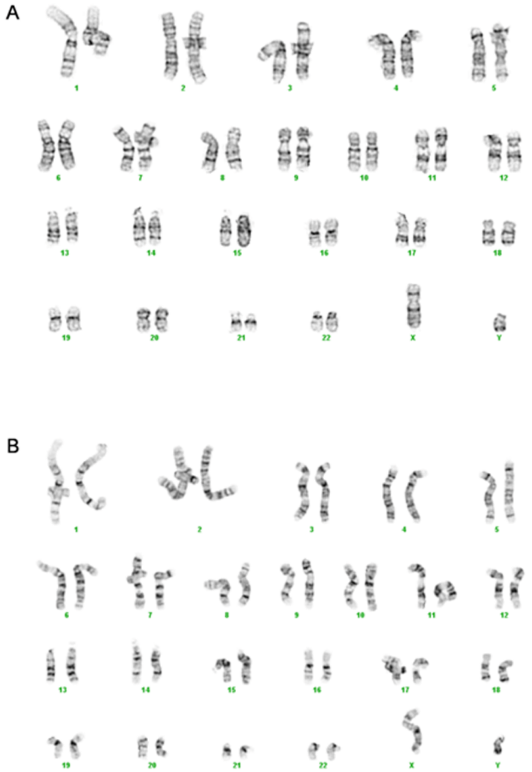
Figure S1

Karyotypic analysis of hAdiPS and hES cells. **(A)** Cytogenetic analysis was performed on 20 G-banded metaphase cells from hAdiPS cell sample. Five were analyzed and two karyotyped with good band resolution using GTL banding technique. All 20 cells demonstrated an apparently normal male karyotype. No abnormal cells were detected. **(B)** Karyotypic analysis of H1 hES cells co-cultured on human amniocyte feeder layers. Cytogenetic analysis was performed on 18 G-banded metaphase cells from a hES cell sample. Twelve were analyzed and 2 karyotyped with good band resolution using GTL banding technique. Sixteen cells demonstrated an apparently normal male karyotype, while 2 cells demonstrated non-clonal chromosome aberrations which are likely technical artifacts. No abnormal cells with trisomy 12 and/or 17 were detected. Analyses were performed by Cell Line Genetics (Madison, WI).


A
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21
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X
Y
B
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X
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Figure S2

Methylation analysis of hAdiPS cells. **(A)** *OCT4* promoter sequence, primers and analyzed CpG islands. **(B)** *NANOG* promoter sequence, primers and analyzed CpG islands.

A

-2244 gcacacgaac agaggcaaca taagagtggg ggaaaagtct caaaagactc a**cg**gatgcca
-2184 ccaagatgaa gacagctggc ca**cg**ggacac ccatcccctt agaaggcaga tagagccact
-2124 gaccccagca gacaagccca ggcagggctg agcctggagc ctgcaatgag aagccttact
-2064 taagt**cg**aca gaggtcag**cg** tgcccagtcc agacctggcc ttctggcctt **cg**aagctgtg
-2004 gggagccctg gcccagagcc ccctctggag cccccagact taccccaggc cctccactga
-1944 gatcaagttt tgggagcaga cagacaaaca tcatccctca cagacaggca ttc**cg**ttggc
-1884 tattctcttg caaacagaat caagcactag accagcagca tgagcctcag gatactcagg
-1824 ccaggcccag aaaaacagac cctgaagggg agcttagggc

Fwd primer GGA TGT TAT TAA GAT GAA GAT AGT TGG

Reverse primer CCT AAA CTC CCC TTC AAA ATC TAT T

cg → Methylation analysis of CpG island

B

-1764 ttggtggcct tgacagcccc cacttaacaa actgtgctga ttaagagaga caggagggca
-1704 agtttttccc ttcttttaaa gaaatcatcc tatttccta**c** **g**agacataga ctatctgcct
-1644 gaagcatgat gtactagccc cactcac**cg**g ctccctgatg cccctatgct taatcttctc
-1584 **cg**gaatggta gtctgagaag aaaaaagatt a**cg**cccaatt tcatttcctt gtttcacatc
-1524 aagcaatact ttt**cg**agtct ttgcattgtg aacaaaagtc agcttgtgtg ggagcaaagc

Fwd primer AGA GAT AGG AGG GTA AGT TTT TTT T

Reverse primer ACT CCC ACA CAA ACT AAC TTT TAT TC

cg → Methylation analysis of CpG island

Figure S3

Analysis of the pairwise correlation data of hAdiPS cell gene expression compared to hES cells demonstrated r^2 = 0.98-0.99 concordance as opposed to r^2 = 0.82-0.85 for human amniocytes relative to hES cells and r^2 = 0.82-0.85 for human amniocytes compared to hAdiPS cells.