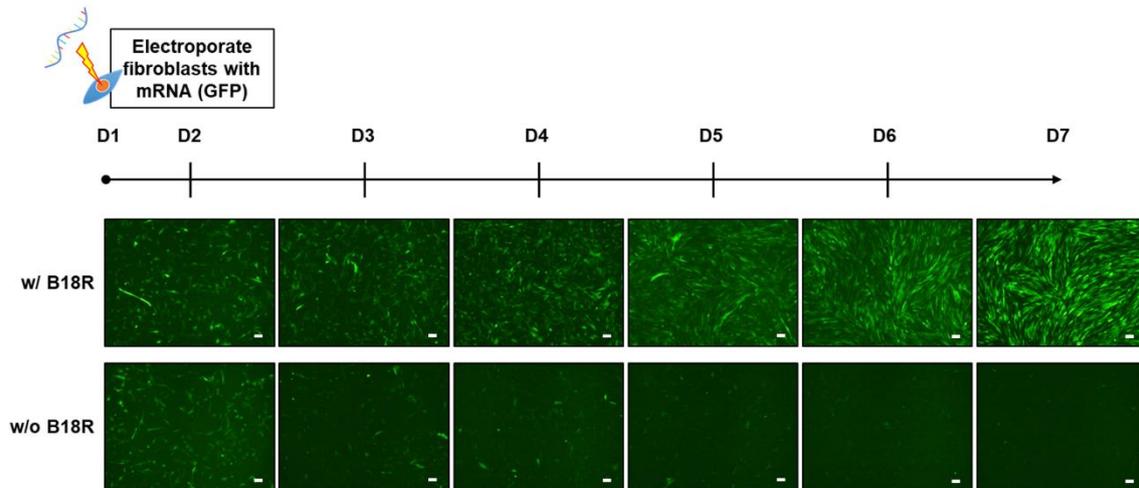
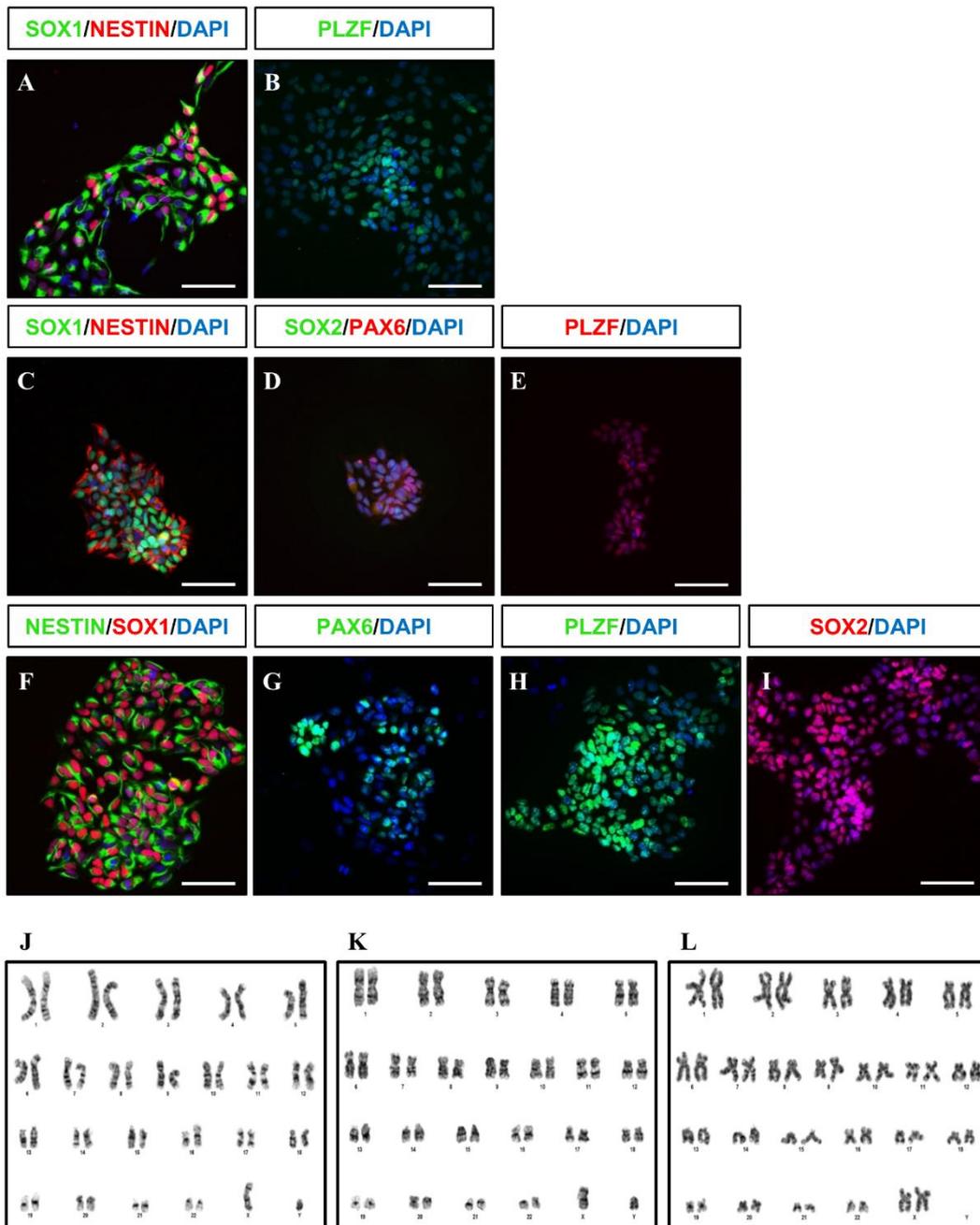


