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4 Figure S1. Morphologies and proliferation rate analysis of naïve iPSCs derived from
5 β-thalassemia fibroblasts.

6 (A), Sequencing results of the β -41/42 mutation sites of HBB gene in fibroblasts.

7 (B), Morphologies of naïve iPSC lines directly derived from human β-thalassemia
8 fibroblasts. Scale bars, 100μm.

9 (C), Proliferation rate analysis of n2-iPSCs and n5-iPSCs at passage 10 and 20.
 2.2X10⁴ cells from each cell line were plated onto feeders and total cell numbers
 were determined every 24h respectively.

1	(D),	Calculation	of	colony	numbers	revealed	l that	the	efficienci	ies of	naïve
2		reprogramm	ing a	nd prim	ned repro	gramming	were	appro	ximately	0.135%	and
3		0.155%.									
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Figure S2

2 Figure S2. Differentiation properties of the naïve iPSCs derived from β-thalassemia
3 fibroblasts.

- 4 (A), Quantitative PCR analysis of expression levels of ESC-specific genes. Data are
 5 shown as mean ± S.E.M., n=3 individual experiments.
- 6 (B), Immunostaining images showed that n2-iPSC and by1-hESC are negative for cell
- 7 surface marker SSEA1. Scale bars, $20\mu m$.
- 8 (C), Morphologies of GFP-labeled pr2-iPSC. Scale bars, 50µm.

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- 2 Figure S3. ChIP-seq tracks for H3K27me3 in pr9-iPSCs, n2-iPSCs and n5-iPSCs at
- 3 genes related to naïve pluripotency and development.







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2	(A), Three sgRNAs were tested by T7E1 assay to detect cleavage efficiency at HBB
3	gene locus.
4	(B), Morphological changes of primed and naïve iPSC lines co-cultured with OP9
5	stromal cells at day 3 and day 9. Primed iPSCs, Pr9-iPSCs; Naïve iPSC lines, n2-
6	iPSCs, n5-iPSCs and n2-c1-iPSCs. Scale bars, 100µm.
7	(C), Flow cytometry analysis of the ratios of human CD34 ⁺ cells differentiated from
8	the two corrected naive iPSC lines.
9	(D), Flow cytometry analysis of human CD34 ⁺ cells derived from n2-iPSCs.
10	(E), Flow cytometry analysis of human CD34 ⁺ cells derived from pr2-iPSCs and pr9-
11	iPSCs.
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1 Figure S4. Hematopoietic differentiation of the naïve iPSCs derived from fibroblasts.