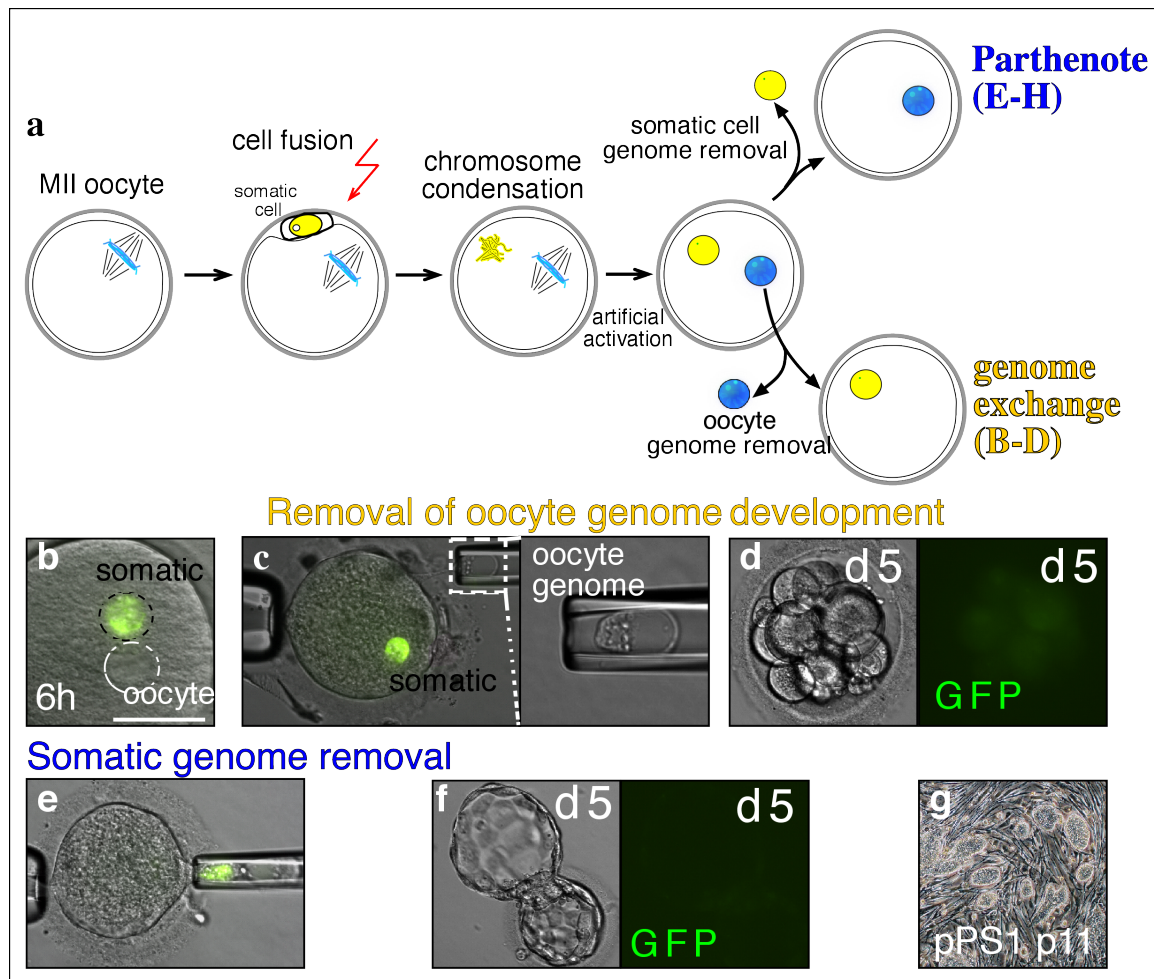
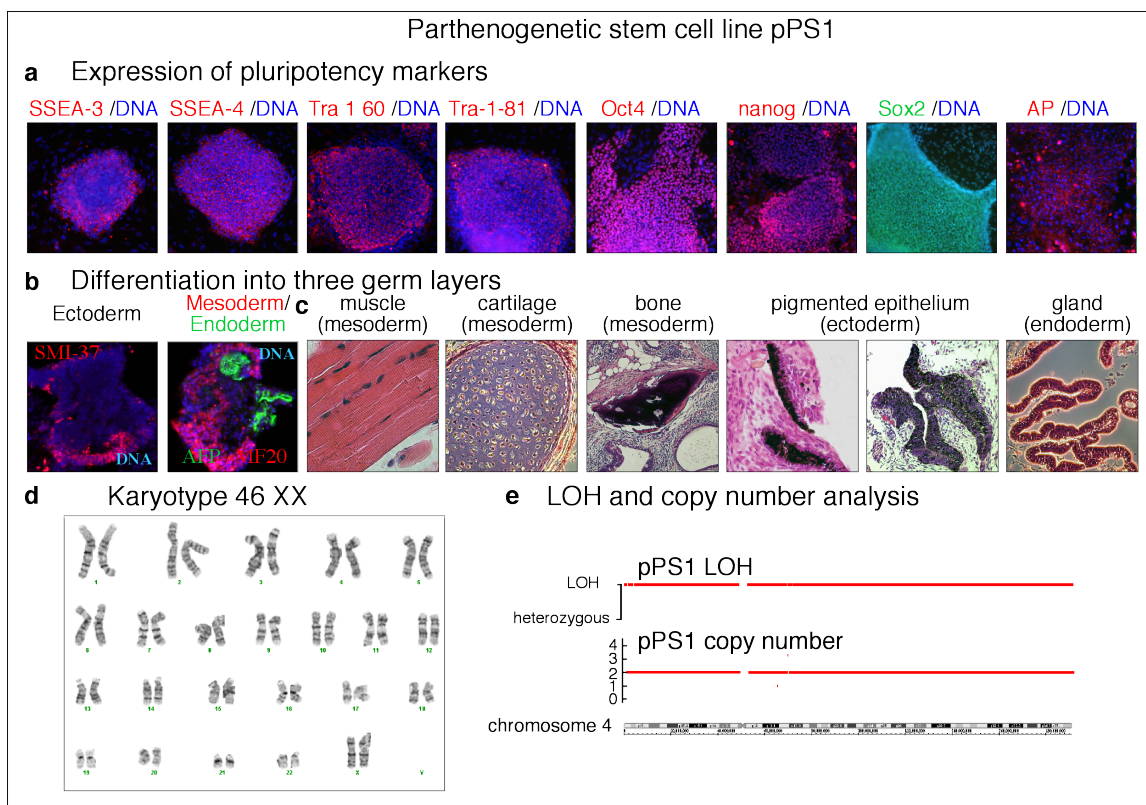


Supplementary Figures and Legends

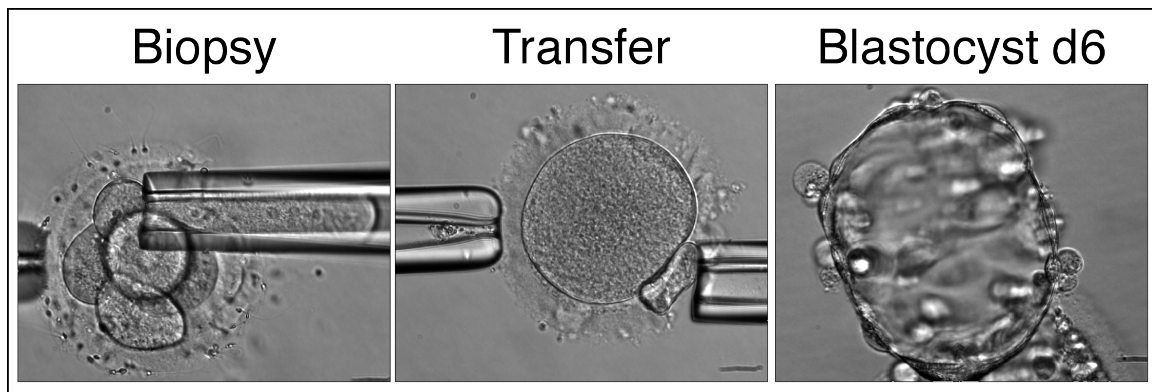


Supplementary Figure 1 | Manipulations and artificial activation are compatible with development to the blastocyst stage and stem cell derivation. **a**, Schematic of somatic cell genome transfer with removal of either the oocyte or the somatic cell genome at the first interphase. **b**, 1-cell stage, 6 hours post activation, containing both the somatic genome (green) as well as the oocyte genome (white circle). Size bar is 50µm. **c**, Specific removal of the oocyte genome 6h post activation, magnified and shown retained in the pipette. **d**, Development after specific removal of the oocyte genome on day 5 after activation. **e**, Specific removal of the somatic cell genome. **f**, parthenote on day 5 after activation. **g**, parthenogenetic pluripotent stem cell line pPS1 at passage 11.

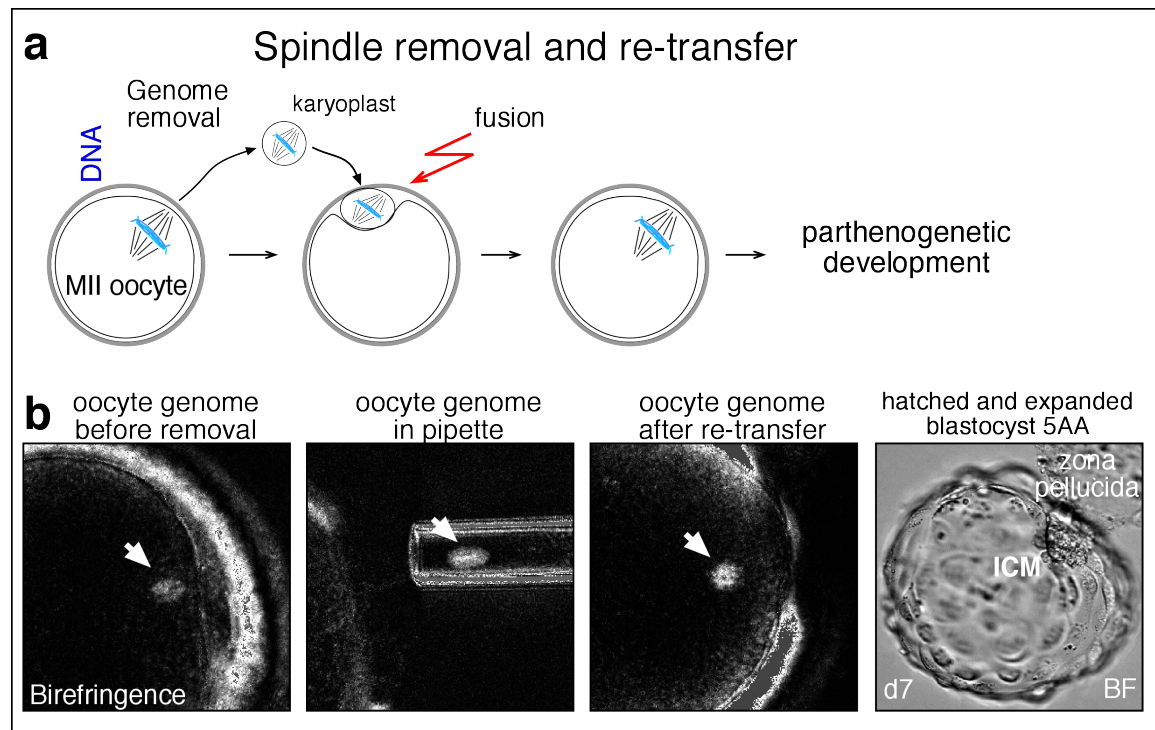


Supplementary Figure 2 | Characterization of a parthenogenetic pluripotent stem cell line