Supplementary Materials



Supplemental Figure S1. Withdrawal of B18R protein diminishes GFP expression induced by synthetic mRNAs. Withdrawal of B18R protein from culture condition diminished the synthetic mRNA-based GFP expression in transfected cells.



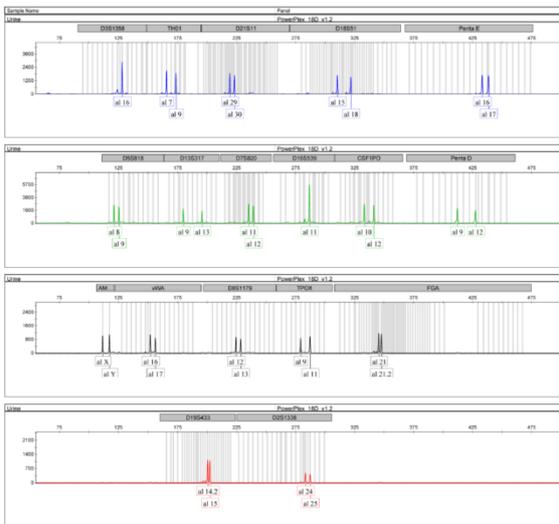
Supplemental Figure S2. Characterization of iNSCs derived from healthy donors. (A, B) NSC marker expression of iNSCs from HUCs, derived from male, 31-year-old. (C-E) NSC marker expression of iNSCs from HUCs, derived from male, 38-year-old. (F-I) NSC marker expression of iNSCs from HUCs, derived from female, 36-year-old. (J) Karyotyping of iNSCs from HUCs, derived from male, 31-year-old. (K) Karyotyping of iNSCs from HUCs, derived from male, 38-year-old. (L) Karyotyping of iNSCs from HUCs, derived from female, 36-year-old. Scale bars, 200 μ m.

