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## Supplemental information

# Improved Sendai viral system for reprogramming to naive pluripotency

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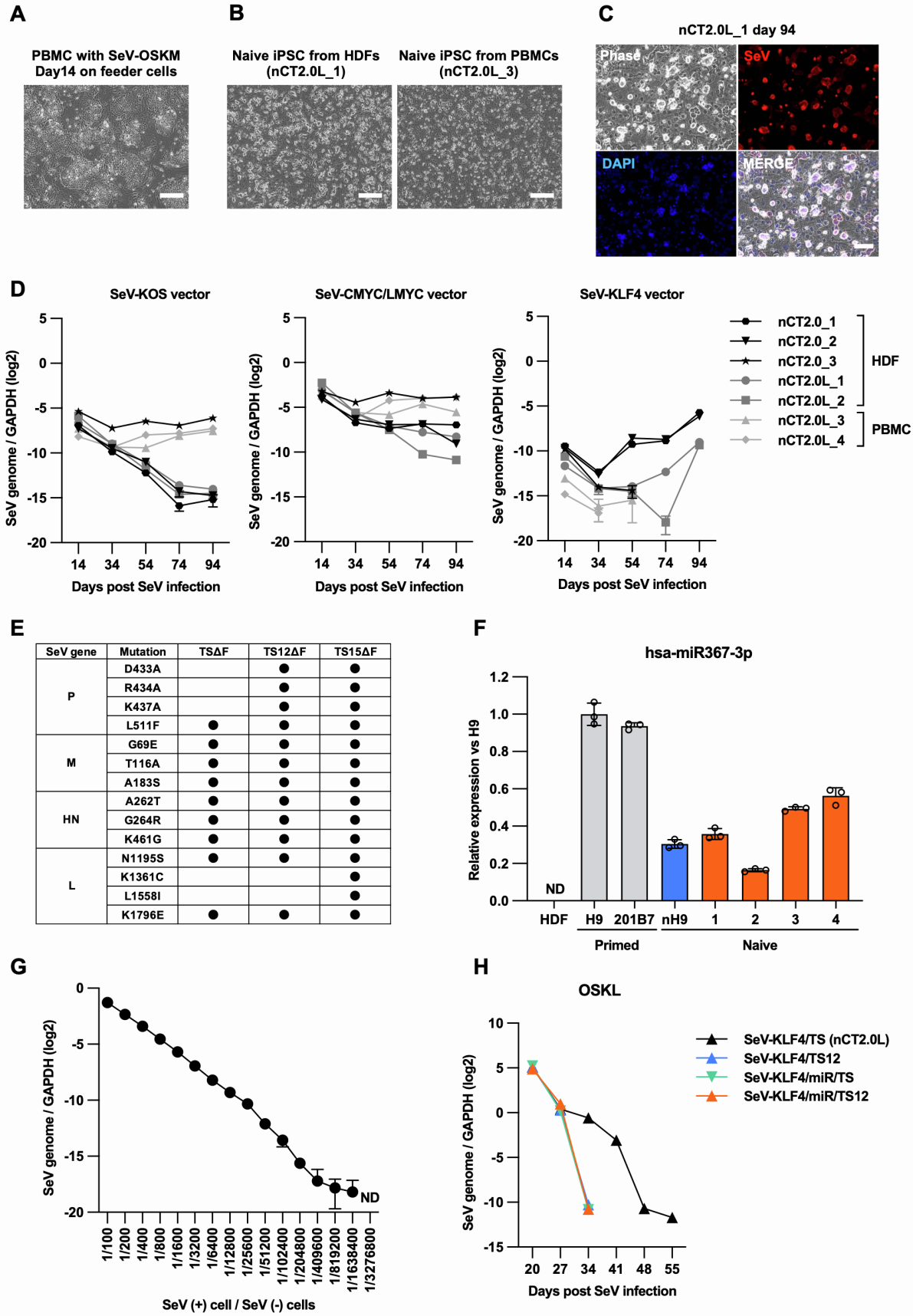
Figure S1




| SeV gene | Mutation | TSΔF | TS12ΔF | TS15ΔF |
|---|---|---|---|---|
| P | D433A | | ● | ● |
| | R434A | | ● | ● |
| | K437A | | ● | ● |
| | L511F | ● | ● | ● |
| M | G69E | ● | ● | ● |
| | T116A | ● | ● | ● |
| | A183S | ● | ● | ● |
| HN | A262T | ● | ● | ● |
| | G264R | ● | ● | ● |
| | K461G | ● | ● | ● |
| L | N1195S | ● | ● | ● |
| | K1361C | | | ● |
| | L1558I | | | ● |
| | K1796E | ● | ● | ● |

**Figure S1 related to Figure 1. Characterization of conventional and modified SeV-KLF4 vectors.**

(A) Representative phase-contrast image of PBMCs 14 days after CytoTune-iPS 2.0 SeV vector infection. Scale bar, 200 μm.