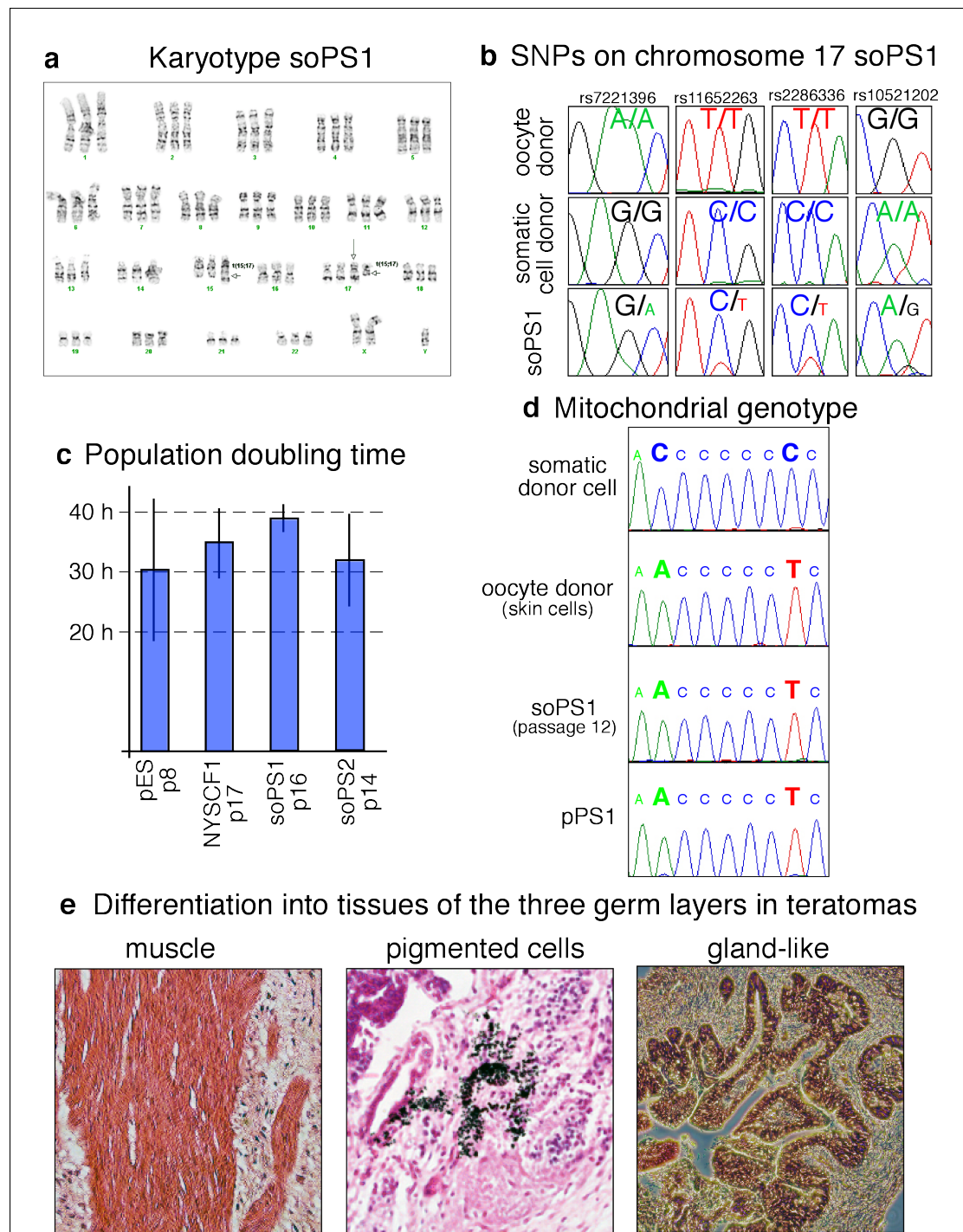
a, pluripotency marker expression. **b,c**, Differentiation into cell types of all three germ layers in vitro (**b**) and in mice (**c**). **d**, Karyotype. **e**, Affymetrix NspI SNP array data showing uniform loss of heterozygosity (LOH) in pPS1 as shown for chromosome 4. Uniform LOH was also observed for all the other chromosomes.



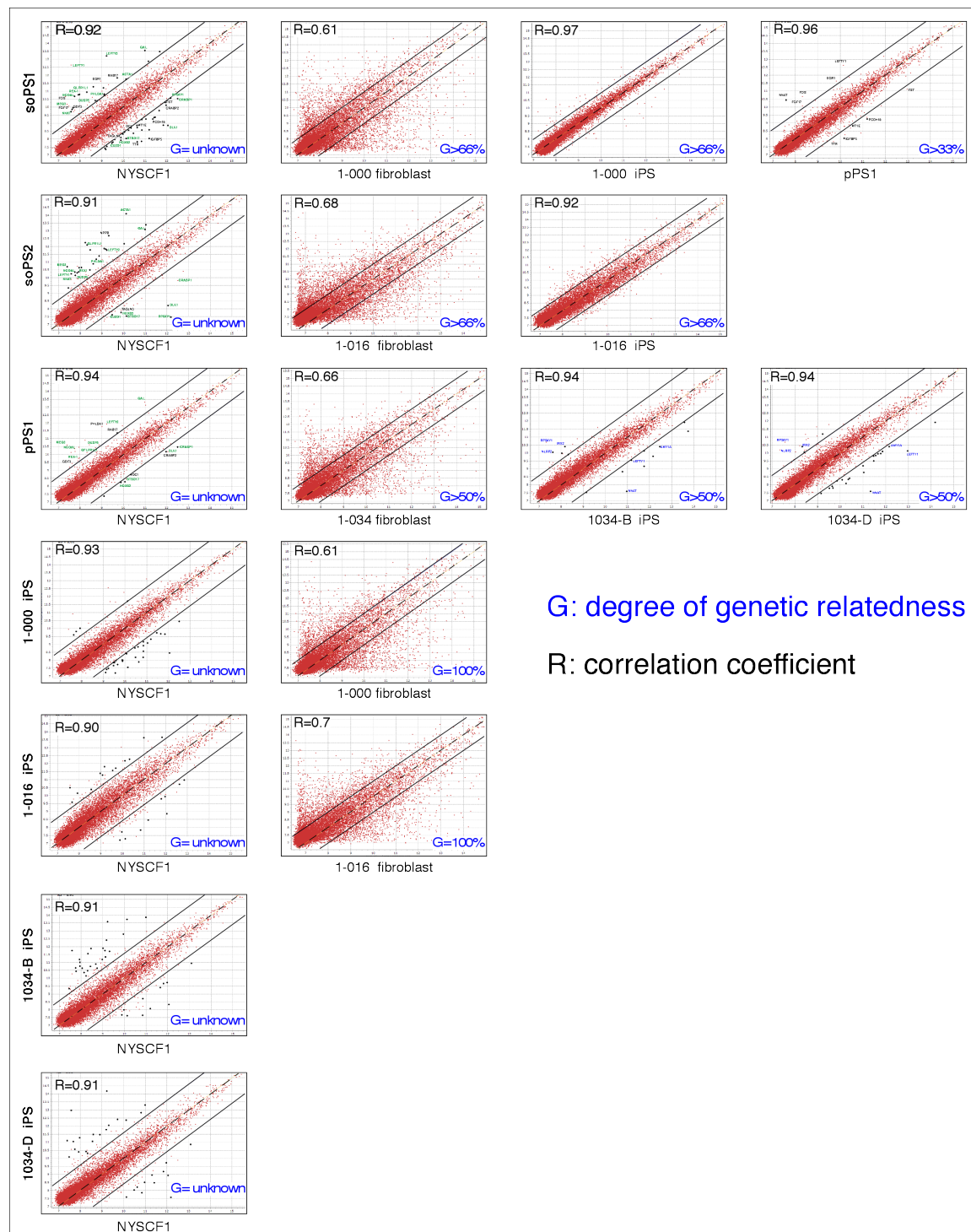
Supplementary Figure 3 | Transfer of blastomere nuclei and development to the blastocyst stage. Transfer of blastomere nuclei was done by aspirating blastomeres from thawed d3 IVF specimen in PGD medium (LifeGlobal, LPGG-050), blastomeres were briefly exposed to HVJ-E diluted 10x in fusion buffer and inserted below the zona pellucida after exposure of the oocyte to ionomycin to avoid chromosome condensation of cells that potentially were in S-phase. After manipulation, cells were kept in 20 μ g/ml puromycin for 4-5 hours, thoroughly washed and cultured in droplets of Global medium covered with mineral oil (IrvineScientific) as described in the methods section.