A

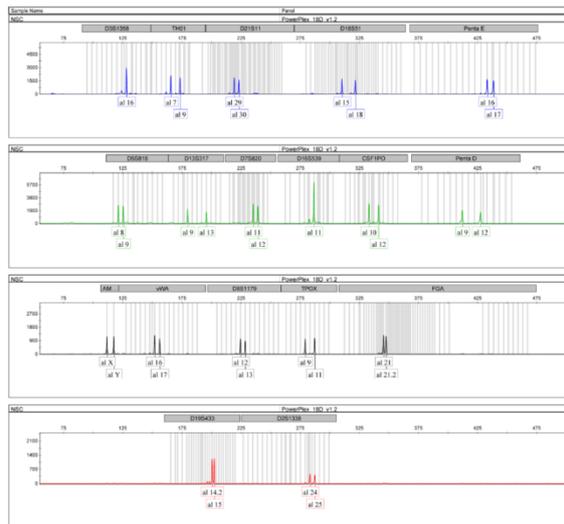
Sample No. 1 2
Match Analysis

Locus	Reference Database Profile		Sample Profile		Shared alleles #
	Database : Urine		Sample Name : NSC		
D5S818	8	9	8	9	2
D13S317	9	13	9	13	2
D7S820	11	12	11	12	2
D16S539	11		11		1
vWA	16	17	16	17	2
TH01	7	9	7	9	2
TPOX	9	11	9	11	2
CSF1PO	10	12	10	12	2
AMEL	X	Y	X	Y	2
D3S1358	16		16		1
D21S11	29	30	29	30	2
D18S51	15	18	15	18	2
D8S1179	12	13	12	13	2
FGA	21	21.2	21	21.2	2
D2S1338	24	25	24	25	2
D19S433	14.2	15	14.2	15	2
Penta D	9	12	9	12	2
Penta E	16	17	16	17	2
Number of shared alleles					34
Total number of alleles in the reference database profile					34
% match					100.0%
Result interpretation					Related

B



C

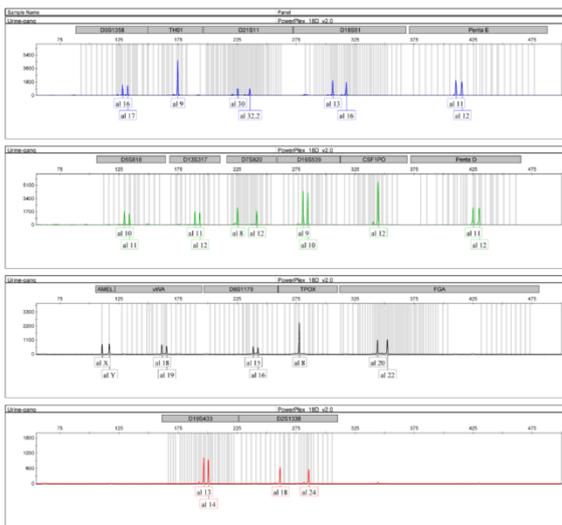


D

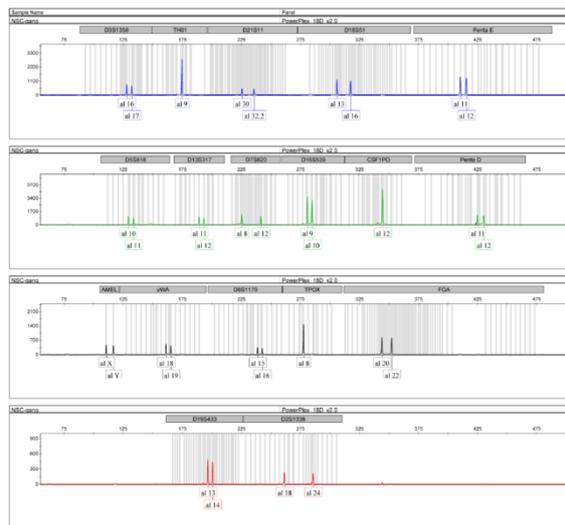
Sample No. 1 2
Match Analysis

Locus	Reference Database Profile		Sample Profile		Shared alleles #
	Database : Urine-gang		Sample Name : NSC-gang		
D5S818	10	11	10	11	2
D13S317	11	12	11	12	2
D7S820	8	12	8	12	2
D16S539	9	10	9	10	2
vWA	18	19	18	19	2
TH01	9		9		1
TPOX	8		8		1
CSF1PO	12		12		1
AMEL	X	Y	X	Y	2
D3S1358	16	17	16	17	2
D21S11	30	32.2	30	32.2	2
D18S51	13	16	13	16	2
D8S1179	15	16	15	16	2
FGA	20	22	20	22	2
D2S1338	18	24	18	24	2
D19S433	13	14	13	14	2
Penta D	11	12	11	12	2
Penta E	11	12	11	12	2
Number of shared alleles					33
Total number of alleles in the reference database profile					33
% match					100.0%
Result interpretation					Related

