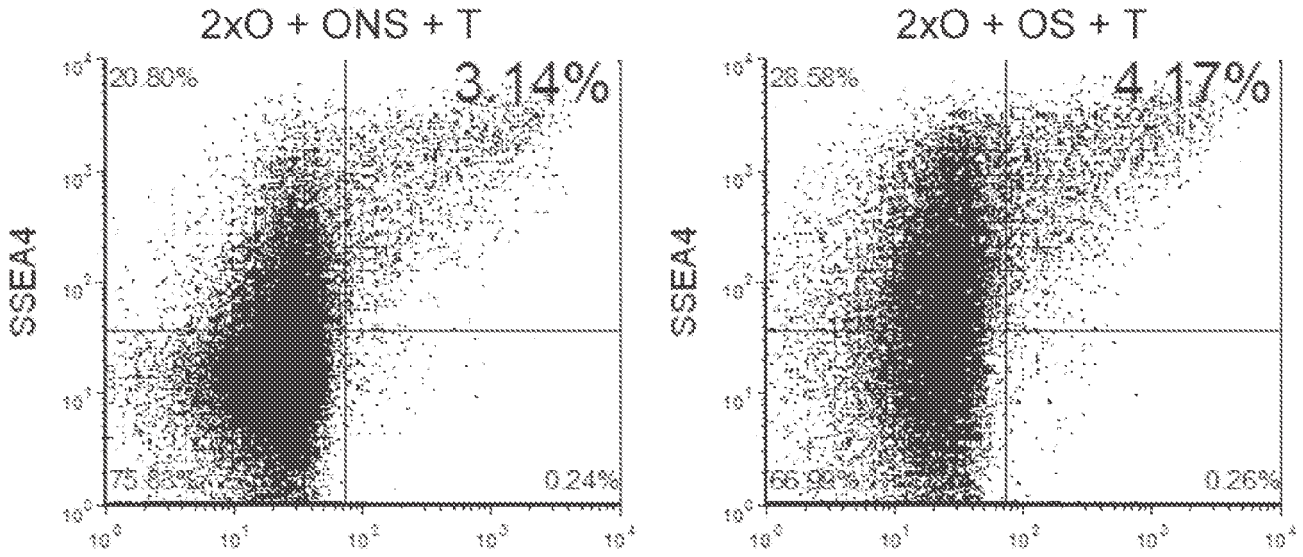


FIG. 11B

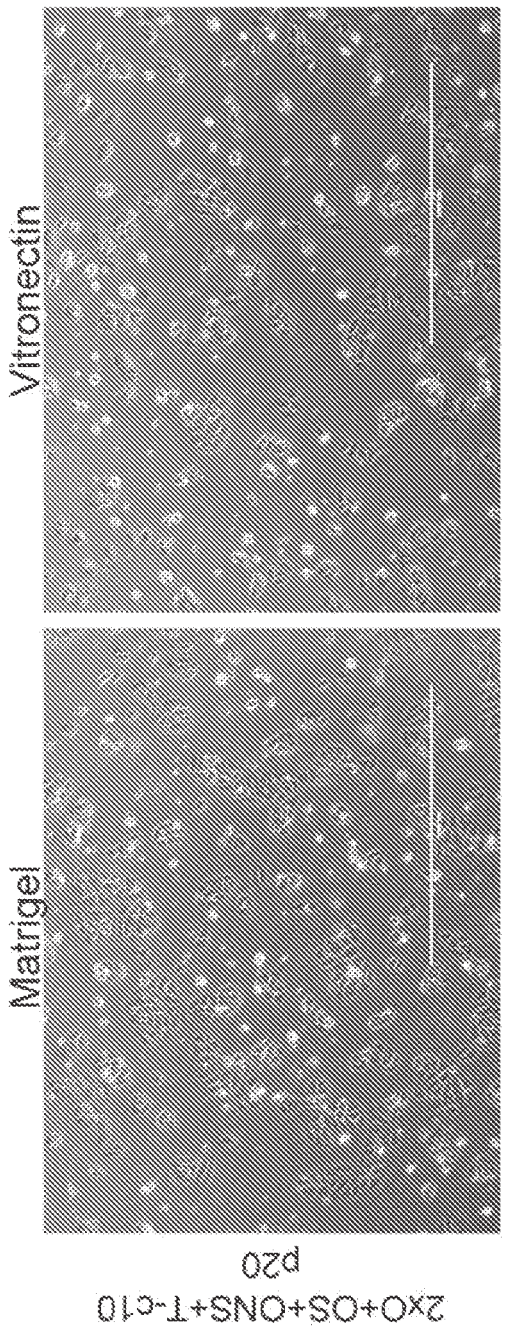


FIG. 11C

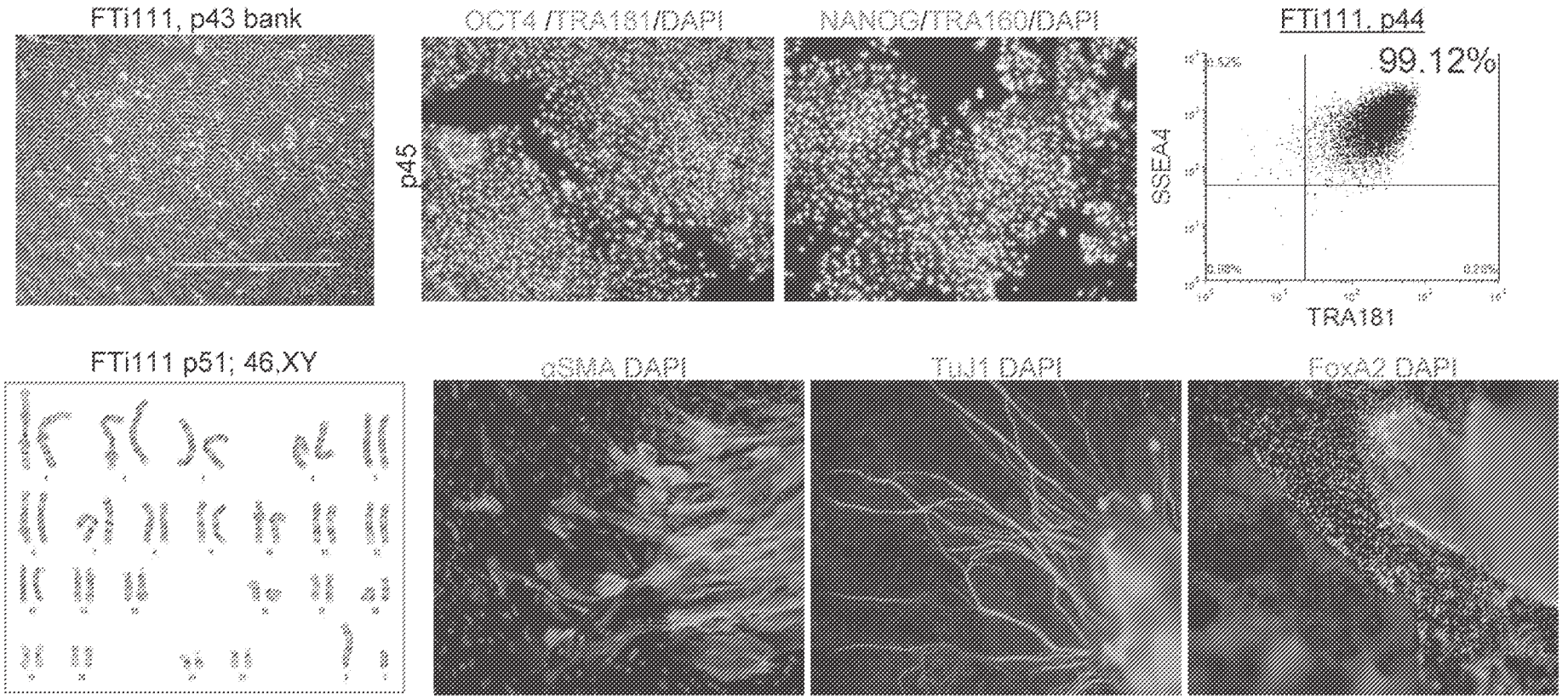

FTi111, p43 bank
OCT4 /TRA181/DAPI
NANOG/TRA160/DAPI
FTi111, p44
99.12%
p45
SSEA4
TRA181
FTi111 p51; 46.XY
αSMA DAPI
TuJ1 DAPI
FoxA2 DAPI

FIG. 12A

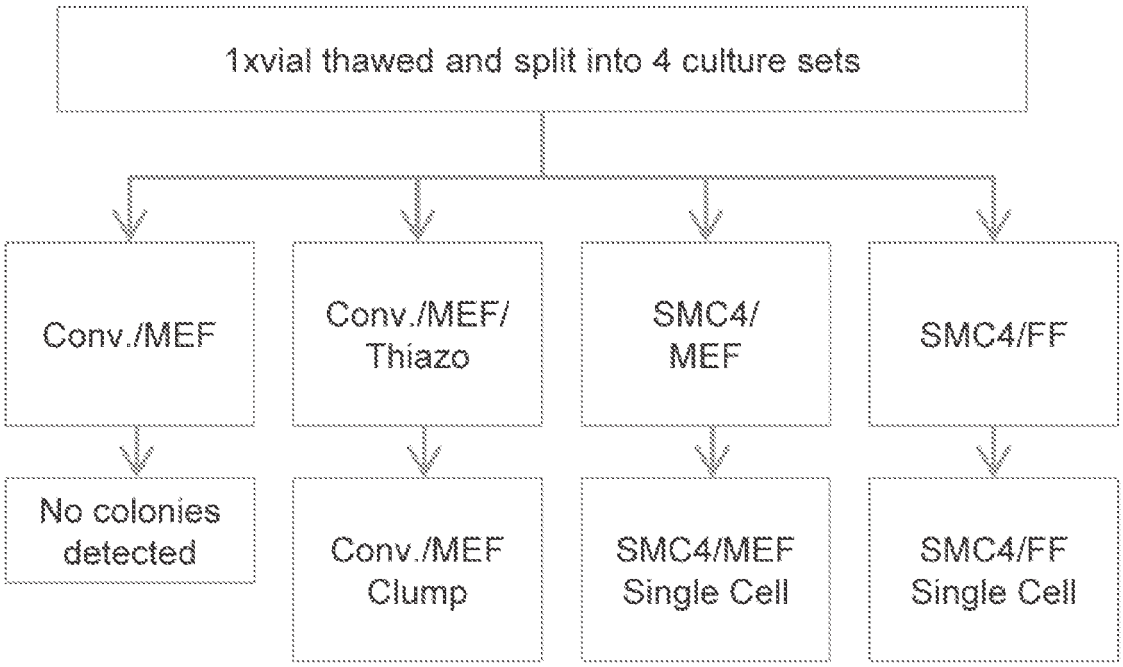

1xvial thawed and split into 4 culture sets
Conv./MEF
Conv./MEF/ Thiazo
SMC4/ MEF
SMC4/FF
No colonies detected
Conv./MEF Clump
SMC4/MEF Single Cell
SMC4/FF Single Cell