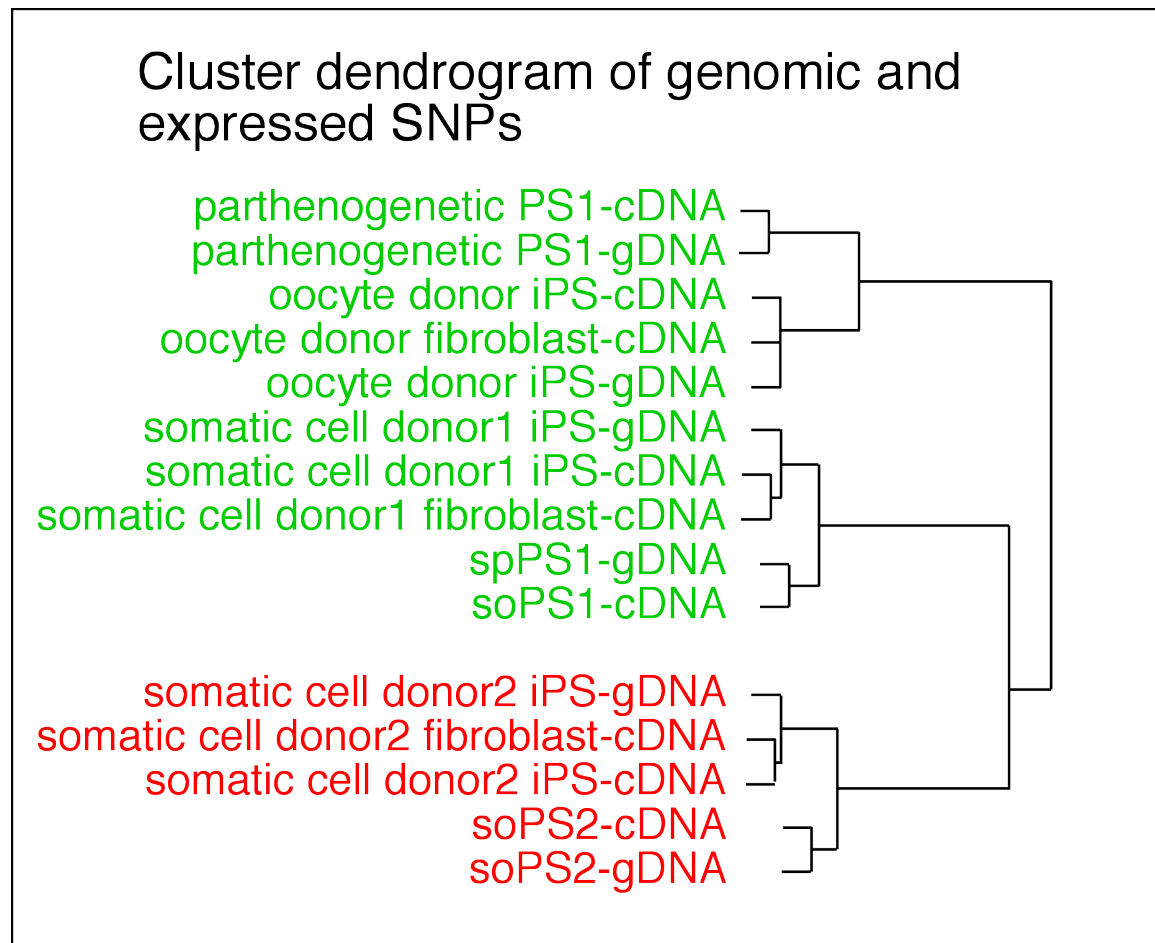
Supplementary Figure 4 | Development to the blastocyst stage after removal and re-transfer of the spindle-chromosome complex. **a**, schematic representation of the experiment. **b**, The spindle-chromosome complex (arrow) was identified by microtubule birefringence. The spindle was aspirated, briefly exposed to HVJ-E diluted 40x with fusion buffer, and placed between zona pellucida and the genome-less oocyte. Spindle birefringence indicated successful fusion. The oocytes were activated and cultured to the blastocyst stage as described in supplementary Fig.4. In both experiments, fragmentation was observed.



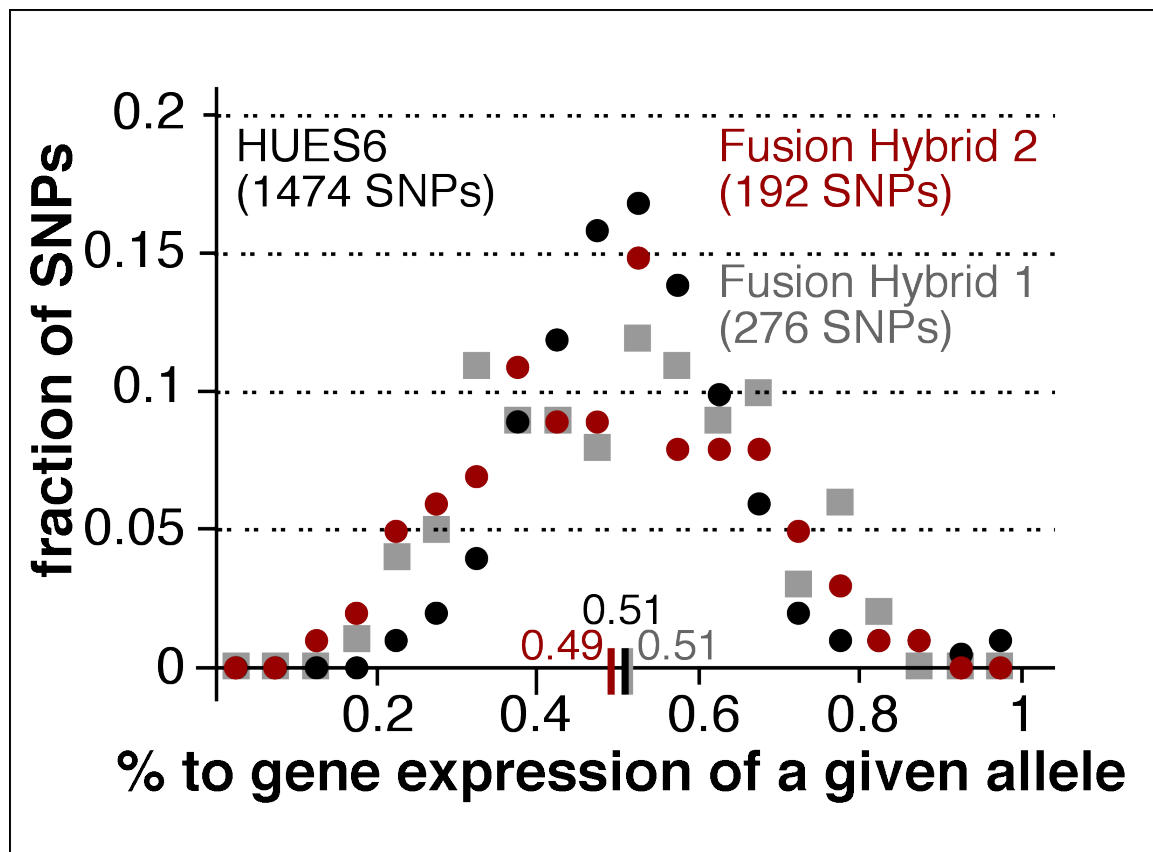
Supplementary Figure 5 | Additional characterization of soPS cells. soPS1 contains the genome of an adult male diabetic individual, soPS2 of a healthy male adult. **a**, Karyotype, **b**, somatic cell origin of the additional chromosome 17. The minor peak from the oocyte indicates that of the four chromosomes 17 present, three originate from the somatic cell and one from the oocyte. **c**, Population doubling time. p= passage number. Standard deviation is indicated. **d**, Sequence of the mitochondrial hypervariable region I. **e**, Differentiation of soPS2 within teratomas into tissues of all three germ layers.



Supplementary Figure 6 | Gene expression analysis of soPS cells. Shown are the scatter plots for the log2 (average signal of expression). Lines indicate thresholds for 3-fold change in expression. Dashed line indicates no difference in expression. Genes indicated in black dots have a P-value of <0.01 and a cutoff of >3x change for differential expression (only applied to comparisons with NYSCF1 and with pPS1). Labeled genes are found differentially expressed in more than a single comparison.

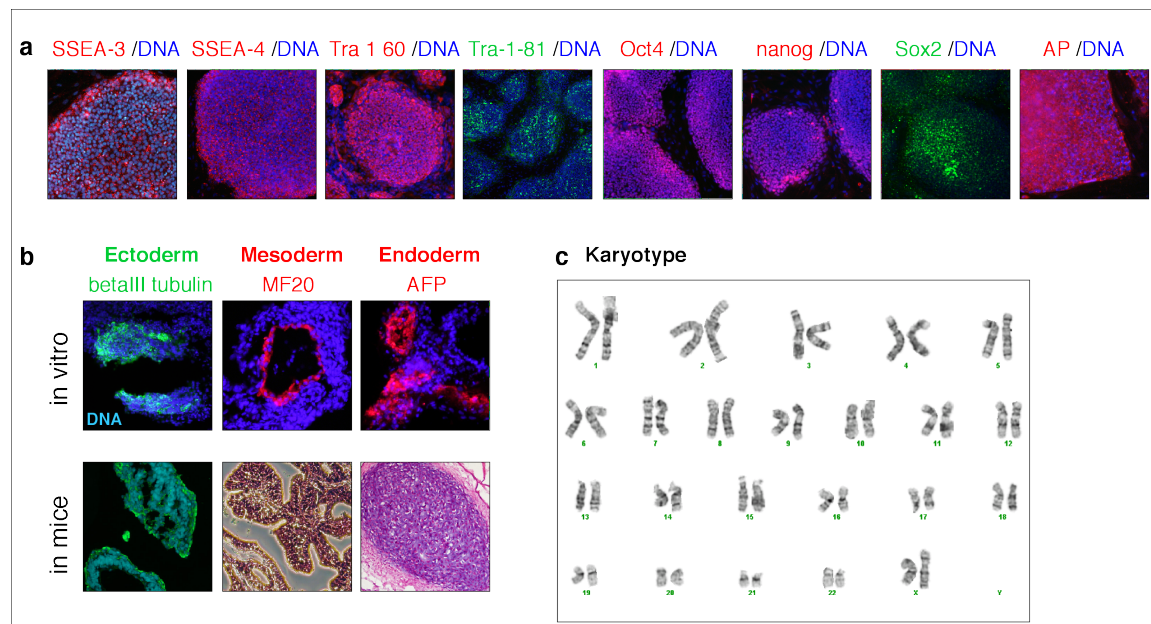


Supplementary Figure 7 | Samples analyzed for genome-wide allelotyping. Samples can be divided into two experimental groups: one group consisting of soPS1, iPS cells and fibroblasts of somatic cell donor 1, parthenogenetic stem cells, iPS cells and fibroblasts of the oocyte donor (colored in green). The second group consists of soPS2, iPS and somatic cells of somatic cell donor 2 (colored in red). The cluster dendrogram groups samples according to their genetic relatedness using SNP sequencing data.



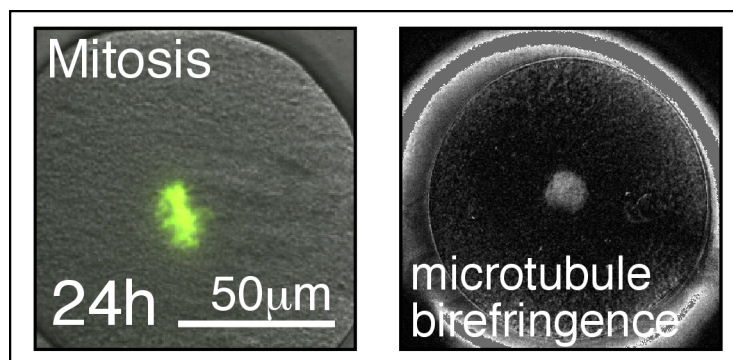
Supplementary Figure 8 | Allelic ratio in human pluripotent stem cell line HUES6 and in reprogrammed somatic cell/HUES6 fusion hybrids².

Horizontal axis represents the allelic ratio for a particular allele, vertical axis represents number of alleles expressed at that ratio of total alleles. For the HUES6/BJ fusion hybrids 1 and 2², quantification refers to the BJ genome (0 corresponds to expression only from the HUES6 genome, 1 corresponds to 100% expression from the BJ genome). In HUES6, the distribution of the allelic ratios in cDNA approximated a Gaussian distribution with a median of 0.51 (Shapiro-Wilk test for normality $W=0.98$). In tetraploid HUES6-somatic cell hybrids², we identified 192 and 176 SNPs in two hybrid cell lines for which the somatic cell genome and HUES6 were, respectively, homozygous. The allelic ratio in cDNA followed a Gaussian distribution with a median of 0.51 for fusion hybrid1 and 0.49 for fusion hybrid2, indicating that the somatic cell-derived genome was expressed proportionally to the HUES6 derived genome.