E



F

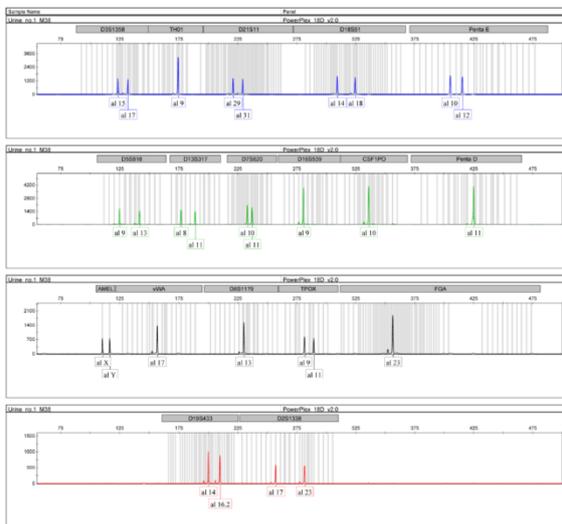


G

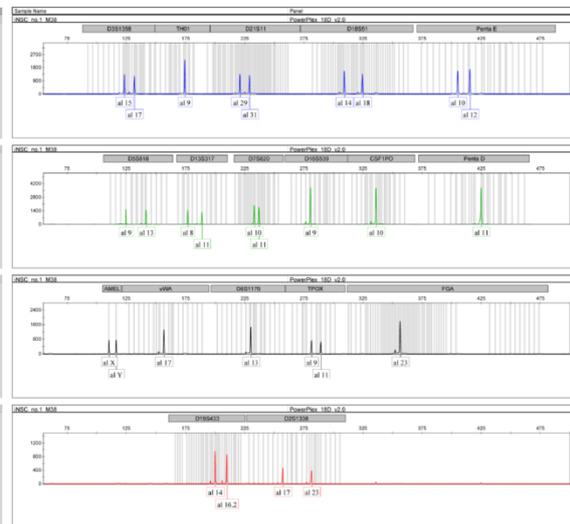
Sample No. 1 2
Match Analysis

Locus	Reference Database Profile		Sample Profile		Shared alleles #
	Database : Urine no.1 M38		Sample Name : iNSC no.1 M38		
D5S818	9	13	9	13	2
D13S317	8	11	8	11	2
D7S820	10	11	10	11	2
D16S539	9		9		1
vWA	17		17		1
TH01	9		9		1
TPOX	9	11	9	11	2
CSF1PO	10		10		1
AMEL	X	Y	X	Y	2
D3S1358	15	17	15	17	2
D21S11	29	31	29	31	2
D18S51	14	18	14	18	2
D8S1179	13		13		1
FGA	23		23		1
D2S1338	17	23	17	23	2
D19S433	14	16.2	14	16.2	2
Penta D	11		11		1
Penta E	10	12	10	12	2
Number of shared alleles					29
Total number of alleles in the reference database profile					29
% match					100.0%
Result interpretation					Related