FIG. 12B

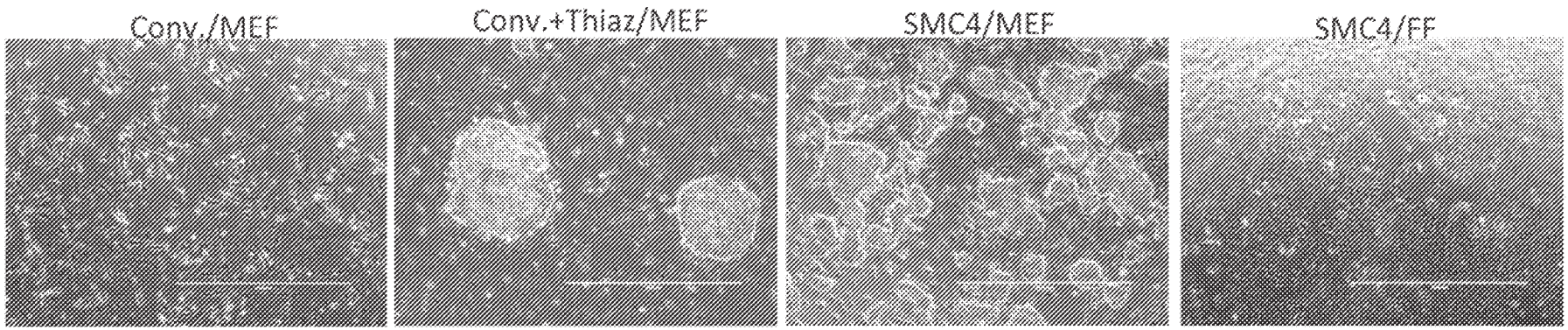


FIG. 12C

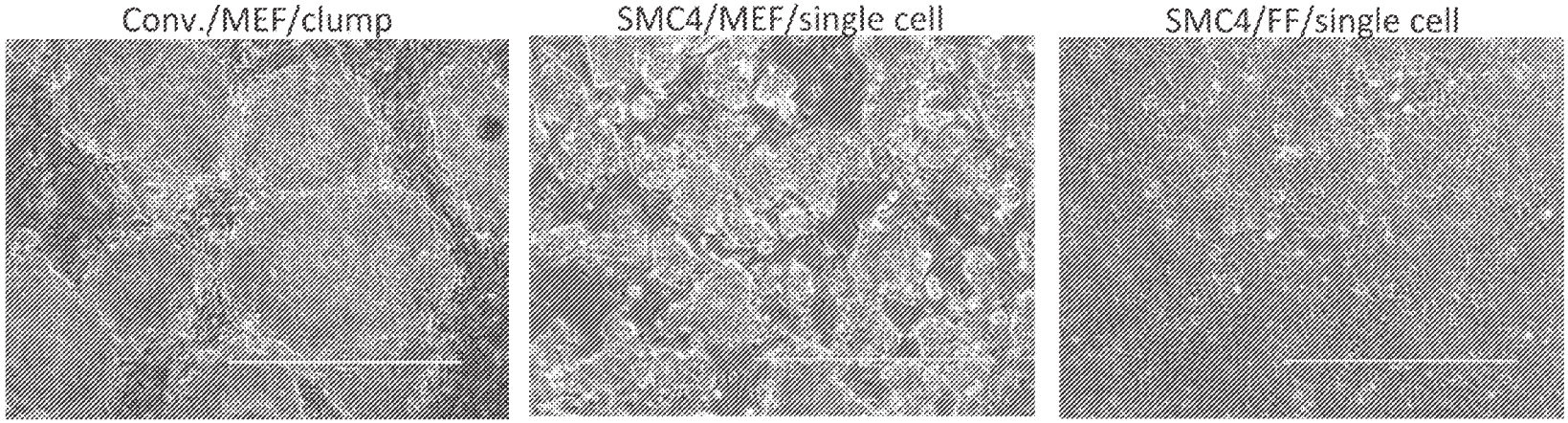


FIG. 12D

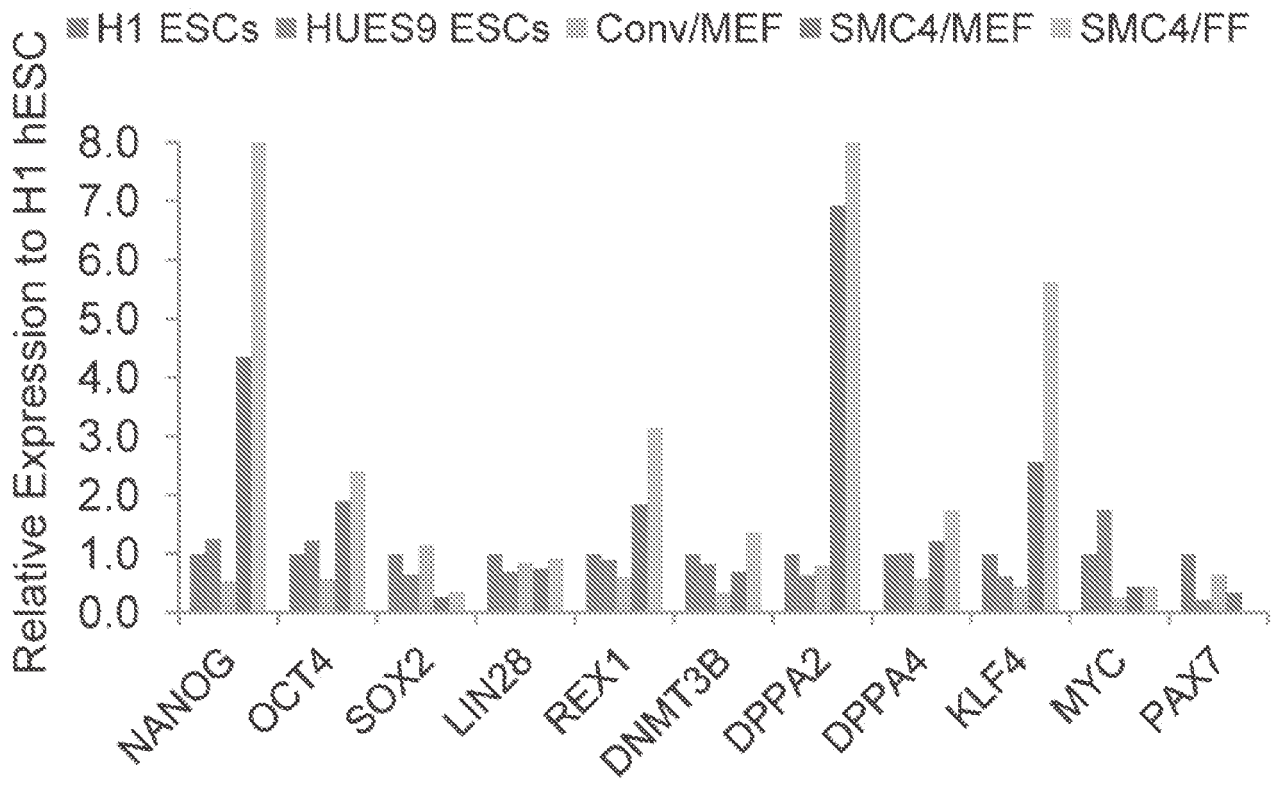

H1 ESCs
HUES9 ESCs
Conv/MEF
SMC4/MEF
SMC4/FF
Relative Expression to H1 hESC
8.0
7.0
6.0
5.0
4.0
3.0
2.0
1.0
0.0
NANOG
OCT4
SOX2
LIN28
REX1
DNMT3B
DPPA2
DPPA4
KLF4
MYC
PAX7

FIG. 12E

Cell Line	Description		Cell Line	Description
FTC016-c28 & -c36	Cord blood parental, episomal-generated and maintained in FRM/FMM		6F Lenti-hiPSC-c1, -c2 & -c3	Fibroblast parental, OSKMNL lentiviral hiPSC clone generated and maintained in conventional hESC culture
FTC007-C21	Fibroblast parental, episomal-generated and maintained in FRM/FMM		3F Lenti-hiPSC-c1 & -c4	Fibroblast parental, OKS lentiviral hiPSC clone generated and maintained in conventional hESC culture
3F Lenti-hiPSC-c2 & -c3	Fibroblast parental, OKS lentiviral hiPSC clone generated and maintained in SMC4			

FIG. 13A

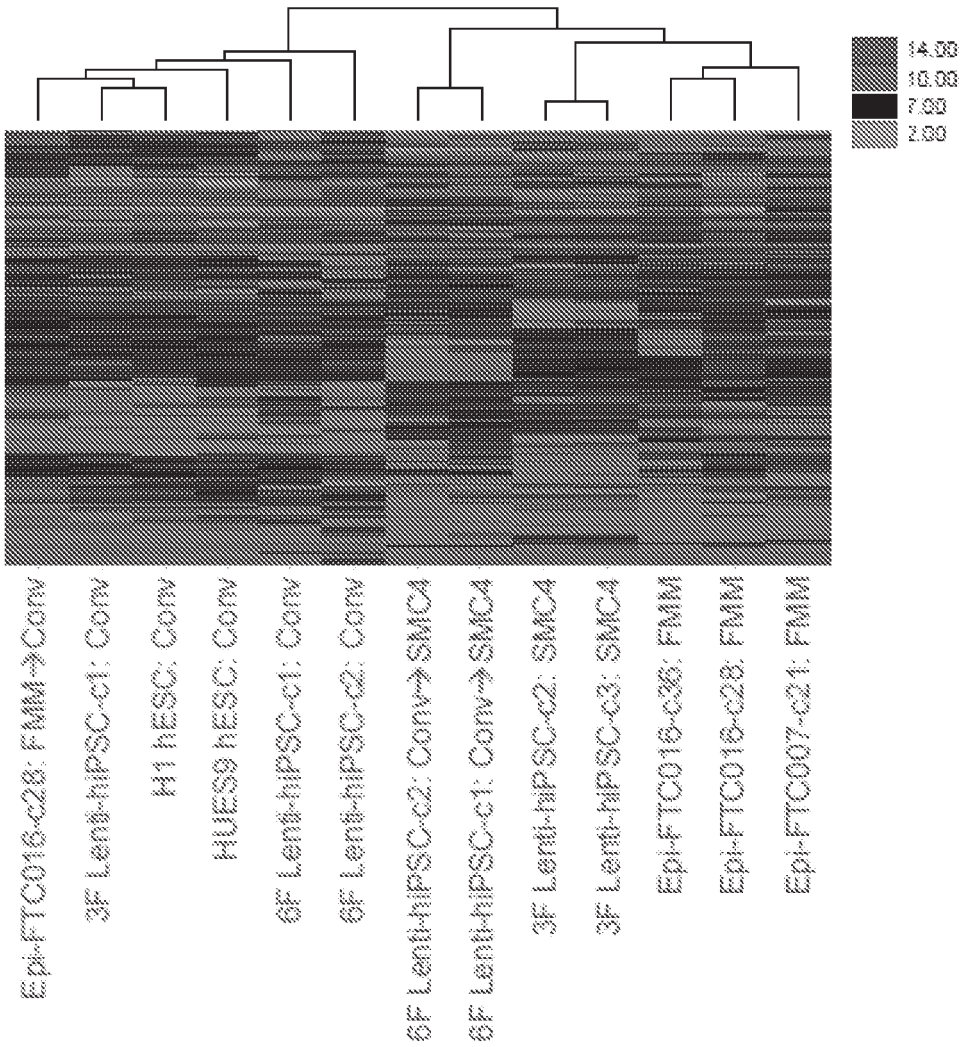

14.00
10.00
7.00
2.00
Epi-FTC016-c28: FMM→Conv
3F Lenti-hiPSC-c1: Conv
H1 hESC: Conv
HUES9 hESC: Conv
6F Lenti-hiPSC-c1: Conv
6F Lenti-hiPSC-c2: Conv
6F Lenti-hiPSC-c2: Conv→SMC4
6F Lenti-hiPSC-c1: Conv→SMC4
3F Lenti-hiPSC-c2: SMC4
3F Lenti-hiPSC-c3: SMC4
Epi-FTC016-c36: FMM
Epi-FTC016-c28: FMM
Epi-FTC007-c21: FMM

FIG. 13B

133 Probe sets upregulated in conventional hESC culture group vs. FMM/SMC4 culture group			
GO ID	GO Term	%	p-value
GO:0007389	pattern specification process	9.7	3.50E-05
GO:0048598	embryonic morphogenesis	8.6	5.90E-04
GO:0001775	cell activation	7.5	2.30E-03
GO:0046649	lymphocyte activation	6.5	2.50E-03
GO:0042110	T cell activation	5.4	3.00E-03
GO:0002521	leukocyte differentiation	5.4	3.40E-03
GO:0030217	T cell differentiation	4.3	3.60E-03
GO:0030097	hemopoiesis	6.5	5.10E-03
GO:0045321	leukocyte activation	6.5	5.70E-03
GO:0007610	behavior	8.6	6.50E-03
GO:0048534	hemopoietic or lymphoid organ development	6.5	7.60E-03
GO:0048568	embryonic organ development	5.4	8.90E-03
GO:0002520	immune system development	6.5	9.80E-03

FIG. 13C

167 Probe sets upregulated in small molecule culture group vs. conventional culture group			
GO ID	GO Term	%	p-value
GO:0042127	regulation of cell proliferation	12.4	5.20E-04
GO:0051205	protein insertion into membrane	2.5	1.50E-03
GO:0009725	response to hormone stimulus	7.4	2.60E-03
GO:0051668	localization within membrane	2.5	4.20E-03
GO:0009719	response to endogenous stimulus	7.4	4.80E-03
GO:0008284	positive regulation of cell proliferation	7.4	5.50E-03
GO:0008406	gonad development	4.1	6.10E-03
GO:0009636	response to toxin	3.3	7.30E-03
GO:0014070	response to organic cyclic substance	4.1	8.00E-03
GO:0043066	negative regulation of apoptosis	6.6	8.20E-03
GO:0048545	response to steroid hormone stimulus	5	8.30E-03
GO:0008585	female gonad development	3.3	8.30E-03
GO:0043069	negative regulation of programmed cell death	6.6	8.80E-03
GO:0060548	negative regulation of cell death	6.6	9.00E-03
GO:0048608	reproductive structure development	4.1	9.20E-03
GO:0045137	development of primary sexual characteristics	4.1	9.40E-03
GO:0046660	female sex differentiation	3.3	1.00E-02
GO:0046545	development of primary female sexual characteristics	3.3	1.00E-02

FIG. 13D

126 Probe sets upregulated in FMM samples group vs. conventional culture group			
GO ID	GO Term	%	p-value
GO:0007267	cell-cell signaling	16.5	8.20E-07
GO:0040008	regulation of growth	10.3	1.10E-04
GO:0042981	regulation of apoptosis	15.5	1.20E-04
GO:0043067	regulation of programmed cell death	15.5	1.30E-04
GO:0010941	regulation of cell death	15.5	1.30E-04
GO:0010817	regulation of hormone levels	7.2	1.90E-04
GO:0045926	negative regulation of growth	6.2	3.60E-04
GO:0031100	organ regeneration	4.1	3.90E-04
GO:0001558	regulation of cell growth	7.2	7.10E-04
GO:0043066	negative regulation of apoptosis	9.3	7.40E-04
GO:0043069	negative regulation of programmed cell death	9.3	8.20E-04
GO:0060548	negative regulation of cell death	9.3	8.30E-04
GO:0016358	dendrite development	4.1	9.40E-04
GO:0006916	anti-apoptosis	7.2	9.70E-04
GO:0045596	negative regulation of cell differentiation	7.2	1.20E-03
GO:0030308	negative regulation of cell growth	5.2	1.70E-03
GO:0050768	negative regulation of neurogenesis	4.1	2.00E-03
GO:0045792	negative regulation of cell size	5.2	2.20E-03
GO:0010721	negative regulation of cell development	4.1	2.40E-03
GO:0042445	hormone metabolic process	5.2	2.80E-03
GO:0032535	regulation of cellular component size	7.2	3.90E-03
GO:0034754	cellular hormone metabolic process	4.1	4.30E-03
GO:0051270	regulation of cell motion	6.2	4.30E-03
GO:0048754	branching morphogenesis of a tube	4.1	5.60E-03
GO:0008361	regulation of cell size	6.2	5.70E-03
GO:0001569	patterning of blood vessels	3.1	5.90E-03
GO:0031099	regeneration	4.1	6.60E-03
GO:0035295	tube development	6.2	7.50E-03
GO:0009991	response to extracellular stimulus	6.2	7.50E-03
GO:0001763	morphogenesis of a branching structure	4.1	8.00E-03
GO:0006917	induction of apoptosis	7.2	8.60E-03
GO:0012502	induction of programmed cell death	7.2	8.70E-03

