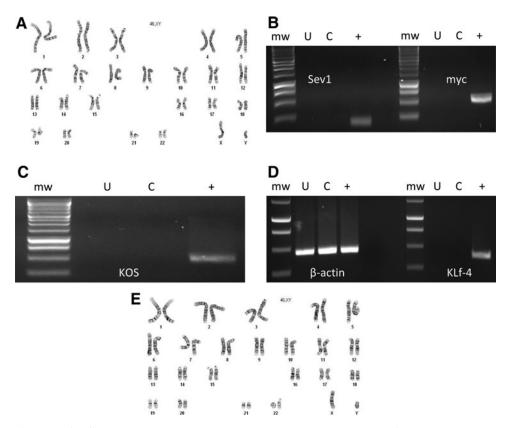
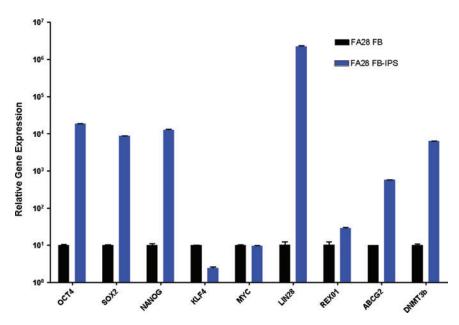
Supplementary Data



SUPPLEMENTARY FIG. S1. Cellular karyotype and Sendai virus clearance. (**A**) Pre reprogramming karyotype. Patient-derived fibroblasts utilized for iPSC generation showed a normal 46, XY karyotype. (**B–D**) Sendai virus genome/reprogramming factor associated clearance. Uncorrected iPSC (labeled "U") or clone 8, gene-corrected iPSC (labeled "C") were assessed for the presence of Sendai viral genome sequences (**B**, Sev1), c-myc, (**C**) Oct3/4, Sox2, Klf4 particles, and (**D**) b-actin and Klf4. Positive controls (labeled "+") are from early passage cells post Sendai virus delivery. (**E**) Post reprogramming Giemsa banding showing 46 XY karyotype. iPSC, induced pluripotent stem cell.

	2 2 2 2 5 4 4 3 6 6 2 7 3 7 5 0	2 2 1 1 1 1 0 9 9 8 0 0 9 5 3 6 3 0 8 5	3 3 2 2 0 0 9 1 2 0 5 5
FA28 FB-1	\bullet \bullet \circ \bullet	$\circ \circ \circ \bullet \bullet$	\bullet \bullet \bullet \circ
FA28 FB-2	\bullet \bullet \circ \circ	• 0000	\bullet \bullet \bullet \circ
FA28 FB-3	\bullet \circ \bullet \circ	0 0 0 0 0	\bullet \bullet \bullet \circ
FA28 FB-4	\bullet \bullet \circ \bullet	\bullet 000 \bullet	\bullet \bullet \bullet \circ
FA28 FB-5	\bullet \bullet \bullet \circ	\bullet \circ \bullet \circ \bullet	\bullet \bullet \bullet \circ
FA28 FB-6	• • • 0	$\circ \circ \bullet \circ \bullet$	• • • •
FA28 IPS-1	0 0 0 0	0 0 0 0 0	0 0 0 0
FA28 IPS-2	0 0 0 0	0 • 0 0 0	0 0 0 0
FA28 IPS-3	0 0 0 0	0 0 0 0 0	0 0 0 0
FA28 IPS-4	$\circ \bullet \circ \bullet$	0 0 0 0 0	$\circ \bullet \circ \circ$
FA28 IPS-5	0 0 0 0	0 0 0 0 0	0 0 0 0
FA28 IPS-6	0 0 0 0	0 0 0 0 0	• 000
	OCT4-2	OCT4-4	NANOG3

SUPPLEMENTARY FIG. S2. FANCI iPSC epigenetic promoter methylation analysis. Sodium bisulfite treated DNA from FANCI patient iPSC was amplified from the *OCT4* and *NANOG* gene promoter CpG islands and sequenced. *Open circles* show unmethylated DNA and *closed circle* indicates methylation. N=6 samples for fibroblasts (FB) and iPSC were analyzed. *Numerical* indicators at *top* represent the CpG sequences in relation to the transcriptional start site.



SUPPLEMENTARY FIG. S3. FANCI iPSC gene expression analysis. TaqMan qRT PCR gene expression analysis (n=3 replicates) of reprogramming associated genes in parental fibroblasts ($black\ bars$) and reprogrammed iPSC ($blue\ bars$). PCR, polymerase chain reaction.