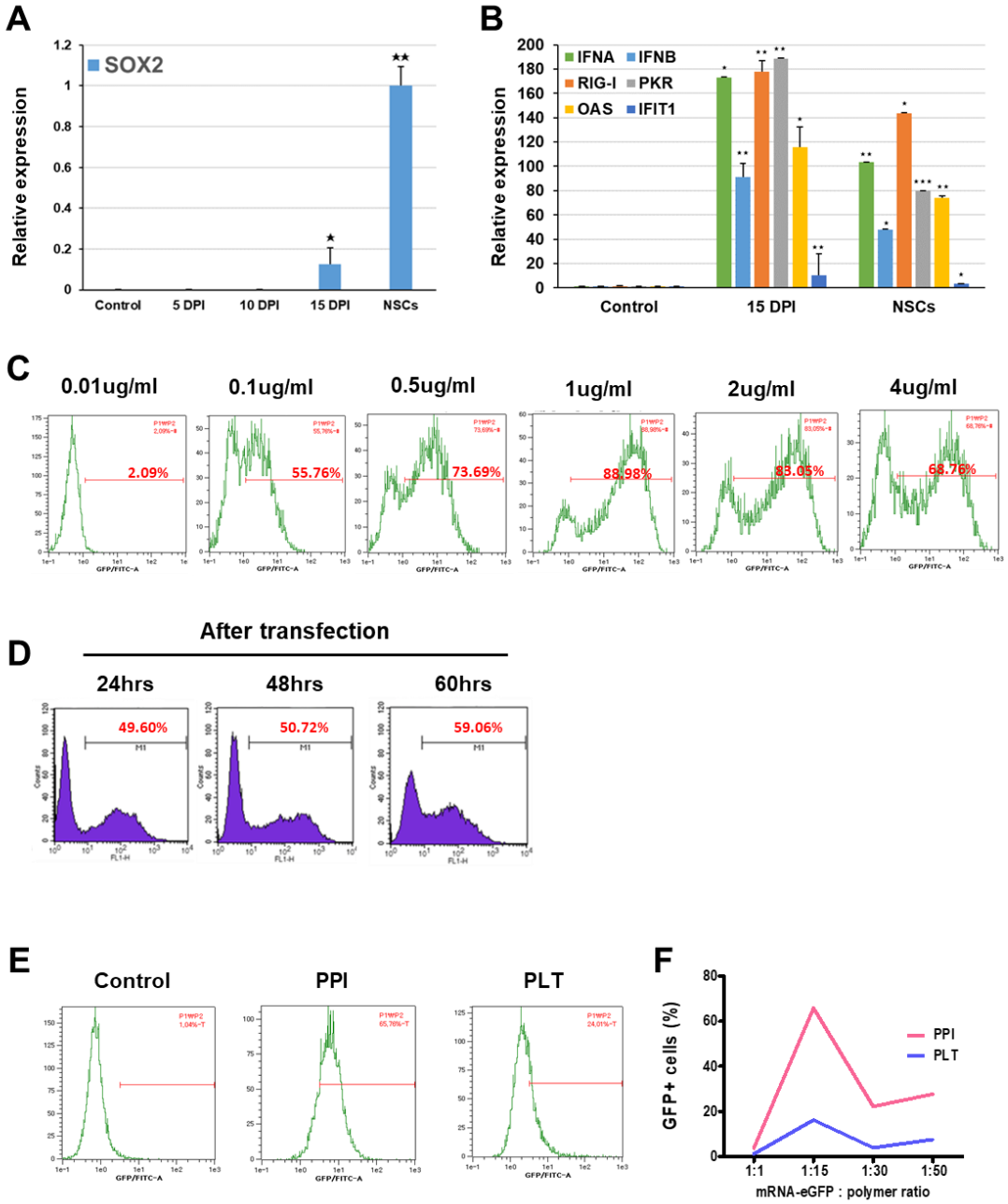
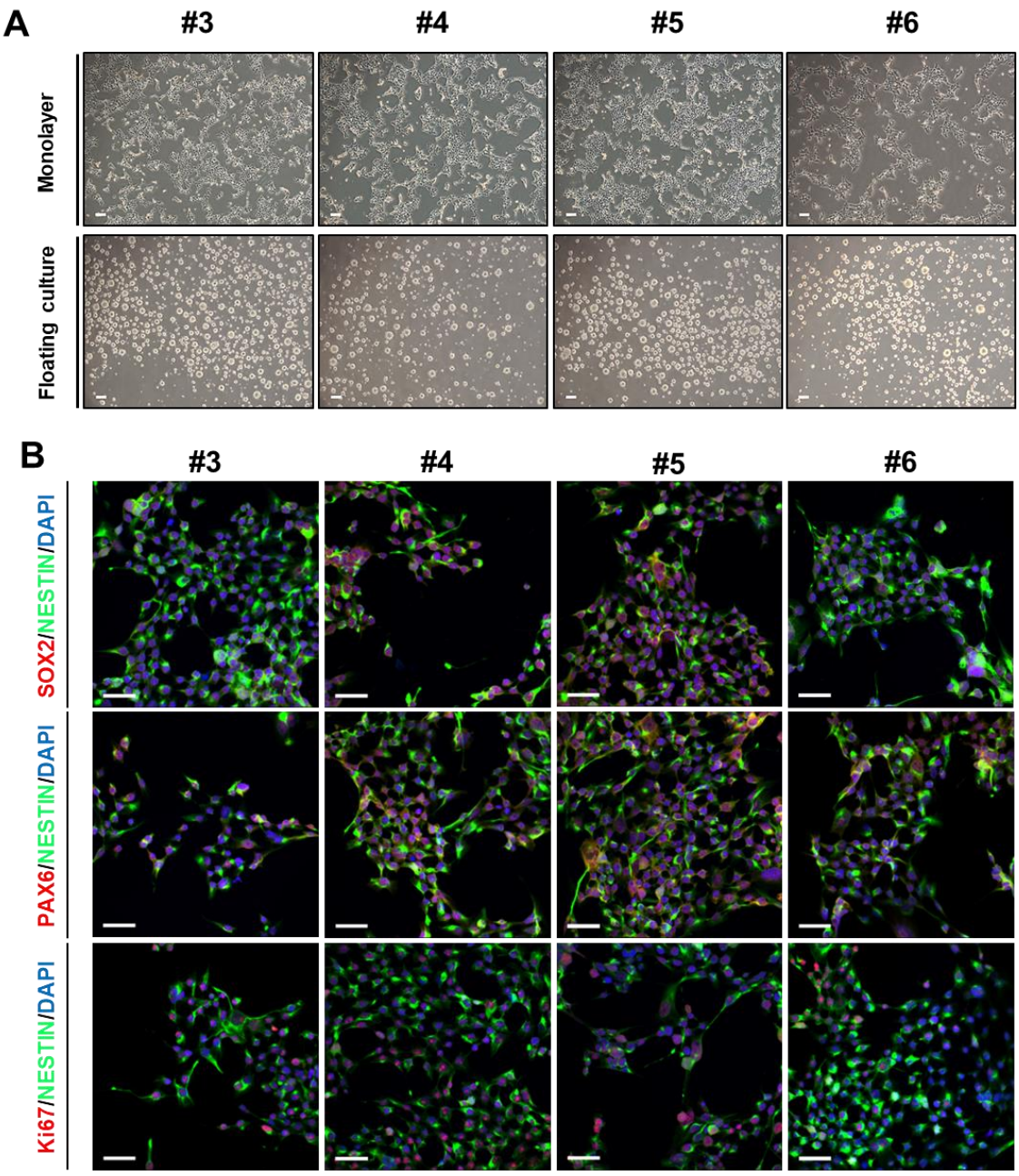
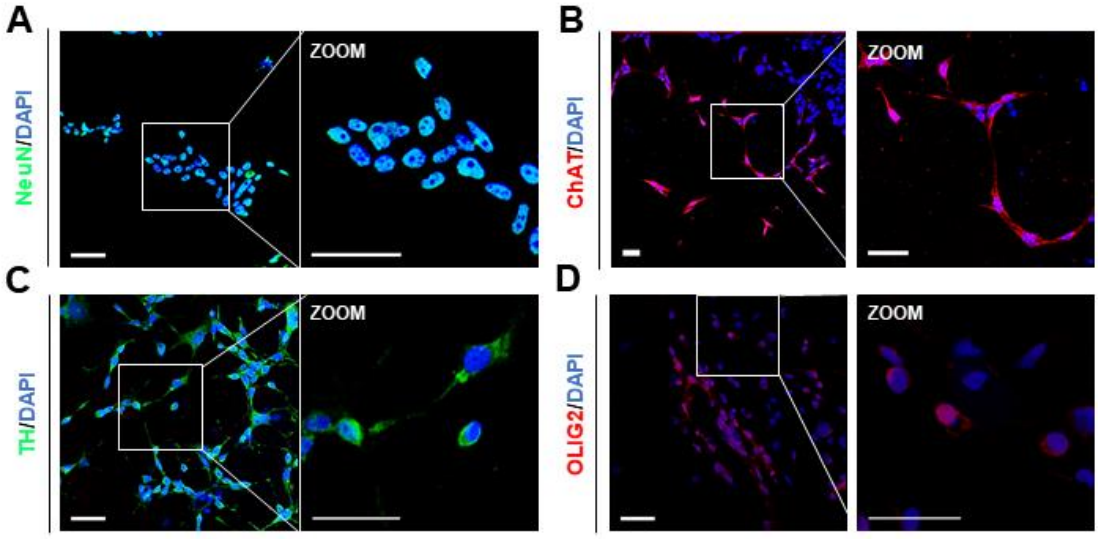
Supplemental Data



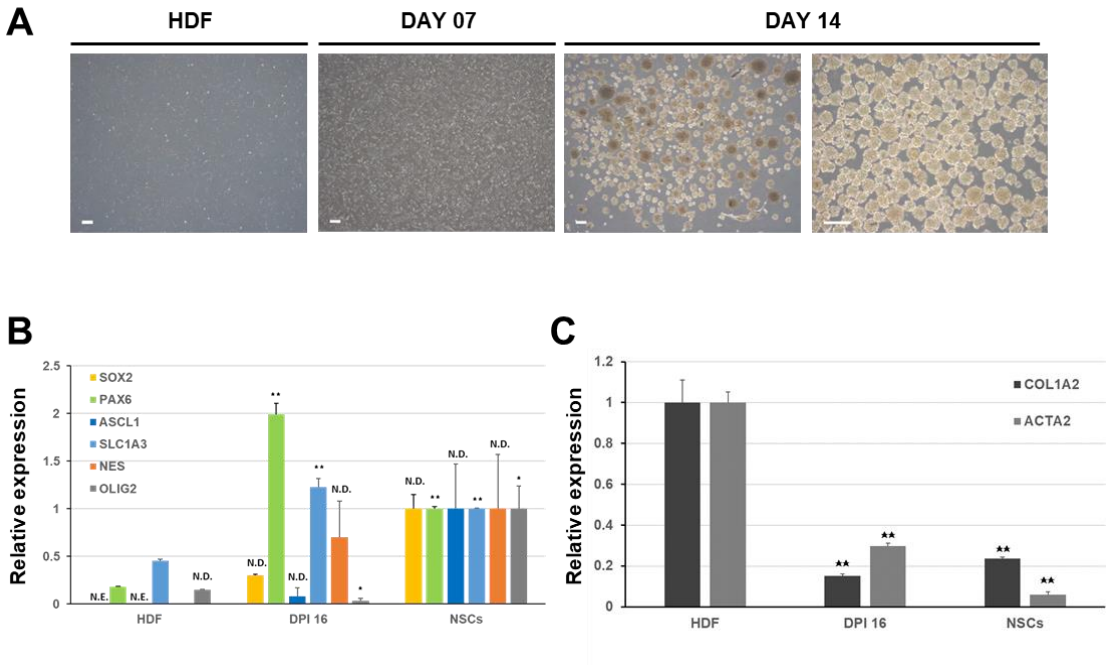
Supplementary Figure S1. (A) The level of endogenous *SOX2* expression after formation of colonies was measured. (B) The expression levels of interferon response genes were measured when colonies formed. (C-D) The percentage of GFP-expressing cells depended on the EGFP mRNA transfection dose and time were analyzed with flow cytometry (related data to the Figure 1E-H). (E) Dose-dependent transfection efficiency test using two types of PEI carriers that are known cationic polymers. (F) The transfection efficiency dependence on the ratio of the mRNA and polymer complexation is presented in the graph. ***P < 0.001; **P < 0.01; *P < 0.05.