FIG. 13E

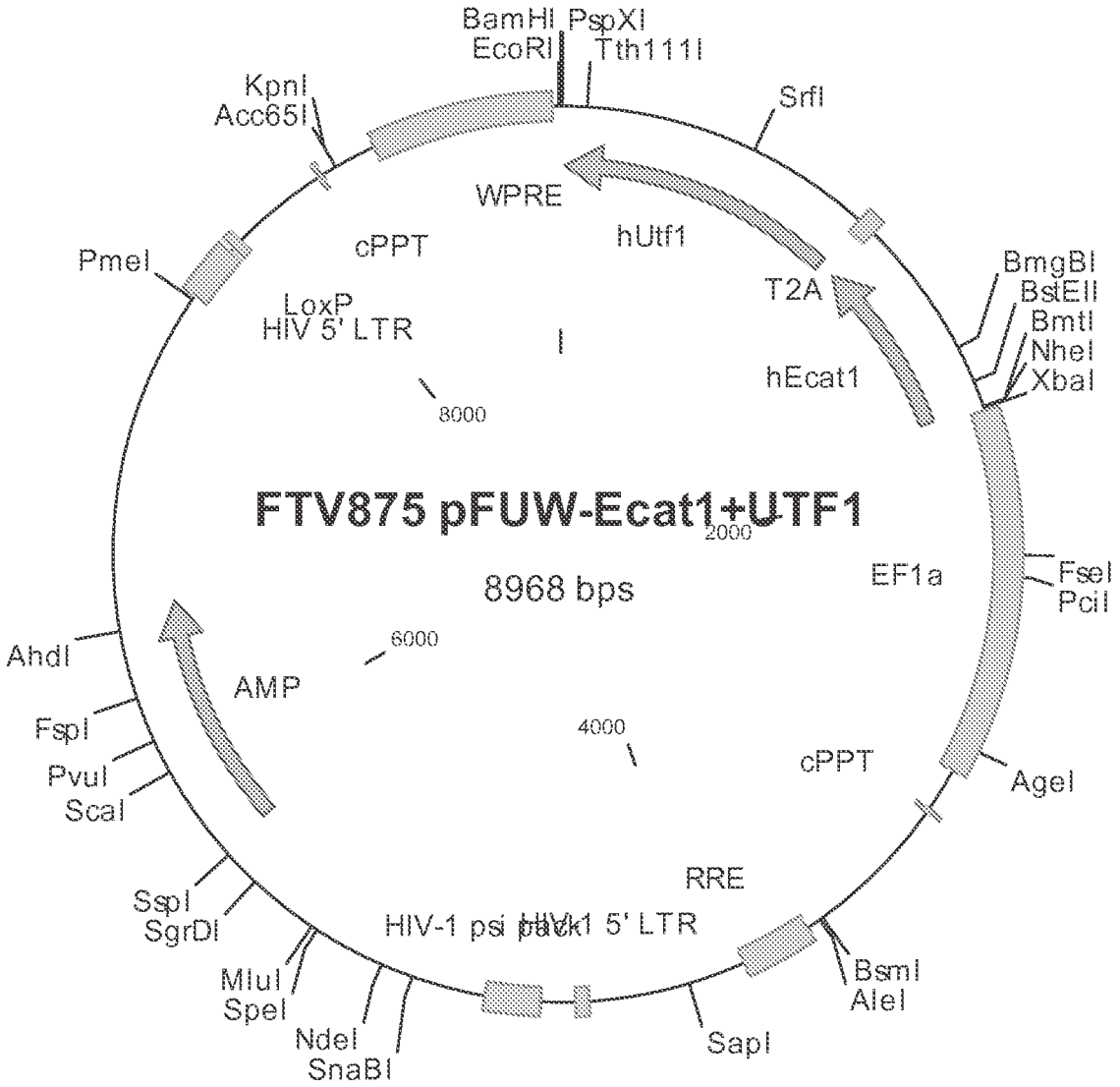

BamHI
EcoRI
PspXI
Tth111I
SrfI
KpnI
Acc65I
WPRE
hUtf1
cPPT
PmeI
T2A
BmgBI
BstEII
BmtI
NheI
XbaI
LoxP
HIV 5' LTR
hEcat1
8000
FTV875 pFUW-Ecat1+UTF1
2000
8968 bps
EF1a
FseI
PciI
AhdI
6000
AMP
4000
cPPT
AgeI
FspI
PvuI
ScaI
RRE
SspI
SgrDI
HIV-1 psi
HIV-1 5' LTR
BsmI
AleI
MluI
SpeI
NdeI
SnaBI
SapI

FIG. 14A

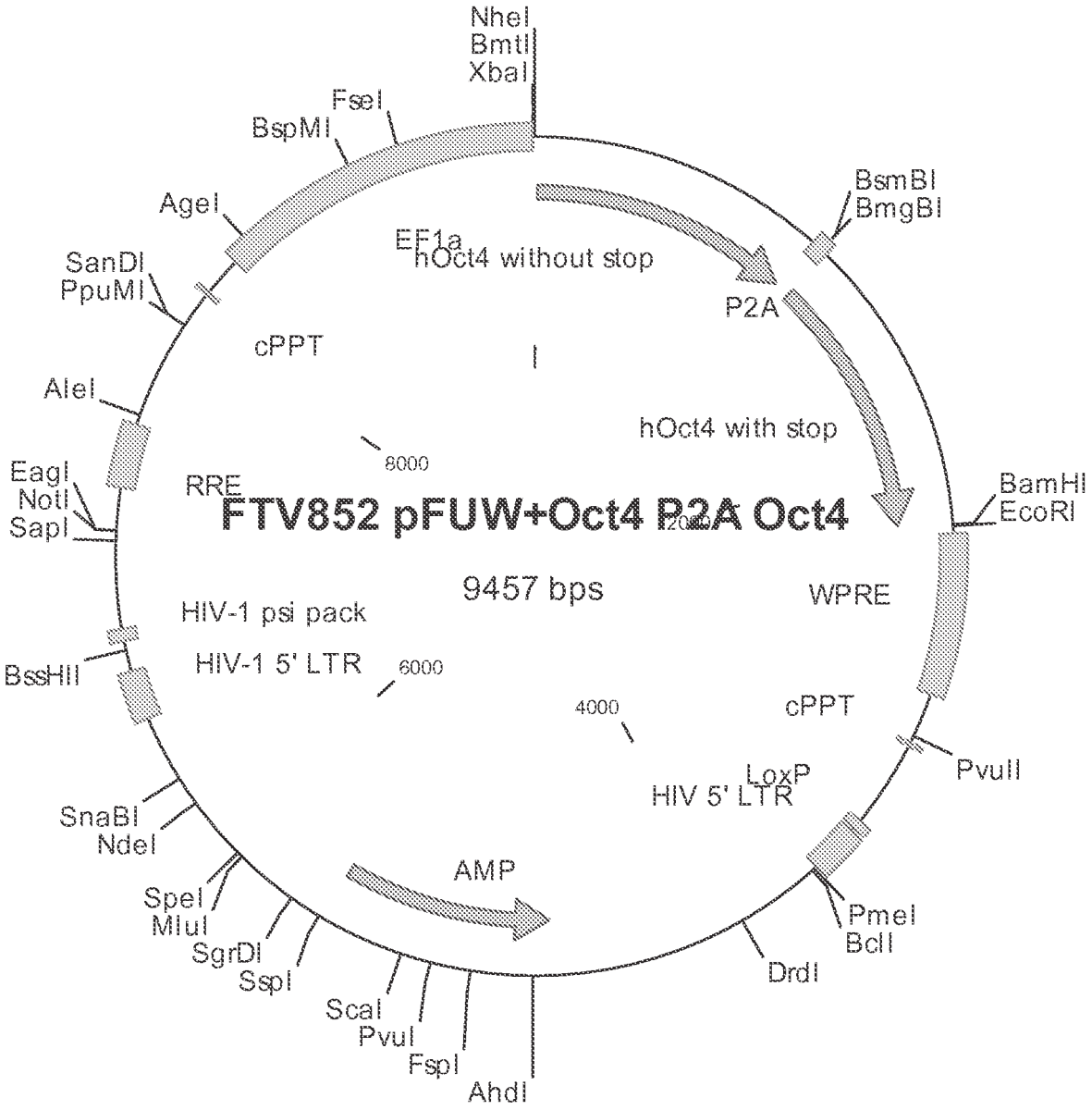

NheI
BmtI
XbaI
FseI
BspMI
AgeI
SanDI
PpuMI
AleI
EagI
NotI
SapI
BssHII
SnaBI
NdeI
SpeI
MluI
SgrDI
SspI
ScaI
PvuI
FspI
AhdI
BsmBI
BmgBI
EF1a
hOct4 without stop
P2A
cPPT
hOct4 with stop
8000
RRE
FTV852 pFUW+Oct4 P2A Oct4
9457 bps
HIV-1 psi pack
HIV-1 5' LTR
6000
4000
cPPT
LoxP
HIV 5' LTR
WPRE
BamHI
EcoRI
PvuII
PmeI
BclI
DrdI
AMP

FIG. 14B

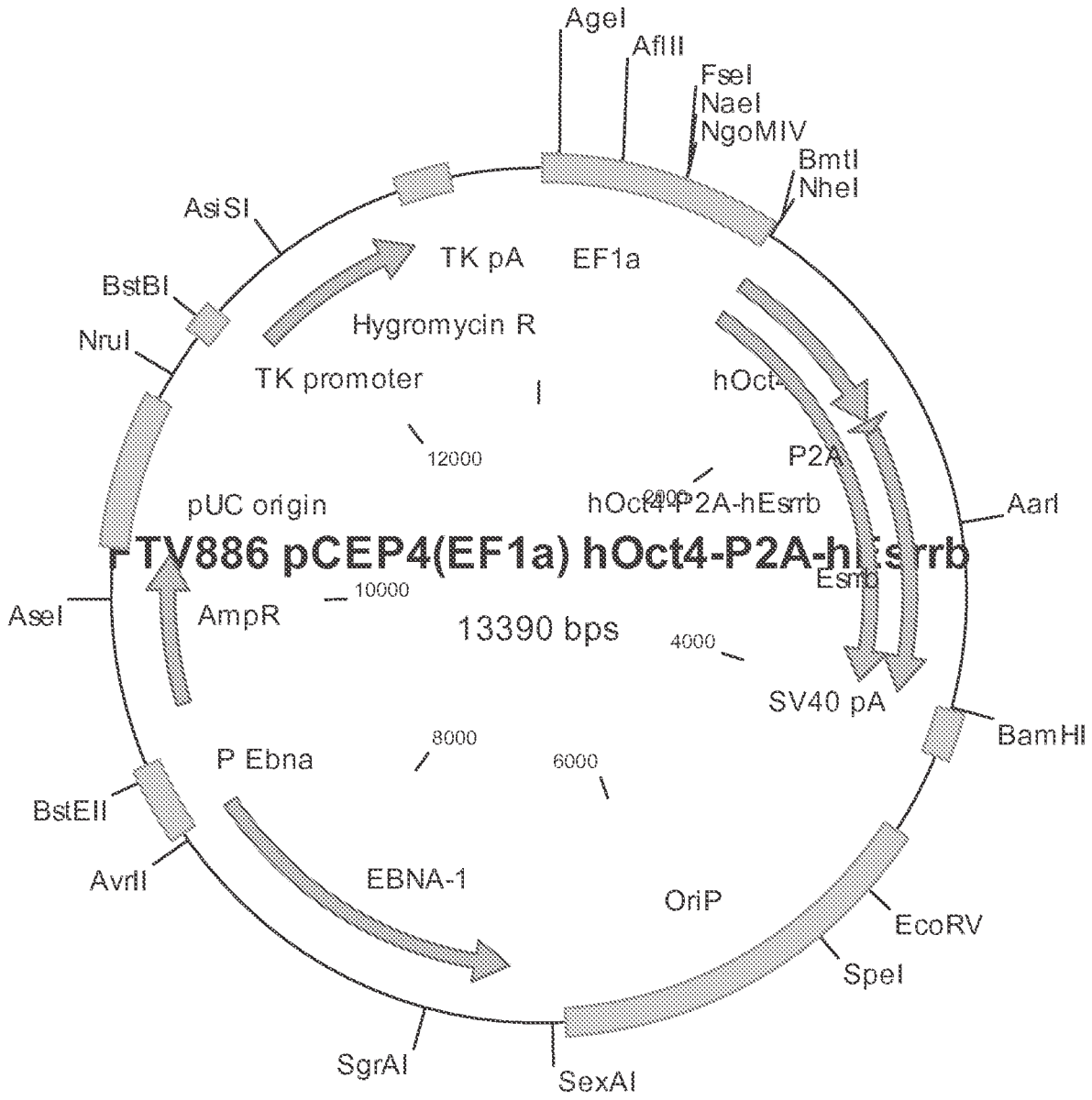

AgeI
AflII
FseI
NaeI
NgoMIV
BmtI
NheI
AsiSI
BstBI
NruI
TK pA
EF1a
Hygromycin R
TK promoter
hOct-
P2A
12000
pUC origin
hOct4-P2A-hEsrrb
AarI
pTV886 pCEP4(EF1a) hOct4-P2A-hEsrrb
Esrrb
AseI
AmpR
10000
13390 bps
4000
SV40 pA
BamHI
P Ebna
8000
6000
BstEII
AvrII
EBNA-1
OriP
EcoRV
SpeI
SgrAI
SexAI