Supplementary Fig. 9 | Characterization of pluripotent stem cell line NYSCF1, derived from an IVF blastocyst.

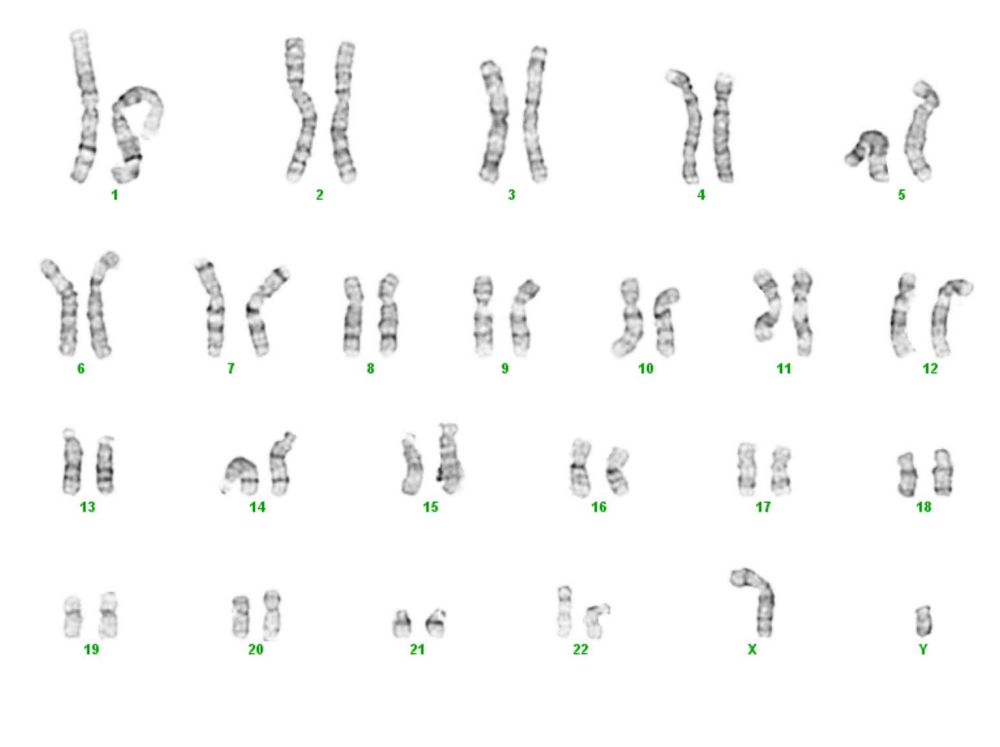
a, pluripotency marker expression, **b**, differentiation in vitro and in vivo, in mice **c**, karyotype 46, XX.



Supplementary Fig. 10 | Spindle assembly after somatic genome transfer. spindle assembly and metaphase alignment of H2B-GFP labeled donor cell chromosomes at the first mitosis, spindle birefringence at the first mitosis. This shows that somatic cell genomes have the ability to assemble into a normal mitotic spindle structure during cleavage development.

Supplementary Karyotypes

These include the files from the analysis of cells shipped as live cultures to Cell Line Genetics. Postal address contained in original files was not included.



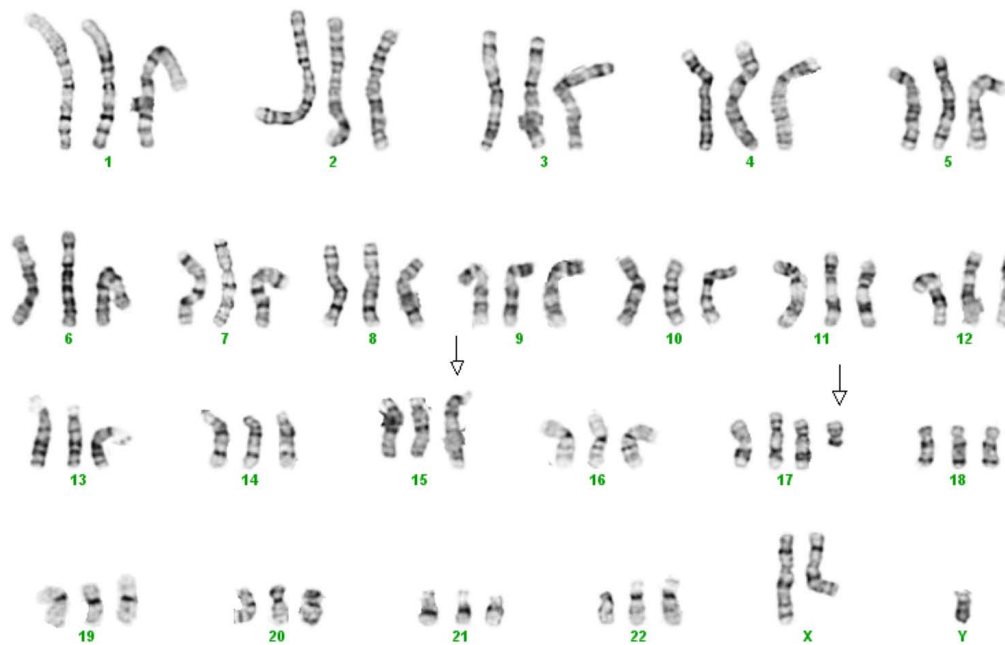
Karyotype skin cell line (fibroblasts) ID 1016, 46, XY



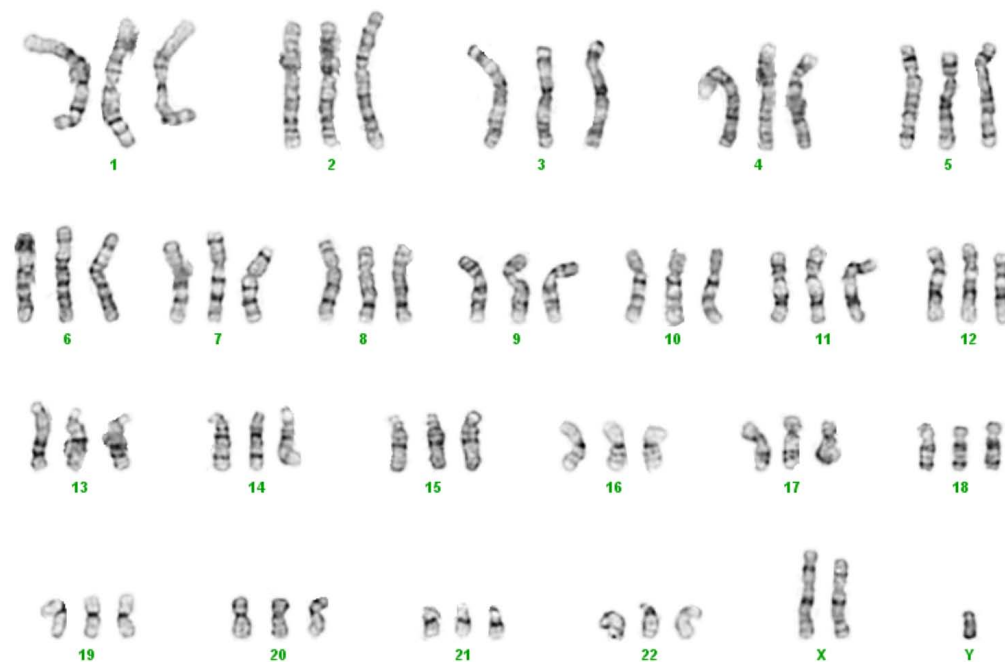
Karyotype oocyte donor skin cell line (fibroblasts) ID 1034. 46, XX



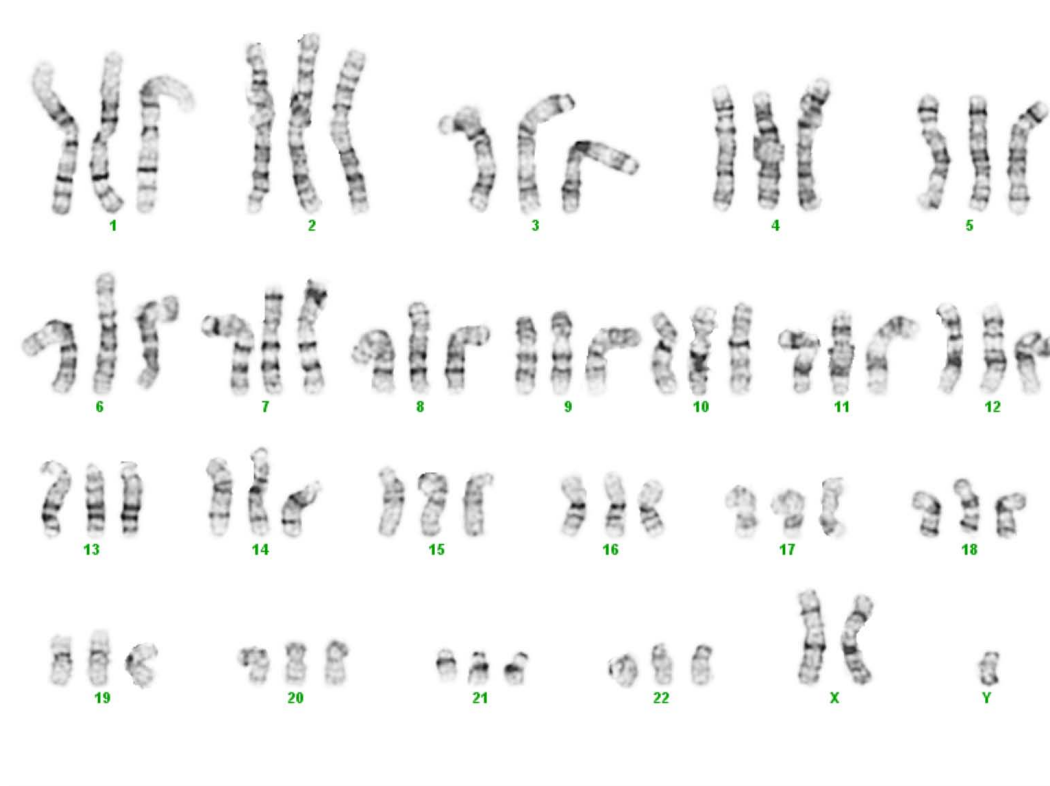
Karyotype skin cell line (fibroblasts) ID 1000, T1D, 46, XY



Karyotype soPS1, p23



Karyotype soPS2 p20



Karyotype soPS2 p3



Cell Line Characterization

Cell Line ID: A2 p11

Passage #: 11

Specimen Type: Human ESC/iPSC Culture

Indication for Study: Routine Culture QC

Lab #: CLG-3599

PI: Scott Noggle

Contact Person: Lauren Bauer

Email: lab@nyscf.org

Test Code: 100,301

Account #: NA

PO #: DE12010SA

Date Received: 12/2/09

Date Reported: 12/21/09

Time in Culture: 1 day

Banding Technique: GTL

Band Resolution: Good

Metaphases Counted: 20

Analyzed: 7

Karyotyped: 2

RESULTS: 46,XX[20]

Apparently NORMAL Female Human Karyotype

Non-clonal Aberrations: none

INTERPRETATION:

Cytogenetic analysis was performed on twenty G-banded metaphase cells from human cell line A2 p11 and all twenty cells demonstrated an apparently normal female karyotype. No abnormal cells with trisomy 12 and/or 17 were detected.