H



I

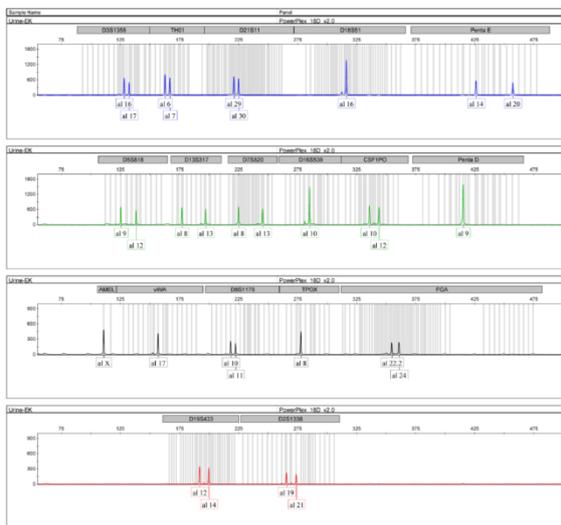


J

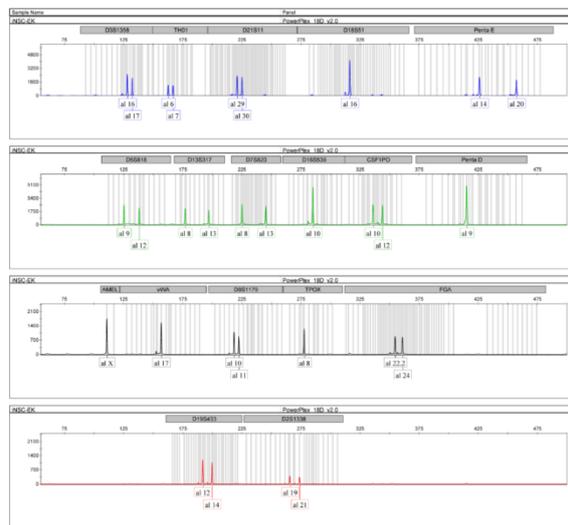
Sample No. 1 2
Match Analysis

Locus	Reference Database Profile		Sample Profile		Shared alleles #
	Database : Urine-EK		Sample Name : iNSC-EK		
D5S818	9	12	9	12	2
D13S317	8	13	8	13	2
D7S820	8	13	8	13	2
D16S539	10		10		1
vWA	17		17		1
TH01	6	7	6	7	2
TPOX	8		8		1
CSF1PO	10	12	10	12	2
AMEL	X		X		1
D3S1358	16	17	16	17	2
D21S11	29	30	29	30	2
D18S51	16		16		1
D8S1179	10	11	10	11	2
FGA	22.2	24	22.2	24	2
D2S1338	19	21	19	21	2
D19S433	12	14	12	14	2
Penta D	9		9		1
Penta E	14	20	14	20	2
Number of shared alleles					30
Total number of alleles in the reference database profile					30
% match					100.0%
Result interpretation					Related