FIG. 14C

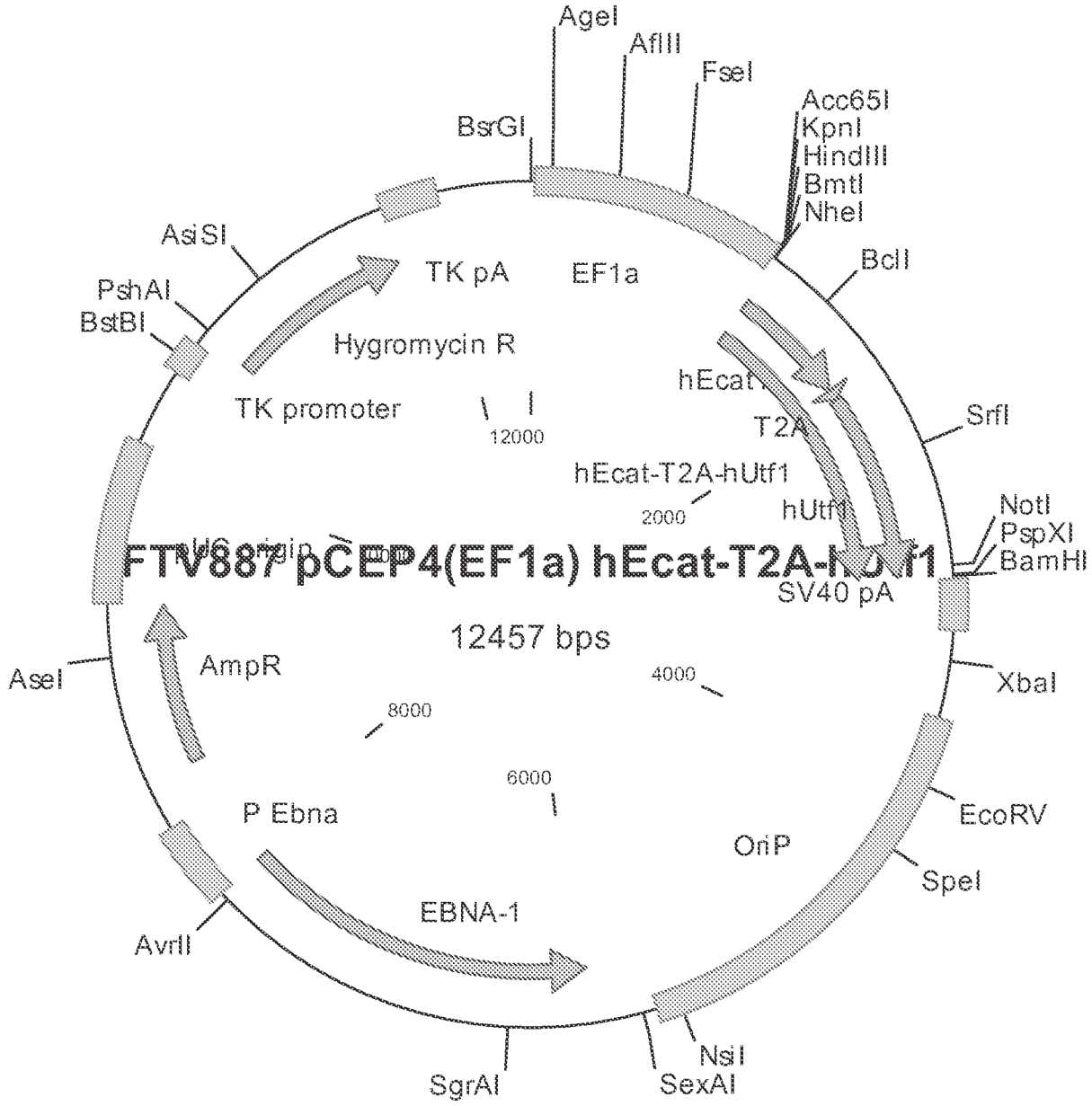

AgeI
AflII
FseI
Acc65I
KpnI
HindIII
BmtI
NheI
BsrGI
AsiSI
PshAI
BstBI
BclI
TK pA
EF1a
Hygromycin R
TK promoter
12000
hEcat
T2A
SrfI
hEcat-T2A-hUtf1
2000
hUtf1
NotI
PspXI
BamHI
FTV887 pCEP4(EF1a) hEcat-T2A-hUtf1
SV40 pA
12457 bps
AseI
AmpR
4000
XbaI
8000
6000
P Ebna
EcoRV
OriP
SpeI
EBNA-1
AvrII
NsiI
SgrAI
SexAI

FIG. 14D

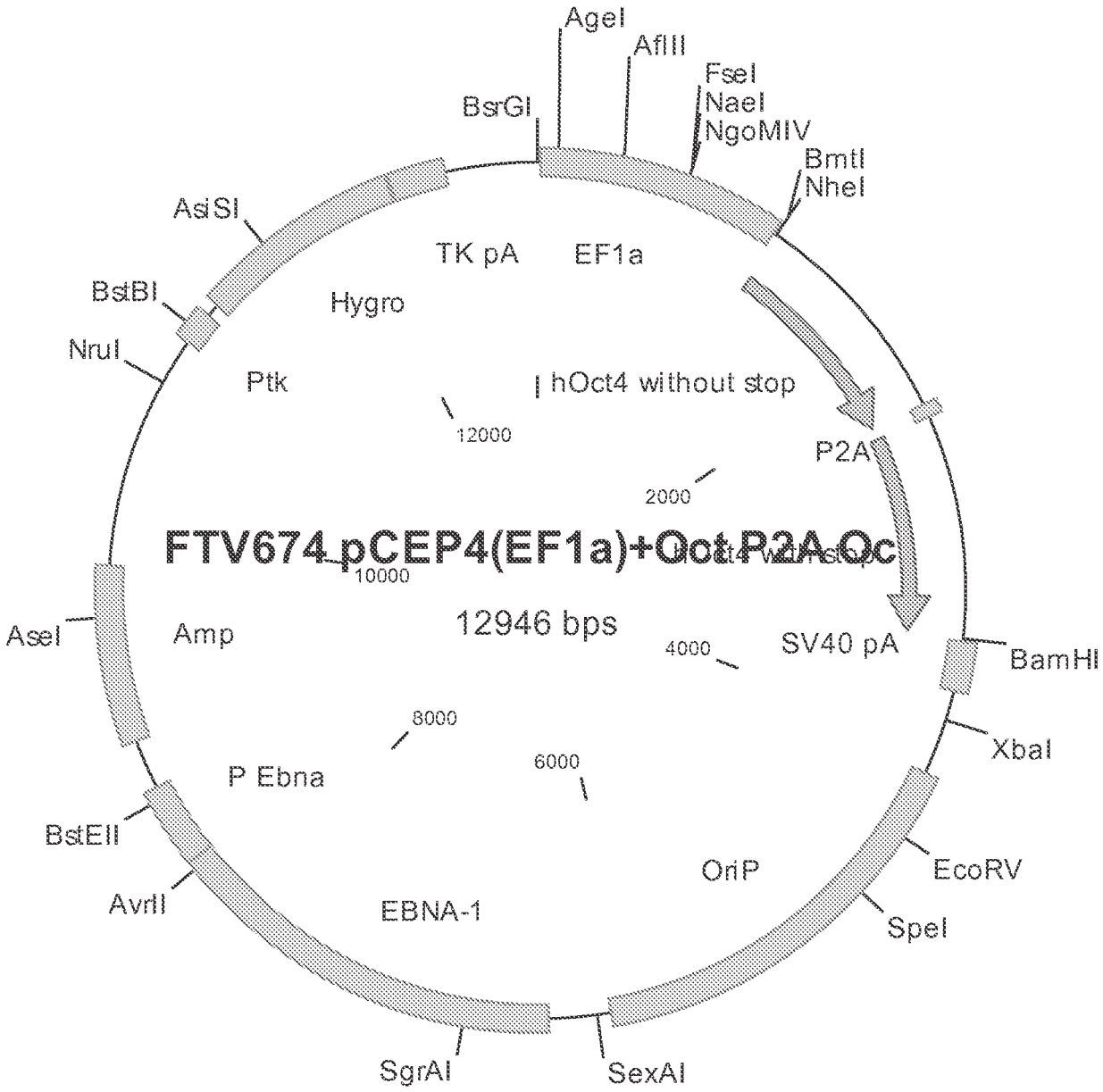

AgeI
AflII
FseI
NaeI
NgoMIV
BmtI
NheI
BsrGI
AsiSI
TK pA
EF1a
BstBI
Hygro
NruI
Ptk
hOct4 without stop
12000
P2A
2000
FTV674_pCEP4(EF1a)+Oct4-P2A-Oc
10000
12946 bps
AseI
Amp
4000
SV40 pA
BamHI
8000
XbaI
6000
P Ebna
BstEII
OriP
EcoRV
AvrII
EBNA-1
SpeI
SgrAI
SexAI

FIG. 14E

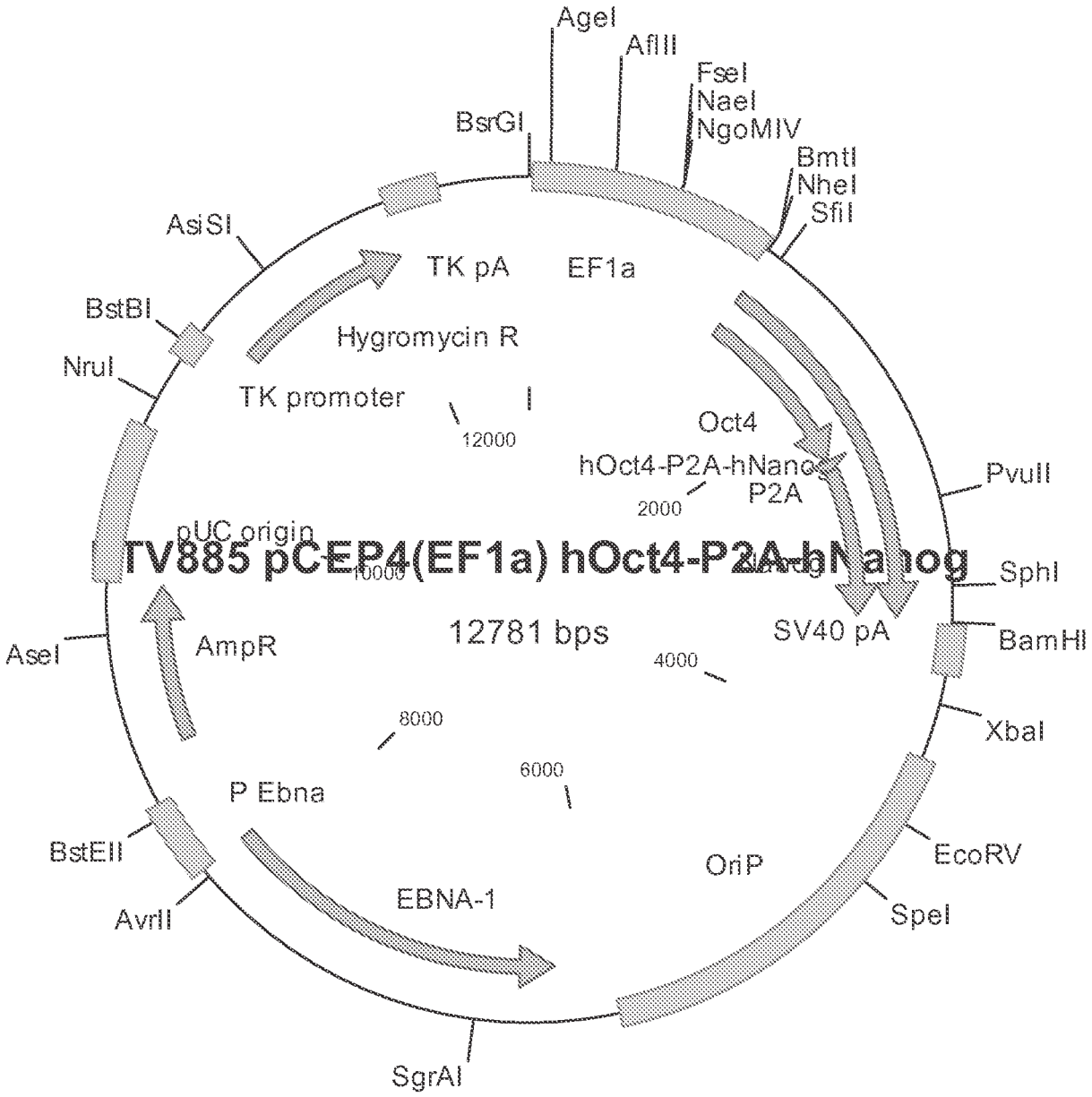

AgeI
AflII
FseI
NaeI
NgoMIV
BmtI
NheI
SfiI
BsrGI
AsiSI
BstBI
NruI
TK pA
EF1a
Hygromycin R
TK promoter
12000
Oct4
hOct4-P2A-hNanog
P2A
2000
PvuII
pUC origin
TV885 pCEP4(EF1a) hOct4-P2A-hNanog
10000
SphI
12781 bps
SV40 pA
BamHI
AseI
AmpR
4000
8000
XbaI
6000
P Ebna
BstEII
EcoRV
OriP
EBNA-1
AvrII
SpeI
SgrAI

