Supporting Information

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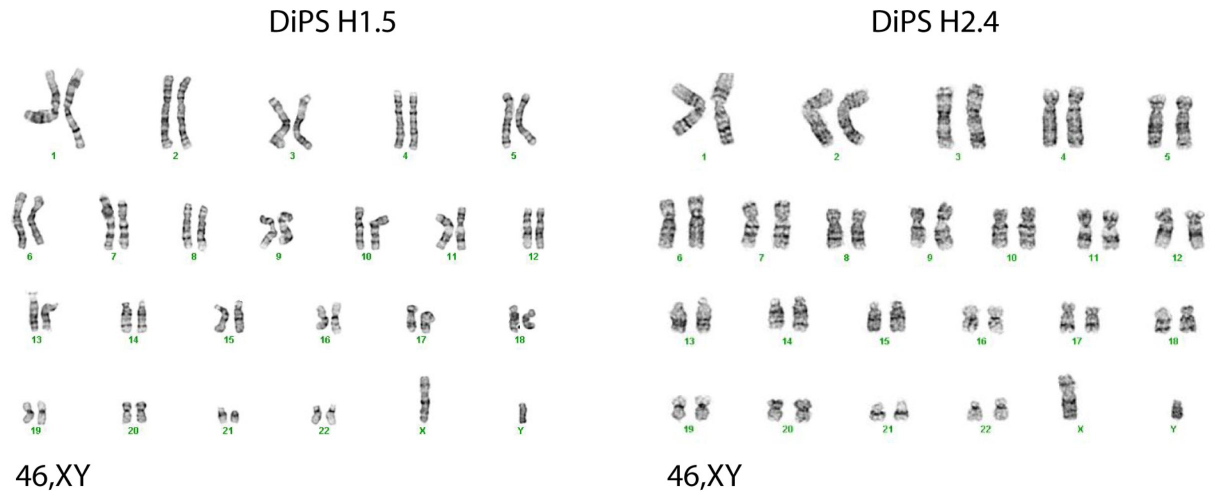

Fig. S1. Representative karyotype analysis of type 1 diabetes-specific induced pluripotent stem (DiPS) cells lines from Patient H1 and H2. Karyotype analysis was conducted on DiPS cells (passages 8–11) at UMass Memorial Medical Center (Worcester, MA).

Table S1. DNA fingerprint of parental fibroblast lines and DiPS lines

	Fibroblasts				DiPS			
	Patient H1		Patient H2		Patient H1		Patient H2	
Amelogenin	X	Y	X	Y	X	Y	X	Y
vWA	17	—	16	18	17	—	16	18
D8S1179	12	15	14	15	12	15	14	15
TPOX	11	—	8	9	11	—	8	9
FGA	24	—	18	23	24	—	18	23
D3S1358	15	18	16	—	15	18	16	—
THO1	9	9.3	9.3	—	9	9.3	9.3	—
D21S11	27	29	30	32.2	27	29	30	32.2
D18S51	14	16	14	18	14	16	14	18
Penta E	5	—	14	16	5	—	14	16
D5S818	11	13	9	12	11	13	9	12
D13S317	11	13	11	13	11	13	11	13
D7S820	10	12	8	10	10	12	8	10
D16S539	11	12	9	11	11	12	9	11
CSF1PO	11	13	11	12	11	13	11	12
Penta D	10	—	12	—	10	—	12	—

Shown here are representative DNA fingerprint results for parental fibroblast and DiPS lines. Analyzed were Amelogenin for sex chromosomes in addition to 15 polymorphic short tandem repeat DNA loci. Analysis was performed by Cell Line Genetics.