K

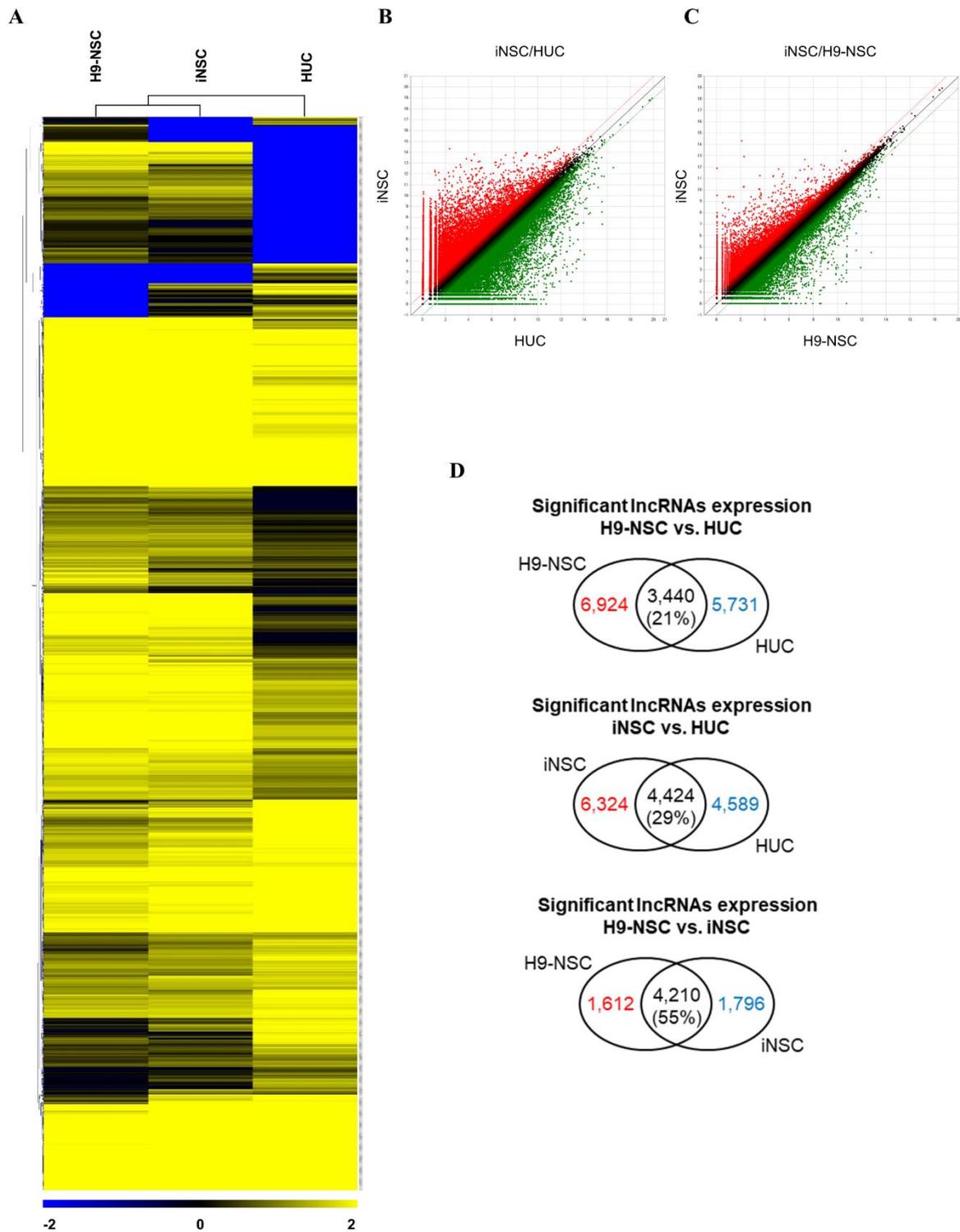


L



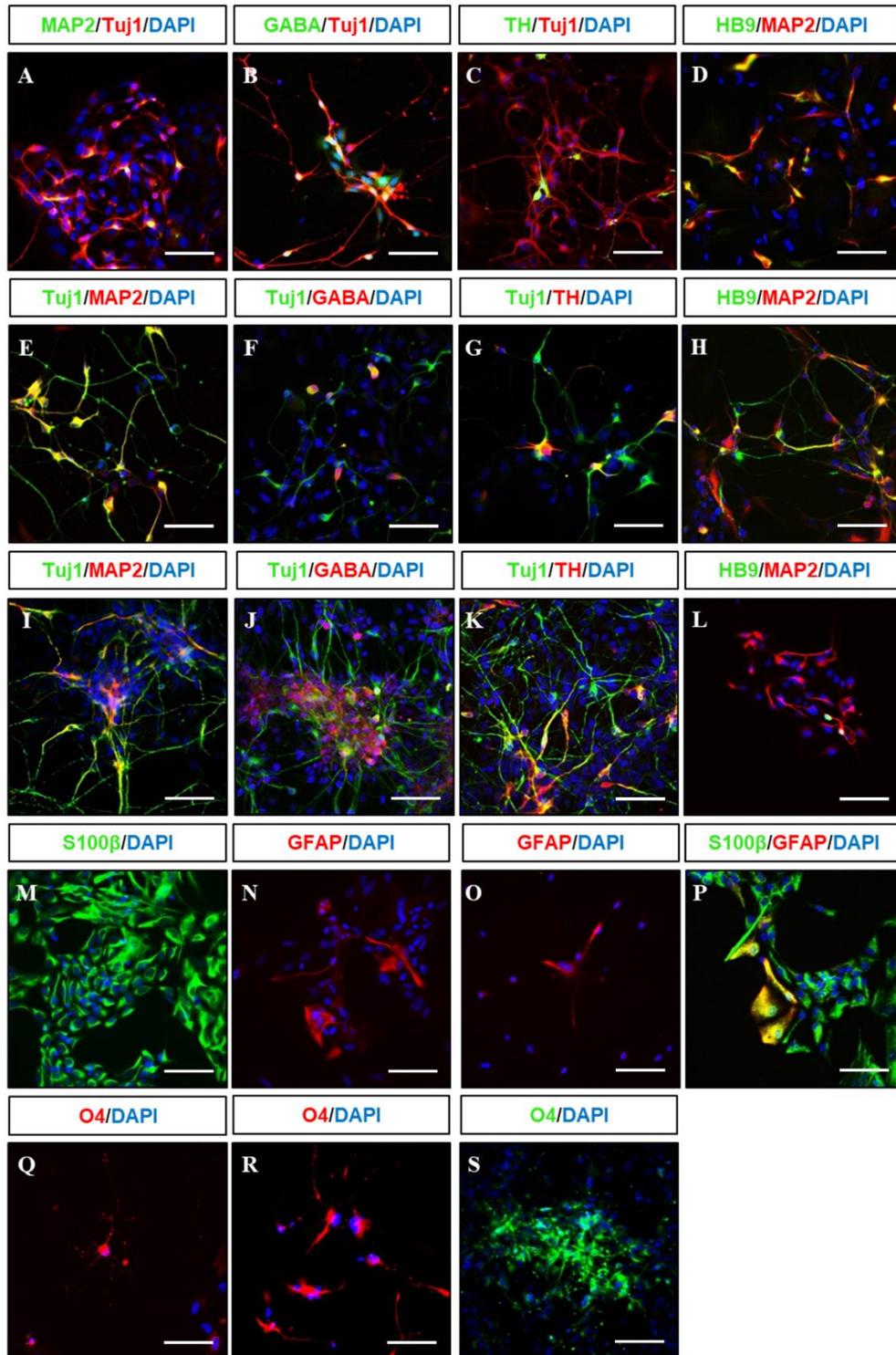
Supplemental Figure S3. STR analysis of iNSCs derived from healthy donors. (A-C) STR DNA profiling analysis of parental HUCs and iNSCs, derived from male, 32-year-old. (B) and (C) are peak data (electropherogram) for parental HUCs and iNSCs, respectively. (D-F) STR DNA profiling analysis of parental HUCs and iNSCs, derived from male, 31-year-old. (E) and (F) are peak data (electropherogram) for parental