FIG. 14F

OCT4/NANOG/ECAT1/UTF1

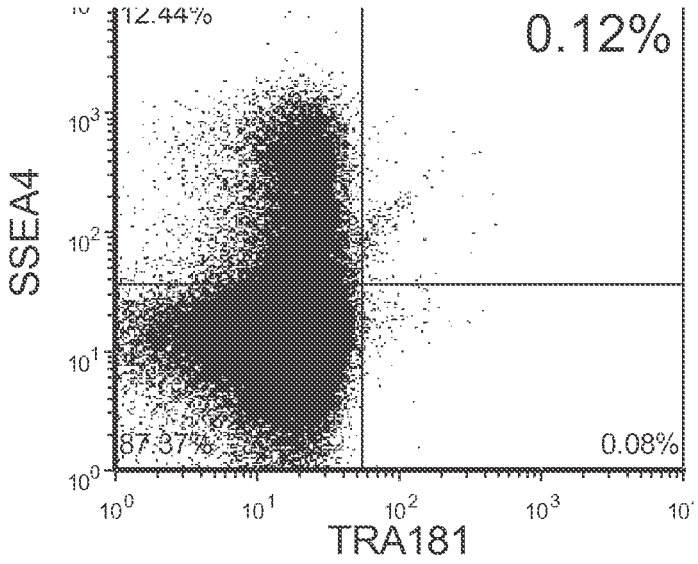


FIG. 15A

OCT4/ESRRB/NANOG/ECAT1/UTF1

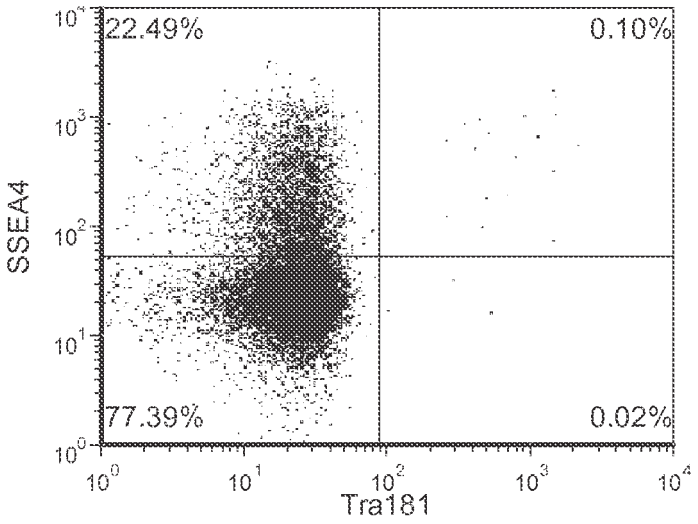


FIG. 15B

OCT4/ESRRB/LIN28/ECAT1/UTF-1

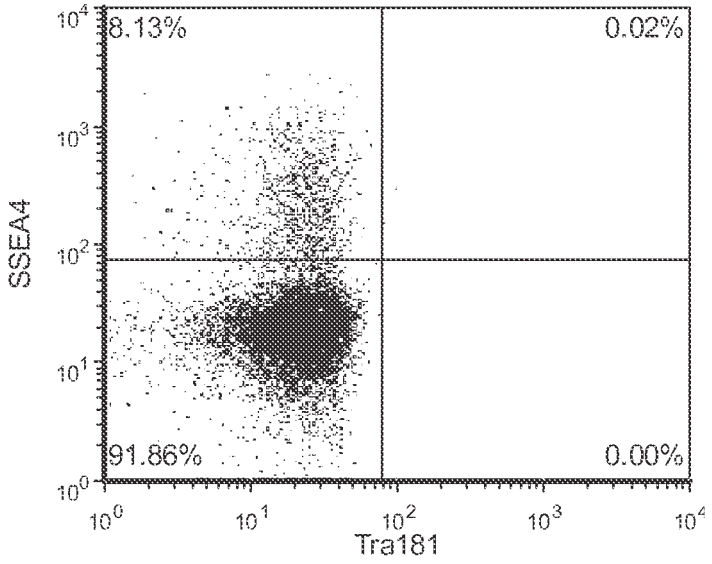


FIG. 15C

OCT4-P2A-OCT4 / NANOG-P2A-ESRRB-P2A-LIN28 / ECAT1-T2A-UTF1

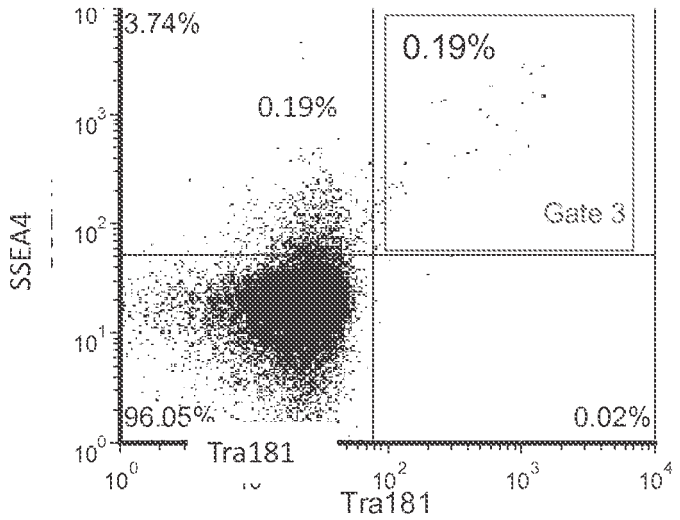
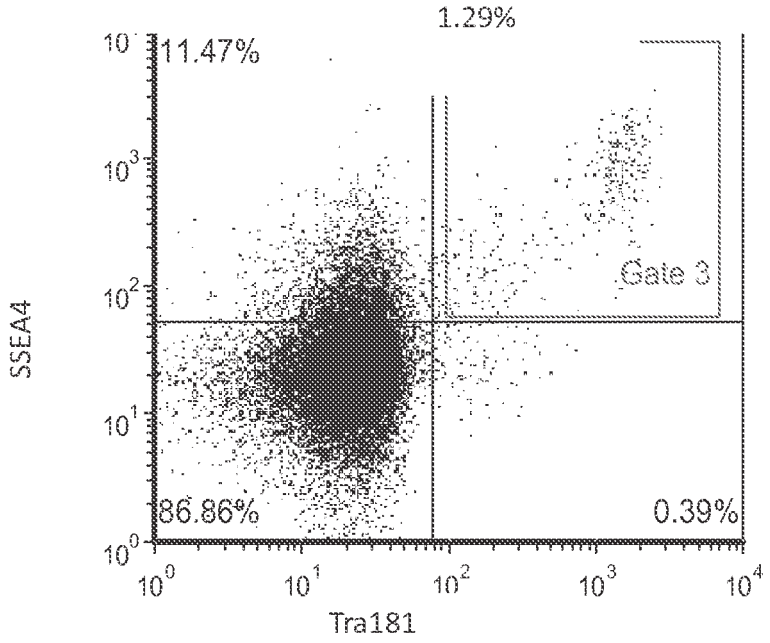


FIG. 16A



FIG. 16B

OCT4-P2A-ESRRB / OCT4-P2A-NANOG / ECAT1-T2A-UTF1



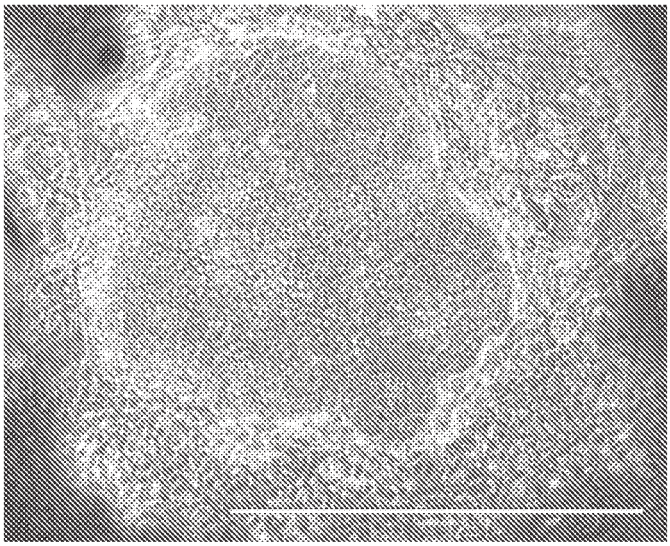
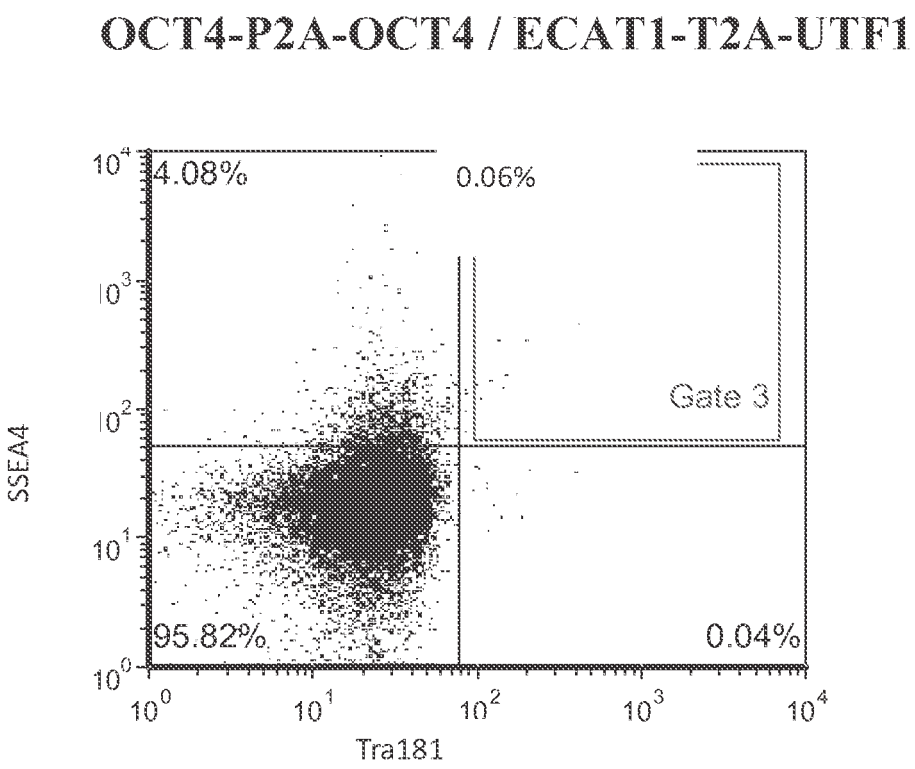


FIG. 16C


OCT4-P2A-OCT4 / ECAT1-T2A-UTF1
4.08%
0.06%
Gate 3
95.82%
0.04%
SSEA4
Tra181
10^0
10^1
10^2
10^3
10^4

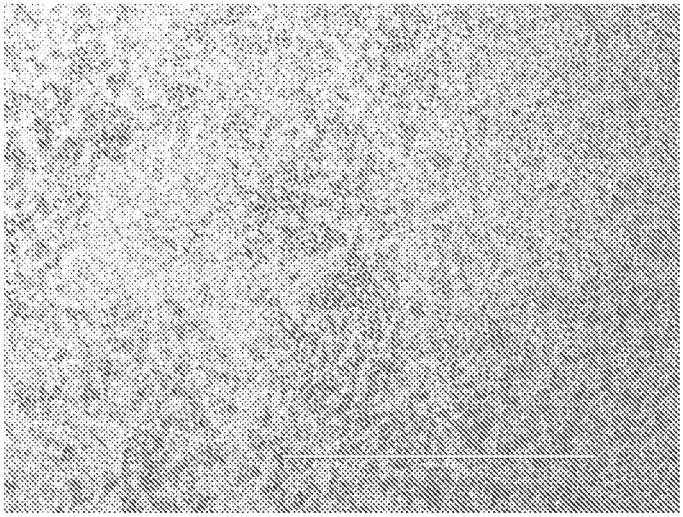
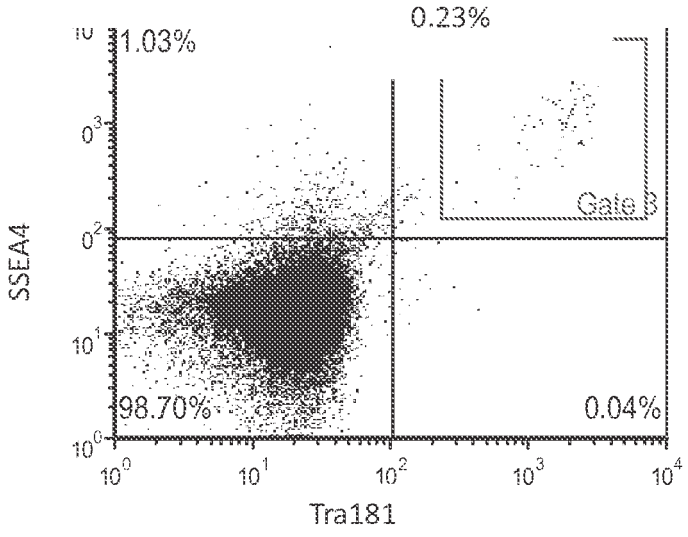