DNA fingerprinting is currently being processed and will be reported separately.

Lorraine Faxon Meisner, Ph.D., FACMG

Julie A. Johnson, M.S., CLSp(CG)



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Cell Line DNA Fingerprint Report

Lab #: CLG-4019
ID: 1000 p11
Passage: 11
Species: human
Cell Type: fibroblast
Feeders: none

T1D
skin cell

Date Received: 3/10/10
Date Reported: 3/18/10
Sample Type: live culture
Reason for Study: cell line DNA STR profile

PO: DE030910E
Test Code: 100,301

Amelogenin	X	Y	D18S51	14	16
vWA	17		Penta E	5	
D8S1179	12	15	D5S818	11	13
TPOX	11		D13S317	11	13
FGA	24		D7S820	10	12
D3S1358	15	18	D16S539	11	12
TH01	9	9.3	CSF1PO	11	13
D21S11	27	29	Penta D	10	

INTERPRETATION: The DNA STR profile for the cell line **1000 p11** is consistent with the presence of a single cell line.

The loci do not match the DNA fingerprint pattern of the cell lines published in the ATCC or NIH website.

Note: This sample was run in duplicate and blinded to the interpreter to confirm the results. We used the Powerplex 16 (Promega) kit to obtain the results.

Lorraine F. Meisner Ph.D. FACMG
Chief Scientific Officer



Cell Line Characterization

Cell Line ID: 1034 p2

Passage #: 2

Specimen Type: Human Fibroblast Culture

Indication for Study: Routine Culture QC

*oocyte donor
skin cell*

Lab #: CLG-4074

PI: Dieter Egli

Contact Person: Lauren Bauer

Email: lab@nyscf.org

Test Code: 100 301

Account #: NA

PO #: de031810a

Date Received: 3/19/10

Date Reported: 3/30/10

Time in Culture: 3 days

Banding Technique: GTL

Band Resolution: Poor

Metaphases Counted: 10

Analyzed: 10

Karyotyped: 3

RESULTS: 46,XX[7]

See Interpretation Below

Non-clonal Aberrations: 45,XX,der(3)t(3;19)(q21;q13.1),-19,frag
46,XX,t(6;15)(q23;q24)
44,XX,-3,-20

INTERPRETATION:

Despite our best efforts, cytogenetic analysis could only be performed on ten G-banded metaphase cells from human cell line 1034 p2 because of a poor mitotic index. Although seven cells demonstrated an apparently normal female karyotype, three cells demonstrated non-clonal aberrations, including two that demonstrated structural aberrations. This could suggest that this cell line is cytogenetically unstable. Therefore, we recommend that this line be tested again.

DNA fingerprinting was also performed. Please see attached report.

Lorraine Faxon Meisner, Ph.D., FACMG

Julie A. Johnson, M.S., CLSp(CG)



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Cell Line DNA Fingerprint Report

Lab #: CLG-4042
 Cell Line ID: Doror Jan18
 Passage: Not specified
 Species: Human
 Cell Type: Not specified
 Feeders: none

Date Received: 3/12/10
 Date Reported: 3/24/10
 Sample Type: DNA
 Reason for Study: cell line authentication

PO: de030510H
 Test Code: 301

oocyte donor & DNA

Amelogenin	X		D18S51	14	16
vWA	14	19	Penta E	18	19
D8S1179	8	16	D5S818	11	12
TPOX	9	11	D13S317	12	13
FGA	21		D7S820	10	11
D3S1358	16		D16S539	11	12
THO1	6	8	CSF1PO	11	12
D21S11	29		Penta D	11	13

INTERPRETATION: The DNA STR profile for the cell line **Doror Jan18** is consistent with the presence of a single cell line.

The loci do not match the DNA fingerprint pattern of the cell lines published in the ATCC or NIH website.

Note: This sample was run in duplicate and blinded to the interpreter to confirm the results. We used the Powerplex 16 (Promega) kit to obtain the results.

Lorraine F. Meisner Ph.D. FACMG
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Cell Line DNA Fingerprint Report

Lab #: CLG-4142
Cell Line ID: 1016A p9
Passage: 9
Species: Human
Cell Type: iPS
Feeders: mouse

*somatic
cell donor
iPS cell*

Date Received: 3/30/10
Date Reported: 4/6/10
Sample Type: live culture
Reason for Study: cell line DNA STR profile

PO: de032510B
Test Code: 100, 301

Amelogenin	X	Y	D18S51	17	
vWA	18		Penta E	11	
D8S1179	10	14	D5S818	12	13
TPOX	10	11	D13S317	8	11
FGA	20	24	D7S820	11	12
D3S1358	16	18	D16S539	11	12
TH01	7	9	CSF1PO	10	11
D21S11	28	30	Penta D	9	12

INTERPRETATION: The DNA STR profile for the cell line **1016A p9** is consistent with the presence of a single cell line.

The loci match the DNA fingerprint pattern of submitted cell line 1016B p8 (CLG-4113).

The loci do not match the DNA fingerprint pattern of the cell lines published in the ATCC or NIH website.

Note: This sample was run in duplicate and blinded to the interpreter to confirm the results. We used the Powerplex 16 (Promega) kit to obtain the results.

Lorraine F. Meisner Ph.D. FACMG
Chief Scientific Officer



Cell Line Characterization

TID skin cell

Cell Line ID: 1000 p11

Passage #: 11

Specimen Type: Human Fibroblast Culture

Indication for Study: Routine Culture QC

Lab #: CLG-4019

PI: Dieter Egli

Contact Person: Lauren Bauer

Email: lab@nyscf.org

Test Code: 100, 301

Date Received: 3/10/10

Account #: NA

Date Reported: 3/18/10

PO #: DE030910E

Time in Culture: 2 days

Banding Technique: GTL

Band Resolution: Fair

Metaphases Counted: 20

Analyzed: 8

Karyotyped: 2

RESULTS: 46,XY[20]

Apparently NORMAL Male Karyotype

Non-clonal Aberrations: none

INTERPRETATION:

Cytogenetic analysis was performed on twenty G-banded metaphase cells from human cell line 1000 p11 and all twenty cells demonstrated an apparently normal male karyotype. No abnormal cells were detected.

DNA fingerprinting was also performed. Please see the attached report.

Lorraine Faxon Meisner, Ph.D., FACMG

Julie A. Johnson, M.S., CLSp(CG)



Cell Line Characterization

Cell Line ID: B4 p23

Passage #: 23

Specimen Type: Human ESC Culture

Indication for Study: Routine Culture QC

so PS1

Lab #: CLG-5618

PI: Dieter Egli

Test Code: 100, 301

Account #: NA

PO #: de112210

Date Received: 11/23/10

Date Reported: 12/10/10

Time in Culture: 1 day

Banding Technique: GTL

Band Resolution: Good

Metaphases Counted: 10 Analyzed: 10 Karyotyped: 10

RESULTS: 71,XXY,+12,t(15;17)(q26.1;q21),+17[3]/70,XXY,t(15;17)(q26.1;q21),+17[5]

ABNORMAL Male Human Karyotype

Non-clonal Aberrations: 69,XXY,-8,t(15;17)(q26.1;q21)
70,XXY,-14,+15,t(15;17)(q26.1;q21)x2,+17

INTERPRETATION:

Cytogenetic analysis was performed on ten G-banded metaphase cells from human cell line B4 p23. Five cells demonstrated an abnormal male triploid karyotype with a balanced translocation between the long arm of chromosome 15 and the long arm of chromosome 17, and an extra copy of chromosome 17, which was also seen in an earlier passage of this line (p12, CLG-3601). Three cells demonstrated an extra copy of chromosome 12 in addition to the t(15;17) and extra copy of chromosome 17, which was not seen in p12. Two cells demonstrated non-clonal chromosome aberrations (listed above) which are most likely technical artifacts.

DNA fingerprinting was also performed. Please see attached report.

Lorraine Faxon Meisner, Ph.D., FACMG

Julie A. Johnson, M.S., CLSp(CG)



Cell Line Characterization

Cell Line ID: B5 p3

Passage #: 3

Specimen Type: Human ESC Culture

Indication for Study: Routine Culture QC

50 PS 2

Lab #: CLG-4021

PI: Dieter Egli

Test Code: 100, 301

Account #: NA

PO #: DE030910A

Date Received: 3/10/10

Date Reported: 3/18/10

Time in Culture: 1 day

Banding Technique: GTL

Band Resolution: Good

Metaphases Counted: 10

Analyzed: 6

Karyotyped: 6

RESULTS: 69,XXY[9]

ABNORMAL Male Human Karyotype Consistent with Triploidy

Non-clonal Aberrations: 69,XXY,-9,+11 (one cell)

INTERPRETATION:

Cytogenetic analysis was performed on ten G-banded metaphase cells from human cell line B5 p3. Nine cells demonstrated a male triploid karyotype with a chromosome count of 69 chromosomes. One cell demonstrated a non-clonal chromosome aberration (listed above) which is most likely a technical artifact. No diploid cells were detected.

DNA fingerprinting was also performed. Please see the attached report.

Lorraine Faxon Meisner, Ph.D., FACMG

Julie A. Johnson, M.S., CLSp(CG)



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Cell Line DNA Fingerprint Report

Lab #: CLG-4021
ID: B5 p3
Passage: 3
Species: human
Cell Type: ESC
Feeders: mouse

sops 2

Date Received: 3/10/10
Date Reported: 3/18/10
Sample Type: live culture
Reason for Study: cell line DNA STR profile

PO: DE030910A
Test Code: 100,301

Amelogenin	X	Y		D18S51	16	17	
vWA	14	18		Penta E	11	18	
D8S1179	8	10	14	D5S818	11	12	13
TPOX	9	10	11	D13S317	8	11	13
FGA	20	21	24	D7S820	10	11	12
D3S1358	16	18		D16S539	11	12	
TH01	7	8	9	CSF1PO	10	11	12
D21S11	28	29	30	Penta D	9	12	13

INTERPRETATION: The DNA STR profile for the cell line **B5 p3** is consistent with the presence of a single cell line.

However, ten loci contain three STRs while six had peaks indicating the presence of a second copy of an existing locus. This suggests that the triploid karyotype originated through fusion of diploid and haploid gametes.

The loci do not match the DNA fingerprint pattern of the cell lines published in the ATCC or NIH website.

Note: This sample was run in duplicate and blinded to the interpreter to confirm the results. We used the Powerplex 16 (Promega) kit to obtain the results.