(B) Representative phase-contrast image of naive human iPSCs derived from HDFs (nCT2.0L_1) and PBMCs (nCT2.0L_3) reprogrammed with CytoTune-iPS 2.0L. Scale bar, 200 μm.

(C) Phase-contrast images of and immunofluorescent staining for SeV in naive human iPSCs (nCT2.0L_1) 94 days after SeV infection. Scale bar, 100 μm.

(D) qRT-PCR analysis of each SeV vector genome expression in naive human iPSCs reprogrammed with CytoTune2.0 or 2.0L normalized to the GAPDH expression. Data are shown as the mean ± s.d. $n$=3 for each point.

(E) Point mutations of SeV genes in the SeV-TSΔF, SeV-TS12ΔF and SeV-TS15ΔF vectors.

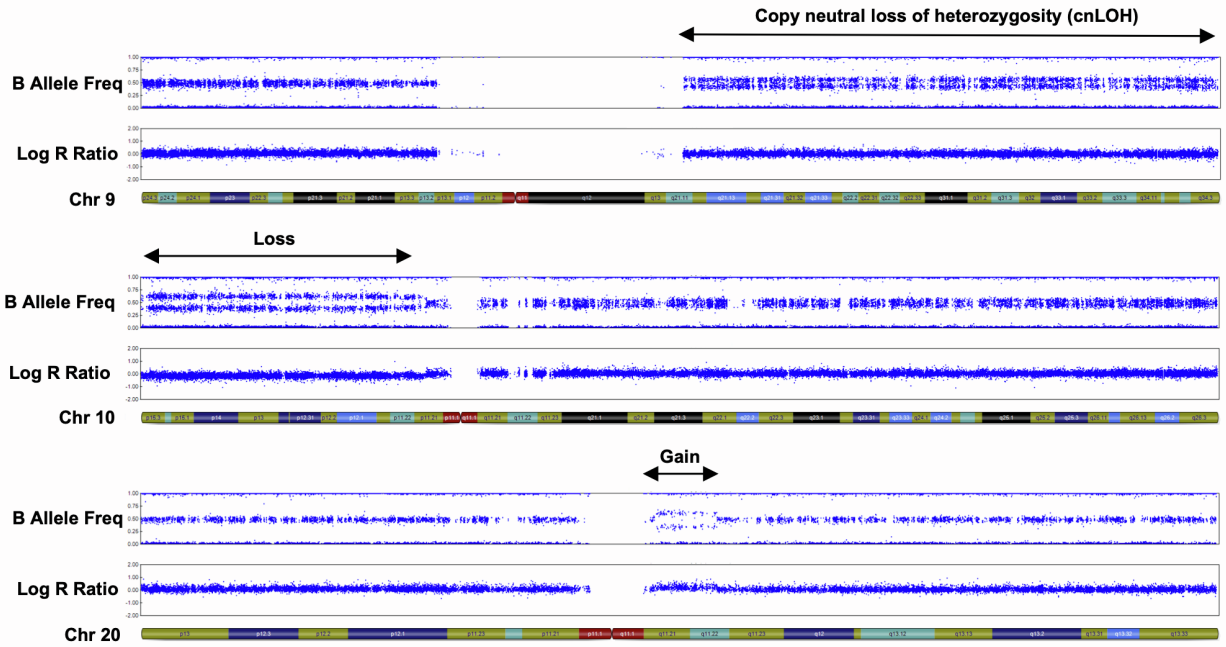
(F) qRT-PCR analysis of hsa-miRNA367-3p expression in HDFs and PSCs normalized to hsa-miRNA423-3p expression using TaqMan probes. Data are shown as the mean ± s.d. $n$=3. ND, not detected even after 40 amplification cycles.

(G) Sensitivity of detection of the SeV genome in cells 14 days after SeV vector infection analyzed by qRT-PCR using TaqMan probes. The X-axis shows the rate of SeV-positive cells among SeV-negative cells.