FIG. 16D

OCT4-P2A-NANOG / ECAT1-T2A-UTF1



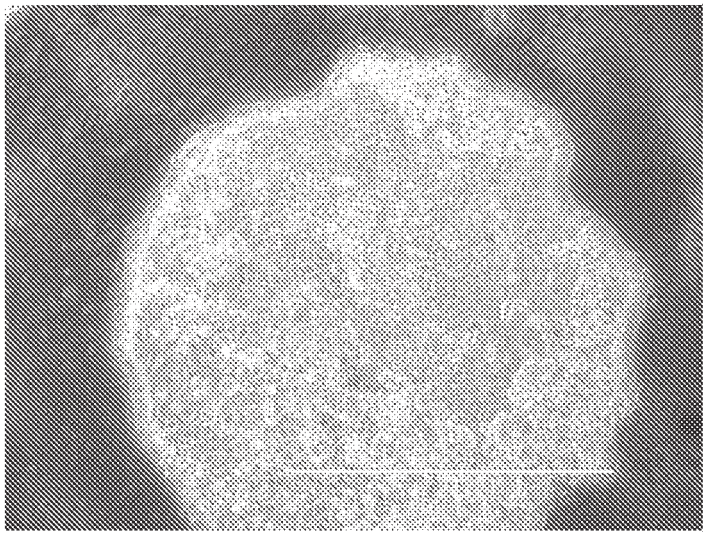
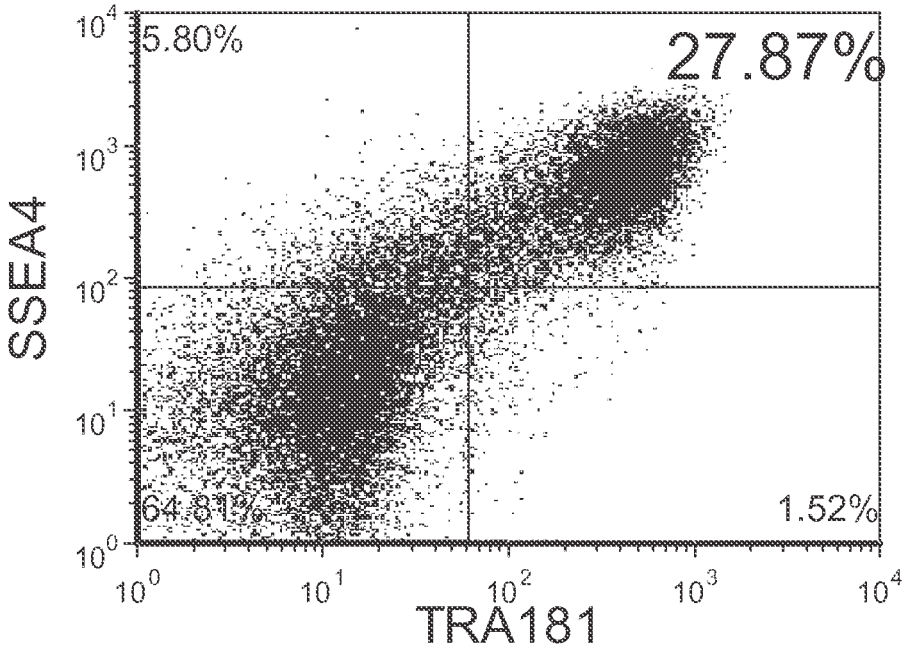


FIG. 17A



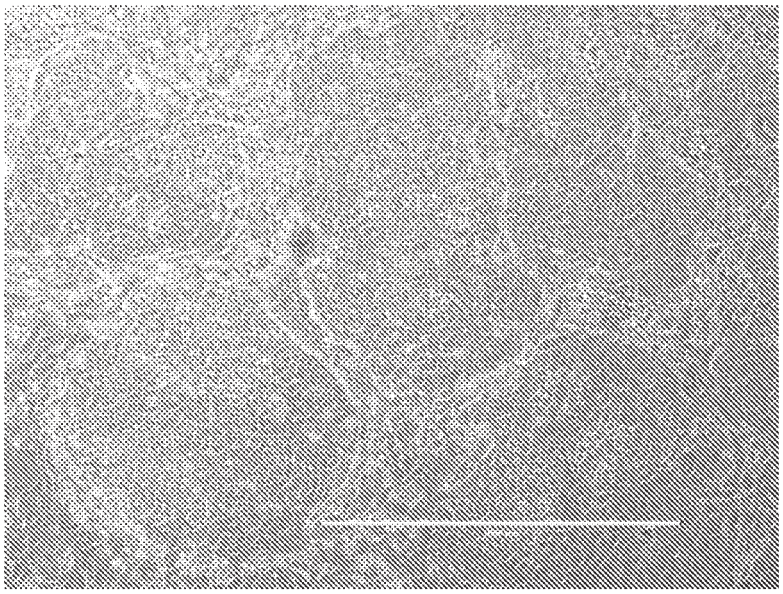
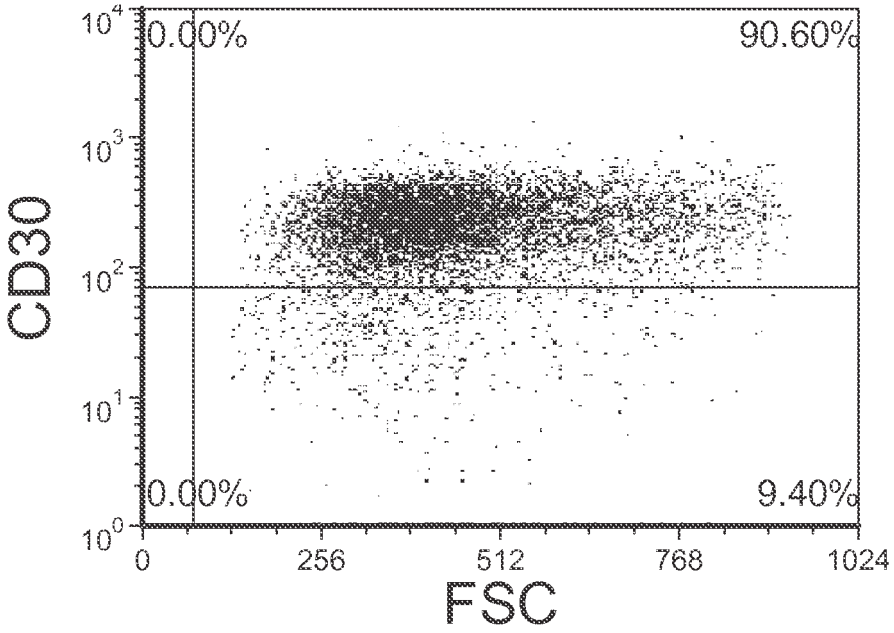


FIG. 17B



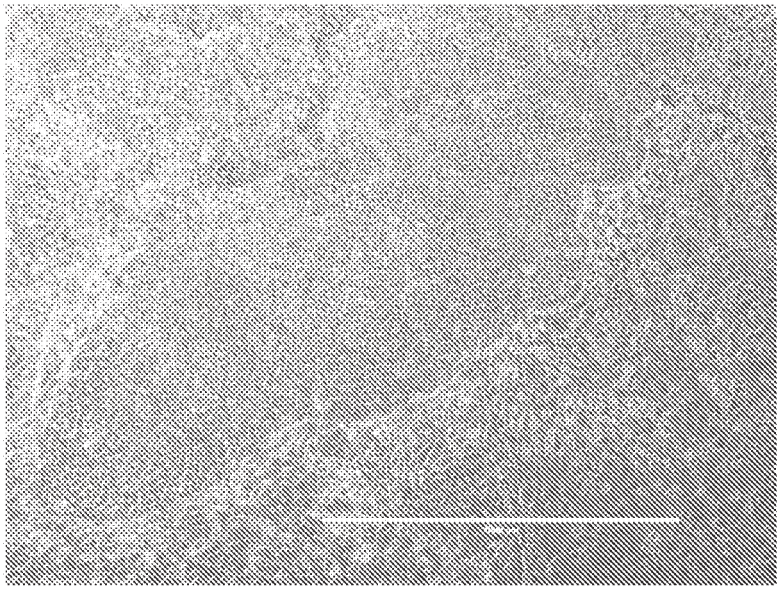
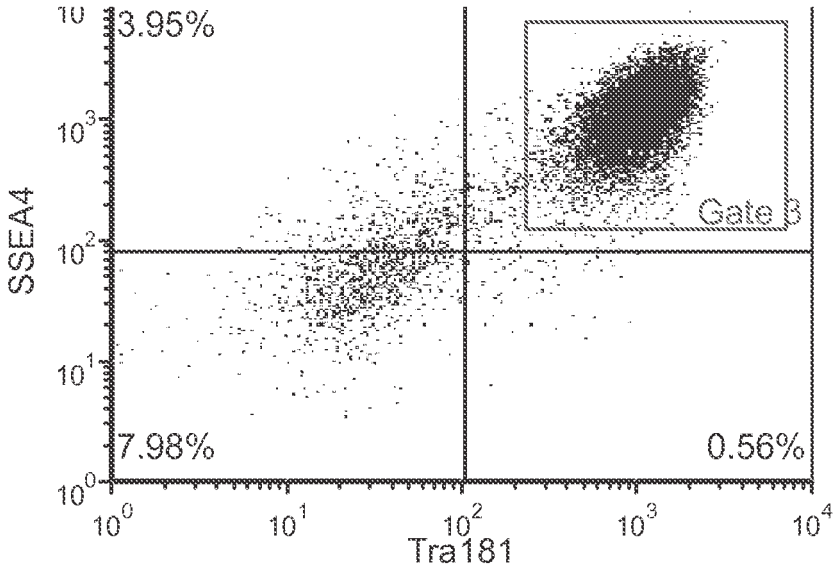


FIG. 18A



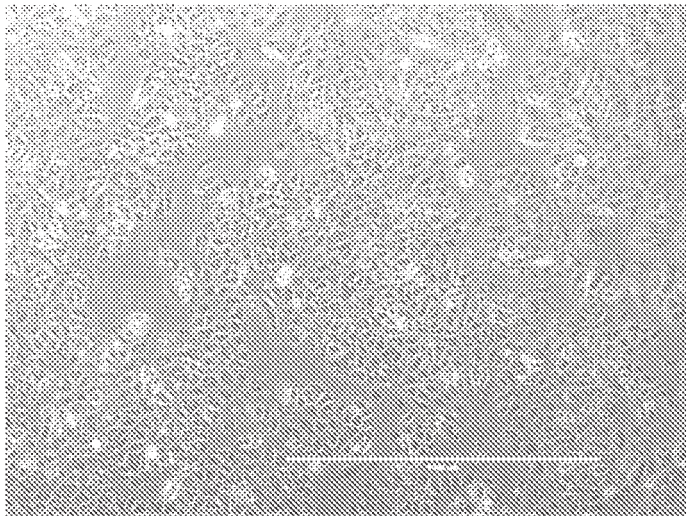
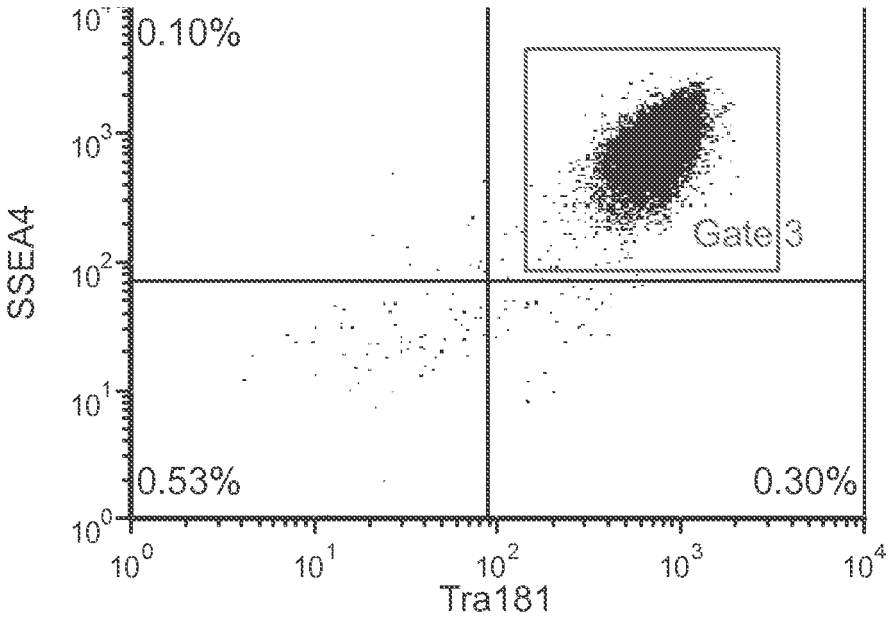


FIG. 18B



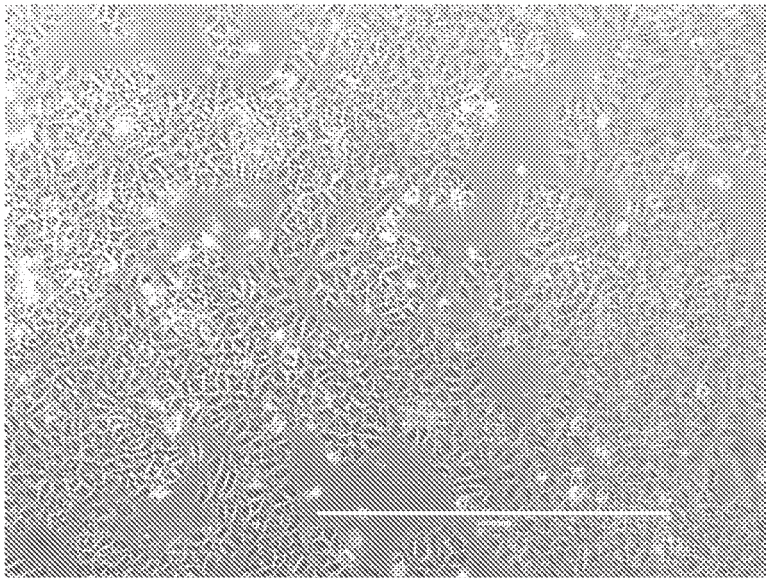
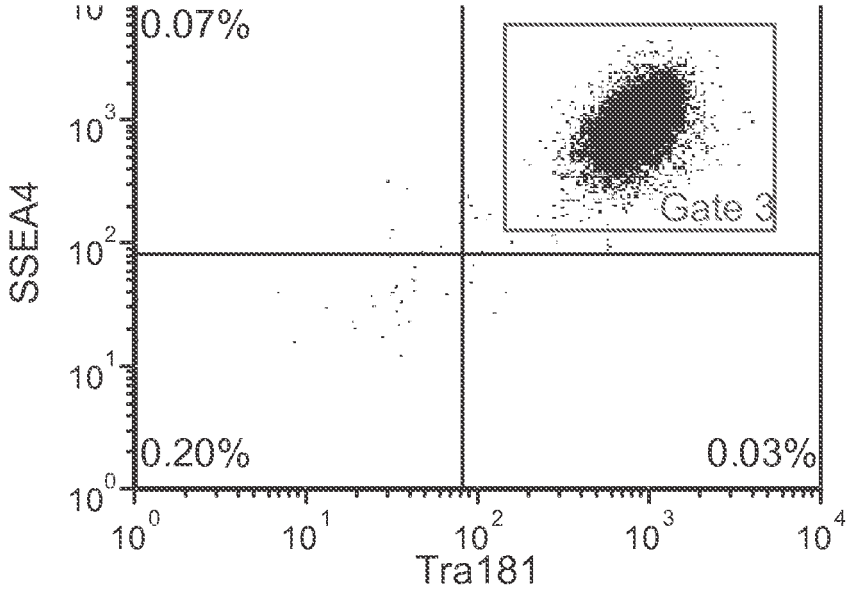