Supplementary Figure S2. (A) Morphologies of additional four UM-iNSC lines (#3, #4, #5, #6) in an adhesion culture and a floating culture condition. Scale bar = 200 μm. (B) Immunocytochemistry analysis of the NSC-enriched markers (SOX2, PAX6 and NESTIN) and a cellular proliferation marker (Ki67) was performed in additional four UM-iNSC lines (#3, #4, #5, #6). Scale bar = 50 μm.



Supplementary Figure S3. UM-iNSCs were further differentiated with specific proper conditions. Immunocytochemistry results revealed mature neuron (NeuN; A), neuronal subtypes (ChAT and TH; B-C) and oligodendrocytes (OLIG2; D). Scale bar = 50 μm.



Supplementary Figure S4. (A) Morphological changes during the reprogramming process from HDFs into iNSCs at 14 DPI. Scale bar = 200 μm. (B) Relative gene expression levels of NSC-related endogenous *SOX2*, *PAX6*, *MASH1*, *SLC1A3*, *NES*, and *OLIG2* and the fibroblast-enriched genes *COL1A2* and *ACTA2* in HDF- and human ESC-derived NSCs (NSCs). N.E.: No Expression. N.D.: Not Determined. Error bars represent the standard deviation of triplicate reactions. ***P < 0.001; **P < 0.01; *P < 0.05.

Supplementary Table 1.

Gene	Primer sequence			
GAPDH	F	5’-AGTCTCCAAGCGACGAAAAA-3’	R	5’-TTTCACGTTTGCAACTGTCC-3’
Endo-SOX2	F	5’-AGTCTCCAAGCGACGAAAAA-3’	R	5’- TTTCACGTTTGCAACTGTCC-3'
Total-SOX2	F	5’-CCAGAAAAACAGCCCGGACC-3'	R	5’-GCTTCTCCGTCTCCGACAAA-3'
PAX6	F	5’-ATTCTGGGCAGGTATTACGAG-3'	R	5’-GATTTCCCAAGCAAAGATGGAC-3'
NES	F	5’-AACAGCGACGGAGGTCTCTA-3'	R	5’-TTCTCTTGTCCCGCAGACTT-3'
SCL1A3	F	5’-CAGATTCGTGCTCCCCGTAG-3'	R	5’-CGGAGGCGATCCCTGATTG-3'
OLIG2	F	5’-CCAGAGCCCGATGACCTTTT-3’	R	5’-CCACTGCCTCCTAGCTTGTC-3’
ASCL1	F	5’-CCCCCAACTACTCCAACGAC-3'	R	5’-AGATGCAGGTTGTGCGATCA-3'
COL1A2	F	5’-ACCACAGGGTGTTCAAGGTG-3'	R	5’-AGGACCAGGGAGACCAAACT-3'
ACTA2	F	5’-AGCGTGGCTATTCCTTCGTT-3'	R	5’-GCCCATCAGGCAACTCGTAA-3'
IVT-tail PCR-F	5’-TTG GAC CCT CGT ACA GAA GCT AAT ACG-3’			
IVT-tail PCR-R	5’-TTT TTT TTT TTT TTT TTT TTT TTT TTT TTT TTT TTT TTT TTT TTT TTT TTT TTT TTT TTT TTT TTT TTT TTT TTT TTT TTT TTT TTT TTT TTT TTT TTT TTT TTT TTT TTT TTT TTT TTT CTT CCT ACT CAG GCT TTA TTC AAA GAC CA-3’			