(H) qRT-PCR analysis of SeV genome expression in primed iPSCs derived from HDFs by the co-infection of SeV-KOS and SeV-LMYC with SeV-KLF4 vectors using TaqMan probe. Data are shown as the mean ± s.d. $n$=3 of each point.

## Figure S2

**A**




**B**

| No. | Type of CNV | Location | Size (bp) | nH9 (p109) | nOSKL_1 (p45) | nOSKL_2 (p29) | nOSKL_3 (p18) | nOSKL_4 (p16) | nOSKL_FF_1 (p21) | nOSKL_FF_2 (p21) |
|---|---|---|---|---|---|---|---|---|---|---|
| 1 | gain | chr1:51,440,093-51,804,731 | 364,639 | - | ○ | - | - | - | ○ | - |
| 2 | loss | chr2:181,333,307-181,967,075 | 633,769 | - | ○ | - | - | - | - | - |
| 3 | loss | chr3:60,305,117-60,518,998 | 213,882 | ○ | - | - | - | - | - | - |
| 4 | cnLOH | chr3:60,542,151-60,597,001 | 54,851 | - | - | - | - | - | ○ | - |
| 5 | cnLOH | chr5:58,428,799-58,620,440 | 191,642 | - | ○ | - | - | - | - | - |
| 6 | loss | chr6:26,198,916-26,237,457 | 38,542 | - | ○ | - | - | - | - | - |
| 7 | loss | chr6:162,392,902-162,914,986 | 522,085 | - | ○ | - | - | - | - | - |
| 8 | cnLOH | chr9:68,167,130-141,066,491 | 72,899,362 | ○ | - | - | - | - | - | - |
| 9 | cnLOH | chr9:71,100,140-141,066,491 | 69,966,352 | - | - | - | - | - | ○ | ○ |
| 10 | loss | chr10:98,087-23,539,203 | 23,441,117 | - | - | ○ | - | - | - | - |
| 11 | loss | chr10:43,530,071-68,593,991 | 25,063,921 | - | ○ | - | - | - | - | - |
| 12 | loss | chr10:68,259,319-68,461,866 | 202,548 | - | - | - | - | - | - | ○ |
| 13 | loss | chr10:98,087-35,901,715 | 35,803,629 | ○ | - | - | - | - | - | - |
| 14 | cnLOH | chr11:125,276,400-125,881,102 | 604,703 | - | ○ | - | - | - | - | - |
| 15 | gain | chr12:191,619-14,939,009 | 14,747,391 | - | ○ | - | - | - | - | - |
| 16 | gain | chr13:42,151,623-42,465,713 | 314,091 | - | ○ | - | - | - | - | - |
| 17 | cnLOH | chr15:22,576,118-87,876,646 | 65,300,529 | ○ | - | - | - | - | - | - |
| 18 | cnLOH | chr15:22,784,095-102,369,711 | 79,585,617 | - | - | - | - | ○ | - | - |
| 19 | gain | chr18:6,873,354-7,688,505 | 815,152 | - | ○ | - | - | - | - | - |
| 20 | gain | chr18:6,912,332-6,951,060 | 38,729 | - | ○ | - | - | - | - | - |
| 21 | cnLOH | chr19:260,912-59,097,160 | 58,836,249 | - | - | - | - | ○ | - | - |
| 22 | gain | chr20:30,183,598-33,720,033 | 3,536,436 | ○ | - | - | - | - | - | - |
| 23 | cnLOH | chr22:43,767,079-51,195,728 | 7,428,650 | ○ | - | - | - | - | - | - |
| 24 | cnLOH | chrX:2,715,425-58,339,545 | 55,624,121 | - | ○ | - | - | - | - | - |
| 25 | loss | chrX:2,760,060-155,123,035 | 152,362,976 | ○ | - | - | - | - | - | - |
| 26 | loss | chrX:32,003,841-32,116,068 | 112,228 | - | ○ | - | - | - | - | ○ |
| 27 | cnLOH | chrX:62,058,620-154,916,845 | 92,858,226 | - | ○ | - | - | - | - | - |

**Figure S2 related to Figure 2. SNP genotyping array results of naive PSCs in this study.**

(A) Representative CNVs found in nH9 ESC:copy neutral loss of heterozygosity (cnLOH) in Chr 9, loss in Chr 10, gain in Chr 20.

(B) All CNVs detected in the naive PSCs after reprogramming.