FIG. 18C



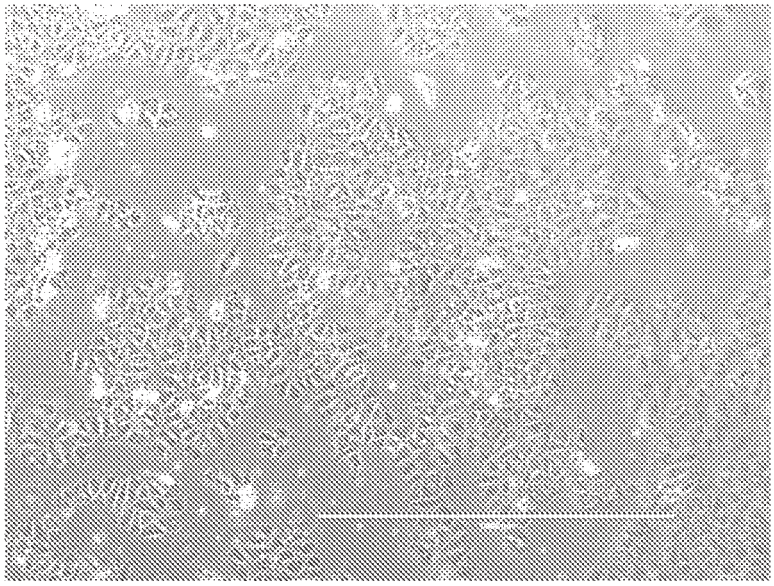
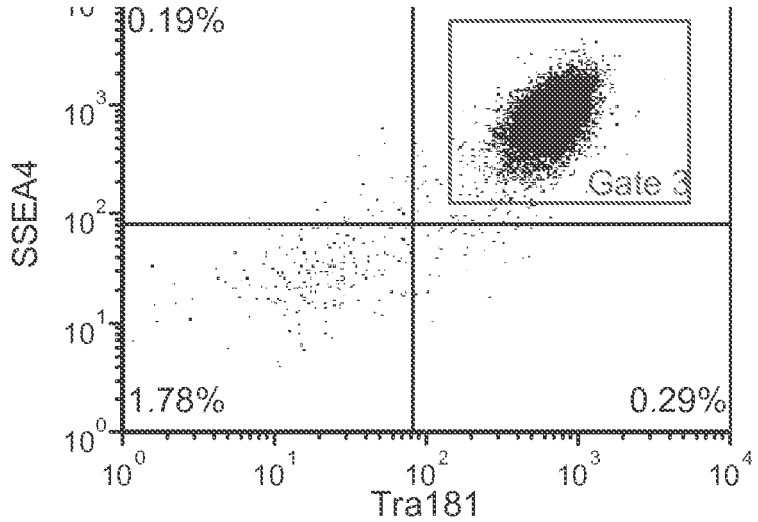