Lorraine F. Meisner Ph.D. FACMG
Chief Scientific Officer



Cell Line Characterization

Cell Line ID: B5 p20

50PS2

Lab #: CLG-5619

Passage #: 20

PI: Dieter Egli

Specimen Type: Human ESC Culture

Indication for Study: Routine Culture QC

Test Code: 100

Date Received: 11/23/10

Account #: NA

Date Reported: 12/13/10

PO #: de112210

Time in Culture: 1 day

Banding Technique: GTL

Band Resolution: Good

Metaphases Counted: 10

Analyzed: 5

Karyotyped: 5

RESULTS: 69,XXY[9]

ABNORMAL Male Human Karyotype Consistent with Triploidy

Non-clonal Aberrations: 68,XX,-Y (one cell)

INTERPRETATION:

Cytogenetic analysis was performed on ten G-banded metaphase cells from human cell line B5 p20. Nine cells demonstrated a male triploid karyotype with a chromosome count of 69 chromosomes. One cell demonstrated a non-clonal chromosome aberration (listed above) which is most likely a technical artifact. No diploid cells were detected.

Lorraine Faxon Meisner, Ph.D., FACMG

Julie A. Johnson, M.S., CLSp(CG)



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Cell Line DNA Fingerprint Report

Lab #: CLG-3600

ID: A3 p14

Passage: 14

Species: human

Cell Type: ES/iPS

Feeders: mouse

NYSCF1

The New York Stem Cell Foundation

Date Received: 12/2/09

Date Reported: 12/22/09

Sample Type: live culture

Reason for Study: cell line DNA STR profile

PO: DE12010SA

Test Code: 100,301

Amelogenin	X		D18S51	14	18
vWA	17	20	Penta E	13	
D8S1179	14		D5S818	10	12
TPOX	8	9	D13S317	11	
FGA	20	22	D7S820	9	13
D3S1358	15	16	D16S539	10	11
TH01	6	8	CSF1PO	9	11
D21S11	27	31.2	Penta D	2.2	13

INTERPRETATION: The DNA STR profile for the cell line A3 p14 is consistent with the presence of a single cell line.

The loci do not match the DNA fingerprint pattern of the cell lines published in the ATCC or NIH website.

Note: This sample was run in duplicate and blinded to the interpreter to confirm the results. We used the Powerplex 16 (Promega) kit to obtain the results.

Lorraine F. Meisner Ph.D. FACMG
Chief Scientific Officer



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Cell Line DNA Fingerprint Report

Lab #: CLG-4074
Cell Line ID: 1034 p2
Passage: 2
Species: Human
Cell Type: fibroblast
Feeders: none

oocyte
donor
skin cell

Date Received: 3/19/10
Date Reported: 3/24/10
Sample Type: genomic DNA
Reason for Study: cell line DNA STR profile

PO: de031810A
Test Code: 100, 301

Amelogenin	X		D18S51	12	15
vWA	17	18	Penta E	15	19
D8S1179	13	15	D5S818	9	10
TPOX	9		D13S317	12	
FGA	23	24	D7S820	8	9
D3S1358	16	17	D16S539	11	12
THO1	9	9.3	CSF1PO	11	12
D21S11	29	30	Penta D	9	12

INTERPRETATION: The DNA STR profile for the cell line **1034 p2** is consistent with the presence of a single cell line.

The loci do not match the DNA fingerprint pattern of the cell lines published in the ATCC or NIH website.

Note: This sample was run in duplicate and blinded to the interpreter to confirm the results. We used the Powerplex 16 (Promega) kit to obtain the results.

Lorraine F. Meisner Ph.D. FACMG
Chief Scientific Officer



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Cell Line DNA Fingerprint Report

Lab #: CLG-3601
ID: B4 p12
Passage: 12
Species: human
Cell Type: ES/iPS
Feeders: mouse

SOPS1
✓

Date Received: 12/2/09
Date Reported: 12/23/09
Sample Type: live culture
Reason for Study: cell line DNA STR profile

PO: DE12010SA
Test Code: 100,301

Amelogenin	X	Y		D18S51	14	15	16
vWA	17	18		Penta E	5	19	
D8S1179	12	15		D5S818	9	11	13
TPOX	9	11		D13S317	11	12	13
FGA	24			D7S820	8	10	12
D3S1358	15	17	18	D16S539	11	12	
TH01	9	9.3		CSF1PO	11	12	13
D21S11	27	29		Penta D	10	12	

INTERPRETATION: The DNA STR profile for the cell line B4 p12 is consistent with the presence of a single cell line.

However, six loci contain three STRs while ten had peaks indicating the presence of a second copy of an existing locus. This suggests that the triploid karyotype originated through fusion of a diploid and haploid cell.

The loci do not match the DNA fingerprint pattern of the cell lines published in the ATCC or NIH website.

Note: This sample was run in duplicate and blinded to the interpreter to confirm the results. We used the Powerplex 16 (Promega) kit to obtain the results.

Lorraine F. Meisner Ph.D. FACMG
Chief Scientific Officer



Cell Line Characterization

Cell Line ID: B4 p12 *soPS1*
Passage #: 12
Specimen Type: Human ES/iPSC Culture
Indication for Study: Routine Culture QC

Lab #: CLG-3601
PI: Scott Noggle
Contact Person: Lauren Bauer
Email: lab@myscf.org

Test Code: 100, 301 Date Received: 12/2/09
Account #: NA Date Reported: 12/21/09
PO #: DE12010SA Time in Culture: 1 day

Banding Technique: GTL Band Resolution: Good
Metaphases Counted: 10 Analyzed: 5 Karyotyped: 5

RESULTS: 70,XXY,t(15;17)(q26.1;q21),+17[8]

ABNORMAL Male Human Karyotype

Non-clonal Aberrations: 68,XXY,-12,-14,t(15;17)(q26.1;q21),+17
69,XXY,t(15;17)(q26.1;q21),-16,+17

INTERPRETATION:

Cytogenetic analysis was performed on ten G-banded metaphase cells from human cell line B4 p12. Eight cells demonstrated an abnormal male karyotype with a triploid chromosome count of 70 chromosomes. These cells demonstrated a balanced translocation between the long arm of chromosome 15 and the long arm of chromosome 17, and an extra copy of chromosome 17. Two cells demonstrated non-clonal chromosome aberrations (listed above) which are most likely technical artifacts.

DNA fingerprinting is currently being processed and will be reported separately.

Lorraine Faxon Meisner, Ph.D., FACMG

Julie A. Johnson, M.S., CLSp(CG)



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Cell Line DNA Fingerprint Report

Lab #: CLG-3599

ID: A2 p11

Passage: 11

Species: human

Cell Type: ES/iPS

Feeders: mouse

pPS1 ✓

Date Received: 12/2/09

Date Reported: 12/22/09

Sample Type: live culture

Reason for Study: cell line DNA STR profile

PO: DE12010SA

Test Code: 100,301

Amelogenin	X	D18S51	15
vWA	18	Penta E	19
D8S1179	13	D5S818	10
TPOX	9	D13S317	12
FGA	24	D7S820	9
D3S1358	16	D16S539	11
THO1	9.3	CSF1PO	11
D21S11	29	Penta D	9

INTERPRETATION: The DNA STR profile for the cell line A2 p11 is consistent with the presence of a single cell line.

However, each locus only contains one STR, which is consistent with uniparental disomy.

The loci do not match the DNA fingerprint pattern of the cell lines published in the ATCC or NIH website.

Note: This sample was run in duplicate and blinded to the interpreter to confirm the results. We used the Powerplex 16 (Promega) kit to obtain the results.

Lorraine F. Meisner Ph.D. FACMG
Chief Scientific Officer



Cell Line Characterization

Cell Line ID: A3 p14

Passage #: 14

Specimen Type: Human ESC/iPSC Culture

Indication for Study: Routine Culture QC

NYS CF1

Lab #: CLG-3600

PI: Scott Noggle

Contact Person: Lauren Bauer

Email: lab@nyscf.org



Test Code: 100, 301

Account #: NA

PO #: DE12010SA

Date Received: 12/2/09

Date Reported: 12/21/09

Time in Culture: 1 day

Additional copies sent to:

Banding Technique: GTL

Band Resolution: Good

Metaphases Counted: 20

Analyzed: 7

Karyotyped: 2

RESULTS: 46,XX[19]

Apparently NORMAL Female Human Karyotype

Non-clonal Aberrations: 46,XX,add(9)(q34) (one cell)

INTERPRETATION:

Cytogenetic analysis was performed on twenty G-banded metaphase cells from human cell line A3 p14. Nineteen cells demonstrated an apparently normal female karyotype, while one cell demonstrated a non-clonal chromosome aberration (listed above) which is most likely a technical artifact. No abnormal cells with trisomy 12 and/or 17 were detected.

DNA fingerprinting is currently being processed and will be reported separately.

Lorraine Faxon Meisner, Ph.D., FACMG

Julie A. Johnson, M.S., CLSp(CG)



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Cell Line DNA Fingerprint Report

Lab #: CLG-5618
ID: B4 p23
Passage: 23
Species: human
Cell Type: ESC
Feeders: mouse

sops1

Date Received: 11/23/10
Date Reported: 12/3/10
Sample Type: live culture
Reason for Study: cell line DNA STR profile

PO: de112210
Test Code: 100,301

Amelogenin	X	Y		D18S51	14	15	16
vWA	17	18		Penta E	5	19	
D8S1179	12	15		D5S818	9	11	13
TPOX	9	11		D13S317	11	12	13
FGA	24			D7S820	8	10	12
D3S1358	15	17	18	D16S539	11	12	
THO1	9	9.3		CSF1PO	11	12	13
D21S11	27	29		Penta D	10	12	

INTERPRETATION: The DNA STR profile for the cell line **B4 p23** is consistent with the presence of a single cell line.

However, six loci contain three STRs while ten had peaks indicating the presence of a second copy of an existing locus. This suggests that the triploid karyotype originated through fusion of a diploid and haploid cell.

The alleles match the DNA fingerprint pattern of previously submitted cell line B4 p12 (CLG-3601).

Note: This sample was run in duplicate and blinded to the interpreter to confirm the results. We used the Powerplex 16 (Promega) kit to obtain the results.