Table S2. Coefficient of determination (r^2 = square of the correlation efficient) values between parental fibroblasts, DiPS, and human ES cells

	Fibroblast H1	Fibroblast H2	HUES 4	HUES 6	HUES 8	DiPS H1.5	DiPS H2.1	DiPS H2.B3	DiPS H2.4
Fibroblast H1	X	—	—	—	—	—	—	—	—
Fibroblast H2	0.98	X	—	—	—	—	—	—	—
HUES 4	0.75	0.75	X	—	—	—	—	—	—
HUES 6	0.72	0.73	0.96	X	—	—	—	—	—
HUES 8	0.73	0.73	0.98	0.97	X	—	—	—	—
DiPS H1.5	**0.73**	0.74	*0.97*	*0.94*	*0.97*	X	—	—	—
DiPS H2.1	0.73	**0.74**	*0.97*	*0.96*	*0.97*	0.98	X	—	—
DiPS H2.3	0.71	**0.72**	*0.97*	*0.95*	*0.97*	0.97	0.98	X	—
DiPS H2.4	0.73	**0.74**	*0.97*	*0.96*	*0.98*	0.99	0.98	0.97	X

The r^2 values between DiPS lines and parental fibroblasts are displayed in bold. The r^2 values between DiPS lines and human ES cell lines are displayed in italics.

Table S3. Primers for quantitative and semiquantitative PCR analysis

Gene name	Forward primer (5′ to 3′)	Reverse primer (5′ to 3′)
OCT4 (transgene)	CCCCAGGGCCCCATTTTGGTACC	TTATCGTCGACCACTGTGCTGCTG
KLF4 (transgene)	ACG ATC GTG GCC CCG GAA AAG GAC C	
SOX2 (transgene)	GGC ACC CCT GGC ATG GCT CTT GGC TC	
OCT4	CTGGGTTGATCCTCGGACCT	CACAGAACTCATACGGCGGG
SOX2	CCCAGCAGACTTCACATGT	CCTCCCATTTCCCTCGTTTT
NANOG	AAAGAATCTTCACCTATGCC	GAAGGAAGAGGAGAGACAGT
REX1	TCTGTTCACACAGGCTCCAG	TTGGAGTGCAATGGTGTGAT
KLF4	TCTCAAGGCACACCTGCGAA	TAGTGCCTGGTCAGTTCATC
GDF3	TCTGGCACAGGTGTCTTCAG	AAATGTTTGTGTTGCGGTCA
TERT	TGTGCACCAACATCTACAAG	GCGTTCTTGGCTTTCAGGAT
Beta-ACTIN	CCAACCGCGAGAGAGTGA	TCCATCACGATGCCAGTG
GAPDH	GTGGACCTGACCTGCCGTCT	GGAGGAGTGGGTGTCGCTGT
PDX1	CCTTTCCCATGGATGAAGTC	CGAACTCCTTCTCCAGCTCTA
HNF6	GTGTTGCCTCTATCCTTCCCAT	CGCTCCGCTTAGCAGCAT
FOXA2	ATTGCTGGTCGTTTGTTGTG	TACGTGTTCATGCCGTTCAT
SOX17	GGCGCAGCAGAATCCAGA	CCACGATTGCCCAGCAT
HNF1β	TCACAGATACCAGCAGCATCAGT	GGGCATCACCAGGCTTGTA
HNF4α	CATGGCCAAGATTGACAACCT	TTCCCATATGTTCCTGCATCAG
HB9	TCCACCGCGGGCATGATCCT	GCGCTTGGGCCGCGACAGCTA
NKX6.1	TCAACAGCTGCGTGATTTTC	CCAAGAAGAAGCAGGACTCG
NKX2.2	ATGTAAACGTTCTGACAACT	TTCCATATTTGAGAAATGTTTGC
INSULIN	GAGGCCATCAAGCACCATCAC	GGCTGCGTCTAGTTGCAGTA
SOMATOSTATIN	GATGCTGTCCTGCCGCCTCC	TGCCATAGCCGGGTTTGA
GLUCAGON	AGGCAGACCCACTCAGTGA	AACAATGGCGACCTCTTCTG