HUCs and iNSCs, respectively. **(G-I)** STR DNA profiling analysis of parental HUCs and iNSCs, derived from male, 38-year-old. **(H)** and **(I)** are peak data (electropherogram) for parental HUCs and iNSCs, respectively. **(J-L)** STR DNA profiling analysis of parental HUCs and iNSCs, derived from female, 36-year-old. **(K)** and **(L)** are peak data (electropherogram) for parental HUCs and iNSCs, respectively.



Supplemental Figure S4. RNA sequencing analysis of the lncRNA expression profile of iNSCs. **(A)** Hierarchical clustering analysis of lncRNA expression in H9-NSCs, iNSCs, and HUCs. 12,655 lncRNAs are selected with significant p-value ($p < 0.05$) and fold change ($FC > 2$). **(B, C)** Scatter plot analysis of lncRNAs in iNSC vs. H9-NSCs or HUCs. **(D)** Venn diagrams show significant lncRNAs expressions of H9-NSCs vs. HUCs, iNSCs vs. HUCs.

HUCs and H9-NSCs vs. iNSCs.



Supplemental Figure S5. Differentiation potential of iNSCs derived from healthy donors. (A-D) Neuronal markers expression in iNSC-derived neurons (male, 31-year-old). (E-H) Neuronal markers expression in iNSC-

derived neurons (male, 38-year-old). **(I-L)** Neuronal markers expression in iNSC-derived neurons (female, 36-year-old). **(M, N)** Astroglial markers expression in iNSC-derived astroglia (male, 31-year-old). **(O)** Astroglial markers expression in iNSC-derived astroglia (male, 38-year-old). **(P)** Astroglial markers expression in iNSC-derived astroglia (female, 36-year-old). **(Q)** Oligodendroglial markers expression in iNSC-derived oligodendroglia (male, 31-year-old). **(R)** Oligodendroglial markers expression in iNSC-derived oligodendroglia (male, 38-year-old). **(S)** Oligodendroglial markers expression in iNSC-derived oligodendroglia (female, 36-year-old). Scale bars, 200 μ m.

Supplemental Table S1. Top 20 up-regulated lncRNAs in iNSCs vs. HUCs.

Top 20 up-regulated lncRNA	lncRNA	Fold change iNSC vs HUC	P-value	Fold change H9-NSC vs HUC	P-value	Chromosome	Start	End	Strand	Proximal gene
1	NONHSAT196622.1	2331.712	0.0000001	1722.544	0.0006476	chr3	181414728	181442487	-	SOX2
2	NONHSAT093477.2	2165.152	0.0000153	1608.971	0.0006533	chr3	181420249	181442508	-	SOX2
3	NONHSAT093478.2	2153.799	0.0000144	1600.403	0.0005219	chr3	181421057	181442486	-	SOX2
4	NONHSAT126980.2	1221.705	0.0000595	1223.597	0.0090088	chr8	65161144	65180341	-	BHLHE22
5	NONHSAT096619.2	1055.934	0.0000384	1185.950	0.0052212	chr4	62117904	62136756	-	ADGRL3
6	NONHSAT058624.2	1001.122	0.0000207	1072.586	0.0000030	chr18	22723490	22778173	-	ZNF521
7	NONHSAT093475.2	818.929	0.0000016	619.977	0.0006395	chr3	181373889	181442508	-	SOX2
8	NONHSAT093476.2	818.929	0.0000016	619.977	0.0006395	chr3	181373889	181442508	-	SOX2
9	NONHSAT123010.2	802.123	0.0010965	1409.944	0.0004956	chr7	121621100	121626826	+	AASS
10	NONHSAT058625.2	772.082	0.0002000	826.394	0.0001181	chr18	22723492	22786873	-	ZNF521
11	NONHSAT178277.1	772.082	0.0002000	826.394	0.0001181	chr18	22723464	22786862	-	ZNF521
12	NONHSAT171697.1	752.393	0.0000179	811.866	0.0038714	chr15	65611231	65655846	-	IGDCC3
13	NONHSAT194978.1	751.779	0.0000183	613.630	0.0008442	chr3	181373888	181442508	+	SOX2
14	NONHSAT058629.2	750.851	0.0007248	872.322	0.0005249	chr18	22784364	22907721	-	ZNF521
15	NONHSAT177503.1	713.078	0.0000104	710.971	0.0042507	chr18	22723487	22797009	+	ZNF521
16	NONHSAT178276.1	682.942	0.0002460	731.430	0.0000116	chr18	22704821	22786859	-	ZNF521
17	NONHSAT162161.1	665.913	0.0005899	757.660	0.0011770	chr12	48385363	48394796	+	COL2A1
18	NONHSAT018342.2	653.464	0.0009344	665.019	0.0074090	chr11	19510892	19524078	-	NAV2
19	NONHSAT006903.2	628.184	0.0000397	441.382	0.0040440	chr1	156641665	156644887	-	NES
20	NONHSAT185419.1	626.346	0.0013783	2108.576	0.0038614	chr2	118061042	118088288	-	DDX18