FIG. 18D



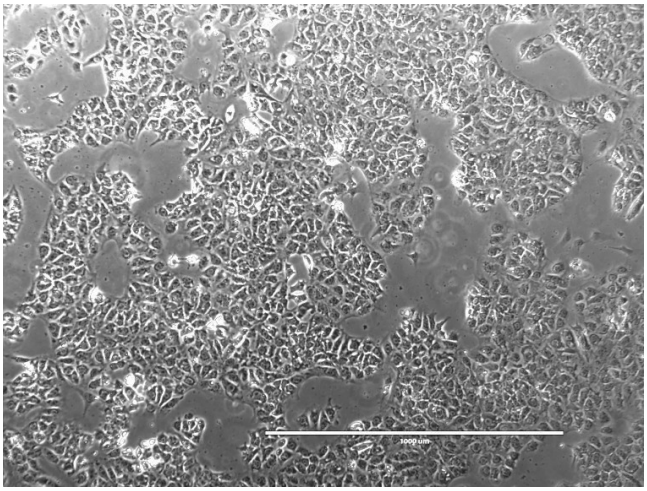


FIG. 19A

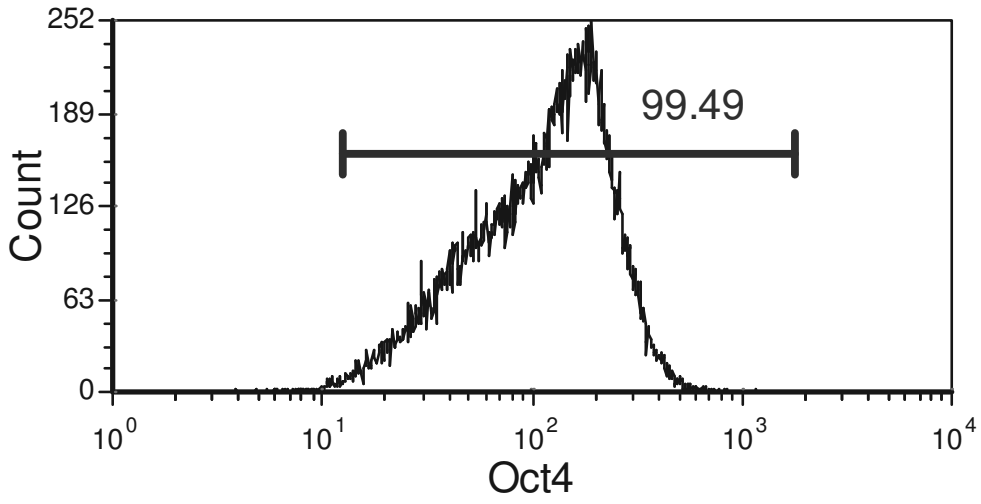


FIG. 19B

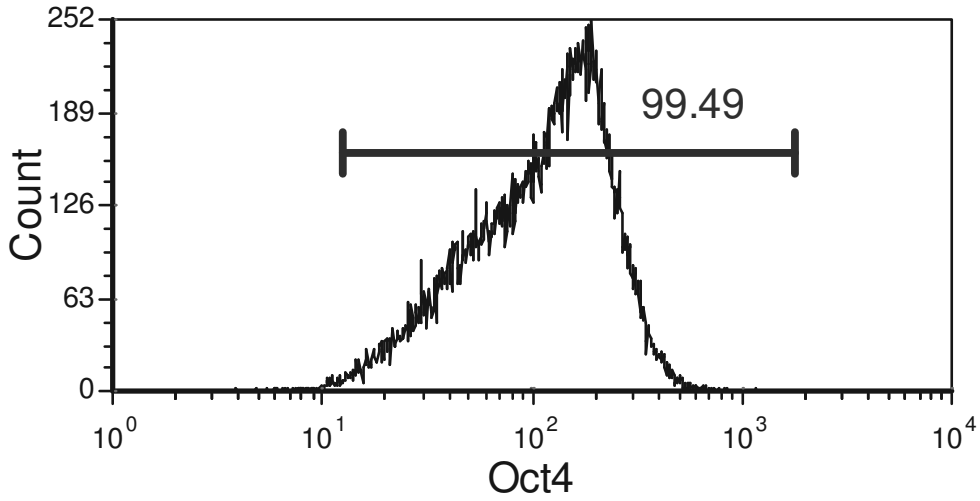


FIG. 20A

Clone 5, Passage 9

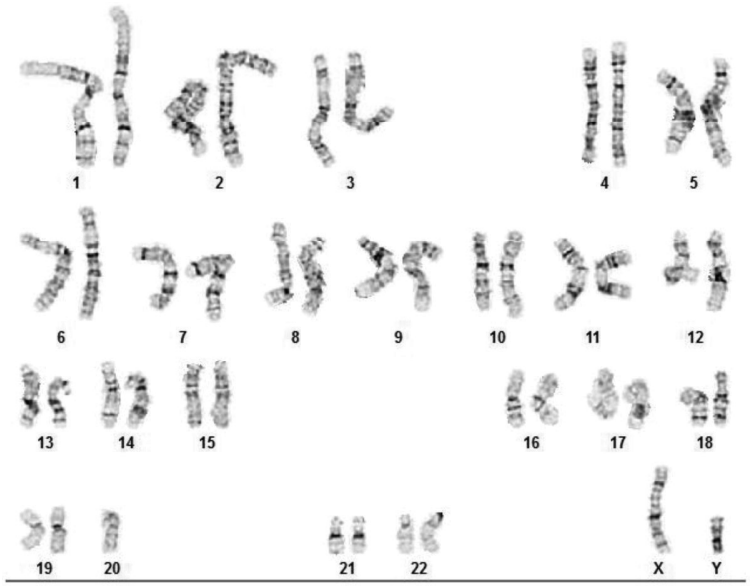


FIG. 20B

Clone 10, Passage 8

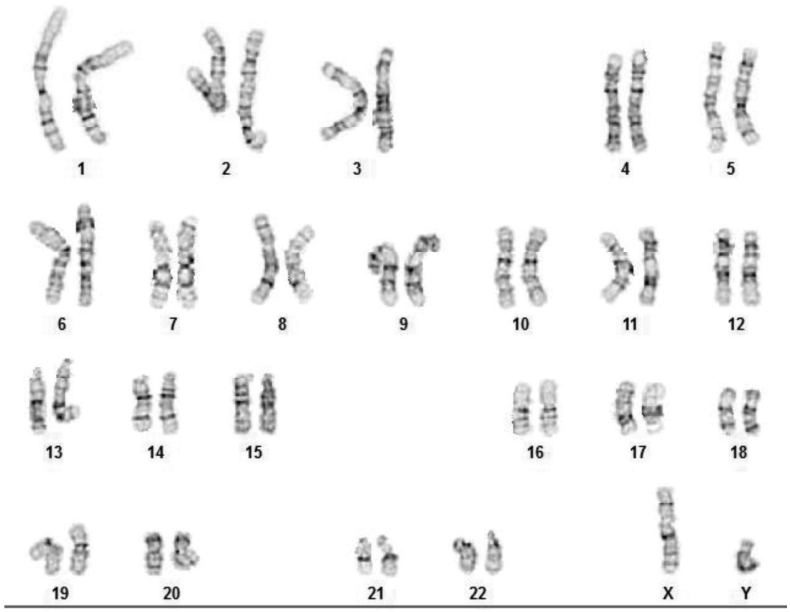


FIG. 20C

Clone 3, Passage 9



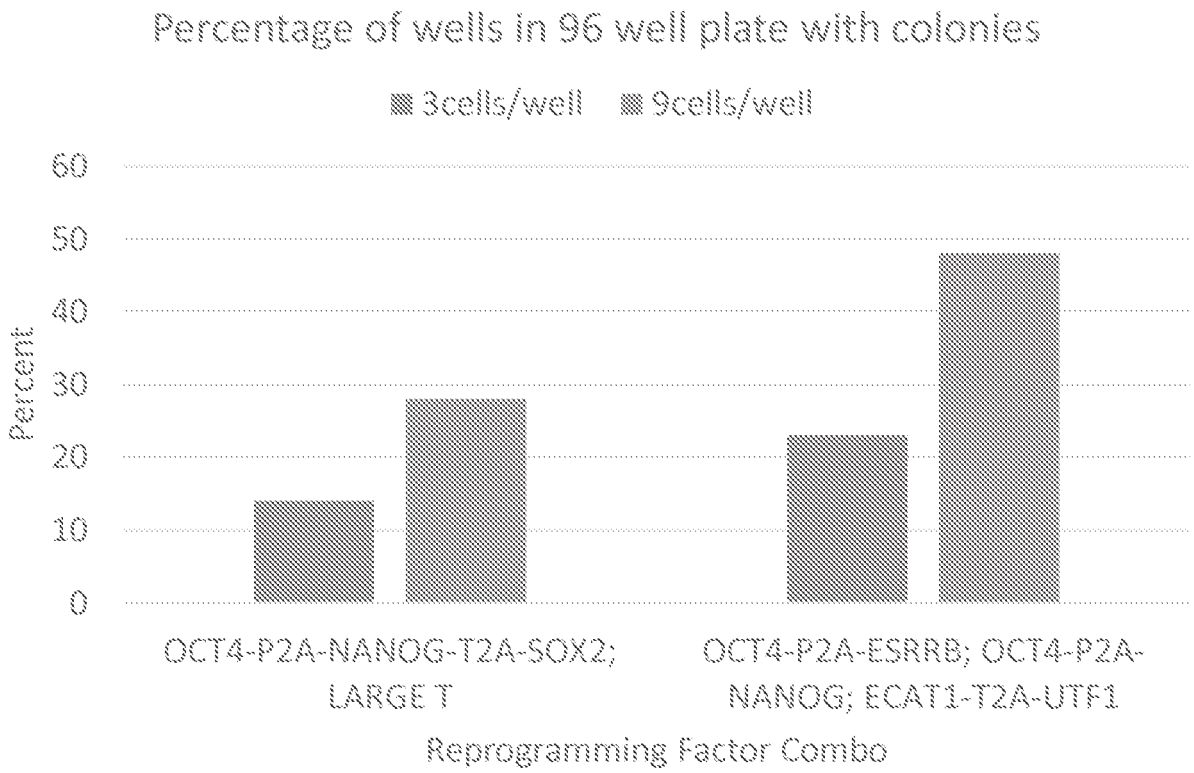


FIG. 21

OCT4-P2A-OCT4 / NANOG-P2A-ESRRB-T2A-LIN28 / ECAT1-T2A-UTF1

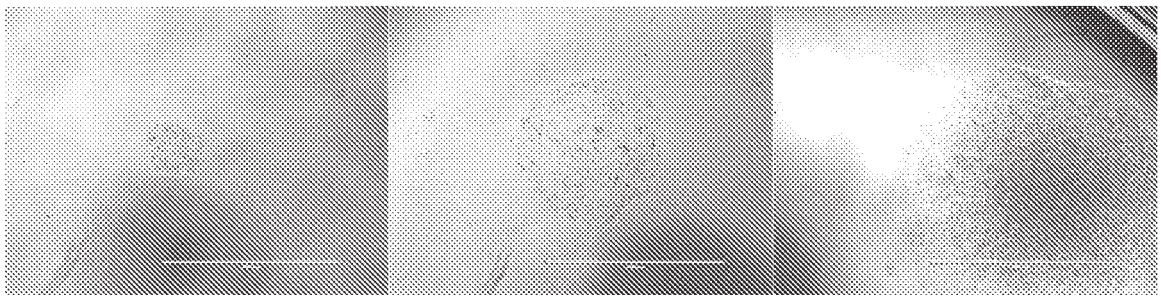


FIG. 22A

OCT4-P2A-ESRRB / OCT4-P2A-NANOG / ECAT1-T2A-UTF1

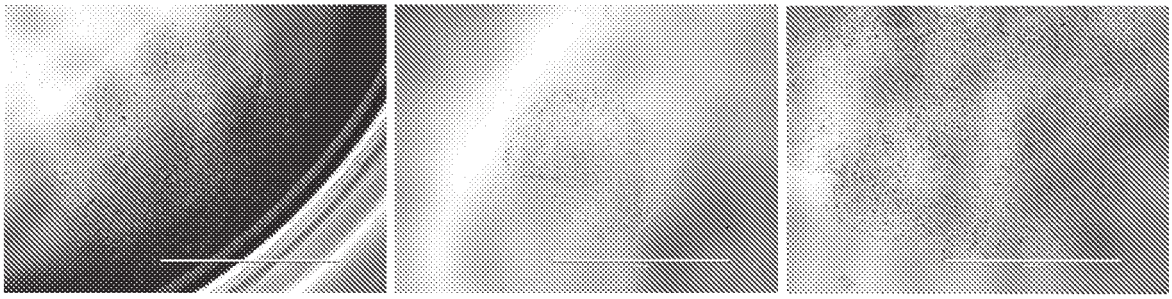


FIG. 22B

Constant Expression	**Selection for**	**SSEA4/Tra181 Positive by flow analysis**
OCT4-P2A-NANOG-T2A-SOX2 SV40 Large T Antigen	No Selection	0.9%
OCT4-P2A-NANOG-T2A-SOX2 SV40 Large T Antigen OCT4-P2A-SOX2-Puro	OCT4/SOX2	0.24%
OCT4-P2A-NANOG-T2A-SOX2 SV40 Large T Antigen OCT4-P2A-NANOG-T2A-SOX2-Puro	OCT4/NANOG/SOX2	0.86%
OCT4-P2A-NANOG-T2A-SOX2 SV40 Large T Antigen OCT2-P2A-OCT4-Puro	OCT4	13.93%

FIG. 23A

OCT4-P2A-NANOG-T2A-SOX2 /SV40 Large T Antigen

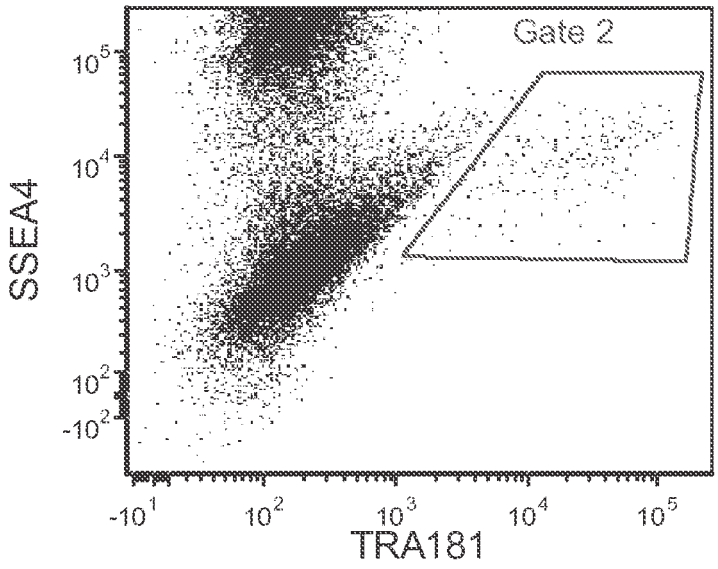


FIG. 23B

OCT4-P2A-NANOG-T2A-SOX2 / SV40 Large T Antigen / OCT2-P2A-OCT4-Puro

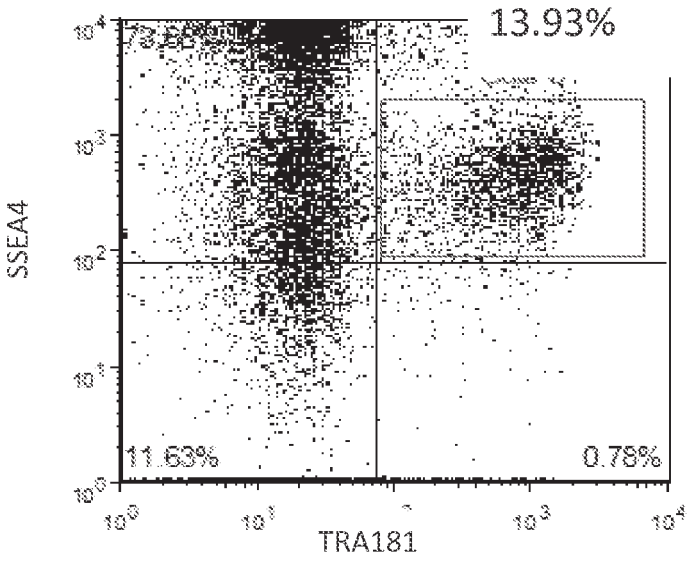


FIG. 23C

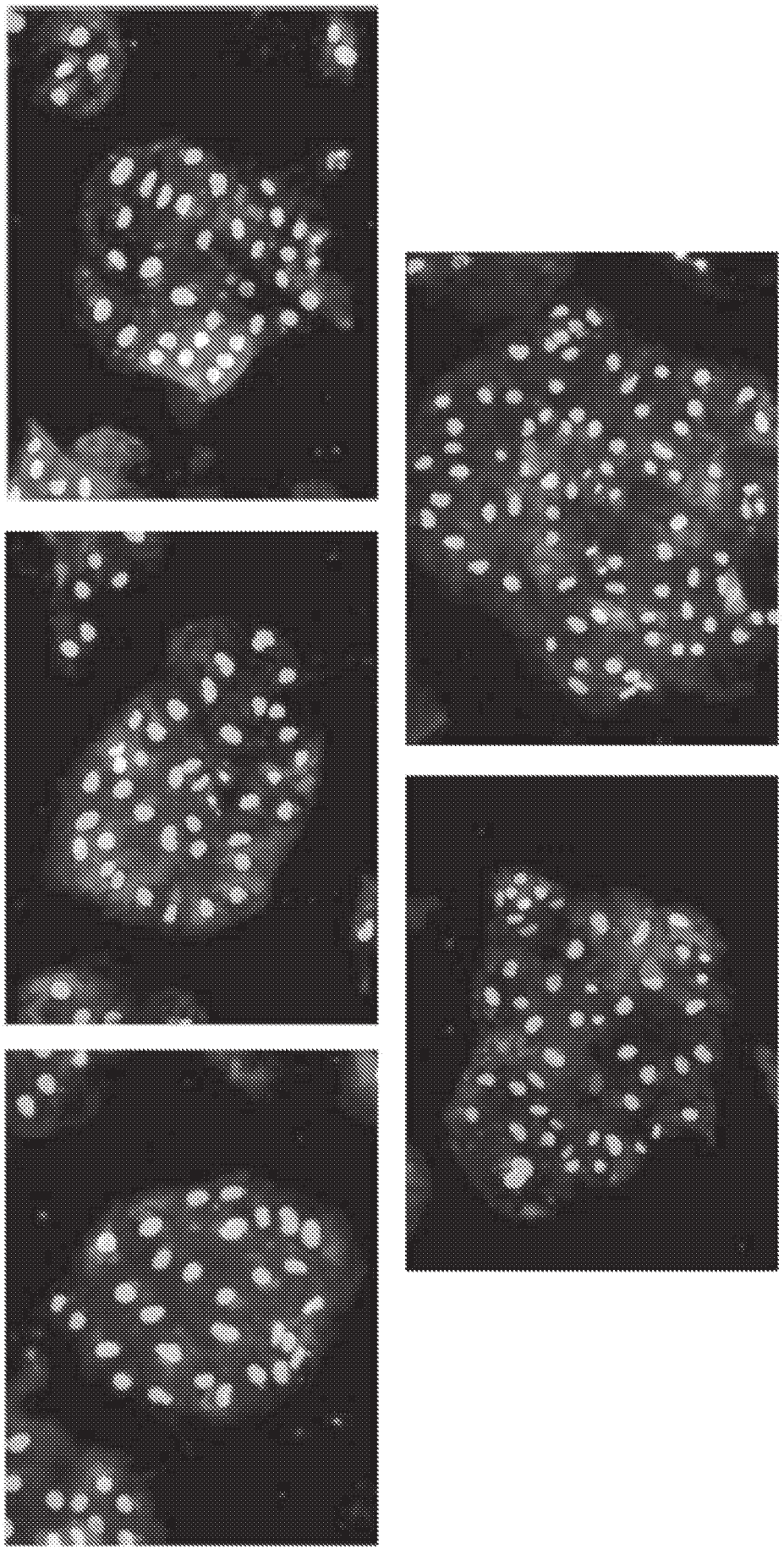


FIG. 24

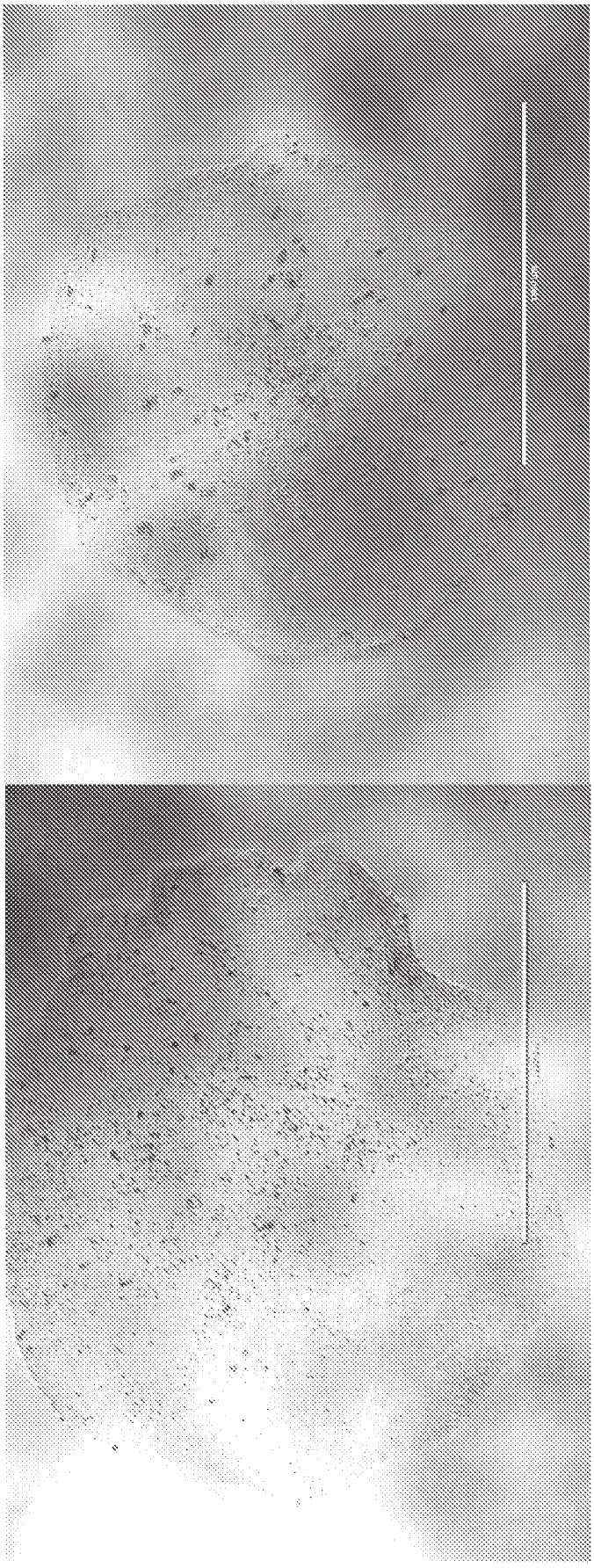


FIG. 25