Supplemental Information

STable 1 Pearson correlation coefficient table (microarray analysis of hiPSC clones derived from adult skin fibroblasts).

	M3-6	M4-8	hESC H1	M4-10	Fibroblast
M3-6	1.00	0.99	0.98	0.97	0.82
M4-8	0.99	1.00	0.98	0.96	0.82
hESC H1	0.98	0.98	1.00	0.96	0.81
M4-10	0.97	0.96	0.96	1.00	0.81
Fibroblast	0.82	0.82	0.81	0.81	1.00

Locus	STR Genotype Repeat #	IMR-90	CFC-1	CFC-2	CFC-3
D16S539	5, 8-15	10,13	10,13	10,13	10,13
D7S820	6-14	9,12	9,12	9,12	9,12
D13S317	7-15	11,13	11,13	11,13	11,13
D5S818	7-15	12,13	12,13	12,13	12,13
CSF1PO	6-15	11,13	11,13	11,13	11,13
TPOX	6-13	8,9	8,9	8,9	8,9
Amelogenin	NA	X,X	X,X	X,X	X,X
TH01	5-11	9.3,9.3	8,9.3	8,9.3	8,9.3
vWA	11, 13-21	16,(19)	16,19	16,19	16,19

STable 2. STR analysis of 3 different colony-forming cells (CFC1-3) obtained from hiPSC (IMR-90)-1 iPSC line



SFigure 1. Characterization of hiPSC clones derived from adult skin fibroblasts (ATCC, Cat. # CRL-2106). (A) Bright-field image of hiPS clone M3-6, p5+p12(7). Scale bar: 0.1 mm. (B) Flow cytometry analysis of hESC-specific cell surface markers: SSEA-3, SSEA-4, Tra-1-60 and Tra-1-81. Fibroblast: p6; hiPS clone M4-8, M4-10 and M3-6: p5+p12(7).
(C) Hematoxylin and eosin staining of teratoma sections of iPS clone M3-6 (9 weeks after injection). Two six-well plates of hiPS clone M3-6 on MEF (~ 60 to 70% confluent) were injected into the hindlimb muscle of two mice. Teratomas were obtained from all three hiPS clones. Shown are neural tissue (ectoderm, upper left), gut epithelium (endoderm, upper right), cartilage (mesoderm, lower left), and bone (mesoderm, lower right). Scale bar: 0.1 mm.

SFigure 2



SFigure 2. (A) Quantitative real time PCR analysis of total and endogenous expression of key pluripotency genes in undifferentiated hiPSC and hiPSC-derived CD43⁺
hematopoietic cells. Following primers were used for amplification: GAPDH (forward: 5'- GTGGACCTGACCTGCCGTCT, reverse: 5'- GGAGGAGTGGGGTGTCGCTGT);

POU5F1 total (forward: 5'- CAGTGCCCGAAACCCACAC, reverse: 5'-GGAGACCCAGCAGCCTCAAA); POU5F1 endogenous (forward: 5'-AGTTTGTGCCAGGGTTTTTG, reverse: 5'- ACTTCACCTTCCCTCCAACC); Nanog total (forward: 5'- CAGAAGGCCTCAGCACCTAC, reverse: 5'-ATTGTTCCAGGTCTGGTTGC); Nanog endogenous (forward: 5'-TTTGGAAGCTGCTGGGGAAG, reverse: 5'- GATGGGAGGAGGGGGAGAGGA; Sox2 total (forward: 5'- TACCTCTTCCTCCCACTCCA, reverse: 5'-GGTAGTGCTGGGACATGTGA); Sox2 endogenous (forward: 5'-AGTCTCCAAGCGACGAAAAA; reverse: 5'- TTTCACGTTTGCAACTGTCC). PCR products were normalized with GAPDH of the same samples and compared with hESC H1 as relative standard as previously described [1]. (B) Flow cytometric analysis of expression of hESC-specific markers in hiPSC- and hESC-derived CD43⁺ hematopoietic and CD31⁺CD43⁻ endothelial cells. In contrast to undifferentiated hiPSCs (see SFig.1), CD43⁺ hematopoietic and CD31⁺CD43⁻ endothelial cells lack of expression of hESC-specific markers.

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SFigure 3



2 31 88 88 88 38 ÷6 38 88 38 ŝε 01 hESC H-1 SK(46)-M4-10 Foreskin-1 IMR90-1

SFigure 3. Karyotype of undifferentiated hESCs and hiPSCs and CD43⁺ cells derived from indicated cell lines.

References.

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1. Yu J, Vodyanik MA, Smuga-Otto K, et al. Induced pluripotent stem cell lines derived from human somatic cells. Science 2007;318: 1917-1920. Epub 2007 Nov 1920.