Supplemental Table S2. . Top 20 down-regulated lncRNAs in iNSCs vs. HUCs.

Top 20 down-regulated lncRNA	lncRNA	Fold change iNSC vs HUC	P-value	Fold change H9-NSC vs HUC	P-value	Chromosome	Start	End	Strand	Proximal gene
1	NONHSAT055470.2	0.0005738	0.0000588	0.0007373	0.0000589	chr17	68101708	68129530	+	KCNJ16
2	NONHSAT090923.2	0.0009164	0.0008068	0.0022107	0.0008098	chr3	101960385	101996532	+	ZPLD1
3	NONHSAT055474.2	0.0009257	0.0001268	0.0018739	0.0001271	chr17	68114411	68135927	+	KCNJ16
4	NONHSAT055460.2	0.0009340	0.0000031	0.0015596	0.0000031	chr17	68101554	68135929	+	KCNJ16
5	NONHSAT055467.2	0.0009342	0.0000035	0.0015597	0.0000035	chr17	68101583	68136002	+	KCNJ16
6	NONHSAT055472.2	0.0009346	0.0000031	0.0015605	0.0000030	chr17	68101563	68133796	+	KCNJ16
7	NONHSAT055465.2	0.0009414	0.0000068	0.0015718	0.0000068	chr17	68101975	68133796	+	KCNJ16
8	NONHSAT073857.2	0.0010438	0.0007494	0.0006061	0.0007487	chr2	113977668	113979984	-	PAX8
9	NONHSAT037288.2	0.0010560	0.0029590	0.0026546	0.0029686	chr14	62117407	62134243	+	HIF1A
10	NONHSAT037289.2	0.0010560	0.0029590	0.0026546	0.0029686	chr14	62117407	62134184	+	HIF1A
11	NONHSAT168547.1	0.0010560	0.0029590	0.0026546	0.0029686	chr14	62117407	62134243	+	HIF1A
12	NONHSAT055457.2	0.0010876	0.0030405	0.0008403	0.0030389	chr17	68096045	68101496	-	KCNJ16
13	NONHSAT055458.2	0.0010885	0.0031414	0.0008410	0.0031398	chr17	68096101	68101496	-	KCNJ16
14	NONHSAT082204.2	0.0011137	0.0003142	0.0014980	0.0003145	chr21	39630270	39726085	+	KCNJ15
15	NONHSAT055464.2	0.0011367	0.0000015	0.0009753	0.0000016	chr17	68101570	68125844	+	KCNJ16
16	NONHSAT055469.2	0.0011388	0.0000075	0.0009771	0.0000076	chr17	68101631	68125840	+	KCNJ16
17	NONHSAT055463.2	0.0011477	0.0000019	0.0009847	0.0000020	chr17	68101567	68125543	+	KCNJ16
18	NONHSAT055468.2	0.0011496	0.0000075	0.0009863	0.0000076	chr17	68101631	68125551	+	KCNJ16
19	NONHSAT175520.1	0.0011508	0.0000165	0.0009874	0.0000166	chr17	68101738	68125790	+	KCNJ16
20	NONHSAT073859.2	0.0012108	0.0003032	0.0006729	0.0003028	chr2	113979568	113983258	+	PAX8