Lorraine F. Meisner Ph.D. FACMG
Chief Scientific Officer

Supplemental Tables

Developmental end-point (cell number)	Description of the experiment								
	Genome-exchange: Oocyte genome removal, somatic cell transfer, activation	Genome-exchange: Oocyte genome removal (no Hoechst), somatic cell transfer, activation	Somatic cell transfer, Activation,	Genome-exchange: somatic cell transfer, activation, oocyte genome removal	Parthenote with manipulation: Somatic cell transfer, activation, somatic cell genome removal	donor IVF	Parthenotes	Genome-exchange: Oocyte genome removal, blastomere transfer, activation	Oocyte genome removal and re-transfer
fragmented	6	5	4	1	-	-	4	6	6
1 cell	3	2	7	1	-	-	2	-	-
2 cells	2	2	5	3	-	-	-	-	-
3 cells	3	-	2	5	-	-	3	-	-
4 cells	3	3	2	6	-	-	8	1	-
5 cells	5	-	4	5	-	1	1	-	-
6 cells	1	-	4	4	-	2	4	-	-
7 cells	4	-	3	3	1	-	5	-	-
8 cells	3	-	2	2	-	-	6	-	-
9 cells	-	-	5	1	-	1	-	-	-
10 cells	1	-	2	-	-	1	4	-	-
11 cells	-	-	-	-	1	-	-	-	-
12 cells	-	-	2	1	1	-	2	-	-
morula	-	-	8	-	-	3	6	2	-
blastocyst	-	-	13	-	4	13	7	1	1
stem cell lines	-	-	2	-	1	n/a	-	nd	nd
Total eggs used	31	12	63	32	7	21	52	10	7

Supplementary Table 1 | Developmental potential of human oocytes upon the indicated experimental treatment. Displayed are the number of times a certain developmental stage was reached. Nd: not determined.

symbol	Fold upregulation compared to oocytes (avg. of 3 NT samples, P<0.01 for each sample)	Fold upregulation compared to d3 IVF (avg of 4 IVF samples)	Fold upregulation compared to skin cells (avg of 2 skin cell samples)
CYP4F2	not detected in oocytes	Not detected in d3 IVF	Not detected in skin cells
TNNI2	not detected in oocytes	Not detected in d3 IVF	Not detected in skin cells
GRAP2	201	Not detected in d3 IVF	Not detected in skin cells
TRIM48	not detected in oocytes	195.4	Not detected in skin cells
FLJ22184	6.5	13	4625
HRASLS	6.9	79.7	763
USP29	not detected in oocytes	62.6	639
GADD45G	16.4	Not detected in d3 IVF	565
GLYATL1	21.7	40.7	419
NXPH1	30.6	41.8	119
FAM19A2	27.6	44.2	81
ZNF571	5.6	13.5	70.7
CDCA7L	9.1	14.2	38.8
SLC12A8	5.1	52.3	27.4
HIST1H2AE	not detected in oocytes	8	17
ZNF222	18.8	57	14.5
CTTNBP2NL	20.7	2993	11.9
SLC41A2	8.2	23.8	5.8
KRT17	not detected in oocytes	10	5.6
PXMP3	not detected in oocytes	5	3
ARHGAP22	9.7	134.6	1.4
S100A6	8.4	38.1	0.2

Supplementary Table 2 | Genes specifically upregulated after transfer of somatic cell genomes into human oocytes in arrested blastomeres.

Locus	Somatic cell donor	Oocyte donor	soPS1	Parthenote pPS1
Amelogenin	X,Y	X	X, X, Y	X
vWA	17	17,18	17, 18, 17	18
D8S1179	12,15	13,15	12, 15, 15	13
TPOX	11	9	9, 11, 11	9
FGA	24	23,24	24, 24, 24	24
D3S1358	15, 18	16,17	15, 17, 18	16
TH01	9, 9.3	9,9.3	9, 9.3, 9	9.3
D21S11	27, 29	29,30	27, 29, 29	29
D18S51	14,16	12,15	14, 15, 16	15
Penta E	5	15,19	5, 19, 5	19
D5S818	11,13	9,10	9, 11, 13	10
D13S317	11,13	12	11, 12, 13	12
D7S820	10,12	8,9	8, 10, 12	9
D16S539	11,12	11,12	11, 12, 12	11
CSF1PO	11,13	11,12	11, 12, 13	11
Penta D	10	9,12	10, 12, 10	9

Supplementary Table 3 | STR analysis of the somatic cell donor, the oocyte donor, a parthenogenetic cell line and the soPS1 cell line made from this oocyte donor. Chromosomes originating from the oocyte donor are marked in **red**, chromosomes originating from the somatic cell donor in **blue**. The pattern is consistent with a haploid genome being contributed by the oocyte donor and a diploid genome contributed by the somatic cell donor ID #1-000. ID #1-000 corresponds to H1.5 of Maehr and colleagues³.

Locus	soPS2	Egg Donor	Somatic cell donor
Amelogenin	XY	X	XY
vWA	14,18,18	14,19	18
D8S1179	8,10,14	8,16	10,14
TPOX	9,10,11	9,11	10,11
FGA	20,21,24	21	20,24
D3S1358	16,18,16	16	16,18
TH01	7,8,9	6,8	7,9
D21S11	28,29,30	29	28,30
D18S51	16,17,17	14,16	17
Penta E	11,18,11	18,19	11
D5S818	11,12,13	11,12	12,13
D13S317	8,11,13	12,13	8,11
D7S820	10,11,12	10,11	11,12
D16S539	11,12,12	11,12	11,12
CSF1PO	10,11,12	11,12	10,11
Penta D	9,12,13	11,13	9,12

Supplementary Table 4 | Short tandem repeat (STR) analysis of soPS2, the egg donor and the somatic cell donor ID# 1-016.

up in soPS2

	fold change to NYSCF1	fold change to pPS1	fold change to somatic donor cell	fold change to iPS cell
COL7A1	16	3	25	10
ACTA1	16	7	170	4
MEG3	14	1	18	12
GLIPR1L1	14	4	33	5
SPP1	11	5	19	2
MYL4	10	9	27	3
NPPB	10	4	70	4
SPP1	9	6	17	2
NNAT	8	8	14	1
ACTC1	7	7	27	2
BHLHB2	6	1	1	5
LEFTY1	6	1	11	1
CAV1	6	2	0	1
NODAL	6	1	11	2
SOX15	6	2	14	2
LEFTY2	6	1	34	3
CYR61	6	2	1	2
CSRP1	5	2	1	2
ZFP42 (Rex1)	5	2	12	1
PLAU	5	2	3	3
SERPINE1	5	1	0	2
ADM	5	1	1	2
FOXQ1	5	3	5	4
FER1L3	5	3	0	3
ANXA1	4	3	0	1
GAL	4	1	93	1
ZNF394	4	2	2	2
FOXD1	4	3	0	2

up in soPS1				
	fold change to NYSCF1	fold change to pPS1	fold change to somatic donor cell	fold change to iPS cell
LEFTY2	16	2	55	2
NODAL	8	1	10	2
ZFP42 (Rex1)	7	2	10	2
EOMES	7	2	13	3
NNAT	7	7	8	2
CLDN7	6	3	14	2
GLIPR1L1	6	2	13	2
GAL	6	1	66	1
CER1	5	2	7	2
GDF3	5	1	5	1
FOXA2	5	2	24	3
LOC100008589	4	2	2	1
RAB17	4	1	22	2
LAD1	4	2	4	2
PSME3	4	2	2	1
IFITM1	4	2	2	1
AK3L1	3	1	3	1
ETV4	3	1	4	1
MAT2A	3	1	2	1
L1TD1	3	2	7	1
AMY1A	3	3	3	3
ACTA1	3	1	22	1
TK1	3	2	6	2
THY1	3	1	0	1

Supplementary Table 5 | Genes differentially expressed in soPS cells in comparison to NYSCF1. Fold differences in average signal are shown in comparison to NYSCF1, pPS1, and the corresponding somatic donor cell, and the corresponding iPS cell. Several of these genes have been described as highly variable in expression in different pluripotent stem cell lines ⁴.

2010 summary	
Sample	# mappable reads
1000iPS_CDNA	8,100,834
1000iPS_CDNA	6,605,941
1016iPS_CDNA	8,307,229
1016s_CDNA	6,519,001
1034iPS_CDNA	8,327,848
1034iPS_GDNA	3,489,012
1034s_CDNA	5,056,563
A2_CDNA	8,791,165
A2_GDNA	7,697,899
B4_CDNA	8,522,632
B4_GDNA	7,515,773
B5_CDNA	5,916,688
B5_GDNA	2,921,777
BJ_CDNA	2,229,285
BJ_GDNA	5,178,951
H1_cDNA	2,739,176
H1_gDNA	1,084,988
Hues6_CDNA	7,494,230
Hues6_GDNA	2,483,989
Total	108,982,981
2009 summary	
Sample	# mappable reads
Hues6-genomic	5537730
Hues6-cDNA	5,209,095
BJ-cDNA	5,226,810
BJ-genomic	6,592,791
H1-genomic	2,311,513
H1-cDNA	5,967,698
H2-genomic	5,261,152
H2-cDNA	6,295,703
Total	40,402,492

Supplementary Table 6 | Summary of sequencing for digital allelotyping. B4 is soPS1, B5 is soPS2, A2 is pPS1, 1016 is somatic cell donor 2, 1000 is somatic cell donor 1, 1034 is oocyte donor1. H1 and H2 are HUES6/BJ fusion hybrids ².

Supplementary Table 7 | allelic ratios of expressed SNPs and fold changes in transcription upon reprogramming. Green is soPS1, red is soPS2

soPS2 expressed SNPs in pluripotency transcripts				fold upregulation (Average signal stem cell/average signal fibroblast donor cell) (Illumina array)	soPS2 Illumina Diffscore	allelic ratio (expression from somatic donor genome/total transcripts)
rs ID	gb_acc	symbol	SEARCH_KEY			
rs2070065	NM_016343	CENPF	ILMN_8225	59.60	55.80	0.29
rs4778	NM_152624	DCP2	ILMN_4971	9.59	44.12	0.63
rs3796386	NM_024046	CAMKV	ILMN_136941	no expression detected in fibroblasts	43.94	0.84
rs7081	NM_021095	SLC5A6	ILMN_880	4.61	43.20	0.76
rs6538644	NM_032147	USP44	ILMN_30293	no expression detected in fibroblasts	41.24	0.58
rs872478	NM_001290	LDB2	ILMN_2220	6.27	39.73	0.71
rs774027	NM_003920	TIMELESS	ILMN_21369	13.05	38.14	0.47
rs2878749	NM_018136	ASPM	ILMN_408	6.10	37.11	0.55
rs910925	NM_015721	GEMIN4	ILMN_15971	4.28	35.01	0.69
rs10793072	NM_173582	PGM2L1	ILMN_15828	6.59	33.96	0.50
rs598869	NM_173582	PGM2L1	ILMN_15828	6.59	33.96	0.33
rs2229571	NM_000465	BARD1	ILMN_1301	6.06	32.64	0.49
rs1049455	NM_004741	NOLC1	ILMN_22590	14.58	32.35	0.80
rs3747420	NM_005278	GPM6B	ILMN_23991	no expression detected in fibroblasts	29.86	0.82
rs12819884	NM_020634	GDF3	ILMN_22815	no expression detected in fibroblasts	29.14	0.44
rs2650492	NM_001024401	SBK1	ILMN_25826	125.13	26.07	0.88
rs7061	NM_005777	RBM6	ILMN_13075	6.52	25.53	0.81
rs6008729	NM_016426	GTSE1	ILMN_23841	5.60	22.70	0.84
rs10887	NM_024808	C13orf34	ILMN_5157	5.80	22.55	0.58
rs16859190	NM_024616	C3orf52	ILMN_22952	5.58	22.11	0.27
				average		0.61
soPS2 expressed SNPs in fibroblast transcripts				fold upregulation (Average signal stem cell/average signal fibroblast donor cell) (Illumina array)	soPS2 Illumina Diffscore	allelic ratio (expression from somatic donor genome/total transcripts)
rs ID	gb_acc	symbol	SEARCH_KEY			
rs1807494	NM_001002034	FAM109B	ILMN_4299	0.05	-23.72	0.68
rs1061494	NM_002160	TNC	ILMN_175221	0.20	-26.44	0.36
rs2274836	NM_002160	TNC	ILMN_175221	0.20	-26.44	0.36
rs3734333	NM_152734	C6orf89	ILMN_6232	0.18	-26.94	0.80
rs7757241	NM_152734	C6orf89	ILMN_6232	0.18	-26.94	0.73
rs2257167	NM_000629	IFNAR1	ILMN_1539	0.10	-29.69	0.38
rs2558	NM_005907	MAN1A1	ILMN_1394	0.21	-32.22	0.75
rs699700	NM_006016	CD164	ILMN_22810	0.20	-34.19	0.76
rs974034	NM_006016	CD164	ILMN_22810	0.20	-34.19	0.65
rs7172548	NM_014862	ARNT2	ILMN_13881	0.05	-38.19	0.76
rs7484	NM_014862	ARNT2	ILMN_13881	0.05	-38.19	0.71
rs5746136	NM_000636	SOD2	ILMN_19880	0.11	-43.35	0.56
rs1064346	NM_014028	OSTM1	ILMN_21496	0.12	-45.90	0.24
rs7572240	NM_000183	HADHB	ILMN_14786	0.19	-48.85	0.72
rs2271031	NM_138389	FAM114A1	ILMN_5266	0.07	-53.06	0.68
rs6922	NM_002526	NT5E	ILMN_28610	0.09	-55.15	0.73
rs8838	NM_012098	ANGPTL2	ILMN_26679	0.09	-56.74	0.45
rs2031131	NM_003851	CREG1	ILMN_11645	0.12	-60.76	0.73
rs10071	NM_018171	APPL2	ILMN_139404	0.13	-63.03	0.57
rs8933	NM_020345	NKIRAS1	ILMN_28229	0.17	-64.05	0.70
rs1059829	NM_003118	SPARC	ILMN_1780	0.11	-75.62	0.76
rs3210714	NM_003118	SPARC	ILMN_1780	0.11	-75.62	0.64
rs13356	NM_016206	VGLL3	ILMN_25235	0.10	-75.99	0.55
rs6789975	NM_016206	VGLL3	ILMN_25235	0.10	-75.99	0.44
				average		0.61
soPS1 expressed SNPs in pluripotency transcripts				fold upregulation (Average signal stem cell/average signal fibroblast donor cell) (Illumina array)	soPS1 Illumina Diffscore	allelic ratio (expression from somatic donor genome/total transcripts)
rs ID	gb_acc	symbol	ILMN_GENE			
rs10521655	NM_005314	GRPR	ILMN_176938	98.12	40.00	0.84
rs3747411	NM_005314	GRPR	ILMN_176938	98.12	39.00	0.87
rs3748697	NM_016343	CENPF	ILMN_8225	14.54	38.53	0.78
rs1048057	NM_016195	KIF20B	ILMN_12022	12.57	34.00	0.65
rs13689	NM_004360	CDH1	ILMN_29401	no expression detected in fibroblasts	33.50	0.67
rs6699932	NM_021190	PTBP2	ILMN_556	5.12	29.77	0.78
rs12974280	NM_032447	FBN3	ILMN_29974	no expression detected in fibroblasts	29.56	0.71
rs465563	NM_013276	SHPK	ILMN_22706	3.99	28.60	0.73
rs730228	NM_024032	C17orf53	ILMN_17950	11.07	28.22	0.82

rs1054685	NM_004720	LPAR2	ILMN_4660	4.92	27.20	0.74
rs8058133	NM_018124	RFWD3	ILMN_3124	8.28	27.12	0.47
rs8058922	NM_018124	RFWD3	ILMN_3124	8.28	27.12	0.63
rs1046650	NM_006617	NES	ILMN_3947	13.38	26.96	0.68
rs11006	NM_001467	SLC37A4	ILMN_24454	7.93	25.00	0.72
rs1377002	NM_006159	NELL2	ILMN_26383	no expression detected in fibroblasts	23.74	0.70
rs1062753	NM_019106	4-Sep	ILMN_4065		10.94	23.11
rs7130899	NM_145018	C11orf82	ILMN_11038	34.99	22.20	0.60
rs920232	NM_015720	PODXL2	ILMN_26815	5.24	21.90	0.64
average						0.71

soPS1 expressed SNPs in fibroblast transcripts

rs ID	gb_acc	symbol	ILMN_GENE	fold upregulation (Avg signal stem cell/average signal fibroblast donor cell) (Illumina array)	soPS1 Illumina	Diffscore	allelic ratio (expression from somatic donor genome/total transcripts)
rs638405	NM_138973	BACE1	ILMN_12354	0.00		-22.57	0.80
rs7083	NM_138973	BACE1	ILMN_12354	0.00		-22.57	0.75
rs1130738	NM_000693	ALDH1A3	ILMN_25111	0.20		-24.00	0.77
rs3803430	NM_000693	ALDH1A3	ILMN_25111	0.20		-24.00	0.54
rs4646690	NM_000693	ALDH1A3	ILMN_25111	0.20		-24.00	0.50
rs867186	NM_006404	PROCR	ILMN_21711	0.01			0.79
rs9262	NM_001009894	C12orf29	ILMN_26574	0.21		-29.00	0.65
rs8665	NM_007107	SSR3	ILMN_19434	0.00		-29.75	0.74
rs13182	NM_015990	KLHL5	ILMN_414	0.15		-31.56	0.71
rs1046210	NM_012105	BACE2	ILMN_14697	0.02		-32.00	0.69
rs11105	NM_006822	RAB40B	ILMN_4889	0.18		-32.38	0.70
rs12595334	NM_005902	SMAD3	ILMN_16351	0.19		-32.50	0.96
rs2228622	NM_004170	SLC1A1	ILMN_14815	0.00		-33.00	0.44
rs7357	NM_203330	CD59	ILMN_1905	0.01		-35.00	0.78
rs842	NM_203330	CD59	ILMN_1905	0.01		-35.00	0.73
rs3829252	NM_030962	SBF2	ILMN_26491	0.00			0.66
rs9862	NM_000362	TIMP3	ILMN_29313	0.10		-40.00	0.72
rs1058212	NM_004334	BST1	ILMN_26226	0.00		-41.00	0.54
rs501231	NM_004748	CCPG1	ILMN_182875	0.11		-44.00	0.72
rs4262	NM_004126	GNNG11	ILMN_8981	0.06		-45.00	0.77
rs2298258	NM_001014796	DDR2	ILMN_21519	0.00		-46.00	0.44
rs11082	NM_020244	CHPT1	ILMN_24076	0.19		-47.95	0.70
rs3769148	NM_016653	ZAK	ILMN_137635	0.13		-45.00	0.84
rs1061157	NM_001204	BMPR2	ILMN_169269	0.07		-51.80	0.68
rs3731696	NM_001204	BMPR2	ILMN_169269	0.07		-51.80	0.90
rs2304035	NM_003062	SLIT3	ILMN_18656	0.00	down		0.88
rs17261110	NM_145305	SLC25A43	ILMN_1479	0.11		-55.50	0.54
rs1045543	NM_016441	CRIM1	ILMN_10588	0.06		-55.99	0.60
rs9009	NM_147781	CTSB	ILMN_6129	0.06		-59.50	0.65
rs2241194	NM_000599	IGFBP5	ILMN_168089	0.02		-62.00	0.69
rs1549317	NM_018357	LARP6	ILMN_25698	0.17		-66.80	0.73
rs1044731	NM_017813	IMPAD1	ILMN_21923	0.14		-68.00	0.72
rs1396117	NM_017813	IMPAD1	ILMN_21923	0.14		-68.00	0.86
rs6655019	NM_015419	MXRA5	ILMN_29922	0.02		-73.00	0.69
rs7149810	NM_152330	FRMD6	ILMN_25287	0.03		-76.50	0.66
rs1983864	NM_032211	LOXL4	ILMN_9214	0.02		-77.34	0.61
rs1071738	NM_016081	PALLD	ILMN_5918	0.29		-78.15	0.66
rs690216	NM_015150	RFTN1	ILMN_29470	0.09		-81.00	0.66
rs690241	NM_015150	RFTN1	ILMN_29470	0.09		-81.00	0.75
rs1050631	NM_001099406	SLC39A6	ILMN_170037	0.01		-85.00	0.76
rs1049337	NM_001753	CAV1	ILMN_178269	0.06		-92.00	0.45
rs753420	NM_001864	COX7A1	ILMN_5679	0.02		-93.00	0.41
rs2810904	NM_003243	TGFBR3	ILMN_22620	0.02		-110.00	0.66
rs1442	NM_000358	TGFB1	ILMN_24587	0.02		-111.00	0.61
rs3098233	NM_138455	CTHRC1	ILMN_7282	0.00		-114.16	0.43
average							0.68

Supplementary Discussion

Analysis of padlock probe data

Padlock probe data analysis of chromosome 17 confirmed that the additional chromosome 17 in soPS1 originates from the somatic cell. The average allelic ratio in the genomic DNA of 22 different SNPs is 0.73 for soPS1 (expected 0.75), and 0.63 for 15 SNPs in soPS2 (expected 0.66). Oocyte origin of the additional chromosome would be expected to yield a ratio close to 0.5. See also supplementary Fig. 5b for Sanger sequencing analysis.

Padlock probe data analysis of expressed genes on the X chromosome was consistent with activity from both X chromosomes. The allelic ratio (somatic genome/(somatic genome plus oocyte genome)) of soPS2 (20 rs loci) was 0.5, and the allelic ratio of soPS1 was 0.64 (14 loci). This suggests that both X chromosomes were active in both soPS cell lines.

Using the data generated from single molecule sequencing, we compared the degree of relatedness of the different cells by performing cluster analysis of the SNPs found in each cell line. Samples of cDNA and genomic DNA clustered together, as did somatic cells and their corresponding iPS cells, as would be expected because of their identical DNA sequences (Supplementary Fig. 7). Sequences of cDNA and genomic DNA of soPS1 and soPS2 clustered/corresponded most closely to the somatic cell used for genome transfer, indicating that most of their transcripts are derived from the fibroblast-derived genome, rather than from the haploid oocyte-derived genome.

Supplementary Reference:

- ¹ Dobson, A.T. *et al.*, The unique transcriptome through day 3 of human preimplantation development. *Hum Mol Genet* 13 (14), 1461-1470 (2004).
- ² Cowan, C.A., Atienza, J., Melton, D.A., & Eggan, K., Nuclear reprogramming of somatic cells after fusion with human embryonic stem cells. *Science* 309 (5739), 1369-1373 (2005).
- ³ Maehr, R. *et al.*, Generation of pluripotent stem cells from patients with type 1 diabetes. *Proc Natl Acad Sci U S A* (2009).
- ⁴ Kim, H. *et al.*, miR-371-3 Expression Predicts Neural Differentiation Propensity in Human Pluripotent Stem Cells. *Cell Stem Cell* 8 (6), 695-706.